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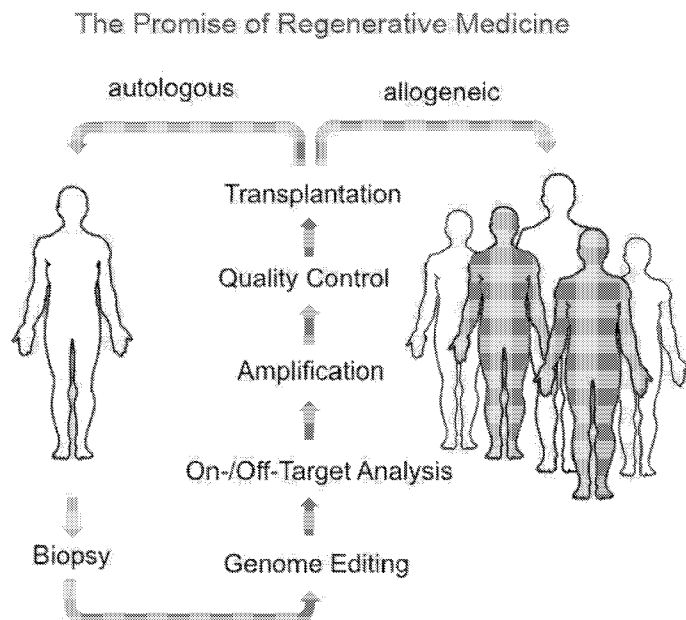


FIG. 1

(57) Abstract: Disclosed herein are universal donor stem cells and related methods of their use and production. The universal donor stem cells disclosed herein are useful for overcoming the immune rejection in cell-based transplantation therapies. In certain embodiments, the universal donor stem cells disclosed herein do not express one or more MHC-I and MHC-II human leukocyte antigens. Similarly, in certain embodiments, the universal donor stem cells disclosed herein do not express one or more human leukocyte antigens (e.g., HLA-A, HLA-B and/or HLA-C) corresponding to MHC-I and MHC-II human leukocyte antigens, thereby rendering such cells hypoinmunogenic.



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UNIVERSAL DONOR STEM CELLS AND RELATED METHODS

CROSS-REFERENCE TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Application No. 62/158,999, filed on May 8, 2015, the contents of which are hereby incorporated by reference in its entirety.

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GOVERNMENT SUPPORT

This invention was made with government support under DK097768 awarded by National Institutes of Health. The government has certain rights in the invention.

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BACKGROUND OF THE INVENTION

Degenerative diseases pose a disproportionate threat to human health. Often age-related, these diseases result in the progressive deterioration of affected tissues and organs and, ultimately, disability and death of the affected subject. The promise of regenerative medicine is to replace diseased or missing cells with new healthy cells. Over the past five years, a new paradigm for regenerative medicine has emerged — the use of human pluripotent stem cells (hPSCs) to generate any adult cell type for transplantation into patients. In principle, hPSC-based cell therapies have the potential to treat most if not all degenerative illnesses, however the success of such therapies may be limited by a subject's immune response.

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Strategies that have been considered to overcome the immune rejection include HLA-matching (e.g. identical twin or umbilical cord banking), the administration of immunosuppressive drugs to the subject, blocking antibodies, bone marrow suppression/mixed chimerism, HLA-matched stem cell repositories and autologous stem cell therapy. Needed are novel approaches, compositions and methods for overcoming immune rejection associated with cell replacement therapies.

SUMMARY OF THE INVENTION

Disclosed herein are efficient strategies to overcome immune rejection in cell-based transplantation therapies by the creation of universal donor stem cell lines that, as quality-controlled cell-based products, will form the base for regenerative cell therapies.

The present inventors have successfully employed genome editing tools such as a TALEN and/or CRISPR system in human pluripotent stem cells to reduce expression or knock out the highly polymorphic classical MHC-I genes (*HLA-A*, *HLA-B* and *HLA-C*) and/or MHC-II genes. In certain aspects, such reduced expression or knock out of the MHC-I and/or MHC-II genes is accomplished by directly and/or indirectly targeting the *NLRC5*, *B2M* and *CIITA* genes and other components of the MHC enhanceosome (e.g., transcriptional regulators of MHC-I or MHC-II).

Disclosed herein are methods of preparing hypoimmunogenic stem cells, the method comprising modulating expression of one or more MHC-I and MHC-II human leukocyte antigens by the stem cell and thereby preparing the hypoimmunogenic stem cell. Also disclosed are methods of modulating expression of one or more MHC-I and MHC-II human leukocyte antigens by a stem cell, comprising deleting one or more genes encoding one or more transcriptional regulators of MHC-I or MHC-II from at least one allele of the cell and thereby modulating expression of the one or more MHC-I and MHC-II human leukocyte antigens.

In certain aspects, modulating expression of the one or more MHC-I and MHC-II human leukocyte antigens comprises reducing, inhibiting and/or interfering

with the expression of the one or more MHC-I and MHC-II human leukocyte antigens. In certain embodiments, modulating expression of the one or more MHC-I and MHC-II human leukocyte antigens comprises deleting one or more genes encoding one or more transcriptional regulators of MHC-I or MHC-II from at least one allele of the cell. For example, in certain embodiments such methods comprise deleting one or more genes encoding one or more of the transcriptional regulators of MHC-I or MHC-II selected from the group consisting of NLRC5, CIITA, B2M and combinations thereof.

In certain aspects, the methods disclosed herein further comprise modulating expression of one or more tolerogenic factors by the stem cell. Modulating expression of the tolerogenic factors may comprises increasing the expression of the tolerogenic factors. Such tolerogenic factors may be inserted into a safe harbor locus (e.g., the AAVS1 locus) of at least one allele of the cell. In certain embodiments, such tolerogenic factors inhibit immune rejection. In certain embodiments, such tolerogenic factors are selected from the group consisting of HLA-C, HLA-E, HLA-G, PD-L1, CTLA-4-Ig, CD47, C1-inhibitor, and IL-35.

Also disclosed herein are methods of preparing a hypoimmunogenic stem cell, the method comprising modulating expression of one or more tolerogenic factors by the stem cell and thereby preparing the hypoimmunogenic stem cell. In certain embodiments, modulating expression of the tolerogenic factors comprises increasing the expression of the tolerogenic factors. Such tolerogenic factors may be inserted into a safe harbor locus (e.g., the AAVS1 locus) of at least one allele of the cell. In certain embodiments, such tolerogenic factors are selected from the group consisting of HLA-C, HLA-E, HLA-G, PD-L1, CTLA-4-Ig, CD47, C1-inhibitor, and IL-35. In certain embodiments, such tolerogenic factors inhibit immune rejection of the stem cell or of a differentiated stem cell prepared therefrom.

In certain aspects, the methods disclosed further comprise modulating expression of one or more MHC-I and MHC-II human leukocyte antigens by the cell, for example, by deleting one or more genes encoding one or more transcriptional regulators of MHC-I or MHC-II from at least one allele of the cell. In certain embodiments, transcriptional regulators of MHC-I or MHC-II from are selected from the group consisting of NLRC5, CIITA, B2M and combinations thereof.

Also disclosed herein are human stem cells that do not express NLRC5 (e.g., a *NLRC5*^{-/-} knockout mutant stem cell). Similarly, also disclosed are human stem cells that do not express CIITA (e.g., a *CIITA*^{-/-} knockout mutant stem cell). Also disclosed are human stem cells that do not express B2M (e.g., a *B2M*^{-/-} knockout mutant stem cell). In certain embodiments, also provided are human stem cells that do not express one or more of NLRC5, CIITA and B2M. In still other embodiments, also disclosed are human stem cells that do not express one or more of HLA-A, HLA-B and HLA-C.

In certain embodiments, the stem cells disclosed herein expresses one or more tolerogenic factors (e.g., one or more tolerogenic factors that inhibit immune rejection). In certain aspects, such tolerogenic factors are inserted into a safe harbor locus (e.g., the AAVS1 locus) of at least one allele of the cell. In certain embodiments, the tolerogenic factors are selected from the group consisting of HLA-C, HLA-E, HLA-G, PD-L1, CTLA-4-Ig, CD47, C1-inhibitor, and IL-35.

In some embodiments, the cell is an embryonic stem cell. In certain embodiments, the cell is a pluripotent stem cell. In certain embodiments, the stem cell is hypoimmunogenic.

In some embodiments, the cell has reduced MHC-I expression relative to the original genotype or relative to a wild-type human stem cell. In certain embodiments, the cell has reduced MHC-II expression relative to the original genotype or relative to a wild-type human stem cell. For example, such cells may have reduced expression of one or more of HLA-A, HLA-B and HLA-C relative to the original genotype or relative to a wild-type human stem cell.

Also disclosed herein are human stem cells that have been altered such that they comprise one or more tolerogenic factors inserted into a safe harbor locus (e.g., the AAVS1 locus) of at least one allele of the cell. In certain embodiments, such tolerogenic factors inhibit immune rejection. In certain embodiments, the tolerogenic factors are selected from the group consisting of HLA-C, HLA-E, HLA-G, PD-L1, CTLA-4-Ig, CD47, C1-inhibitor, and IL-35. In certain aspects, such cells do not express one or more of NLRC5, CIITA and B2M. In certain aspects, such cells do not express one or more of HLA-A, HLA-B and HLA-C. In certain embodiments, such cells have reduced expression of one or more of HLA-A, HLA-B and HLA-C relative to a wild-type human stem cell.

Also disclosed herein are methods of using the hypoimmunogenic cells disclosed herein for cell replacement therapy. For example, the universal stem cells disclosed herein may be incubated under appropriate conditions and differentiated into hypoimmunogenic cardiomyocytes, endothelial cells, hepatocytes or pancreatic beta cells.

Also disclosed herein are methods for producing hypoimmunogenic stem cells, the method comprising contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 36353-81239, thereby editing the NLRC5 gene to reduce or eliminate NLRC5 surface expression and/or activity in the cell.

Also disclosed are methods for producing hypoimmunogenic stem cells, the method comprising contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 5184-36352, thereby editing the CIITA gene to reduce or eliminate CIITA surface expression and/or activity in the cell.

Also disclosed are methods for producing hypoimmunogenic stem cells, the method comprising contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 81240-85644, thereby editing the B2M gene to reduce or eliminate B2M surface expression and/or activity in the cell.

Also disclosed herein are methods for producing a hypoimmunogenic stem cell, the method comprising: (a) contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 36353-81239, thereby editing the NLRC5 gene to reduce or eliminate NLRC5 surface expression and/or activity in the cell; (b) contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a second pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 5184-36352, thereby editing the CIITA gene to reduce or eliminate CIITA surface expression and/or

activity in the cell; and/or (c) contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a third pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 81240-85644, thereby editing the B2M gene to reduce or eliminate B2M surface expression and/or activity in the cell.

Also disclosed are methods for producing hypoimmunogenic stem cells, the method comprising contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a first ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 36353-81239, thereby editing the NLRC5 gene to reduce or eliminate NLRC5 surface expression and/or activity in the cell.

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Also disclosed herein are methods for producing hypoimmunogenic stem cells, the method comprising: (a) contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a first ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 36353-81239, thereby editing the NLRC5 gene to reduce or eliminate NLRC5 surface expression and/or activity in the cell; (b) contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a second ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 5184-36352, thereby editing the CIITA gene to reduce or eliminate CIITA surface expression and/or activity in the cell; and/or (c) contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas

protein and a third ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 81240-85644, thereby editing the B2M gene to reduce or eliminate B2M surface expression and/or activity in the cell.

Also disclosed herein are hypoimmunogenic stem cells comprising a modified genome comprising a first genomic modification in which the NLRC5 gene has been edited to reduce or eliminate NLRC5 surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 36353-81239.

Also disclosed are hypoimmunogenic stem cells comprising a modified genome comprising a first genomic modification in which the CIITA gene has been edited to reduce or eliminate CIITA surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 5184-36352.

Also disclosed are hypoimmunogenic stem cells comprising a modified genome comprising a first genomic modification in which the B2M gene has been edited to reduce or eliminate B2M surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 81240-85644.

Also disclosed herein are hypoimmunogenic stem cells comprising a modified genome comprising: (a) a first genomic modification in which the NLRC5 gene has been edited to reduce or eliminate NLRC5 surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 36353-81239; (b) a second genomic modification in which the CIITA gene has been edited to reduce or eliminate CIITA surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 5184-36352; and/or (c) a third genomic modification in which the B2M gene has been edited to reduce or eliminate B2M surface expression and/or activity in the

cell by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 81240-85644.

Also disclosed are hypoimmunogenic stem cells comprising a modified genome comprising a first genomic modification in which the NLRC5 gene has been edited to delete a first contiguous stretch of genomic DNA, thereby reducing or eliminating NLRC5 surface expression and/or activity in the cell, wherein the first contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 36353-81239.

Also disclosed are hypoimmunogenic stem cells comprising a modified genome comprising a first genomic modification in which the CIITA gene has been edited to delete a first contiguous stretch of genomic DNA, thereby reducing or eliminating CIITA surface expression and/or activity in the cell, wherein the first contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 5184-36352.

Also disclosed are hypoimmunogenic stem cells comprising a modified genome comprising a first genomic modification in which the B2M gene has been edited to delete a first contiguous stretch of genomic DNA, thereby reducing or eliminating B2M surface expression and/or activity in the cell, wherein the first contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 81240-85644.

Also disclosed herein are hypoimmunogenic stem cells comprising a modified genome comprising: (a) a first genomic modification in which the NLRC5 gene has been edited to delete a first contiguous stretch of genomic DNA, thereby reducing or eliminating NLRC5 surface expression and/or activity in the cell, wherein the first contiguous stretch of genomic DNA has been deleted by contacting the cell with a

Cas protein or a nucleic acid encoding a Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 36353-81239; (b) a second genomic modification in which the CIITA gene has been edited to delete a first contiguous stretch of genomic DNA, thereby reducing or eliminating CIITA surface expression and/or activity in the cell, wherein the first contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 5184-36352; and/or (c) a third genomic modification in which the B2M gene has been edited to delete a first contiguous stretch of genomic DNA, thereby reducing or eliminating B2M surface expression and/or activity in the cell, wherein the first contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 81240-85644.

The above discussed, and many other features and attendant advantages of the present inventions will become better understood by reference to the following detailed description of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication with color drawings will be provided by the Office upon request and payment of the necessary fee.

FIG. 1 illustrates the promise of regenerative medicine.

FIGS. 2A-2B graphically depict the HLA barrier in transplantation. FIG. 2A graphically illustrates MHC-I and MHC-II surface molecules that define donor compatibility during organ transplant. FIG. 2B illustrates the HLA region 6p21.1-21.3.

FIGS. 3A-3B illustrate targeting of transcriptional regulators of antigen presentation. FIG. 3A illustrates a model of the MHC-II enhanceosome. FIG. 3B depicts a model of the NLRC5 enhanceosome at the MHC-I promoter.

FIG. 4 illustrates MHC-I expression in WT HuES9 and the indicated modified mutant cell lines. Cells were stimulated for 48 hrs. with IFN γ and MHC-I expression was assessed by FACS.

FIGS. 5A-5C illustrate that *CIITA*-deficient stem cell-derived macrophage lack MHC-II expression. FIG. 5A depicts a time line of macrophage differentiation. FIG. 5B shows a bright-field image of stem cell-derived macrophages on day 5 of M-CSF medium. FIG. 5C shows MHC-II expression in induced macrophages, as assessed by qPCR 48 hrs. post stimulation with IFN γ , and evidences reduced MHC-II expression relative to wild-type cells. As illustrated in FIG. 5C, MHC-II expression can be efficiently abrogated by targeting the first coding exon of the *CIITA* gene depicted in FIGS. 10A-10B.

FIG. 6 illustrates a time line of the teratoma rejection study disclosed herein in which humanized NSG mice - BLT mice are given 3 months to fully reconstitute a human immune system before injection of the indicated genome-edited stem cell lines.

FIG. 7 demonstrates improved engraftment of genome-edited stem cells in humanized mice. Illustrated are the quantification of teratoma type observed following the teratoma rejection study depicted in FIG. 6. Upon review of the morphology of the teratoma samples, a clear phenotype that correlates with the levels of MHC-I expression was observed.

FIGS. 8A-8C demonstrate that proliferation of infiltrating CD8⁺ T cell indicates immune rejection. FIGS. 8A and 8B illustrate immunostaining of teratoma-infiltrating CD3⁺ lymphocytes. FIG. 8C illustrates co-staining of CD8 and Ki67, which is a proliferation marker, and highlights proliferating CD8⁺ T cells (white arrows). Nuclear DAPI staining is shown in blue.

FIGS. 9A-9D demonstrate that the deletion of *NLRC5* using TALENs results in reduced MHC-I expression in induced pluripotent stem cell-derived hepatocyte-like cells (HLCs). FIG. 9A illustrates the *NLRC5* locus. FIG. 9B shows targeting of the *NLRC5* locus to abrogate *NLRC5* expression. FIGS. 9C-9D illustrate reduced MHC-I expression in *NLRC5*^{-/-} HLCs.

FIGS. 10A-10B illustrate targeting of the first coding exon of the *CIITA* gene. FIG. 10A depicts the *CIITA* locus. FIG. 10B shows the targeting of the *CIITA* locus to abrogate MHC-II expression.

FIGS. 11A-11C demonstrate that tolerogenic factors, such as PD-L1 and HLA-G, can be expressed from a safe harbor locus.

FIG. 12 shows an exemplary amino acid sequence of a Cas protein. Yellow highlights indicate Ruv-C-like domain. Underlining indicates HNH nuclease domain.

FIG. 13 illustrates a comparison of the MHC-II and MHC-I enhanceosomes.

FIGS. 14A-14J demonstrates the targeting of HLA-A, HLA-B and HLA-C. FIG. 14A depicts an HLA-B and HLA-C knock-out strategy. Two short guide RNAs (sgRNAs) were designed upstream of the HLA-B locus and downstream of HLA-C, which allow excision of the HLA-B and HLA-C genes. sgRNA #1 and sgRNA #2 target the HLA-B upstream region, and sgRNA #3 and sgRNA #4 target HLA-C the downstream region. FIG. 14B shows that PCR screening confirms clone 1D as a homozygous knock-out clone. FIG. 14B includes a schematic showing the PCR verification strategy for successful deletion of HLA-B and HLA-C. Two pairs of wild-type (WT) primers were designed flanking each cutting site, with predicted amplicon sizes of 545 bp and 472 bp. Clone 1D was identified as a homozygous knock-out clone by the presence of about 680 bp PCR band generated with KO primers and the absence of bands using the two different sets of WT primers.

Genomic DNA was isolated from the indicated targeted HuES8 clones. FIG. 14C provides a schematic showing sequence confirmation of HLA-B, HLA-C deletion in 1D KO clone. The sequencing results of 1D PCR product demonstrated successful deletion of HLA-B and HLA-C genes in HuES8. FIG. 14D shows that RT-PCR confirms the loss of HLA-B and HLA-C mRNA expression in HuES8 cells. RT-PCR with HLA-B and HLA-C specific primers demonstrated the mRNA expressions of HLA-B and HLA-C in clone 1D are eliminated. GAPDH, TOP1 and HPRT1 were used as internal controls. FIG. 14E provides a schematic showing sequence confirmation of HLA-B RT-PCR bands obtained from WT and clone 1D. WT and 1D RT-PCR products amplified with HLA-B primers were sequenced and identified as HLA-B and HLA-A mRNAs, respectively using BLAST. These results demonstrated that in the absence of the HLA-B gene, the HLA-B specific primers will

amplify HLA-A mRNA in HuES8 clone 1D. FIG. 14F shows the karyotyping of HuES8 clone 1D by NanoString nCounter. HuES8 clone 1D displays a normal karyotype as assessed by NanoString nCounter set. FIG. 14G provides a schematic showing HLA-A knockout strategy using the dual sgRNA approach. The schematic shows the positions of the two sgRNAs (sgRNA #5 and sgRNA #6) that were designed to bind upstream and downstream of HLA-A. FIG. 14H shows the on-target cutting efficiency of HLA-A sgRNA using TIDE. The cutting efficiency of sgRNA #5 and sgRNA #6 was determined in 293T cells using TIDE. FIG. 14I demonstrates that PCR screening confirmed clone 4E as a heterozygous HLA-A knockout clone. PCR screening strategy confirmed deletion of HLA-A in HuES8. KO primers were designed with one primer annealing upstream and one primer annealing downstream of the cutting sites. Upon HLA-A deletion, the resulting amplicon is observed as 220 bp on a 2% agarose gel. Two pairs of WT primers were designed flanking each cutting site, with predicted amplicons sizes of 589 bp and 571 bp. Clone 4E was identified as heterozygous clone due to the presence of bands generated with KO primers and WT primers amplified from genomic DNA. FIG. 14J includes a schematic showing that sequencing confirms successful deletion of HLA-A in HuES8 cells. Sequencing of the PCR product amplified from genomic DNA of clone 4E using KO primers demonstrates successful deletion of HLA-A in HuES8.

FIGS. 15A-15D show TALEN-induced CIITA and NLRC5 mutations in BJ-RIPSCs and HuES9 cells. FIG. 15A provides a schematic of TALEN-induced CIITA mutations in BJ-RIPSCs. FIG. 15B provides a schematic of TALEN-induced NLRC5 mutations in BJ-RIPSCs. FIG. 15C provides a schematic of TALEN-induced NLRC5 mutations in HuES9s. FIG. 15D provides a schematic of TALEN-induced CIITA mutations in HuES9s.

FIGS. 16A-16G demonstrate targeting of NLRC5 and CIITA utilizing a CRISPR system to achieve a reduction in MHC class I expression and complete loss of MHC class II expression. FIG. 16A shows reduced MHC-I expression in NLRC5^{-/-} Thp1 cells, including a NLRC5 targeting strategy in Thp1 cells. The + indicates 48 hours of IFN γ stimulation. FIG. 16B provides schematics of multiple targeting strategies. FIG. 16B provides a schematic of targeting NLRC5 using CRISPR, a schematic of targeting B2M using CRISPR, a schematic of targeting CIITA using

TALENs and a schematic of targeting CIITA using CRISPR. FIG. 16C shows reduced MHC class I expression in HuES9 cells following targeting with NLRC5 or B2M CRISPRs. The graph shows low basal MHC-I expression in stem cells. The MHC-I expression can be increased by IFN γ stimulation. About a 50% reduction of MHC-I expression occurs in IFN γ -treated NLRC5-/- cells. A complete loss of MHC-I surface expression is shown in B2M-/- cells. FIG. 15D shows a lentiviral transduction of Thp-1. A dual-vector lentiviral GeCKO system is used. The two component system includes Lenti-Cas9-Blasticidin, which acts to establish stable Thp-1 Cas9 cell line, and Lenti-Guide-puro, which acts to bring in the guide. FIG. 16E identifies various CRISPRs used for the lentiviral transduction of Thp-1. CRISPRs targeting CIITA, NLRC5 and IRF1 are provided. FIG. 16F shows that CIITA and NLRC5 act independently on MHC-II and MHC-I, respectively. Thp1 was transduced with lentivirus encoding NLRC5 and CIITA. A B2M CRISPR is used as a positive control. All cells were stimulated ON with 50U IFN γ to boost HLA expression. HLA-A2 1:200; DR 1:100. FIG. 16G shows targeting of IRF1 results in loss of MHC-II expression. Thp1, 10 days post CRISPR transduction. All cells were stimulated ON with 50U IFN γ . HLA-A2 1:200; DR 1:100.

FIGS. 17A-17K demonstrate targeting of IRF1 utilizing a CRISPR system to achieve reduced MHC class I expression in human pluripotent stem cells (HuES9) and Thp-1 cells. FIG. 17A shows a dual CRISPR strategy targeting the *IRF1* locus. Three different CRISPRs are identified. FIG. 17B demonstrates the testing of different *IRF1* guide combinations. Screening results of different guide combinations are provided. FIG. 17C demonstrates a 'dual guide strategy' for the targeted deletion of *IRF1*. Screening results of the dual guide strategy are provided. FIG. 17D provides a schematic showing sequence confirmation of *IRF-1* CRISPR induced deletion. FIG. 17E provides the screening results of *IRF-1* targeted HuES9 cells. The screening is of a dual CRISPR strategy using CRISPRs #2 and #3. The presence of the PCR band suggests successful targeting. FIG. 17F demonstrated reconfirmation of IRF-1 clones. Screening results using primers KYM07 and TM377 are provided. FIG. 17G demonstrates genotypes of IRF-1 clones. Screening results are provided. FIG. 17H provides a schematic showing sequence confirmation of IRF-1 CRISPR induced deletion in clone 12. FIG. 17I provides a schematic showing sequence

confirmation of IRF-1 CRISPR induced deletion in clone 17. FIG. 17J provides a schematic showing sequence confirmation of IRF-1 CRISPR induced deletion in clone 21. FIG. 17K shows impaired MHC class I induction in IRF1^{-/-} HuES9 clones following IFN γ treatment. P42 are WT; C7 are B2M KO; + identifies 48 hours IFN γ treatment.

FIGS. 18A-18H demonstrate targeting of RFX5, RFX-ANK and RFX-AP in 293T cells utilizing CRISPR results in reduced MHC class I expression. FIG. 18A demonstrates dual guide targeting of RFX5 in 293T cells. Combinations of four different CRISPRs were examined. FIG. 18B shows that the targeting of RFX5 results in reduced MHC class I expression. FIG. 18C demonstrates dual guide targeting of RFX-ANK in 293T cells. Combinations of four different CRISPRs were examined. FIG. 18D shows that the targeting of RFX-ANK results in reduced MHC class I expression. FIG. 18E shows that targeting RFX5 and RFX-ANK results in reduced MHC class I expression. FIG. 18F provides a bar graph showing that targeting RFX5 and RFX-ANK results in reduced MHC class I expression. FIG. 18G demonstrates dual guide targeting of RFX-AP in 293T cells. Combinations of four different CRISPRs were examined. FIG. 18H shows that the targeting of RFX-AP results in reduced MHC class I expression.

FIGS. 19A-19E demonstrate targeting of NFY-A, NFY-B and NFY-C utilizing CRISPR results in reduced MHC class I expression. FIG. 19A demonstrates dual guide targeting of NFY-A in 293T cells. Combinations of four different CRISPRs were examined. FIG. 19B demonstrates dual guide targeting of NFY-C in 293T cells. Combinations of four different CRISPRs were examined. FIG. 19C shows that the targeting of NFY-C and NFY-A results in reduced MHC class I expression. FIG. 19D demonstrates dual guide targeting of NFY-B in 293T cells. Combinations of four different CRISPRs were examined. FIG. 19E shows that the targeting of NFY-B results in reduced MHC class I expression.

FIGS. 20A-20D show that surface trafficking of MHC class I molecules can be suppressed by disrupting the TAP1 gene, an ER-resident peptide transporter. FIG. 20A shows TAP1 CRISPR expression reduces MHC-I surface expression in Jurkat T cells. Combinations of four different CRISPRs was examined. FIG. 20B demonstrates TAP1 CRISPR expression reduces MHC-I surface expression in Jurkat

T cells. FIG. 20C demonstrates eliminating HLA surface expression in Jurkat (Cas9) T cells. The Jurkat cell line was established from the peripheral blood of a 14 year old having acute T cell leukemia by Schneider et al. FIG. 20D shows eliminating HLA surface expression in Jurkat (Cas9) T cells. The cells were treated with IFN γ for 48 hours.

FIGS. 21A-21D demonstrate the use of a CRISPR gRNA identified as an HLA Razor that allows simultaneous deletion of all MHC class I alleles by targeting a conserved region in the HLA genes. FIG. 21A provides a schematic showing the targeting of a conserved sequence found in all HLAs by CRISPR or TALENs using an HLA Razor. The two violet boxes indicate the binding sites for the panHLA TALEN pair. The blue arrow indicates the pan-HLA CRISPR tested; the PAM is boxed in blue. FIG. 21B shows the expression of pan-HLA TALENs in 293T and HuES9 cells 72 hours post transfection. FIG. 21C shows HLA-Razor CRISPR blunts MHC class I expression. The 293T cells were co-transfected with Cas9-GFP. The results are shown 72 hours post transfection. FIG. 21D provides a schematic showing a comparison of the activity of two different HLA Razors. Two HLA Razor guides are identified.

FIGS. 22A-22F show the results of a PD-L1 and HLA-G knock-in strategy. FIG. 22A provides a schematic showing PD-L1 and HLA-G knock-in strategy. WT primers and knock-in (KI) primers for clone screening were designed. The amplicon with WT primers is predicted as 488 bp, and the amplicons with KI primers are predicted as 403 bp and 915 bp. FIG. 22B depicts the design of the knock-in donor plasmid. The design of the knock-in donor plasmid shows that the reading frames of PD-L1 and HLA-G are linked by T2A and their expression is driven by a CAGGS promoter. Puromycin was used as a drug resistance marker following the SA-2A gene trap element. FIG. 22C demonstrates ectopic PD-L1 and HLA-G expression in 293T cells. The expression of PD-L1 and HLA-G were examined in the donor plasmid-transfected 293T cells by FACS analysis. APC-conjugated PD-L1 antibody and FITC-conjugated HLA-G antibody were used. FIG. 22D shows ectopic HLA-G expression in JEG-3 cells. Donor plasmid was transfected into an HLA-G $^{-}$ -JEG-3 cell line, and ectopic HLA-G expression was examined by FACS analysis 48 hours post-transfection. A PE-conjugated HLA-G antibody (MEM/G9) was used to detect

surface HLA-G surface expression. FIG. 22E provides PCR screening results that confirm clone 1G as a heterozygous KI clone for PD-L1/HLA-G. Clone 1G was identified as a heterozygous KI clone by the presence of bands using both WT primers and KI-specific primers amplified from genomic DNA of targeted HuES8 cells. FIG. 22F shows stable PD-L1 and HLA-G expression from a safe harbor locus in HuES8. The expression of PD-L1 was verified in HuES8 KI clone 1G by FACS analysis using an APC-conjugated PD-L1 antibody.

FIG. 23 demonstrates expression of CD47 in 293T cells and hPSCs using a knock-in strategy. Human CD47 was cloned into an expression plasmid driven by a CAG promoter, which in addition contains an IRES-GFP. 293T cells already express high levels of CD47, the human 'don't eat me' signal, which prevents engulfment of cells from macrophages. Expression can be increased by overexpression of CD47 in both 293T cells, as well as in human pluripotent stem cells (HuES9), as detected by FACS using a CD47-specific antibody. Overexpression of CD47 will assist engraftment of stem cell-derived transplants by protecting cells from macrophage engulfment.

FIG. 24 demonstrates that deletion of TRAC and TRBC in HuES9 disrupts TCR expression. A dual guide RNA approach was used to introduce deletions into the TRAC and TRBC loci in HuES9 cells. TCRA wt band is 249 bp, and is 209 bp after deletion. TCRB wt band is 162 bp, and is 140 bp after deletion. Bands identified with a * are TCRB KO in HuES9 cells; bands identified with a ** are TCRA KO in HuES9 cells; and bands identified with a *** are TCRA KO in HuES9 B2M^{-/-}CIITA^{-/-} cells. TCRA KO in HuES9 B2M^{-/-}CIITA^{-/-} cells is a triple knock-out stem cell line for B2M^{-/-}, CIITA^{-/-} and TCR^{-/-}. Upon differentiation into T cells this triple knock out stem cell line will be devoid of MHC-I, MHC-II and TCR surface expression.

FIGS. 25A-25D demonstrate targeting of CD274/B7-H1/PD-L1 in a variety of cell lines. FIG. 25A identifies an example of a CRISPR guide sequence that may be used when targeting CD274/B7-H1/PD-L1. CD274/B7-H1/PD-L1 knock out cell lines are identified. FIG. 25B shows the screening of targeted B7-H1 colonies in JEG-3 cells. The screening identified a CRISPR cutting efficiency of 22/265 or about

8.3%. FIG. 25C demonstrates the reconfirmation of 501 melanoma knock-out clones. FIG. 25D demonstrates the reconfirmation of MalMe melanoma knock-out clones.

FIGS. 26A-26P demonstrate targeting of co-inhibitory/co-stimulatory receptors or their ligands. For each target, the indicated four CRISPRs have been cloned and tested for on-target activity in 293T cells. The expected size of the PCR band, when cutting of both CRISPRs occurs, is indicated below the gel picture. FIG. 26A shows co-stimulatory/co-inhibitory molecules and their receptors on T cells. FIG. 26B demonstrates dual guide targeting of TIGIT in 293T cells. All four CRISPRs were found to work. FIG. 26C demonstrates dual guide targeting of TIM3 in 293T cells. All four CRISPRs were found to work. FIG. 26D demonstrates dual guide targeting of HVEM in 293T cells. All four CRISPRs were found to work. FIG. 26E demonstrates dual guide targeting of 2B4/CD244 in 293T cells. All four CRISPRs were found to work. FIG. 26F demonstrates dual guide targeting of CD28 in 293T cells. CRISPRs #1, #2 and #3 were found to work. FIG. 26G demonstrates dual guide targeting of OX40 in 293T cells. CRISPRs #1, #2 and #4 were found to work. FIG. 26H demonstrates dual guide targeting of B71 in 293T cells. CRISPRs #1, #3 and #4 were found to work. FIG. 26I demonstrates dual guide targeting of CD226 in 293T cells. CRISPRs #1 and #2 were found to work. FIG. 26J demonstrates dual guide targeting of CD2 in 293T cells. CRISPRs #1, #2 and #3 were found to work. FIG. 26K demonstrates dual guide targeting of LAG3 in 293T cells. CRISPRs #2 and #3 were found to work. FIG. 26L demonstrates dual guide targeting of BTLA in 293T cells. All four CRISPRs were found to work. FIG. 26M demonstrates dual guide targeting of ICOS in 293T cells. CRISPRs #2, #3 and #4 were found to work. FIG. 26N demonstrates dual guide targeting of CD27 in 293T cells. CRISPRs #1 and #2 were found to work. FIG. 26O demonstrates dual guide targeting of ST2 in 293T cells. All four CRISPRs were found to work. FIG. 26P demonstrates dual guide targeting of GITR in 293T cells. CRISPRs #1 and #3 were found to work.

FIG. 27 depicts various cell lines tested and with which targets the cells lines were tested. HuES8 and HuES9 are human ES cell lines. BJ-RiPSCs is an iPSC line. All other enhanceosome components not shown in the table (e.g., RFX and NFY) were only tested in HEK293T cells.

FIGS. 28A-28J provides that modified ES cells can be differentiated into various different cell types with reduced or absent HLA expression. FIG. 28A provides that the modified ES cell can be differentiated into Mesenchymal Progenitor Cells (MPCs), endothelial cells (ECs), macrophages, hepatocytes, beta-cells and neural progenitor cells (NPCs). FIG. 28B shows reduced MHC-I expression in NLRC5^{-/-} human ES cells. There is low basal MHC-I expression in stem cells. The expression can be increased by IFN γ stimulation. About a 50% reduction in MHC-I expression occurs in IFN γ -treated NLRC5^{-/-} cells. FIG. 28C shows reduced MHC-I expression in NLRC5^{-/-} human mesenchymal progenitor cells (MPCs). A comparison is provided of HuES9 cells and MPCs. FIG. 28D shows reduced MHC-I expression in stem cell-derived NLRC5^{-/-} endothelial cells (ECs). FIG. 28E demonstrates that ECs exhibit similar differentiation efficiency. FIG. 28F shows loss of HLA expression in B2M^{-/-}CIITA^{-/-}ECs. N=3, 48 hours of IFN γ treatment. FIG. 28G demonstrates reduced MHC class I expression in NLRC5^{-/-} hepatocyte-like cells. A schematic is included demonstrating the targeting strategy and CRISPR design. The HLCs are derived from BJ-RiPSCs, day 7 of final hepatocyte differentiation. FIG. 28H demonstrates that mutation of *CIITA* abrogates MHC class II expression in hESC-derived macrophages. A schematic is included demonstrating the targeting strategy and CRISPR design. The HuES9-derived iM Φ s, day 5 M-CSF. FIG. 28I shows neural progenitor cell (NPC) differentiation. B2M^{-/-}CIITA^{-/-}-HuES9 form Nestin⁺ neural rosettes (white arrow). FIG. 28J demonstrates the adaptation of stem cells to spin culture for beta-cell differentiation. This is the first step in the beta-cell differentiation protocol.

FIG. 29A-29B provide *in vivo* data in a teratoma model. FIG. 29A provides that 'hypoinmunogenic' DKO cell lines were generated. The cell lines generated include WT HuES9, NLRC5^{-/-}CIITA^{-/-} HuES9 and B2M^{-/-}CIITA^{-/-} HuES9. The WT cell lines exhibited MHC-I and MHC-II expression. The NLRC5^{-/-}CIITA^{-/-} cells lines exhibited reduced MHC-I expression and no MHC-II expression. The B2M^{-/-}CIITA^{-/-} cell lines exhibited no MHC-I and MHC-II expression. FIG. 29B shows improved engraftment of genome-edited stem cells in humanized mice. The three cell lines tested were WT HuES9, NLRC5^{-/-}CIITA^{-/-} HuES9 and B2M^{-/-}CIITA^{-/-} HuES9.

FIGS. 30A-30D demonstrates CRISPR targeting of B7-H3 in JEG-3 cells. FIG. 30A provides a CRISPR guide sequence for targeting B7-H3. FIG. 30B shows a screening of targeted B7-H3 colonies in JEG-3 cells. The CRISPR cutting efficiency is shown to be 15/80 or about 18.7%. FIG. 30C shows confirmation of B7-H3 knock-outs through sequencing. FIG. 30D demonstrates loss of B7-H3 surface expression in targeted JEG3 clones.

FIG. 31 shows loss of MHC class I surface expression in B2M^{-/-} Jurkat Cas9 T cells. The B2M^{-/-} Jurkat Cas9 T cells are compared to Jurkat Cas9 T cells that do not include a knock out of B2M.

FIGS. 32A-32H demonstrate targeting clinically relevant loci in human cells using CRISPR/Cas9. FIG. 32A is a schematic of gRNAs targeting *B2M*. FIG. 32B is a histogram of B2M surface expression in HEK293T cells. FIG. 32C shows B2M deletion efficiency with various gRNAs in HEK293T cells; n=3 (mean±SEM). FIG. 32D is a schematic of gRNAs targeting *CCR5*. Orange and green arrows represent primer pairs used to amplify the region for analysis. FIG. 32E shows results of Surveyor assays of each gRNA targeting *CCR5* in K562 cells. % InDels is indicated under each guide. FIG. 32F illustrates B2M deletion efficiency of selected gRNAs in primary CD4⁺ T cells in comparison to 293T cells; n=6 (mean±SEM). FIG. 32G shows results of surveyor assay of crCCR5_A and crCCR5_B targeting *CCR5* in K562 cells and HSPCs. FIG. 32H illustrates clonal deletion efficiency of crCCR5_A and crCCR5_B targeting of *CCR5* in HSPCs (n=2) as determined by Sanger sequencing. (Note: crB2M_14 is not depicted in panel A schematic, as it is located 20 Kb downstream of coding sequence.).

FIGS. 33A-33E demonstrate an evaluation of on target mutational efficiencies of various gRNAs targeting B2M. FIG. 33A shows B2M deletion efficiency for all gRNAs targeting *B2M* locus in HEK293T cells as measured by flow cytometry. Pooled data from 3 independent experiments shown as mean±SEM. FIG. 33B shows B2M deletion efficiencies of selected guides in HEK293T cells, measured as % InDels by CEL Surveyor assay. FIG. 33C is a comparison of B2M surface expression in HEK293T cells and primary CD4⁺ T cells when transfected with Cas9 and guide crB2M_13. FIG. 33D shows B2M deletion efficiency for selected guides targeting the *B2M* locus in primary CD4⁺ T-cells, as measured by flow cytometry. FIG. 33E shows

B2M deletion efficiencies of selected guides in primary CD4⁺ T cells, measured as % InDels by CEL Surveyor assay.

FIGS. 34A-34E depict a dual gRNA approach for CRISPR/Cas9 genome editing in primary human hematopoietic stem and effector cells. FIG. 34A is a schematic of dual gRNA approach for targeting the *B2M* locus. gRNA pairs are in red. The offset in base pairs between Cas9 sites for each gRNA combination (right panel). FIG. 34B shows B2M deletion efficiency in CD4⁺ T cells for 6 dual gRNA combinations (n=3; mean $\pm$ SEM). FIG. 34C is a FACS plots showing loss of B2M expression of either crB2M_13 or crB2M_8 alone or in combination in primary CD4⁺ T cells. FIG. 34D is a schematic of dual gRNA approach for targeting *CCR5*. gRNA pairs are shown in red. Orange and green arrowheads represent primer pairs used to amplify the region. The offset between the Cas9 sites of each gRNA pair (right panel). FIG. 34E is a gel electrophoresis image of CD34⁺ HSPCs derived clones targeted with crCCR5_D+Q analyzed by PCR. Note the deletion of the 205 bp region between the two gRNA cutting sites (top panel; WT: wild type; Δ CCR5: deleted; green * denotes a WT clone; orange * denotes a heterozygous clone; and red * denotes a homozygous deleted clone). Clonal deletion efficiency for three dual gRNA combinations targeting *CCR5* in CD34⁺ HSPCs (n=4; % mean $\pm$ SEM; bottom panel).

FIGS. 35A-35G demonstrate the targeting efficiency of dual gRNA combinations. FIG. 35A shows B2M deletion efficiency for 6 dual gRNA combinations from three independent donors as measured by flow cytometry. FIG. 35B are FACS plots showing loss of MHC class I surface expression (bottom panel) following *B2M* deletion (top panel). FIG. 35C is a schematic of the single cell nested PCR strategy for the *B2M* locus (left panel), black and gray arrowheads: control primer pairs, orange and green arrowheads: primer pairs flanking targeting region. % B2M null single cells is shown (right panel, n=301). FIG. 35D is a Sanger sequencing chromatogram showing predicted deletion of targeted region at *B2M* locus. FIG. 35E shows clonal *CCR5* deletion efficiency for three dual gRNA combinations in CD34⁺ HSPC-mPB obtained from multiple donors. DNA isolated from individual colony was analyzed by PCR and gel electrophoresis. FIG. 35F is a schematic of the single cell nested PCR strategy (left panel) for determining deletion of *CCR5* in primary CD4⁺ T

cells. % *CCR5* null single cells is shown (right panel, n=363). FIG. 35G shows Sanger sequencing chromatogram shows predicted deletion at targeted region.

FIG. 36 demonstrates B2M deletion efficiencies of selected guides in 293T cells. Arrows on the Surveyor assays show nuclease cleavage bonds.

5 FIG. 37 demonstrates a comparison of B2M surface expression in 293T cells when transfected with AsCpf1 and guide crB2M.

FIG. 38 demonstrates a comparison of B2M surface expression in 293T cells when transfected with LbCpf1 and guide crB2M.

FIG. 39 depicts Cpf1 crRNA design and cloning information.

10 FIGS. 40A-40G demonstrate generation and characterization of B2M KO JEG3 cells using TALENs. FIG. 40A depicts a design of B2M TALEN and induced mutations. FIG. 40B depicts an analysis of B2M at the transcript and protein levels. FIG. 40C demonstrates an analysis of B2M at the surface expression level. FIG. 40D demonstrates that Δ B2M clones are devoid of MHC-I surface expression. FIG. 40E demonstrates that Δ B2M clones are devoid of HLA-G surface expression. FIG. 40F demonstrates that Δ B2M clones are devoid of HLA-C surface expression. FIG. 40G demonstrates that Δ B2M clones are devoid of HLA-E surface expression.

20 FIG. 41 demonstrates an exemplary TCR targeting strategy of the present invention. FIG. 41 is a schematic illustration depicting the location of the CRISPR gRNAs targeting the first coding exons of the TCRalpha and TCRbeta chains, respectively.

25 FIGS. 42A-42B demonstrate deletion of T cell receptor in Jurkat T cells. FIG. 42A depicts the results of a FACS analysis employing an anti-CD3 antibody, which reveals successful TCR deletion in Jurkat T cells that stably express the Cas9 nuclease. FIG. 42B shows the results of a SURVEYORTM assay confirming cutting at the TCRA and TCRB loci.

30 FIGS. 43A-43B demonstrate TCR Deletion in Primary Human CD3⁺ T Cells. FIG. 43A shows the results of a SURVEYORTM assay demonstrating CRISPR cutting at the TCRA and TCRB loci in CD3⁺ T cells obtained from two independent donors. FIG. 43B shows the loss of TCR surface expression demonstrated by FACS analysis.

FIGS. 44A-44C demonstrate an exemplary PD-1 locus targeting strategy of the present invention. FIG. 44A is a schematic representation of the *PD-1* targeting strategy. FIG. 44B demonstrates that the double CRISPR strategy results in cutting by both CRISPRs targeting the PD-1 locus in HEK293T cells. FIG. 44C is a schematic representation of sequencing, which confirmed the predicted deletion in the PD-1 locus after transfection of two CRISPRs targeting the PD-1 gene (*PDCDI*).

FIGS. 45A-45B demonstrate the loss of PD-1 expression in Jurkat T cells. FIG. 45A shows the results of FACS analysis, demonstrating the loss of PD-1 expression in activated Jurkat T cells. FIG. 45B shows the results of a SURVEYORTM assay confirming cutting at the PD-1 locus.

FIGS. 46A-46C demonstrate an exemplary CTLA4 locus targeting strategy of the present invention. FIG. 46A is a schematic representation of the *CTLA4* targeting strategy. FIG. 46B demonstrates that the double CRISPR strategy results in cutting by both CRISPRs targeting the CTLA4 locus in HEK293T cells. FIG. 46C is a schematic representation of sequencing, which confirmed the predicted deletion in the CTLA4 locus after transfection of two CRISPRs targeting the CTLA4 gene (*CTLA4*).

FIGS. 47A-47B demonstrate cutting at the CTLA-4 locus in Jurkat T cells. FIG. 47A demonstrates that the double CRISPR strategy results in cutting by both CRISPRs targeting the CTLA4 locus in Jurkat T cells. FIG. 47B shows the results of a SURVEYORTM assay, demonstrating successful cutting by both CTLA4 CRISPRs in Jurkat T cells.

The following Tables 8-55 are submitted herewith as Appendices 1-47, respectively:

Table 8 – exemplary gRNA sequences useful for targeting HLA-A;

Table 9 – exemplary gRNA sequences useful for targeting HLA-B;

Table 10 - exemplary gRNA sequences useful for targeting HLA-C;

Table 11 - exemplary gRNA sequences useful for targeting RFX-ANK;

Table 12 - exemplary gRNA sequences useful for targeting CIITA;

Table 13 - exemplary gRNA sequences useful for targeting NFY-A;

Table 14 - exemplary gRNA sequences useful for targeting NLRC5;

Table 15 - exemplary gRNA sequences useful for targeting B2M;

Table 16 - exemplary gRNA sequences useful for targeting RFX5;

	Table 17 - exemplary gRNA sequences useful for targeting RFX-AP;
	Table 18 - exemplary gRNA sequences useful for targeting HLA-G;
	Table 19 - exemplary gRNA sequences useful for targeting HLA-E;
	Table 20 - exemplary gRNA sequences useful for targeting NFY-B;
5	Table 21 - exemplary gRNA sequences useful for targeting PD-L1;
	Table 22 - exemplary gRNA sequences useful for targeting NFY-C;
	Table 23 - exemplary gRNA sequences useful for targeting IRF1;
	Table 24 - exemplary gRNA sequences useful for targeting TAP1;
	Table 25 - exemplary gRNA sequences useful for targeting GITR;
10	Table 26 - exemplary gRNA sequences useful for targeting 41BB;
	Table 27 - exemplary gRNA sequences useful for targeting CD28;
	Table 28 - exemplary gRNA sequences useful for targeting B7-1;
	Table 29 - exemplary gRNA sequences useful for targeting CD47;
	Table 30 - exemplary gRNA sequences useful for targeting B7-2;
15	Table 31 - exemplary gRNA sequences useful for targeting OX40;
	Table 32 - exemplary gRNA sequences useful for targeting CD27;
	Table 33 - exemplary gRNA sequences useful for targeting HVEM;
	Table 34 - exemplary gRNA sequences useful for targeting SLAM;
	Table 35 - exemplary gRNA sequences useful for targeting CD226;
20	Table 36 - exemplary gRNA sequences useful for targeting ICOS;
	Table 37 - exemplary gRNA sequences useful for targeting LAG3;
	Table 38 - exemplary gRNA sequences useful for targeting TIGIT;
	Table 39 - exemplary gRNA sequences useful for targeting TIM3;
	Table 40 - exemplary gRNA sequences useful for targeting CD160;
25	Table 41 - exemplary gRNA sequences useful for targeting BTLA;
	Table 42 - exemplary gRNA sequences useful for targeting CD244;
	Table 43 - exemplary gRNA sequences useful for targeting LFA-1;
	Table 44 - exemplary gRNA sequences useful for targeting ST2;
	Table 45 - exemplary gRNA sequences useful for targeting HLA-F;
30	Table 46 - exemplary gRNA sequences useful for targeting CD30;
	Table 47 - exemplary gRNA sequences useful for targeting B7-H3;
	Table 48 - exemplary gRNA sequences useful for targeting VISTA;

Table 49 - exemplary gRNA sequences useful for targeting TLT;

Table 50 - exemplary gRNA sequences useful for targeting PD-L2;

Table 51 - exemplary gRNA sequences useful for targeting CD58;

Table 52 - exemplary gRNA sequences useful for targeting CD58;

5 Table 53 - exemplary gRNA sequences useful for targeting CD2; and

Table 54 - exemplary gRNA sequences useful for targeting HELIOS.

The material submitted herewith in electronic (.txt) form and comprising
Appendices 1-47 (Tables 8-54, respectively) is incorporated herein by reference,
specifically:

10 Appendix 1 (file name: Table8.txt; date created: May 9, 2016; file size:
223,026 bytes);

Appendix 2 (file name: Table9.txt; date created: May 9, 2016; file size:
327,895 bytes);

15 Appendix 3 (file name: Table10.txt; date created: May 9, 2016; file size:
280,849 bytes);

Appendix 4 (file name: Table11.txt; date created: May 9, 2016; file size:
998,046 bytes);

Appendix 5 (file name: Table12.txt; date created: May 9, 2016; file size
4,717,823 bytes);

20 Appendix 6 (file name: Table13.txt; date created: May 9, 2016; file size
2,813,407 bytes);

Appendix 7 (file name: Table14.txt; date created: May 9, 2016; file size
6,568,742 bytes);

25 Appendix 8 (file name: Table15.txt; date created: May 9, 2016; file size
728,685 bytes);

Appendix 9 (file name: Table16.txt; date created: May 9, 2016; file size
766,106 bytes);

Appendix 10 (file name: Table17.txt; date created: May 9, 2016; file size
874,435 bytes);

30 Appendix 11 (file name: Table18.txt; date created: May 9, 2016; file size
232,536 bytes);

Appendix 12 (file name: Table19.txt; date created: May 9, 2016; file size 539,932 bytes);

Appendix 13 (file name: Table20.txt; date created: May 9, 2016; file size 2,256,084 bytes);

5 Appendix 14 (file name: Table21.txt; date created: May 9, 2016; file size 1,303,081 bytes);

Appendix 15 (file name: Table22.txt; date created: May 9, 2016; file size 6,821,299 bytes);

10 Appendix 16 (file name: Table23.txt; date created: May 9, 2016; file size 1,095,386 bytes);

Appendix 17 (file name: Table24.txt; date created: May 9, 2016; file size 941,281 bytes);

Appendix 18 (file name: Table25.txt; date created: May 9, 2016; file size 378,368 bytes);

15 Appendix 19 (file name: Table26.txt; date created: May 9, 2016; file size 2,706,509 bytes);

Appendix 20 (file name: Table27.txt; date created: May 9, 2016; file size 3,578,977 bytes);

20 Appendix 21 (file name: Table28.txt; date created: May 9, 2016; file size 3,638,039 bytes);

Appendix 22 (file name: Table29.txt; date created: May 9, 2016; file size 5,083,645 bytes);

Appendix 23 (file name: Table30.txt; date created: May 9, 2016; file size 4,481,092 bytes);

25 Appendix 24 (file name: Table31.txt; date created: May 9, 2016; file size 393,567 bytes);

Appendix 25 (file name: Table32.txt; date created: May 9, 2016; file size 675,503 bytes);

30 Appendix 26 (file name: Table33.txt; date created: May 9, 2016; file size 1,002,258 bytes);

Appendix 27 (file name: Table34.txt; date created: May 9, 2016; file size 454,540 bytes);

Appendix 28 (file name: Table35.txt; date created: May 9, 2016; file size 10,463,522 bytes);

Appendix 29 (file name: Table36.txt; date created: May 9, 2016; file size 2,755,910 bytes);

5 Appendix 30 (file name: Table37.txt; date created: May 9, 2016; file size 733,191 bytes);

Appendix 31 (file name: Table38.txt; date created: May 9, 2016; file size 1,674,331 bytes);

10 Appendix 32 (file name: Table39.txt; date created: May 9, 2016; file size 2,622,419 bytes);

Appendix 33 (file name: Table40.txt; date created: May 9, 2016; file size 2,049,613 bytes);

Appendix 34 (file name: Table41.txt; date created: May 9, 2016; file size 4,016,813 bytes);

15 Appendix 35 (file name: Table42.txt; date created: May 9, 2016; file size 4,177,884 bytes);

Appendix 36 (file name: Table43.txt; date created: May 9, 2016; file size 4,326,759 bytes);

20 Appendix 37 (file name: Table44.txt; date created: May 9, 2016; file size 1,007,674 bytes);

Appendix 38 (file name: Table45.txt; date created: May 9, 2016; file size 1,690,144 bytes);

Appendix 39 (file name: Table46.txt; date created: May 9, 2016; file size 5,427,706 bytes);

25 Appendix 40 (file name: Table47.txt; date created: May 9, 2016; file size 3,510,941 bytes);

Appendix 41 (file name: Table48.txt; date created: May 9, 2016; file size 3,043,135 bytes);

30 Appendix 42 (file name: Table49.txt; date created: May 9, 2016; file size 274,899,026 bytes);

Appendix 43 (file name: Table50.txt; date created: May 9, 2016; file size 7,273,026 bytes);

Appendix 44 (file name: Table51.txt; date created: May 9, 2016; file size 2,336,524 bytes);

Appendix 45 (file name: Table52.txt; date created: May 9, 2016; file size 274,899,026 bytes);

5 Appendix 46 (file name: Table53.txt; date created: May 9, 2016; file size 1,820,108 bytes); and

Appendix 47 (file name: Table54.txt; date created: May 9, 2016; file size 17,165,777 bytes).

10 DETAILED DESCRIPTION OF THE INVENTION

Recent advances in stem cell biology have made it possible to contemplate the use of a subject's own cells as an unlimited source for transplantation, as generally depicted, for example, in FIG. 1. Unfortunately, genome editing and the generation of
15 induced pluripotent stem cells (iPSCs) followed by the differentiation of such iPSCs remains a costly, time consuming and highly variable process, with regards to pluripotency, epigenetic status, capacity for differentiation, and genomic stability. Moreover, changes occurring during genome editing and prolonged culturing have been found to trigger an adaptive immune response, resulting in immune rejection of
20 even autologous stem cell-derived transplants. To overcome the problem of a subject's immune rejection of stem cell-derived transplants, the present inventors have developed and disclose herein a universal donor stem cell that represents a viable source for any transplantable cell type. Advantageously, the universal stem cells disclosed herein are not rejected by the recipient subject's immune system,
25 regardless of the subject's genetic make-up.

The inventions disclosed herein employ genome editing technologies (e.g., the CRISPR/Cas or TALEN systems) to reduce or eliminate expression of critical immune genes (e.g., by deleting genomic DNA of critical immune genes) or, in certain instances, insert tolerance-inducing factors, in human ES cells and iPSCs,
30 rendering them and the differentiated cells prepared therefrom hypoinmunogenic and less prone to immune rejection by a subject into which such cells are transplanted. As used herein to characterize a cell, the term "hypoinmunogenic" generally means that

such cell is less prone to immune rejection by a subject into which such cells are transplanted. For example, relative to an unaltered wild-type cell, such a hypoinmunogenic cell may be about 2.5%, 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95%, 97.5%, 99% or more less prone to immune rejection by a subject into which such cells are transplanted. In some aspects, genome editing technologies (e.g., the CRISPR/Cas or TALEN systems) are used to modulate (e.g., reduce or eliminate) the expression of MHC-I and MHC-II genes.

In certain embodiments, the inventions disclosed herein relate to a stem cell, the genome of which has been altered to reduce or delete critical components of HLA expression. Similarly, in certain embodiments, the inventions disclosed herein relate to a stem cell, the genome of which has been altered to insert one or more tolerance inducing factors. The present invention contemplates altering target polynucleotide sequences in any manner which is available to the skilled artisan, for example, utilizing a TALEN or a CRISPR/Cas system. Such CRISPR/Cas systems can employ a variety of Cas proteins (Haft et al. PLoS Comput Biol. 2005;1(6)e60). In some embodiments, the CRISPR/Cas system is a CRISPR type I system. In some embodiments, the CRISPR/Cas system is a CRISPR type II system. In some embodiments, the CRISPR/Cas system is a CRISPR type V system. It should be understood that although examples of methods utilizing CRISPR/Cas (e.g., Cas9 and Cpf1) and TALEN are described in detail herein, the invention is not limited to the use of these methods/systems. Other methods of targeting polynucleotide sequences to reduce or ablate expression in target cells known to the skilled artisan can be utilized herein.

The present inventions contemplate altering, e.g., modifying or cleaving, target polynucleotide sequences in a cell for any purpose, but particularly such that the expression or activity of the encoded product is reduced or eliminated. For example, CRISPR/Cas systems may be used to target transcriptional regulators of antigen presentation to produce a hypoinmunogenic stem cell. In some embodiments, the target polynucleotide sequence in a cell (e.g., ES cells or iPSCs) is altered to produce a mutant cell. As used herein, a “mutant cell” generally refers to a cell with a resulting genotype that differs from its original genotype or the wild-type cell. In some instances, a “mutant cell” exhibits a mutant phenotype, for example

when a normally functioning stem gene is altered using the CRISPR/Cas systems. In some embodiments, the target polynucleotide sequence in a cell is altered to correct or repair a genetic mutation (e.g., to restore a normal phenotype to the cell). In some embodiments, the target polynucleotide sequence in a cell is altered to induce a genetic mutation (e.g., to disrupt the function of a gene or genomic element).

In some embodiments, the alteration is an indel. As used herein, "indel" refers to a mutation resulting from an insertion, deletion, or a combination thereof. As will be appreciated by those skilled in the art, an indel in a coding region of a genomic sequence will result in a frameshift mutation, unless the length of the indel is a multiple of three. In some embodiments, the alteration is a point mutation. As used herein, "point mutation" refers to a substitution that replaces one of the nucleotides. A CRISPR/Cas system can be used to induce an indel of any length or a point mutation in a target polynucleotide sequence.

In some embodiments, the alteration results in a knock out of the target polynucleotide sequence or a portion thereof. For example, knocking out a target polynucleotide sequence in a cell can be performed *in vitro*, *in vivo* or *ex vivo* for both therapeutic and research purposes. Knocking out a target polynucleotide sequence in a cell can be useful for treating or preventing a disorder associated with expression of the target polynucleotide sequence (e.g., by knocking out a mutant allele in a cell *ex vivo* and introducing those cells comprising the knocked out mutant allele into a subject).

As used herein, "knock out" includes deleting all or a portion of the target polynucleotide sequence in a way that interferes with the function of the target polynucleotide sequence or its expression product.

In some embodiments, the alteration results in reduced expression of the target polynucleotide sequence. The terms "decrease," "reduced," "reduction," and "decrease" are all used herein generally to mean a decrease by a statistically significant amount. However, for avoidance of doubt, "decreased," "reduced," "reduction," "decrease" includes a decrease by at least 10% as compared to a reference level, for example a decrease by at least about 20%, or at least about 30%, or at least about 40%, or at least about 50%, or at least about 60%, or at least about 70%, or at least about 80%, or at least about 90% or up to and including a 100%

decrease (i.e. absent level as compared to a reference sample), or any decrease between 10-100% as compared to a reference level.

The terms “increased,” “increase” or “enhance” or “activate” are all used herein to generally mean an increase by a statically significant amount; for the avoidance of any doubt, the terms “increased”, “increase” or “enhance” or “activate” means an increase of at least 10% as compared to a reference level, for example an increase of at least about 20%, or at least about 30%, or at least about 40%, or at least about 50%, or at least about 60%, or at least about 70%, or at least about 80%, or at least about 90% or up to and including a 100% increase or any increase between 10-100% as compared to a reference level, or at least about a 2-fold, or at least about a 3-fold, or at least about a 4-fold, or at least about a 5-fold or at least about a 10-fold increase, or any increase between 2-fold and 10-fold or greater as compared to a reference level.

The term “statistically significant” or “significantly” refers to statistical significance and generally means a two standard deviation (2SD) below normal, or lower, concentration of the marker. The term refers to statistical evidence that there is a difference. It is defined as the probability of making a decision to reject the null hypothesis when the null hypothesis is actually true. The decision is often made using the p-value.

In some embodiments, the alteration is a homozygous alteration. In some embodiments, the alteration is a heterozygous alteration.

In some embodiments, the alteration results in correction of the target polynucleotide sequence from an undesired sequence to a desired sequence. CRISPR/Cas systems can be used to correct any type of mutation or error in a target polynucleotide sequence. For example, CRISPR/Cas systems can be used to insert a nucleotide sequence that is missing from a target polynucleotide sequence due to a deletion. CRISPR/Cas systems can also be used to delete or excise a nucleotide sequence from a target polynucleotide sequence due to an insertion mutation. In some instances, CRISPR/Cas systems can be used to replace an incorrect nucleotide sequence with a correct nucleotide sequence (e.g., to restore function to a target polynucleotide sequence that is impaired due to a loss of function mutation).

CRISPR/Cas systems can alter target polynucleotides with surprisingly high efficiency. In certain embodiments, the efficiency of alteration is at least about 5%. In certain embodiments, the efficiency of alteration is at least about 10%. In certain embodiments, the efficiency of alteration is from about 10% to about 80%. In certain
5 embodiments, the efficiency of alteration is from about 30% to about 80%. In certain
embodiments, the efficiency of alteration is from about 50% to about 80%. In some
embodiments, the efficiency of alteration is greater than or equal to about 80%. In
some embodiments, the efficiency of alteration is greater than or equal to about 85%.
In some embodiments, the efficiency of alteration is greater than or equal to about
10 90%, about 91%, about 92%, about 93%, about 94%, about 95%, about 96%, about
97%, about 98%, or about 99%. In some embodiments, the efficiency of alteration is
equal to about 100%.

In some embodiments, the target polynucleotide sequence is a genomic
sequence. In some embodiments, the target polynucleotide sequence is a human
15 genomic sequence. In some embodiments, the target polynucleotide sequence is a
mammalian genomic sequence. In some embodiments, the target polynucleotide
sequence is a vertebrate genomic sequence.

In some embodiments, CRISPR/Cas systems include a Cas protein or a nucleic
acid sequence encoding the Cas protein and at least one to two ribonucleic acids (e.g.,
20 gRNAs) that are capable of directing the Cas protein to and hybridizing to a target
motif of a target polynucleotide sequence. In some embodiments, CRISPR/Cas
systems include a Cas protein or a nucleic acid sequence encoding the Cas protein and
a single ribonucleic acid or at least one pair of ribonucleic acids (e.g., gRNAs) that are
capable of directing the Cas protein to and hybridizing to a target motif of a target
25 polynucleotide sequence. As used herein, “protein” and “polypeptide” are used
interchangeably to refer to a series of amino acid residues joined by peptide bonds
(i.e., a polymer of amino acids) and include modified amino acids (e.g.,
phosphorylated, glycosylated, glycosolated, etc.) and amino acid analogs. Exemplary
polypeptides or proteins include gene products, naturally occurring proteins,
30 homologs, paralogs, fragments and other equivalents, variants, and analogs of the
above.

In some embodiments, a Cas protein comprises one or more amino acid substitutions or modifications. In some embodiments, the one or more amino acid substitutions comprise a conservative amino acid substitution. In some instances, substitutions and/or modifications can prevent or reduce proteolytic degradation and/or extend the half-life of the polypeptide in a cell. In some embodiments, the Cas protein can comprise a peptide bond replacement (e.g., urea, thiourea, carbamate, sulfonyl urea, etc.). In some embodiments, the Cas protein can comprise a naturally occurring amino acid. In some embodiments, the Cas protein can comprise an alternative amino acid (e.g., D-amino acids, beta-amino acids, homocysteine, phosphoserine, etc.). In some embodiments, a Cas protein can comprise a modification to include a moiety (e.g., PEGylation, glycosylation, lipidation, acetylation, end-capping, etc.).

In some embodiments, a Cas protein comprises a core Cas protein. Exemplary Cas core proteins include, but are not limited to Cas1, Cas2, Cas3, Cas4, Cas5, Cas6, Cas7, Cas8 and Cas9. In some embodiments, a Cas protein comprises a Cas protein of an E. coli subtype (also known as CASS2). Exemplary Cas proteins of the E. Coli subtype include, but are not limited to Cse1, Cse2, Cse3, Cse4, and Cas5e. In some embodiments, a Cas protein comprises a Cas protein of the Ypest subtype (also known as CASS3). Exemplary Cas proteins of the Ypest subtype include, but are not limited to Csy1, Csy2, Csy3, and Csy4. In some embodiments, a Cas protein comprises a Cas protein of the Nmeni subtype (also known as CASS4). Exemplary Cas proteins of the Nmeni subtype include, but are not limited to Csn1 and Csn2. In some embodiments, a Cas protein comprises a Cas protein of the Dvulg subtype (also known as CASS1). Exemplary Cas proteins of the Dvulg subtype include Csd1, Csd2, and Cas5d. In some embodiments, a Cas protein comprises a Cas protein of the Tneap subtype (also known as CASS7). Exemplary Cas proteins of the Tneap subtype include, but are not limited to, Cst1, Cst2, Cas5t. In some embodiments, a Cas protein comprises a Cas protein of the Hmari subtype. Exemplary Cas proteins of the Hmari subtype include, but are not limited to Csh1, Csh2, and Cas5h. In some embodiments, a Cas protein comprises a Cas protein of the Apern subtype (also known as CASS5). Exemplary Cas proteins of the Apern subtype include, but are not limited to Csa1, Csa2, Csa3, Csa4, Csa5, and Cas5a. In some embodiments, a Cas

protein comprises a Cas protein of the Mtube subtype (also known as CASS6). Exemplary Cas proteins of the Mtube subtype include, but are not limited to Csm1, Csm2, Csm3, Csm4, and Csm5. In some embodiments, a Cas protein comprises a RAMP module Cas protein. Exemplary RAMP module Cas proteins include, but are not limited to, Cmr1, Cmr2, Cmr3, Cmr4, Cmr5, and Cmr6.

In some embodiments, the Cas protein is a *Streptococcus pyogenes* Cas9 protein or a functional portion thereof. In some embodiments, the Cas protein is a *Staphylococcus aureus* Cas9 protein or a functional portion thereof. In some embodiments, the Cas protein is a *Streptococcus thermophilus* Cas9 protein or a functional portion thereof. In some embodiments, the Cas protein is a *Neisseria meningitidis* Cas9 protein or a functional portion thereof. In some embodiments, the Cas protein is a *Treponema denticola* Cas9 protein or a functional portion thereof. In some embodiments, the Cas protein is Cas9 protein from any bacterial species or functional portion thereof. Cas9 protein is a member of the type II CRISPR systems which typically include a trans-coded small RNA (tracrRNA), endogenous ribonuclease 3 (rnc) and a Cas protein. Cas 9 protein (also known as CRISPR-associated endonuclease Cas9/Csn1) is a polypeptide comprising 1368 amino acids. An exemplary amino acid sequence of a Cas9 protein (SEQ ID NO: 1) is shown in FIG. 12. Cas 9 contains 2 endonuclease domains, including an RuvC-like domain (residues 7-22, 759-766 and 982-989) which cleaves target DNA that is noncomplementary to crRNA, and an HNH nuclease domain (residues 810-872) which cleave target DNA complementary to crRNA. In FIG. 12, the RuvC-like domain is highlighted in yellow and the HNH nuclease domain is underlined.

In some embodiments, the Cas protein is Cpf1 protein or a functional portion thereof. In some embodiments, the Cas protein is Cpf1 from any bacterial species or functional portion thereof. In some aspects, Cpf1 is a *Francisella novicida* U112 protein or a functional portion thereof. In some aspects, Cpf1 is a *Acidaminococcus* sp. BV3L6 protein or a functional portion thereof. In some aspects, Cpf1 is a *Lachnospiraceae* bacterium ND2006 protein or a functional portion thereof. Cpf1 protein is a member of the type V CRISPR systems. Cpf1 protein is a polypeptide comprising about 1300 amino acids. Cpf1 contains a RuvC-like endonuclease domain. Cpf1 cleaves target DNA in a staggered pattern using a single ribonuclease

domain. The staggered DNA double-stranded break results in a 4 or 5-nt 5' overhang.

As used herein, "functional portion" refers to a portion of a peptide which retains its ability to complex with at least one ribonucleic acid (e.g., guide RNA (gRNA)) and cleave a target polynucleotide sequence. In some embodiments, the functional portion comprises a combination of operably linked Cas9 protein functional domains selected from the group consisting of a DNA binding domain, at least one RNA binding domain, a helicase domain, and an endonuclease domain. In some embodiments, the functional portion comprises a combination of operably linked Cpf1 protein functional domains selected from the group consisting of a DNA binding domain, at least one RNA binding domain, a helicase domain, and an endonuclease domain. In some embodiments, the functional domains form a complex. In some embodiments, a functional portion of the Cas9 protein comprises a functional portion of a RuvC-like domain. In some embodiments, a functional portion of the Cas9 protein comprises a functional portion of the HNH nuclease domain. In some embodiments, a functional portion of the Cpf1 protein comprises a functional portion of a RuvC-like domain.

It should be appreciated that the present invention contemplates various ways of contacting a target polynucleotide sequence with a Cas protein (e.g., Cas9). In some embodiments, exogenous Cas protein can be introduced into the cell in polypeptide form. In certain embodiments, Cas proteins can be conjugated to or fused to a cell-penetrating polypeptide or cell-penetrating peptide. As used herein, "cell-penetrating polypeptide" and "cell-penetrating peptide" refers to a polypeptide or peptide, respectively, which facilitates the uptake of molecule into a cell. The cell-penetrating polypeptides can contain a detectable label.

In certain embodiments, Cas proteins can be conjugated to or fused to a charged protein (e.g., that carries a positive, negative or overall neutral electric charge). Such linkage may be covalent. In some embodiments, the Cas protein can be fused to a superpositively charged GFP to significantly increase the ability of the Cas protein to penetrate a cell (Cronican et al. ACS Chem Biol.2010;5(8):747-52). In certain embodiments, the Cas protein can be fused to a protein transduction domain (PTD) to facilitate its entry into a cell. Exemplary PTDs include Tat, oligoarginine,

and penetratin. In some embodiments, the Cas9 protein comprises a Cas9 polypeptide fused to a cell-penetrating peptide. In some embodiments, the Cas9 protein comprises a Cas9 polypeptide fused to a PTD. In some embodiments, the Cas9 protein comprises a Cas9 polypeptide fused to a tat domain. In some embodiments, the Cas9 protein comprises a Cas9 polypeptide fused to an oligoarginine domain. In some
5 embodiments, the Cas9 protein comprises a Cas9 polypeptide fused to a penetratin domain. In some embodiments, the Cas9 protein comprises a Cas9 polypeptide fused to a superpositively charged GFP. In some embodiments, the Cpf1 protein comprises a Cpf1 polypeptide fused to a cell-penetrating peptide. In some
10 embodiments, the Cpf1 protein comprises a Cpf1 polypeptide fused to a PTD. In some embodiments, the Cpf1 protein comprises a Cpf1 polypeptide fused to a tat domain. In some
embodiments, the Cpf1 protein comprises a Cpf1 polypeptide fused to an oligoarginine domain. In some embodiments, the Cpf1 protein comprises a Cpf1 polypeptide fused to a penetratin domain. In some
15 embodiments, the Cpf1 protein comprises a Cpf1 polypeptide fused to a superpositively charged GFP.

In some embodiments, the Cas protein can be introduced into a cell containing the target polynucleotide sequence in the form of a nucleic acid encoding the Cas protein (e.g., Cas9 or Cpf1). The process of introducing the nucleic acids into cells can be achieved by any suitable technique. Suitable techniques include calcium
20 phosphate or lipid-mediated transfection, electroporation, and transduction or infection using a viral vector. In some embodiments, the nucleic acid comprises DNA. In some embodiments, the nucleic acid comprises a modified DNA, as described herein. In some embodiments, the nucleic acid comprises mRNA. In some
embodiments, the nucleic acid comprises a modified mRNA, as described herein (e.g.,
25 a synthetic, modified mRNA).

In some embodiments, nucleic acids encoding Cas protein and nucleic acids encoding the at least one to two ribonucleic acids are introduced into a cell via viral transduction (e.g., lentiviral transduction).

In some embodiments, the Cas protein is complexed with one to two
30 ribonucleic acids. In some embodiments, the Cas protein is complexed with two ribonucleic acids. In some embodiments, the Cas protein is complexed with one

ribonucleic acid. In some embodiments, the Cas protein is encoded by a modified nucleic acid, as described herein (e.g., a synthetic, modified mRNA).

The methods of the present invention contemplate the use of any ribonucleic acid that is capable of directing a Cas protein to and hybridizing to a target motif of a target polynucleotide sequence. In some embodiments, at least one of the ribonucleic acids comprises tracrRNA. In some embodiments, at least one of the ribonucleic acids comprises CRISPR RNA (crRNA). In some embodiments, a single ribonucleic acid comprises a guide RNA that directs the Cas protein to and hybridizes to a target motif of the target polynucleotide sequence in a cell. In some embodiments, at least one of the ribonucleic acids comprises a guide RNA that directs the Cas protein to and hybridizes to a target motif of the target polynucleotide sequence in a cell. In some embodiments, both of the one to two ribonucleic acids comprise a guide RNA that directs the Cas protein to and hybridizes to a target motif of the target polynucleotide sequence in a cell. The ribonucleic acids of the present invention can be selected to hybridize to a variety of different target motifs, depending on the particular CRISPR/Cas system employed, and the sequence of the target polynucleotide, as will be appreciated by those skilled in the art. The one to two ribonucleic acids can also be selected to minimize hybridization with nucleic acid sequences other than the target polynucleotide sequence. In some embodiments, the one to two ribonucleic acids hybridize to a target motif that contains at least two mismatches when compared with all other genomic nucleotide sequences in the cell. In some embodiments, the one to two ribonucleic acids hybridize to a target motif that contains at least one mismatch when compared with all other genomic nucleotide sequences in the cell. In some embodiments, the one to two ribonucleic acids are designed to hybridize to a target motif immediately adjacent to a deoxyribonucleic acid motif recognized by the Cas protein. In some embodiments, each of the one to two ribonucleic acids are designed to hybridize to target motifs immediately adjacent to deoxyribonucleic acid motifs recognized by the Cas protein which flank a mutant allele located between the target motifs.

In some embodiments, at least one of the one to two ribonucleic acids comprises a sequence selected from the group consisting of the ribonucleic acid sequences of SEQ ID NOs: 2-817976. In some embodiments, at least one ribonucleic

acid comprises a sequence selected from the group consisting of the ribonucleic acid sequences of SEQ ID NOs: 2-817976.

In some embodiments, at least one of the one to two ribonucleic acids comprises a sequence with a single nucleotide mismatch to a sequence selected from the group consisting of the ribonucleic acid sequences of SEQ ID NOs: 2-817976. In some embodiments, at least one ribonucleic acid comprises a sequence with a single nucleotide mismatch to a sequence selected from the group consisting of the ribonucleic acid sequences of SEQ ID NOs: 2-817976.

In some embodiments, each of the one to two ribonucleic acids comprises guide RNAs that directs the Cas protein to and hybridizes to a target motif of the target polynucleotide sequence in a cell. In some embodiments, one or two ribonucleic acids (e.g., guide RNAs) are complementary to and/or hybridize to sequences on the same strand of a target polynucleotide sequence. In some embodiments, one or two ribonucleic acids (e.g., guide RNAs) are complementary to and/or hybridize to sequences on the opposite strands of a target polynucleotide sequence. In some embodiments, the one or two ribonucleic acids (e.g., guide RNAs) are not complementary to and/or do not hybridize to sequences on the opposite strands of a target polynucleotide sequence. In some embodiments, the one or two ribonucleic acids (e.g., guide RNAs) are complementary to and/or hybridize to overlapping target motifs of a target polynucleotide sequence. In some embodiments, the one or two ribonucleic acids (e.g., guide RNAs) are complementary to and/or hybridize to offset target motifs of a target polynucleotide sequence.

In some embodiments, the target motif is a 17 to 23 nucleotide DNA sequence. In some embodiments, the target motif is at least 20 nucleotides in length. In some embodiments, the target motif is a 20-nucleotide DNA sequence. In some embodiments, the target motif is a 17 to 23-nucleotide DNA sequence and immediately precedes an NRG motif. In some aspects, the NRG motif is NGG or NAG. In some embodiments, the target motif is a 20-nucleotide DNA sequence and immediately precedes an NGG motif recognized by the Cas protein. In some embodiments, the target motif is a 20-nucleotide DNA sequence and immediately precedes an NAG motif recognized by the Cas protein. In some embodiments, the target motif is a 20-nucleotide DNA sequence beginning with G and immediately

precedes an NGG motif recognized by the Cas protein. In some embodiments, the target motif is G(N)19NGG. In some embodiments, the target motif is (N)20NGG.

In some embodiments, the target motif is a 17 to 23-nucleotide DNA sequence and immediately precedes an NNGRRT motif. In some embodiments, the target motif is a 20 nucleotide DNA sequence and immediately precedes an NNGRRT motif. In some embodiments, the target motif is a 17 to 23-nucleotide DNA sequence and immediately precedes an NNNRRT motif. In some embodiments, the target motif is a 20 nucleotide DNA sequence and immediately precedes an NNNRRT motif. In some embodiments, the target motif is a 17 to 23-nucleotide DNA sequence and immediately precedes an NNAGAAW motif. In some embodiments, the target motif is a 20 nucleotide DNA sequence and immediately precedes an NNAGAAW motif. In some embodiments, the target motif is a 17 to 23-nucleotide DNA sequence and immediately precedes an NNNNGATT motif. In some embodiments, the target motif is a 20 nucleotide DNA sequence and immediately precedes an NNNNGATT motif. In some embodiments, the target motif is a 17 to 23-nucleotide DNA sequence and immediately precedes an NAAAAC motif. In some embodiments, the target motif is a 20 nucleotide DNA sequence and immediately precedes an NAAAAC motif. In some embodiments, the target motif is a 17 to 23-nucleotide DNA sequence having a 5' T-rich region (e.g., TTTN motif). In some embodiments, the target motif is a 20 nucleotide DNA sequence having a 5' T-rich region (e.g., TTTN motif).

In some embodiments, the target motif is a 17 to 23-nucleotide DNA sequence and immediately precedes an NRG motif (e.g., NGG or NAG) recognized by a *S. pyogenes* Cas9 protein. In some embodiments, the target motif is a 17 to 23-nucleotide DNA sequence and immediately precedes an NNGRRT motif recognized by a *S. aureus* Cas9 protein. In some embodiments, the target motif is a 17 to 23-nucleotide DNA sequence and immediately precedes an NNNRRT motif recognized by a *S. aureus* Cas9 protein. In some embodiments, the target motif is a 17 to 23-nucleotide DNA sequence and immediately precedes an NNAGAAW motif recognized by a *S. thermophilus* Cas9 protein. In some embodiments, the target motif is a 17 to 23-nucleotide DNA sequence and immediately precedes an NNNNGATT motif recognized by *N. meningitides* Cas9 protein. In some embodiments, the target motif is a 17 to 23-nucleotide DNA sequence and immediately precedes an NAAAAC

motif recognized by *T. denticola* Cas9 protein. In some embodiments, the target motif is a 17 to 23-nucleotide DNA sequence having a 5' T-rich region (e.g., TTTN motif) recognized by *Acidaminococcus* or *Lachnospiraceae* Cpf1 protein.

In some embodiments, the one to two ribonucleic acids hybridize to a target motif that contains at least two mismatches when compared with all other genomic nucleotide sequences in the cell. In some embodiments, the one to two ribonucleic acids hybridize to a target motif that contains at least one mismatch when compared with all other genomic nucleotide sequences in the cell. Those skilled in the art will appreciate that a variety of techniques can be used to select suitable target motifs for minimizing off-target effects (e.g., bioinformatics analyses). In some embodiments, the one to two ribonucleic acids are designed to hybridize to a target motif immediately adjacent to a deoxyribonucleic acid motif recognized by the Cas protein. In some embodiments, each of the one to two ribonucleic acids are designed to hybridize to target motifs immediately adjacent to deoxyribonucleic acid motifs recognized by the Cas protein which flank a mutant allele located between the target motifs.

In some aspects, the target polynucleotide sequence in a cell is altered to reduce or eliminate expression and/or activity of one or more critical immune genes in the cell using a genetic editing system (e.g., TALENs, CRISPR/Cas, etc.). In some embodiments, the present disclosure provides that the target polynucleotide sequence in a cell is altered to delete a contiguous stretch of genomic DNA (e.g., delete one or more critical immune genes) from one or both alleles of the cell (e.g., using a CRISPR/Cas system). In some embodiments, the target polynucleotide sequence in a cell is altered to insert a genetic mutation in one or both alleles of the cell (e.g., using a CRISPR/Cas system). In still other embodiments, the universal stem cells disclosed herein may be subject to complementary genome editing approaches (e.g., using a CRISPR/Cas system), whereby such stem cells are modified to both delete contiguous stretches of genomic DNA (e.g., critical immune genes) from one or both alleles of the cell, as well as to insert one or more tolerance-inducing factors, such as HLA-G or PD-L1, into one or both alleles of the cells to locally suppress the immune system and improve transplant engraftment.

The universal stem cells disclosed herein may be differentiated into relevant cell types to assess HLA expression, as well as the evaluation of immunogenicity of the universal stem cell lines, for example, in a pre-clinical humanized mouse model. For example, the universal stem cells disclosed herein may be incubated under
5 appropriate conditions and differentiated into mesenchymal progenitors cells (MPCs), hypoinmunogenic cardiomyocytes, endothelial cells (ECs), macrophages, hepatocytes, beta cells (e.g., pancreatic beta cells), or neural progenitor cells (NPCs).

The universal stem cells and methods disclosed herein will have an enormous impact on regenerative medicine by leading the way to rigorously tested universal
10 donor stem cell lines that could be grown up and differentiated into a very large numbers of cells, made widely available to all medical institutions, and used on demand to treat patients suffering from degenerative illnesses, and thereby make it unnecessary to use a patient's own cells on a case-by-case basis as a source for autologous transplantation. Moreover, as the resulting cell products will be protected
15 from immune attack, they will represent a new form of treatment for autoimmune diseases such as MS (multiple sclerosis) and diabetes, where autologous cells would still be prone to immune attack. Immunoprivileged universal donor stem cell-derived cell products, however, will be protected from autoimmune rejection.

The universal stem cells disclosed herein may be used, for example, to
20 diagnose, monitor, treat and/or cure the presence or progression of a disease or condition in a subject. As used herein, a "subject" means a human or animal. In certain embodiments, the subject is a human. In certain embodiments, the subject is an adolescent. In certain embodiments, the subject is treated *in vivo*, *in vitro* and/or *in utero*. In certain aspects, a subject in need of treatment in accordance with the
25 methods disclosed herein has a condition or is suspected or at increased risk of developing such condition.

As depicted in FIG. 2A, HLA represents an immunologic barrier to the successful transplantation of stem cells or differentiated stem cells in a subject. Disclosed herein are novel compositions, cells and related methods that are useful for
30 overcoming the HLA immunologic barrier to transplantation. As illustrated in FIG. 2B, major histocompatibility complex (MHC) is a locus on human Chr. 6p21, which encodes a highly polymorphic gene family of surface molecules that define donor

compatibility during organ transplantation. MHC class I (MHC-I) and MHC class II (MHC-II) play essential roles in the activation of adaptive immune responses by presenting antigens to T lymphocytes. A comparison of the MHC-II and MHC-I enhanceosomes is provided in FIG. 13. Humans have three classical MHC-Ia molecules (HLA-A, HLA-B, and HLA-C), which are vital to the detection and elimination of viruses, cancerous cells, and transplanted cells. In addition, there are three non-classical MHC-Ib molecules (HLA-E, HLA-F, and HLA-G), which have immune regulatory functions. While MHC's serve a vital cellular function, in certain contexts, such as cell-based transplantation therapies, they may also contribute to immune rejection. Provided herein are novel cells, compositions and methods that are useful for addressing such HLA-based immune rejection of transplanted cells.

Knock-outs

In certain aspects, the inventions disclosed herein relate to genomic modifications of one or more targeted polynucleotide sequences of the stem cell genome that regulates the expression of MHC-I and/or MHC-II. In some aspects, a genetic editing system is used to modify one or more targeted polynucleotide sequences. In some aspects, a CRISPR/Cas system is used to delete the one or more targeted polynucleotide sequences. MHC-I molecules are composed of MHC-encoded heavy chains and the invariant subunit β 2-microglobulin (B2M). Antigen-derived peptides are presented by MHC-I-B2M complexes at the cell surface to CD8 T cells carrying an antigen-specific T cell receptor. Peptides are mostly produced from the degradation of cytoplasmic proteins by a specialized proteasome or immunoproteasome, which is optimized to generate MHC class I peptides and contains several IFN- γ -inducible subunits. Unlike MHC-II, which is found mainly in antigen-presenting cells, MHC-Ia is ubiquitously expressed in almost all nucleated cells (Pamer, *et al.*, Annu Rev Immunol (1998) 16:323-358.). Both MHC-I and MHC-II genes are highly inducible by IFN- γ stimulation.

The efficient removal of the HLA barrier can be accomplished by one or more of the following: (1) targeting the polymorphic HLA alleles (HLA-A, -B, -C) and MHC-II genes directly; (2) removal of B2M, which will prevent surface trafficking of all MHC-I molecules; and/or (3) deletion of components of the MHC enhanceosomes,

such as NLRC5, RFX-5, -ANK, and -AP, IRF1, NF-Y, and CIITA that are critical for HLA expression.

In certain embodiments, HLA expression is interfered with. In some aspects, HLA expression is interfered with by targeting individual HLAs (e.g., knocking out
5 expression of HLA-A, HLA-B and/or HLA-C), targeting transcriptional regulators of HLA expression (e.g., knocking out expression of NLRC5, CIITA, RFX5, RFXAP, RFXANK, NFY-A, NFY-B, NFY-C and/or IRF-1), blocking surface trafficking of MHC class I molecules (e.g., knocking out expression of B2M and/or TAP1), and/or targeting HLA-Razor.

10 In certain aspects, the stem cells disclosed herein do not express one or more human leukocyte antigens (e.g., HLA-A, HLA-B and/or HLA-C) corresponding to MHC-I and/or MHC-II and are thus characterized as being hypoimmunogenic. For example, in certain aspects, the stem cells disclosed herein have been modified such that the stem cell or a differentiated stem cell prepared therefrom do not express or
15 exhibit reduced expression of one or more of the following MHC-I molecules: HLA-A, HLA-B and HLA-C. In some aspects, one or more of HLA-A, HLA-B and HLA-C may be “knocked-out” of a cell. A cell that has a knocked-out HLA-A gene, HLA-B gene, and/or HLA-C gene may exhibit reduced or eliminated expression of each knocked-out gene. See FIGS. 13A-J.

20 In some aspects, the present disclosure provides a stem cell (e.g., hypoimmunogenic stem cell) or population thereof comprising a genome in which the HLA-A gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating surface expression of MHC class I molecules in the cell or population thereof. The contiguous stretch of genomic DNA can be deleted by
25 contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 2-1418.

In certain aspects, the present disclosure provides a method for altering a target HLA-A sequence in a cell comprising contacting the HLA-A sequence with a
30 clustered regularly interspaced short palindromic repeats-associated (Cas) protein and at least one ribonucleic acid or at least one pair of ribonucleic acids, wherein the ribonucleic acids direct Cas protein to and hybridize to a target motif of the target

HLA-A polynucleotide sequence, wherein the target HLA-A polynucleotide sequence is cleaved, and wherein the at least one ribonucleic acid or the at least one pair of ribonucleic acids is selected from the group consisting of SEQ ID NOs: 2-1418.

In some aspects, the present disclosure provides a stem cell (e.g.,
5 hypoimmunogenic stem cell) or population thereof comprising a genome in which the HLA-B gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating surface expression of MHC class I molecules in the cell or population thereof. The contiguous stretch of genomic DNA can be deleted by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding
10 the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 1419-3277.

In certain aspects, the present disclosure provides a method for altering a target HLA-B sequence in a cell comprising contacting the HLA-B sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and
15 at least one ribonucleic acid or at least one pair of ribonucleic acids, wherein the ribonucleic acids direct Cas protein to and hybridize to a target motif of the target HLA-B polynucleotide sequence, wherein the target HLA-B polynucleotide sequence is cleaved, and wherein the at least one ribonucleic acid or the at least one pair of ribonucleic acids is selected from the group consisting of SEQ ID NOs: 1419-3277.

In some aspects, the present disclosure provides a stem cell (e.g.,
20 hypoimmunogenic stem cell) or population thereof comprising a genome in which the HLA-C gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating surface expression of MHC class I molecules in the cell or population thereof. The contiguous stretch of genomic DNA can be deleted by
25 contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 3278-5183.

In certain aspects, the present disclosure provides a method for altering a target HLA-C sequence in a cell comprising contacting the HLA-C sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and
30 at least one ribonucleic acid or at least one pair of ribonucleic acids, wherein the ribonucleic acids direct Cas protein to and hybridize to a target motif of the target

HLA-C polynucleotide sequence, wherein the target HLA-C polynucleotide sequence is cleaved, and wherein the at least one ribonucleic acid or the at least one pair of ribonucleic acids is selected from the group consisting of SEQ ID NOs: 3278-5183.

In certain embodiments, the expression of MHC-I or MHC-II is modulated by targeting and deleting a contiguous stretch of genomic DNA thereby reducing or eliminating expression of a target gene, for example, NLRC5. As used herein, the term “modulate” is used consistently with its use in the art, i.e., meaning to cause or facilitate a qualitative or quantitative change, alteration, or modification in a process, pathway, or phenomenon of interest. Without limitation, such change may be an increase, decrease, or change in relative strength or activity of different components or branches of the process, pathway, or phenomenon. In certain aspects, the target gene is NLRC5, CIITA, RFX5, RFXAP, RFXANK, NFY-A, NFY-B, NFY-C or IRF-1.

In certain aspects, the inventions disclosed herein modulate (e.g., reduce or eliminate) the expression of MHC-II genes by targeting and modulating (e.g., reducing or eliminating) Class II transactivator (CIITA) expression. In some aspects, the modulation occurs using a CRISPR/Cas system. CIITA is a member of the NLR or nucleotide binding domain (NBD) leucine-rich repeat (LRR) family of proteins and regulates the transcription of MHC-II by associating with the MHC enhanceosome. The expression of CIITA is induced in B cells and dendritic cells as a function of developmental stage and is inducible by IFN- γ in most cell types. Aside from CIITA, NLR proteins are localized in the cytoplasm and contribute to the innate immune response by recognizing microbial products and exogenous danger signals, leading to inflammation and/or cell death.

In some aspects, the present disclosure provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof comprising a genome in which the Class II transactivator (CIITA) gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating surface expression of MHC class II molecules in the cell or population thereof.

The contiguous stretch of genomic DNA can be deleted by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein

and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 5184-36352.

The present invention contemplates genomically editing human cells to cleave CIITA gene sequences, as well as editing the genome of such cells to alter one or
5 more additional target polynucleotide sequences (e.g., NLRC5 and/or B2M). It should be appreciated that cleaving a CIITA genomic sequence using one or more gRNAs or gRNA pairs described herein and a Cas protein could result in partial or complete deletion of the target CIITA genomic sequence, depending on the number of gRNAs or gRNA pairs selected, as well as their targets.

10 In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising a genomic modification in which the CIITA gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating MHC Class II molecule surface expression and/or activity in the cell. In some embodiments, the
15 contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and a pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 5184-36352.

In some aspects, the invention provides a method for altering a target CIITA polynucleotide sequence in a cell comprising contacting the CIITA polynucleotide
20 sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and from one to two ribonucleic acids, wherein the ribonucleic acids direct Cas protein to and hybridize to a target motif of the target CIITA polynucleotide sequence, wherein the target CIITA polynucleotide sequence is cleaved, and wherein at least one of the one to two ribonucleic acids are selected from
25 the group consisting of SEQ ID NOs: 5184-36352.

In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising:
a genomic modification in which the CIITA gene has been edited to reduce or eliminate CIITA surface expression and/or activity in the cell by contacting the cell
30 with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 5184-36352.

In some aspects, the invention provides a method for altering a target CIITA polynucleotide sequence in a cell comprising contacting the CIITA polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and at least one ribonucleic acid, wherein the ribonucleic acid directs
5 Cas protein to and hybridizes to a target motif of the target CIITA polynucleotide sequence, wherein the target CIITA polynucleotide sequence is cleaved, and wherein the at least one ribonucleic acid is selected from the group consisting of SEQ ID NOs: 5184-36352.

In certain aspects, the inventions disclosed herein modulate (e.g., reduce or
10 eliminate) the expression of MHC-I genes by targeting and modulating (e.g., reducing or eliminating) expression of the NLR family, CARD domain containing 5/NOD27/CLR16.1 (NLRC5). In some aspects, the modulation occurs using a CRISPR/Cas system. NLRC5 is a critical regulator of MHC-I-mediated immune responses and, similar to CIITA, NLRC5 is highly inducible by IFN- γ and can
15 translocate into the nucleus. NLRC5 activates the promoters of MHC-I genes and induces the transcription of MHC-I as well as related genes involved in MHC-I antigen presentation.

In some aspects, the present disclosure provides a stem cell (e.g.,
hypoimmunogenic stem cell) or population thereof comprising a genome in which the
20 NLRC5 gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating surface expression of MHC class I molecules in the cell or population thereof.

The contiguous stretch of genomic DNA can be deleted by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein
25 and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 36353-81239.

The present invention contemplates genomically editing human cells to cleave NLRC5 gene sequences, as well as editing the genome of such cells to alter one or more additional target polynucleotide sequences (e.g., CIITA and/or B2M). It should
30 be appreciated that cleaving a NLRC5 genomic sequence using one or more gRNAs or gRNA pairs described herein and a Cas protein could result in partial or complete

deletion of the target NLRC5 genomic sequence, depending on the number of gRNAs or gRNA pairs selected, as well as their targets.

In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising a genomic modification in which the NLRC5 gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating MHC Class I molecule surface expression and/or activity in the cell. In some embodiments, the contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and a pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 36353-81239.

In some aspects, the invention provides a method for altering a target NLRC5 polynucleotide sequence in a cell comprising contacting the NLRC5 polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and from one to two ribonucleic acids, wherein the ribonucleic acids direct Cas protein to and hybridize to a target motif of the target NLRC5 polynucleotide sequence, wherein the target NLRC5 polynucleotide sequence is cleaved, and wherein at least one of the one to two ribonucleic acids are selected from the group consisting of SEQ ID NOs: 36353-81239.

In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising: a genomic modification in which the NLRC5 gene has been edited to reduce or eliminate MHC Class I molecule surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 36353-81239.

In some aspects, the invention provides a method for altering a target NLRC5 polynucleotide sequence in a cell comprising contacting the NLRC5 polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and at least one ribonucleic acid, wherein the ribonucleic acid directs Cas protein to and hybridizes to a target motif of the target NLRC5 polynucleotide sequence, wherein the target NLRC5 polynucleotide sequence is cleaved, and wherein

the at least one ribonucleic acid is selected from the group consisting of SEQ ID NOs: 36353-81239.

In certain embodiments, the inventions disclosed herein modulate (e.g., reduce or eliminate) the expression of MHC-I genes by targeting and modulating (e.g.,
5 reducing or eliminating) expression of the accessory chain B2M. In some aspects, the modulation occurs using a CRISPR/Cas system. By modulating (e.g., reducing or deleting) expression of B2M, surface trafficking of MHC-I molecules is blocked and the cell rendered hypoimmunogenic.

In some aspects, the present disclosure provides a stem cell (e.g.,
10 hypoimmunogenic stem cell) or population thereof comprising a genome in which the β 2-microglobulin (B2M) gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating surface expression of MHC class I molecules in the cell or population thereof.

The contiguous stretch of genomic DNA can be deleted by contacting the cell
15 or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 81240-85644.

The present invention contemplates genomically editing human cells to cleave B2M gene sequences, as well as editing the genome of such cells to alter one or more
20 additional target polynucleotide sequences (e.g., NLRC5 and/or CIITA). It should be appreciated that cleaving a B2M genomic sequence using one or more gRNAs or gRNA pairs described herein and a Cas protein could result in partial or complete deletion of the target B2M genomic sequence, depending on the number of gRNAs or gRNA pairs selected, as well as their targets.

In some aspects, the invention provides a stem cell (e.g., hypoimmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising a genomic modification in which the B2M gene has been edited to delete a contiguous
25 stretch of genomic DNA, thereby reducing or eliminating MHC Class I molecule surface expression and/or activity in the cell. In some embodiments, the contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and a pair of ribonucleic acids having
30 sequences selected from the group consisting of SEQ ID NOs: 81240-85644.

In some aspects, the invention provides a method for altering a target B2M polynucleotide sequence in a cell comprising contacting the B2M polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and from one to two ribonucleic acids, wherein the ribonucleic acids
5 direct Cas protein to and hybridize to a target motif of the target B2M polynucleotide sequence, wherein the target B2M polynucleotide sequence is cleaved, and wherein at least one of the one to two ribonucleic acids are selected from the group consisting of SEQ ID NOs: 81240-85644.

In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising:
10 a genomic modification in which the B2M gene has been edited to reduce or eliminate MHC Class I molecule surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid having a sequence selected from the group consisting of SEQ ID
15 NOs: 81240-85644.

In some aspects, the invention provides a method for altering a target B2M polynucleotide sequence in a cell comprising contacting the B2M polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and at least one ribonucleic acid, wherein the ribonucleic acid directs
20 Cas protein to and hybridizes to a target motif of the target B2M polynucleotide sequence, wherein the target B2M polynucleotide sequence is cleaved, and wherein the at least one ribonucleic acid is selected from the group consisting of SEQ ID NOs: 81240-85644.

In certain aspects, the inventions disclosed herein modulate (e.g., reduce or
25 eliminate) the expression of MHC-I genes by targeting and modulating (e.g., reducing or eliminating) expression of one or more of RFX5. In some aspects, the modulation occurs using a CRISPR/Cas system.

In some aspects, the present disclosure provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof comprising a genome in which the
30 RFX5 gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating surface expression of MHC class I molecules in the cell or population thereof.

The contiguous stretch of genomic DNA can be deleted by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 85645-90115.

5 The present invention contemplates genomically editing human cells to cleave RFX5 gene sequences, as well as editing the genome of such cells to alter one or more additional target polynucleotide sequences. It should be appreciated that cleaving a RFX5 genomic sequence using one or more gRNAs or gRNA pairs described herein and a Cas protein could result in partial or complete deletion of the target RFX5
10 genomic sequence, depending on the number of gRNAs or gRNA pairs selected, as well as their targets.

In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising a genomic modification in which the RFX5 gene has been edited to delete a
15 contiguous stretch of genomic DNA, thereby reducing or eliminating MHC Class I molecule surface expression and/or activity in the cell. In some embodiments, the contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and a pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 85645-90115.

20 In some aspects, the invention provides a method for altering a target RFX5 polynucleotide sequence in a cell comprising contacting the RFX5 polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and from one to two ribonucleic acids, wherein the ribonucleic acids direct Cas protein to and hybridize to a target motif of the target RFX5 polynucleotide
25 sequence, wherein the target RFX5 polynucleotide sequence is cleaved, and wherein at least one of the one to two ribonucleic acids are selected from the group consisting of SEQ ID NOs: 85645-90115.

In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising:
30 a genomic modification in which the RFX5 gene has been edited to reduce or eliminate MHC Class I molecule surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and at

least one ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 85645-90115.

In some aspects, the invention provides a method for altering a target RFX5 polynucleotide sequence in a cell comprising contacting the RFX5 polynucleotide
5 sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and at least one ribonucleic acid, wherein the ribonucleic acid directs Cas protein to and hybridizes to a target motif of the target RFX5 polynucleotide sequence, wherein the target RFX5 polynucleotide sequence is cleaved, and wherein the at least one ribonucleic acid is selected from the group consisting of SEQ ID NOs:
10 85645-90115.

In certain aspects, the inventions disclosed herein modulate (e.g., reduce or eliminate) the expression of MHC-I genes by targeting and modulating (e.g., reducing or eliminating) expression of one or more of RFXAP. In some aspects, the modulation occurs using a CRISPR/Cas system.

15 In some aspects, the present disclosure provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof comprising a genome in which the RFXAP gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating surface expression of MHC class I molecules in the cell or population thereof.

20 The contiguous stretch of genomic DNA can be deleted by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 90116-95635.

The present invention contemplates genomically editing human cells to cleave
25 RFXAP gene sequences, as well as editing the genome of such cells to alter one or more additional target polynucleotide sequences. It should be appreciated that cleaving a RFXAP genomic sequence using one or more gRNAs or gRNA pairs described herein and a Cas protein could result in partial or complete deletion of the target RFXAP genomic sequence, depending on the number of gRNAs or gRNA pairs
30 selected, as well as their targets.

In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising

a genomic modification in which the RFXAP gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating MHC Class I molecule surface expression and/or activity in the cell. In some embodiments, the contiguous stretch of genomic DNA has been deleted by contacting the cell with a
5 Cas protein or a nucleic acid encoding the Cas protein and a pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 90116-95635.

In some aspects, the invention provides a method for altering a target RFXAP polynucleotide sequence in a cell comprising contacting the RFXAP polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated
10 (Cas) protein and from one to two ribonucleic acids, wherein the ribonucleic acids direct Cas protein to and hybridize to a target motif of the target RFXAP polynucleotide sequence, wherein the target RFXAP polynucleotide sequence is cleaved, and wherein at least one of the one to two ribonucleic acids are selected from the group consisting of SEQ ID NOs: 90116-95635.

15 In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising: a genomic modification in which the RFXAP gene has been edited to reduce or eliminate MHC Class I molecule surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and at
20 least one ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 90116-95635.

In some aspects, the invention provides a method for altering a target RFXAP polynucleotide sequence in a cell comprising contacting the RFXAP polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated
25 (Cas) protein and at least one ribonucleic acid, wherein the ribonucleic acid directs Cas protein to and hybridizes to a target motif of the target RFXAP polynucleotide sequence, wherein the target RFXAP polynucleotide sequence is cleaved, and wherein the at least one ribonucleic acid is selected from the group consisting of SEQ ID NOs: 90116-95635.

30 In certain aspects, the inventions disclosed herein modulate (e.g., reduce or eliminate) the expression of MHC-I genes by targeting and modulating (e.g., reducing

or eliminating) expression of one or more of RFXANK. In some aspects, the modulation occurs using a CRISPR/Cas system.

In some aspects, the present disclosure provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof comprising a genome in which the RFXANK gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating surface expression of MHC class I molecules in the cell or population thereof.

The contiguous stretch of genomic DNA can be deleted by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 95636-102318.

The present invention contemplates genomically editing human cells to cleave RFXANK gene sequences, as well as editing the genome of such cells to alter one or more additional target polynucleotide sequences. It should be appreciated that cleaving a RFXANK genomic sequence using one or more gRNAs or gRNA pairs described herein and a Cas protein could result in partial or complete deletion of the target RFXANK genomic sequence, depending on the number of gRNAs or gRNA pairs selected, as well as their targets.

In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising a genomic modification in which the RFXAP gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating MHC Class I molecule surface expression and/or activity in the cell. In some embodiments, the contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and a pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 95636-102318.

In some aspects, the invention provides a method for altering a target RFXANK polynucleotide sequence in a cell comprising contacting the RFXANK polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and from one to two ribonucleic acids, wherein the ribonucleic acids direct Cas protein to and hybridize to a target motif of the target RFXANK polynucleotide sequence, wherein the target RFXANK polynucleotide

sequence is cleaved, and wherein at least one of the one to two ribonucleic acids are selected from the group consisting of SEQ ID NOs: 95636-102318.

In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising:
5 a genomic modification in which the RFXANK gene has been edited to reduce or eliminate MHC Class I molecule surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 95636-102318.

10 In some aspects, the invention provides a method for altering a target RFXANK polynucleotide sequence in a cell comprising contacting the RFXANK polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and at least one ribonucleic acid, wherein the ribonucleic acid directs Cas protein to and hybridizes to a target motif of the target
15 RFXANK polynucleotide sequence, wherein the target RFXANK polynucleotide sequence is cleaved, and wherein the at least one ribonucleic acid is selected from the group consisting of SEQ ID NOs: 95636-102318.

In certain aspects, the inventions disclosed herein modulate (e.g., reduce or eliminate) the expression of MHC-I genes by targeting and modulating (e.g., reducing
20 or eliminating) expression of one or more of NFY-A. In some aspects, the modulation occurs using a CRISPR/Cas system.

In some aspects, the present disclosure provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof comprising a genome in which the NFY-A gene has been edited to delete a contiguous stretch of genomic DNA, thereby
25 reducing or eliminating surface expression of MHC class I molecules in the cell or population thereof.

The contiguous stretch of genomic DNA can be deleted by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from
30 the group consisting of SEQ ID NOs: 102319-121796.

The present invention contemplates genomically editing human cells to cleave NFY-A gene sequences, as well as editing the genome of such cells to alter one or

more additional target polynucleotide sequences. It should be appreciated that cleaving a NFY-A genomic sequence using one or more gRNAs or gRNA pairs described herein and a Cas protein could result in partial or complete deletion of the target NFY-A genomic sequence, depending on the number of gRNAs or gRNA pairs selected, as well as their targets.

In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising a genomic modification in which the NFY-A gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating MHC Class I molecule surface expression and/or activity in the cell. In some embodiments, the contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and a pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 102319-121796.

In some aspects, the invention provides a method for altering a target NFY-A polynucleotide sequence in a cell comprising contacting the NFY-A polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and from one to two ribonucleic acids, wherein the ribonucleic acids direct Cas protein to and hybridize to a target motif of the target NFY-A polynucleotide sequence, wherein the target NFY-A polynucleotide sequence is cleaved, and wherein at least one of the one to two ribonucleic acids are selected from the group consisting of SEQ ID NOs: 102319-121796.

In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising: a genomic modification in which the NFY-A gene has been edited to reduce or eliminate MHC Class I molecule surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 102319-121796.

In some aspects, the invention provides a method for altering a target NFY-A polynucleotide sequence in a cell comprising contacting the NFY-A polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated

(Cas) protein and at least one ribonucleic acid, wherein the ribonucleic acid directs Cas protein to and hybridizes to a target motif of the target NFY-A polynucleotide sequence, wherein the target NFY-A polynucleotide sequence is cleaved, and wherein the at least one ribonucleic acid is selected from the group consisting of SEQ ID NOs: 102319-121796.

In certain aspects, the inventions disclosed herein modulate (e.g., reduce or eliminate) the expression of MHC-I genes by targeting and modulating (e.g., reducing or eliminating) expression of one or more of NFY-B. In some aspects, the modulation occurs using a CRISPR/Cas system.

In some aspects, the present disclosure provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof comprising a genome in which the NFY-B gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating surface expression of MHC class I molecules in the cell or population thereof.

The contiguous stretch of genomic DNA can be deleted by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 121797-135112.

The present invention contemplates genomically editing human cells to cleave NFY-B gene sequences, as well as editing the genome of such cells to alter one or more additional target polynucleotide sequences. It should be appreciated that cleaving a NFY-B genomic sequence using one or more gRNAs or gRNA pairs described herein and a Cas protein could result in partial or complete deletion of the target NFY-B genomic sequence, depending on the number of gRNAs or gRNA pairs selected, as well as their targets.

In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising a genomic modification in which the NFY-B gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating MHC Class I molecule surface expression and/or activity in the cell. In some embodiments, the contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and a pair of ribonucleic acids

having sequences selected from the group consisting of SEQ ID NOs: 121797-135112.

In some aspects, the invention provides a method for altering a target NFY-B polynucleotide sequence in a cell comprising contacting the NFY-B polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and from one to two ribonucleic acids, wherein the ribonucleic acids direct Cas protein to and hybridize to a target motif of the target NFY-B polynucleotide sequence, wherein the target NFY-B polynucleotide sequence is cleaved, and wherein at least one of the one to two ribonucleic acids are selected from the group consisting of SEQ ID NOs: 121797-135112.

In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising: a genomic modification in which the NFY-B gene has been edited to reduce or eliminate MHC Class I molecule surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 121797-135112.

In some aspects, the invention provides a method for altering a target NFY-B polynucleotide sequence in a cell comprising contacting the NFY-B polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and at least one ribonucleic acid, wherein the ribonucleic acid directs Cas protein to and hybridizes to a target motif of the target NFY-B polynucleotide sequence, wherein the target NFY-B polynucleotide sequence is cleaved, and wherein the at least one ribonucleic acid is selected from the group consisting of SEQ ID NOs: 121797-135112.

In certain aspects, the inventions disclosed herein modulate (e.g., reduce or eliminate) the expression of MHC-I genes by targeting and modulating (e.g., reducing or eliminating) expression of one or more of NFY-C. In some aspects, the modulation occurs using a CRISPR/Cas system.

In some aspects, the present disclosure provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof comprising a genome in which the NFY-C gene has been edited to delete a contiguous stretch of genomic DNA, thereby

reducing or eliminating surface expression of MHC class I molecules in the cell or population thereof.

The contiguous stretch of genomic DNA can be deleted by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein
5 and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 135113-176601.

The present invention contemplates genomically editing human cells to cleave NFY-C gene sequences, as well as editing the genome of such cells to alter one or more additional target polynucleotide sequences. It should be appreciated that
10 cleaving a NFY-C genomic sequence using one or more gRNAs or gRNA pairs described herein and a Cas protein could result in partial or complete deletion of the target NFY-C genomic sequence, depending on the number of gRNAs or gRNA pairs selected, as well as their targets.

In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising
15 a genomic modification in which the NFY-C gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating MHC Class I molecule surface expression and/or activity in the cell. In some embodiments, the contiguous stretch of genomic DNA has been deleted by contacting the cell with a
20 Cas protein or a nucleic acid encoding the Cas protein and a pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 135113-176601.

In some aspects, the invention provides a method for altering a target NFY-C polynucleotide sequence in a cell comprising contacting the NFY-C polynucleotide
25 sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and from one to two ribonucleic acids, wherein the ribonucleic acids direct Cas protein to and hybridize to a target motif of the target NFY-C polynucleotide sequence, wherein the target NFY-C polynucleotide sequence is
30 cleaved, and wherein at least one of the one to two ribonucleic acids are selected from the group consisting of SEQ ID NOs: 135113-176601.

In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising:

a genomic modification in which the NFY-C gene has been edited to reduce or eliminate MHC Class I molecule surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 135113-176601.

In some aspects, the invention provides a method for altering a target NFY-C polynucleotide sequence in a cell comprising contacting the NFY-C polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and at least one ribonucleic acid, wherein the ribonucleic acid directs Cas protein to and hybridizes to a target motif of the target NFY-C polynucleotide sequence, wherein the target NFY-C polynucleotide sequence is cleaved, and wherein the at least one ribonucleic acid is selected from the group consisting of SEQ ID NOs: 135113-176601.

In certain aspects, the inventions disclosed herein modulate (e.g., reduce or eliminate) the expression of MHC-I genes by targeting and modulating (e.g., reducing or eliminating) expression of one or more of IRF-1. In some aspects, the modulation occurs using a CRISPR/Cas system.

In some aspects, the present disclosure provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof comprising a genome in which the IRF-1 gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating surface expression of MHC class I molecules in the cell or population thereof.

The contiguous stretch of genomic DNA can be deleted by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 176602-182813.

The present invention contemplates genomically editing human cells to cleave IRF-1 gene sequences, as well as editing the genome of such cells to alter one or more additional target polynucleotide sequences. It should be appreciated that cleaving a IRF-1 genomic sequence using one or more gRNAs or gRNA pairs described herein and a Cas protein could result in partial or complete deletion of the target IRF-1

genomic sequence, depending on the number of gRNAs or gRNA pairs selected, as well as their targets.

In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising a genomic modification in which the IRF-1 gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating MHC Class I molecule surface expression and/or activity in the cell. In some embodiments, the contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and a pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 176602-182813.

In some aspects, the invention provides a method for altering a target IRF-1 polynucleotide sequence in a cell comprising contacting the IRF-1 polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and from one to two ribonucleic acids, wherein the ribonucleic acids direct Cas protein to and hybridize to a target motif of the target IRF-1 polynucleotide sequence, wherein the target IRF-1 polynucleotide sequence is cleaved, and wherein at least one of the one to two ribonucleic acids are selected from the group consisting of SEQ ID NOs: 176602-182813.

In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising: a genomic modification in which the IRF-1 gene has been edited to reduce or eliminate MHC Class I molecule surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 176602-182813.

In some aspects, the invention provides a method for altering a target IRF-1 polynucleotide sequence in a cell comprising contacting the IRF-1 polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and at least one ribonucleic acid, wherein the ribonucleic acid directs Cas protein to and hybridizes to a target motif of the target IRF-1 polynucleotide sequence, wherein the target IRF-1 polynucleotide sequence is cleaved, and wherein

the at least one ribonucleic acid is selected from the group consisting of SEQ ID NOs: 176602-182813.

In some aspects, the present disclosure provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof comprising a genome in which the TAP1 gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating surface expression of MHC class I molecules in the cell or population thereof.

The contiguous stretch of genomic DNA can be deleted by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 182814-188371.

The present invention contemplates genomically editing human cells to cleave TAP1 gene sequences, as well as editing the genome of such cells to alter one or more additional target polynucleotide sequences. It should be appreciated that cleaving a TAP1 genomic sequence using one or more gRNAs or gRNA pairs described herein and a Cas protein could result in partial or complete deletion of the target TAP1 genomic sequence, depending on the number of gRNAs or gRNA pairs selected, as well as their targets.

In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising a genomic modification in which the TAP1 gene has been edited to delete a contiguous stretch of genomic DNA, thereby reducing or eliminating MHC Class I molecule surface expression and/or activity in the cell. In some embodiments, the contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and a pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 182814-188371.

In some aspects, the invention provides a method for altering a target TAP1 polynucleotide sequence in a cell comprising contacting the TAP1 polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and from one to two ribonucleic acids, wherein the ribonucleic acids direct Cas protein to and hybridize to a target motif of the target TAP1 polynucleotide

sequence, wherein the target TAP1 polynucleotide sequence is cleaved, and wherein at least one of the one to two ribonucleic acids are selected from the group consisting of SEQ ID NOs: 182814-188371.

5 In some aspects, the invention provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof, each cell comprising a modified genome comprising: a genomic modification in which the TAP1 gene has been edited to reduce or eliminate MHC Class I molecule surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid having a sequence selected from the group consisting of
10 SEQ ID NOs: 182814-188371.

In some aspects, the invention provides a method for altering a target TAP1 polynucleotide sequence in a cell comprising contacting the TAP1 polynucleotide sequence with a clustered regularly interspaced short palindromic repeats-associated (Cas) protein and at least one ribonucleic acid, wherein the ribonucleic acid directs
15 Cas protein to and hybridizes to a target motif of the target TAP1 polynucleotide sequence, wherein the target TAP1 polynucleotide sequence is cleaved, and wherein the at least one ribonucleic acid is selected from the group consisting of SEQ ID NOs: 182814-188371.

In certain embodiments, gRNAs that allow simultaneous deletion of all MHC class I alleles by targeting a conserved region in the HLA genes are identified as HLA Razors. In some aspects, the gRNAs are part of a CRISPR system. In alternative aspects, the gRNAs are part of a TALEN system. In one aspect, an HLA Razor targeting an identified conserved region in HLAs is depicted in FIG. 21A. In other aspects, multiple HLA Razors targeting identified conserved regions are utilized. It is
20 generally understood that any guide that targets a conserved region in HLAs can act as an HLA Razor.
25

Knock-in

30 In certain embodiments, tolerogenic factors can be inserted or reinserted into genome-edited stem cell lines to create immune-privileged universal donor stem cell lines. In certain embodiments, the universal stem cells disclosed herein have been further modified to express one or more tolerogenic factors. Exemplary tolerogenic

factors include, without limitation, one or more of HLA-C, HLA-E, HLA-F, HLA-G, PD-L1, CTLA-4-Ig, CD47, C1-inhibitor, and IL-35.

The present inventors have used genome editing systems, such as the CRISPR/Cas system, to facilitate the insertion of tolerogenic factors, such as the tolerogenic factors shown in Table 2 below, into a safe harbor locus, such as the AAVS1 locus, to actively inhibit immune rejection. As evidenced in **FIGS. 11A-11C**, the present inventors have successfully expressed tolerogenic factors, such as PD-L1 and HLA-G, from a safe harbor locus.

TABLE 2 – Tolerogenic factors that can be (re)introduced into genome edited stem cell lines to create immune-privileged universal donor stem cell lines.

Gene	Receptor	Target Cell
HLA-G*	KIR2DL4	NK cells
HLA-C*	KIR2DS1/L1	NK cells
HLA-E*	NKG2A/C	NK cells
PD-L1	PD-1	T cells
CTLA4-Ig	CD28	APC/T cells
CD47	SIRP α	Macrophages
C1-inhibitor	Complement	
IL-35	IL35R	T reg
* in the form of a peptide-B2M-HLA fusion construct, when (re)introduced into a B2M ^{-/-} cell line		

In some aspects, the present disclosure provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof comprising a genome in which the stem cell genome has been modified to express HLA-G. In some aspects, the present disclosure provides a method for altering a stem cell genome to express HLA-G. In certain aspects at least one ribonucleic acid or at least one pair of ribonucleic acids may be utilized to facilitate the insertion of HLA-G into a stem cell line. In certain embodiments, the at least one ribonucleic acid or the at least one pair of ribonucleic acids is selected from the group consisting of SEQ ID NOs: 188372-189858.

In some aspects, the present disclosure provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof comprising a genome in which the stem cell genome has been modified to express HLA-C. In some aspects, the present disclosure provides a method for altering a stem cell genome to express HLA-C. In certain aspects at least one ribonucleic acid or at least one pair of ribonucleic acids may be utilized to facilitate the insertion of HLA-C into a stem cell line. In certain embodiments, the at least one ribonucleic acid or the at least one pair of ribonucleic acids is selected from the group consisting of SEQ ID NOs: 3278-5183.

In some aspects, the present disclosure provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof comprising a genome in which the stem cell genome has been modified to express HLA-E. In some aspects, the present disclosure provides a method for altering a stem cell genome to express HLA-E. In certain aspects at least one ribonucleic acid or at least one pair of ribonucleic acids may be utilized to facilitate the insertion of HLA-E into a stem cell line. In certain embodiments, the at least one ribonucleic acid or the at least one pair of ribonucleic acids is selected from the group consisting of SEQ ID NOs: 189859-193183.

In some aspects, the present disclosure provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof comprising a genome in which the stem cell genome has been modified to express PD-L1. In some aspects, the present disclosure provides a method for altering a stem cell genome to express PD-L1. In certain aspects at least one ribonucleic acid or at least one pair of ribonucleic acids may be utilized to facilitate the insertion of PD-L1 into a stem cell line. In certain embodiments, the at least one ribonucleic acid or the at least one pair of ribonucleic acids is selected from the group consisting of SEQ ID NOs: 193184-200783.

In some aspects, the present disclosure provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof comprising a genome in which the stem cell genome has been modified to express CD-47. In some aspects, the present disclosure provides a method for altering a stem cell genome to express CD-47. In certain aspects at least one ribonucleic acid or at least one pair of ribonucleic acids may be utilized to facilitate the insertion of CD-47 into a stem cell line. In certain embodiments, the at least one ribonucleic acid or the at least one pair of ribonucleic acids is selected from the group consisting of SEQ ID NOs: 200784-231885.

In some aspects, the present disclosure provides a stem cell (e.g., hypoinmunogenic stem cell) or population thereof comprising a genome in which the stem cell genome has been modified to express HLA-F. In some aspects, the present disclosure provides a method for altering a stem cell genome to express HLA-F. In certain aspects at least one ribonucleic acid or at least one pair of ribonucleic acids may be utilized to facilitate the insertion of HLA-F into a stem cell line. In certain embodiments, the at least one ribonucleic acid or the at least one pair of ribonucleic acids is selected from the group consisting of SEQ ID NOs: 688808-399754.

Other target modifications

In some embodiments, additional targets can be modified and/or deleted in universal cells, such as universal T cells, to improve their function and/or tailor them to a specific therapeutic approach.

In some aspects, genes encoding for co-stimulatory molecules/receptors that engage cytotoxic T cells can be deleted by genome editing (Table 3). Deletion of co-stimulatory molecules/receptors may occur to prevent autoimmunity. In other aspects, genes encoding for co-inhibitory molecules/receptors can be deleted by genome editing (Table 4). Deletion of co-inhibitory molecules/receptors may occur to prevent T cell inhibition by cancer cells, and may be useful in T cell-based cancer immunotherapy.

Table 3 – Co-stimulatory molecules that will be deleted to prevent autoimmunity (e.g., to block interaction of transplanted cells with T cells).

Ligand on Cancer cells	Receptor on T cells
Ox40L	Ox40
GITRL	GITR
4-1BBL	4-1BB
CD58	CD2
B7-1, -2	CD28
B2-2	ICOS
CD70	CD27
LIGHT	HVEM

SLAM	SLAM
CD155, CD112	CD226

Table 4 – Co-inhibitory molecules/receptors that will be deleted to prevent T cell inhibition by cancer cells. Useful in T cell-based cancer immunotherapy

Ligand on Cancer cells	Receptor on T cells
B7/H1PD-L1	PD1
B7-1/B7-2	CTLA4
MHC	LAG3
CD155, CD112, CD113	TIGIT
Galectin 9	TIM3
B7-1	B7-H1/PD-L1
PD-L2	PD-1
B7-H3	TLT-2
CD153	CD30
VISTA	?
HVEM	CD160
HVEM	BTLA
Collagen	LAIR1
CD48	2B4/CD244

5 In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the OX40 gene has been edited to modify (e.g., delete) a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target OX40 sequence in a cell. The contiguous stretch of genomic DNA can be modified (e.g., deleted) by contacting the
10 cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 231886-234210.

15 In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the GITR gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target GITR sequence in a cell. The contiguous

stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 234211-236445.

5 In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the 4-1BB gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target 4-1BB sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof
10 with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 234211-236445.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the CD28 gene has been edited to modify a
15 contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target CD28 sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group
20 consisting of SEQ ID NOs: 252807-274181.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the B7-1 gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target B7-1 sequence in a cell. The contiguous
25 stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 274182-295529.

In some aspects, the present disclosure provides a stem cell or population
30 thereof comprising a genome in which the B7-2 gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target B7-2 sequence in a cell. The contiguous

stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 295530-324177.

5 In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the ICOS gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target ICOS sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof
10 with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 324178-339974.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the CD27 gene has been edited to modify a
15 contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target CD27 sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group
20 consisting of SEQ ID NOs: 339975-344266.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the HVEM gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target HVEM sequence in a cell. The contiguous
25 stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 344267-350722.

In some aspects, the present disclosure provides a stem cell or population
30 thereof comprising a genome in which the SLAM gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target SLAM sequence in a cell. The contiguous

stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 350723-353590.

5 In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the CD226 gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target CD226 sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof
10 with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 353591-416840.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the PD1 gene has been edited to modify a
15 contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target PD1 sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of
20 sequences numbered 196-531 and 4047-9101 in US Application No. 15/083,021, which is incorporated herein by reference.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the CTLA4 gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure
25 provides a method for altering a target CTLA4 sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of sequences numbered 1-195 and 797-4046 in US Application No.
30 15/083,021, which is incorporated herein by reference.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the LAG3 gene has been edited to modify a

contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target LAG3 sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one
5 ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 416841-421195.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the TIGIT gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure
10 provides a method for altering a target TIGIT sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 421196-432039.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the TIM3 gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target TIM3 sequence in a cell. The contiguous
15 stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 432040-447610.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the CD160 gene has been edited to modify a
20 contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target CD160 sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group
25 consisting of SEQ ID NOs: 447611-459294.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the BTLA gene has been edited to modify a

contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target BTLA sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one
5 ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 459295-482454.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the CD244 gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure
10 provides a method for altering a target CD244 sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 482455-504169.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the CD244 gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure
15 provides a method for altering a target CD244 sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group
20 consisting of SEQ ID NOs: 482455-504169.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the CD30 gene has been edited to modify a
25 contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target CD30 sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group
30 consisting of SEQ ID NOs: 699755-731993.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the TLT gene has been edited to modify a

contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target TLT sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 731994-739957.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the VISTA gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target VISTA sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 739958-757515.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the B7-H3 gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target B7-H3 sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 757516-777888.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the PD-L2 gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target PD-L2 sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 777889-817976.

In some embodiments, lymphocyte adhesion is blocked to prevent autoimmunity. In certain aspects, target genes can be edited by genome editing to block lymphocyte adhesion (Table 5).

Table 5 – Blocking lymphocyte adhesion to prevent autoimmunity.

Ligand on Cancer cells	Receptor on T cells
ICAM-1, ICAM-2	LFA-1
CD58/LFA-3	CD2
CD-SIGN	ICAM-3

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the LFA-1 gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target LFA-1 sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 504170-526670.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the CD2 gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target CD2 sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 526671-536704.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the CD58 gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target CD58 sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one

ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 536705-570967.

In some embodiments, genes encoding for T cell receptors can be deleted by genome editing. Deletion of T cell receptor genes may occur to prevent autoimmune attack in T cell therapy. In some aspects, the gene encoding the T cell receptor is a T cell receptor alpha locus (TCRA), or a homolog, ortholog, or variant thereof (Gene ID: 5133, also known as IMD7, TCRD, TRA@, TRAC, and referred to herein as TCRA, TCRA, TCRalpha, and the like). In some aspects, the gene encoding the T cell receptor is a T cell receptor alpha locus (TCRB), or a homolog, ortholog, or variant thereof (Gene ID: 6957, also known as TCRB; TRB@, and referred to herein as TCRb, TCRB, TCRbeta, and the like). In some aspects, the T cell receptor gene is modified by genome editing as described in US Application No. 15/083,021 and PCT Application No. PCT/US2016/024554, both of which are incorporated herein by reference.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the TRAC gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target TRAC sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of sequences numbered 532-609 and 9102-9797, as described in US Application No. 15/083,021, incorporated herein by reference.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the TRBC gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target TRBC sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of sequences numbered 610-765 and 9798-10573, as described in US Application No. 15/083,021 and incorporated herein by reference.

In some embodiments, genes involved in regulatory T cell (T reg) function can be deleted by genome editing (Table 6). Deletion of genes involved in regulatory T cell (T reg) function may occur to break tolerance in T cell therapy.

Table 6 – Deletion of genes involved in regulatory T cell (T reg) function to break tolerance in T cell therapy.

Gene	Function
FOXP3	T reg development
HELIOS	T reg maintenance
ST2	IL-33 receptor

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the FOXP3 gene has been edited to modify (e.g., delete) a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target FOXP3 sequence in a cell. The contiguous stretch of genomic DNA can be modified (e.g., deleted) by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 570968-584068.

In some aspects, the present disclosure provides a stem cell or population thereof comprising a genome in which the HELIOS gene has been edited to modify a contiguous stretch of genomic DNA. In certain aspects, the present disclosure provides a method for altering a target HELIOS sequence in a cell. The contiguous stretch of genomic DNA can be modified by contacting the cell or population thereof with a Cas protein or a nucleic acid encoding the Cas protein and at least one ribonucleic acid or at least one pair of ribonucleic acids selected from the group consisting of SEQ ID NOs: 683033-688807.

The capacity of the CRISPR/Cas system for multiplexing also allows the generation of disease-specific universal donor cell lines that harbor one or more genomic alterations that will improve their applicability to treat a certain disease or condition. A list of potential diseases that can be addressed can be found in Table 7.

Table 7 – Additional targets that can be modified using the CRISPR/Cas system in order to generate universal donor cell lines tailored to a specific disease or application.

Gene	Disease
<i>TCR</i>	T cell therapy
<i>PD-1</i>	T cell therapy
<i>CTLA4</i>	T cell therapy
<i>LAG-3</i>	T cell therapy
<i>TIGIT</i>	T cell therapy
<i>TIM3</i>	T cell therapy
<i>CCR5</i>	HIV resistance
<i>PCSK9</i>	Cardiovascular disease
<i>APOC3</i>	Cardiovascular disease

It is to be understood that the inventions disclosed herein are not limited in their application to the details set forth in the description or as exemplified. The invention encompasses other embodiments and is capable of being practiced or carried out in various ways. Also, it is to be understood that the phraseology and terminology employed herein is for the purpose of description and should not be regarded as limiting.

While certain compositions, methods and assays of the present invention have been described with specificity in accordance with certain embodiments, the following examples serve only to illustrate the methods and compositions of the invention and are not intended to limit the same.

The articles “a” and “an” as used herein in the specification and in the claims, unless clearly indicated to the contrary, should be understood to include the plural referents. Claims or descriptions that include “or” between one or more members of a group are considered satisfied if one, more than one, or all of the group members are present in, employed in, or otherwise relevant to a given product or process unless indicated to the contrary or otherwise evident from the context. The invention includes embodiments in which exactly one member of the group is present in, employed in, or otherwise relevant to a given product or process. The invention also

includes embodiments in which more than one, or the entire group members are present in, employed in, or otherwise relevant to a given product or process. Furthermore, it is to be understood that the invention encompasses all variations, combinations, and permutations in which one or more limitations, elements, clauses, descriptive terms, etc., from one or more of the listed claims is introduced into another claim dependent on the same base claim (or, as relevant, any other claim) unless otherwise indicated or unless it would be evident to one of ordinary skill in the art that a contradiction or inconsistency would arise. Where elements are presented as lists, (e.g., in Markush group or similar format) it is to be understood that each subgroup of the elements is also disclosed, and any element(s) can be removed from the group. It should be understood that, in general, where the invention, or aspects of the invention, is/are referred to as comprising particular elements, features, etc., certain embodiments of the invention or aspects of the invention consist, or consist essentially of, such elements, features, etc. For purposes of simplicity those embodiments have not in every case been specifically set forth in so many words herein. It should also be understood that any embodiment or aspect of the invention can be explicitly excluded from the claims, regardless of whether the specific exclusion is recited in the specification. The publications and other reference materials referenced herein to describe the background of the invention and to provide additional detail regarding its practice are hereby incorporated by reference.

Examples:*Cell lines*

The inventors have targeted various genes in a variety of cell lines. The various cell lines utilized include HuES8, HuES9, BJ-RiPSCs, Thp1, Jurkat, Primary T cells and HEK293T cells (FIG. 27). HuES8 and HuES9 are human ES cell lines. BJ-RiPSC is an iPSC line.

Knock-out of HLA-A, HLA-B, and HLA-C

Knock-out targeting of HLAs was examined. Initially, an HLA-B and HLA-C knock-out strategy was examined. Two short guide RNAs (sgRNAs) were designed upstream of the HLA-B locus and downstream of HLA-C, which allowed for excision

of the HLA-B and HLA-C genes (FIG. 14A). sgRNA #1 and sgRNA #2 target the HLA-B upstream region, and sgRNA #3 and sgRNA #4 target the HLA-C downstream region.

PCR screening was performed and confirmed that clone 1D was a homozygous knock-out clone. A schematic showing the PCR verification strategy for successful deletion of HLA-B and HLA-C is shown in FIG. 13B. Two pairs of wild-type (WT) primers were designed flanking each cutting site, with predicted amplicons sizes of 545 bp and 472 bp. Clone 1D was identified as a homozygous knock-out clone by the presence of ~680 pb PCR band generated with KO primers and the absence of bands using the two different sets of WT primers (FIG. 14B). In addition, genomic DNA was isolated from the indicated targeted HuES8 clones. Sequencing results of the clone 1D PCR product demonstrated successful deletion of HLA-B and HLA-C genes in HuES9 (FIG. 14C).

Further, RT-PCR with HLA-B and HLA-C specific primers demonstrated the mRNA expression of HLA-B and HLA-C in clone 1D was eliminated (FIG. 14D). GAPDH, TOP1 and HPRT1 were used as internal controls. WT and clone 1D RT-PCR products amplified with HLA-B primers were sequenced and identified as HLA-B and HLA-A mRNAs, respectively using BLAST (FIG. 14E). These results demonstrated that in the absence of the HLA-B gene, the HLA-B specific primers will amplify HLA-A mRNA in HuES8 clone 1D. HuES8 clone 1D displays a normal karyotype as assessed by NanoString nCounter set (FIG. 14F).

A schematic demonstrating an HLA-A knockout strategy using the dual sgRNA approach is provided in FIG. 14G. The schematic shows the position of the two sgRNAs (#5 and #6) that were designed to bind upstream and downstream of HLA-A. The on-target cutting efficiency of sgRNA #5 and #6 was determined in 293T cells using TIDE (FIG. 14H).

PCR screening confirmed that clone 4E was a heterozygous HLA-A knockout clone (FIG. 14I). The PCR screening strategy confirmed deletion of HLA-A in HuES8. KO primers were designed with one primer annealing upstream and one primer annealing downstream of the cutting sites. Upon HLA-A deletion, the resulting amplicon was observed as 220 bp on a 2% agarose gel. Two pairs of WT primers were designed flanking each cutting site, with predicted amplicon sizes of

589 bp and 571 bp. Clone 4E was identified as a heterozygous clone due to the presence of bands generated with KO primers and WT primers amplified from genomic DNA (FIG. 14I). Sequencing of the PCR product amplified from the genomic DNA of clone 4E using KO primers demonstrated successful deletion of HLA-A in HuES8 (FIG. 14J).

Knock-out of transcriptional regulators

As illustrated in FIGS. 3A-3B, in certain aspects, the inventions disclosed herein target the transcriptional regulators of antigen presentation (e.g., CIITA and/or NLRC5). The inventors have discovered that targeting and/or modulating the expression of such transcriptional regulators of antigen presentation provides a means to efficiently modulate (e.g., reduce or eliminate) the expression of the three classical MHC-Ia molecules, HLA-A, HLA-B, and HLA-C, and thereby produce hypoinmunogenic universal stem cell lines that are useful for cell replacement therapy. As evidenced in FIG. 4, the present inventors have demonstrated that such genome-edited cells are characterized by reduced MHC-I expression relative to the WT HuES9 cells, as assessed by FACS. Reduced or eliminated MHC-I surface expression was observed in those stem cells in which the expression of NLRC5, CIITA and B2M was modulated using the CRISPR/Cas system. In particular, FIG. 4 evidences low basal MHC-I expression in stem cells which can be increased by IFN- γ , that an approximately 50% reduction of MHC-I surface expression was observed in the IFN- γ -treated *NLRC5*^{-/-} stem cells and that a complete loss of MHC-I surface expression was observed in the *B2M*^{-/-} stem cells.

Similar results were observed on MHC-II expression following modulation of the expression of CIITA. The present inventors differentiated the genome-edited *CIITA*^{-/-} stem cell line into macrophage, which are antigen presenting cells. As depicted in FIG. 5C, the CIITA-deficient stem cell-derived macrophage lacked MHC-II expression, thus clearly showcasing the expected phenotype. In particular, by targeting the first coding exon of the *CIITA* gene (FIGS. 10A-10B), the foregoing results evidence that MHC-II expression can be efficiently abrogated.

The functional consequences of reduced HLA expression in the genome-edited cells were next evaluated in a humanized mouse model that was prepared by

reconstituting an immunocompromised mice model with a human immune system (FIG. 6). As illustrated in Table 1 below, a comparable number of teratomas formed in all cases, irrespective of the genotype and the whole colony had to be sacrificed. Similarly, no differences in the failure rates of teratoma formation was observed. The inventors looked more closely at the overall morphology of the teratoma samples and a clear cut phenotype that correlates with the levels of MHC-I expression was identified. NLRC5, reduced, B2M absent MHC-I on the surface. FIG. 7 illustrates the quantification of the resulting teratoma types. FIGS. 8A-8C further demonstrate CD8+ T cell proliferation in wild-type cells and suggests immune rejection of the wild-type teratomas and improved engraftment of the genome-edited cells in the humanized mouse model.

Table 1

	Genotype	#tumors (injections)
p42	WT	21 (24)
E4	NLRC5-/-CIITA-/-	21 (24)
C7	B2M-/-CIITA-/-	20 (24)
C6	NLRC5-/-CIITA-/-	18 (20)

The foregoing results therefore demonstrate successful targeting of *NLRC5*, *CIITA* and *B2M* in HuES9 and BJ RiPSCs and further evidence that genome-edited cells can be differentiated into a variety of different cell types that are characterized by reduced HLA expression.

The inventors have used both a TALENs system and a CRISPR/Cas system to facilitate the targeting of transcriptional regulators of HLA expression (i.e., the MHC enhanceosome). TALEN-induced *CIITA* and *NLRC5* mutations in BJ-RIPSCs and HuES9 are illustrated in FIGS. 15A-D. In addition, *NLRC5* and *CIITA* can also be targeted utilizing CRISPRs to achieve a reduction in MHC class I expression and complete loss of MHC class II expression, respectively.

NLRC5 was targeted in Thp1 cells using CRISPR and it was demonstrated that MHC-I expression in *NLRC5*-/- Thp1 cells was reduced (FIG. 16A). Examples of CRISPR and/or TALENs systems targeting *NLRC5*, *CIITA* and *B2M* are provided

in FIG. 16B. Reduced MHC class I expression in HuES9 was shown following targeting with NLRC5 or B2M CRISPRs. For example, about 50% reduction was shown in IFN γ -treated NLRC5 $^{-/-}$ cells and complete loss of MHC-I surface expression was shown in B2M $^{-/-}$ cells (FIG. 16C).

5 A lentiviral transduction of Thp-1 was conducted using a two component (e.g., dual vector) system (FIG. 16D). The two component system included Lenti-Cas9-Blasticidin and Lenti-Guide-puro. Examples of the different CRISPRs used for the lentiviral transduction of Thp-1 are provided in FIG. 16E. Thp-1 was transduced with lentivirus encoding NLRC5 and CIITA. A B2M CRISPR was used as a positive control. All of the cells were stimulated ON with 50U IFN γ to boost HLA expression (HLA-A2 was 1:200 and HLA-DR was 1:100). It was demonstrated that CIITA and NLRC5 act independently on MHC-II and MHC-I, respectively (FIG. 16F). At ten days post CRISPR transduction, when the Thp1 cells were all stimulated ON with 50U IFN γ (HLA-A2 is 1:200 and HLA-DR is 1:100), it was demonstrated that
10 targeting IRF1 results in a loss of MHC-II expression (FIG. 16G).

The inventors further examined targeting of IRF1 and the resultant reduced MHC class I expression in human pluripotent stem cells (HuES9) and Thp-1 cells. A schematic demonstrating a dual CRISPR strategy for targeting the *IRF1* locus is provided in FIG. 17A. Testing of different *IRF1* guide combinations was conducted (FIG. 17B) and a 'dual guide strategy' for the targeted deletion of *IRF1* was identified (FIG. 17C). After the dual guide strategy for the targeted deletion of *IRF1* was applied, a sequence confirmation of *IRF1* CRISPR induced deletion was provided (FIG. 17D), followed by screening of *IRF1*-targeted HuES9 cells (FIG. 17E). The presence of the PCR bands suggests successful targeting using the dual CRISPR
20 strategy.

The inventors then reconfirmed (FIG. 17F) and genotyped (FIG. 17G) the IRF1 clones. Sequencing confirmed IRF1 CRISPR induced deletion in clone 12 (FIG. 17H), clone 17 (FIG. 17I) and clone 21 (FIG. 17J). The IRF1 $^{-/-}$ HuES9 clones exhibited impaired MHC class I induction following IFN γ treatment for 48 hours (FIG. 17K).
25

The inventors also examined targeting of additional enhanceosome components. The impact on MHC-I expression by targeting additional enhanceosome
30

components in 293T cells was examined, but it is expected that the targeting of these additional enhanceosome components will also affect MHC-II levels in cells that actually express it, e.g., Thp1 cells or other APCs. For example, the inventors examined CRISPR targeting of RFX5 (FIG. 18A), RFX-ANK (FIG. 18C) and RFX-AP (FIG. 18G) in 293T cells using a dual guide strategy. The targeting results demonstrated reduced MHC class I expression of RFX5 (FIG. 18B, FIGS. 18E-18F), RFX-ANK (FIG. 18D, FIGS. 18E-F) and RFX-AP (FIG. 18H). The inventors also examined CRISPR dual guide targeting of NFY-A (FIG. 19A), NFY-B (FIG. 19D) and NFY-C (FIG. 19B) in 293T cells. The targeting results demonstrated reduced MHC class I expression of NFY-A (FIG. 19C), NFY-B (FIG. 19E) and NFY-C (FIG. 19C).

Blocking surface trafficking of MHC class I

The successful targeting of B2M utilizing TALENs and/or CRISPR has previously been described in PCT Patent Application No. PCT/US2015/059621, which is incorporated herein by reference and is shown in FIGS. 32-40. It has further been demonstrated that surface expression of MHC class I molecules is reduced or eliminated, thereby blocking the surface trafficking of MHC-I molecules. For example, loss of MHC class I surface expression in B2M^{-/-} Jurkat Cas9 T cells was shown in comparison to MHC class I surface expression in Jurkat Cas9 T cells in FIG. 31.

In addition, the inventors have demonstrated that surface trafficking of MHC class I molecules can be suppressed by disrupting the TAP1 gene, an ER-resident peptide transporter. For example, TAP1 CRISPR expression reduces MHC-I surface expression in Jurkat cells (FIG. 20A), as well as in Jurkat T cells (FIG. 20B), following 48 hour treatment with IFN γ . It was further demonstrated that HLA surface expression in Jurkat (Cas9) T cells could be eliminated (FIG. 20C and FIG. 20D). The Jurkat T cells were established from the peripheral blood of a 14 year old boy who had acute T cell leukemia.

HLA Razor

The inventors examined CRISPR guide RNAs that allow simultaneous deletion of all MHC class I alleles by targeting a conserved region in the HLA genes. A TALEN pair of guides that target the same conserved region in MHC class I genes were also identified. Any guide that targets the conserved regions may be identified or classified as an HLA Razor. The targeting of a conserved sequence found in all HLAs by CRISPR or TALENS was demonstrated in FIG. 21A. The two violet boxes indicate the binding sites for the pan-HLA TALEN pair. The blue arrow indicates the pan-HLA CRISPR tested pair, with the PAM being boxed in blue. The expression of pan-HLA-TALENs in 293T and HuES9 cells was shown in FIG. 21B at 72 hours post transfection. The HLA-Razor CRISPR blunts MHC class I expression in 293T cells as demonstrated in FIG. 21C. The 293T cells were also co-transfected with Cas9-GFP. FIG. 21D provides a comparison of the activity of two different HLA Razors targeting two different conserved regions of the HLAs.

Knock-in of PD-L1 and HLA-G

The present inventors have used a CRISPR/Cas system to facilitate the insertion of tolerogenic factors, such as the tolerogenic factors shown in Table 2, into an AAVS1 locus, to actively inhibit immune rejection. As evidenced in FIGS. 11A-11C, tolerogenic factors, such as PD-L1 and HLA-G, have been successfully expressed from the AAVS1 locus.

A schematic of the PD-L1 and HLA-G knock-in strategy is shown in FIG. 22A. Wild type (WT) and knock-in (KI) primers for clone screening were designed. The amplicon with WT primers is predicted as 488 bp, and the amplicons with KI primers are predicted as 403 bp and 915 bp. A design of a knock-in donor plasmid (FIG. 22B) shows that the reading frames of PD-L1 and HLA-G are linked by T2A and their expression is driven by a CAGGS promoter. Puromycin was used as a drug resistance marker following the SA-2A gene trap element.

The expression of PD-L1 and HLA-G was examined in the donor plasmid-transfected 293T cells by FACS analysis. FIG. 22C shows the ectopic PD-L1 and HLA-G expression in 293T cells. APC-conjugated PD-L1 antibody and FITC-conjugated HLA-G antibody were used. In addition, the expression of ectopic HLA-G expression in JEG-3 cells is shown in FIG. 22D. The donor plasmid was

transfected into an HLA-G^{-/-} JEG-3 cell line, and ectopic HLA-G expression was examined by FACS analysis 48 hours post-transfection. A PE-conjugated HLA-G antibody (MEM/G9) was used to detect surface HLA-G surface expression.

PCR screening was performed, which confirmed that clone 1G was a heterozygous KI clone for PD-L1/HLA-G (FIG. 22E). Clone 1G was identified as a heterozygous KI clone by the presence of bands using both WT primers and KI-specific primers amplified from genomic DNA of targeted HuES8. The expression of PD-L1 was verified in HuES8 KI clone 1G by FACS analysis using an APC-conjugated PD-L1 antibody (FIG. 22F).

Knock-in of CD-47

In addition, a CD47 knock-in strategy was also examined. Human CD47 was cloned into an expression plasmid driven by a CAG promoter, which also contained an IRES-GFP. 293T cells already express high levels of CD47 (the human “don’t eat me” signal), which prevents engulfment of cells from macrophages. Expression can be increased by overexpression of CD47 in both 293T cells, as well as in human pluripotent stem cells (HuES9), as detected by FACS using a CD47-specific antibody (FIG. 23). It is expected that overexpression of CD47 will assist engraftment of stem cell-derived transplants by protecting cells from macrophage engulfment.

Additional targets to be modified in Universal Donor Cells

Additional targets may be modified in universal donor cells to tailor them to a specific application. For example, additional targets may be modified in universal donor cells to tailor them to be used as universal CAR T cells. In one instance, the inventors deleted TRAC and TRBC in HuES9 to disrupt TCR expression (FIG. 24). A dual guide RNA approach was used to introduce deletions into the TRAC and TRBC loci in HuES9 cells. The TCRA wild type band is 249 bp and after deletion is 209 bp. The TCRB wild type band is 162 bp and after deletion is 140 bp. The inventors additionally targeted TCRA in HuES9 B2M^{-/-}CIITA^{-/-} to create a triple knock-out stem cell line for B2M^{-/-}, CIITA^{-/-} and TCR^{-/-}, which upon differentiation into T cells will be devoid of MHC-I and -II and exhibit no TCR surface expression.

In another instance, the inventors targeted PD-L1 (FIG. 25A). It was identified that CRISPRs targeting Cd274/B7-H1/PD-L1 were very useful in breaking tolerance in cancer immunotherapy. PD-L1 knock out was demonstrated in multiple cell types, including JEG-3, a choriocarcinoma cell line, and in two melanoma cell lines, 501 and MalMe (FIGS. 25B-25D). Screening of targeted B7-H1 colonies was conducted, and it was identified that there was an 8.3% CRISPR cutting efficiency in JEG-3 cells (FIG. 25B). Additionally, reconfirmation of 501 melanoma knock out clones was shown in FIG. 25C, and reconfirmation of MalMe melanoma knock out clones was shown in FIG. 25D.

Targeting co-inhibitor/co-stimulatory receptors or their ligands

The inventors examined multiple targets utilizing CRISPR. An illustration of co-stimulatory/inhibitory molecules and their receptors on T cells is provided in FIG. 26A. For each target examined, the indicated four CRISPRs have been cloned and tested for on-target activity in 293T cells. The expected size of the PCR band, when cutting of both CRISPRs occurs, is indicated below each individual gel picture (FIGS. 26B-26P). Dual guide targeting in 293T cells was demonstrated for TIGIT (FIG. 26B), TIM3 (FIG. 26C), HVEM (FIG. 26D), 2B4/CD244 (FIG. 26E), CD28 (FIG. 26F), OX40 (FIG. 26G), B71 (FIG. 26H), CD226 (FIG. 26I), CD2 (FIG. 26J), LAG3 (FIG. 26K), BTLA (FIG. 26L), ICOS (FIG. 26M), CD27 (FIG. 26N), ST2 (FIG. 26O) and GITR (FIG. 26P).

CRISPR targeting of B7-H3 was examined in JEG-3 cells (FIGS. 30A-30D). FIG. 30B shows a screening of targeted B7-H3 colonies in JEG-3 cells and identifies a CRISPR cutting efficiency of 15/80 or about 18.7%. Confirmation of the B7-H3 knock-outs through sequencing was performed (FIG. 30C) and the loss of B7-H3 surface expression in targeted Jeg3 clones was provided in FIG. 30D.

Differentiation of modified embryonic stem cells

Modified embryonic stem cells may be differentiated into a variety of different cell types, with reduced or absent HLA expression (FIG. 28A). Examples of such cell types include mesenchymal progenitors cells (MPCs), hypoinmunogenic

cardiomyocytes, endothelial cells (ECs), macrophages, hepatocytes, beta cells (e.g., pancreatic beta cells), or neural progenitor cells (NPCs).

Initially, the inventors demonstrated reduced MHC-I expression in NLRC5^{-/-} human ES cells in FIG. 28B. Low basal MHC-I expression was seen in stem cells, but expression could be increased by IFN γ stimulation. There is about a 50% reduction in IFN γ -treated NLRC5^{-/-} cells.

The inventors then examined MHC-I expression in various differentiated cell types. For example, FIG. 28C shows reduced MHC-I expression in NLRC5^{-/-} human mesenchymal progenitor cells (MPCs). The graphs included in FIG. 28C demonstrate the differences between MHC-I expression in HuES9 cells and MPC cells. FIG. 28D shows reduced MHC-I expression in stem cell-derived NLRC5^{-/-} endothelial cells (ECs). Similar differentiation efficiency for ECs was shown in FIG. 28E, and a loss of HLA expression in B2M^{-/-} CIITA^{-/-} ECs was shown in FIG. 28F. Next, reduced MHC class I expression in NLRC5^{-/-} hepatocyte-like cells (HLCs) was provided (FIG. 28G). The HLCs were derived from BJ-RIPSCs.

At FIG. 28H it is shown that a mutation of *CIITA* abrogates MHC class II expression in hESC-derived macrophages. Additionally, neural progenitor cells (NPCs) are differentiated from an embryonic stem cell (FIG. 28I). It was shown that B2M^{-/-} CIITA^{-/-} HuES9 cells form Nestin⁺ neural rosettes (white arrows in figure) as a result of differentiation. Finally, the inventors have adapted modified embryonic stem cells to spin culture so as to be utilized for beta-cell differentiation (FIG. 28J).

In vivo data

Finally, the inventors have generated 'hypoimmunogenic' DKO cell lines (FIG. 29A). The cells lines examined were WT HuES9 cells, NLRC5^{-/-} C2TA^{-/-} HuES9 cells and B2M^{-/-} C2TA^{-/-} HuES9 cells. The different cells lines showed different levels of MHC-I and MHC-II expression (FIG. 29A). For example, WT HuES9 cells exhibited expression of MHC-I and MHC-II. The NLRC5^{-/-} C2TA^{-/-} HuES9 cells exhibited reduced MHC-I expression and no MHC-II expression. The B2M^{-/-} C2TA^{-/-} HuES9 cells exhibited no MHC-I and MHC-II expression. These cells lines were then examined in humanized mice and improved engraftment of genome-edited stem cells in humanized mice was shown in FIG. 29B.

CLAIMS

What is claimed is:

1. A stem cell comprising modulated expression of one or more MHC-I and MHC-II human leukocyte antigens relative to a wild-type stem cell.
2. A stem cell comprising modulated expression of one or more MHC-I and MHC-II human leukocyte antigens relative to a wild-type stem cell, wherein the hypoimmunogenic stem cell has one or more genes encoding one or more transcriptional regulators of MHC-I or MHC-II deleted from at least one allele of the cell.
3. The stem cell of claims 1-2, wherein the modulated expression of the one or more MHC-I and MHC-II human leukocyte antigens comprises reduced expression of the one or more MHC-I and MHC-II human leukocyte antigens.
4. The stem cell of claims 1-2, wherein the modulated expression of the one or more MHC-I and MHC-II human leukocyte antigens comprises inhibited expression of the one or more MHC-I and MHC-II human leukocyte antigens.
5. The stem cell of claims 1-2, wherein the modulated expression of the one or more MHC-I and MHC-II human leukocyte antigens comprises interfered with expression of the one or more MHC-I and MHC-II human leukocyte antigens.
6. The stem cell of claim 1, wherein the modulated expression of the one or more MHC-I and MHC-II human leukocyte antigens comprises one or more genes encoding one or more transcriptional regulators of MHC-I or MHC-II being deleted from at least one allele of the cell.
7. The stem cell of claim 6, wherein the transcriptional regulators of MHC-I or MHC-II are selected from the group consisting of NLRC5, CIITA and B2M.

8. The stem cell of claim 6, wherein the transcriptional regulator of MHC-I or MHC-II comprises NLRC5.
9. The stem cell of claim 6, wherein the transcriptional regulator of MHC-I or MHC-II comprises CIITA.
10. The stem cell of claim 6, wherein the transcriptional regulator of MHC-I or MHC-II comprises B2M.
11. The stem cell of claim 1, further comprising modulated expression of one or more tolerogenic factors relative to a wild-type stem cell.
12. The stem cell of claim 11, wherein the modulated expression of the tolerogenic factors comprises increased expression of the tolerogenic factors.
13. The stem cell of claim 11, wherein the tolerogenic factors are inserted into a safe harbor locus of at least one allele of the cell.
14. The stem cell of claim 11, wherein the safe harbor locus comprises an AAVS1 locus.
15. The stem cell of claim 11, wherein the tolerogenic factors inhibit immune rejection.
16. The stem cell of claim 11, wherein the tolerogenic factors are selected from the group consisting of HLA-C, HLA-E, HLA-G, PD-L1, CTLA-4-Ig, CD47, C1-inhibitor, and IL-35.
17. The stem cell of claims 1-2, wherein the stem cell is an embryonic stem cell.
18. The stem cell of claims 1-2, wherein the stem cell is a pluripotent stem cell.

19. The stem cell of claims 1-2, wherein the stem cell is hypoimmunogenic.
20. The stem cell of claims 1-2, wherein the stem cell is a human stem cell.
21. The stem cell of claims 1-2, wherein the cell does not express one or more of NLRC5, CIITA and B2M.
22. The stem cell of claims 1-2, wherein the cell does not express one or more of HLA-A, HLA-B and HLA-C.
23. The stem cell of claims 1-2, wherein the cell has reduced expression of one or more of HLA-A, HLA-B and HLA-C relative to a wild-type stem cell.
24. A stem cell comprising modulated expression of one or more tolerogenic factors relative to a wild-type human stem cell.
25. The stem cell of claim 24, wherein the modulated expression of the tolerogenic factors comprises increased expression of the tolerogenic factors.
26. The stem cell of claim 24, wherein the tolerogenic factors are inserted into a safe harbor locus of at least one allele of the cell.
27. The stem cell of claim 26, wherein the safe harbor locus comprises an AAVS1 locus.
28. The stem cell of claim 24, wherein the tolerogenic factors inhibit immune rejection.
29. The stem cell of claim 24, wherein the stem cell is an embryonic stem cell.
30. The stem cell of claim 24, wherein the stem cell is a pluripotent stem cell.

31. The stem cell of claim 24, wherein the stem cell is hypoimmunogenic.
32. The stem cell of claim 24, wherein the stem cell is a human stem cell.
33. The stem cell of claim 24, wherein the tolerogenic factors are selected from the group consisting of HLA-C, HLA-E, HLA-G, PD-L1, CTLA-4-Ig, CD47, C1-inhibitor, and IL-35.
34. The stem cell of claim 24, further comprising modulated expression of one or more MHC-I and MHC-II human leukocyte antigens relative to a wild-type stem cell.
35. The stem cell of claim 34, wherein the modulated expression of the one or more MHC-I and MHC-II human leukocyte antigens comprises one or more genes encoding one or more transcriptional regulators of MHC-I or MHC-II deleted from at least one allele of the cell.
36. The stem cell of claim 24, further comprising one or more genes encoding one or more transcriptional regulators of MHC-I or MHC-II deleted from at least one allele of the cell.
37. The stem cell of claims 35-36, wherein the transcriptional regulators of MHC-I or MHC-II are selected from the group consisting of NLRC5, CIITA and B2M.
38. The stem cell of claims 35-36, wherein the transcriptional regulators of MHC-I or MHC-II comprise NLRC5.
39. The stem cell of claims 35-36, wherein the transcriptional regulators of MHC-I or MHC-II comprise CIITA.

40. The stem cell of claims 35-36, wherein the transcriptional regulators of MHC-I or MHC-II comprise B2M.
41. A human stem cell that does not express NLRC5.
42. The cell of claim 41, wherein the cell is a *NLRC5*^{-/-} knockout stem cell.
43. A human stem cell that does not express CIITA.
44. The cell of claim 43, wherein the cell is a *CIITA*^{-/-} knockout stem cell.
45. A human stem cell that does not express B2M.
46. The cell of claim 45, wherein the cell is a *B2M*^{-/-} knockout stem cell.
47. A human stem cell that does not express one or more of NLRC5, CIITA and B2M.
48. A human stem cell that does not express one or more of HLA-A, HLA-B and HLA-C.
49. The cell of claims 41-48, wherein the cell expresses one or more tolerogenic factors.
50. The cell of claim 49, wherein the tolerogenic factors inhibit immune rejection.
51. The cell of claim 49, wherein the tolerogenic factors are inserted into a safe harbor locus of at least one allele of the cell.
52. The cell of claims 51, wherein the safe harbor locus comprises an AAVS1 locus.

53. The cell of claim 51, wherein the tolerogenic factors are selected from the group consisting of HLA-C, HLA-E, HLA-G, PD-L1, CTLA-4-Ig, CD47, C1-inhibitor, and IL-35.
54. The cell of claims 41-48, wherein the cell is an embryonic stem cell.
55. The cell of claims 41-48, wherein the cell is a pluripotent stem cell.
56. The cell of claims 41-48, where in the stem cell is hypoinmunogenic.
57. The cell of claims 41-48, wherein the cell has reduced MHC-I expression relative to a wild-type human stem cell.
58. The cell of claims 41-48, wherein the cell has reduced MHC-II expression relative to a wild-type human stem cell.
59. The cell of claims 41-48, wherein the cell has reduced expression of one or more of HLA-A, HLA-B and HLA-C relative to a wild-type human stem cell.
60. A method of using the cell of claims 41-48 for cell replacement therapy.
61. A human stem cell comprising one or more tolerogenic factors inserted into a safe harbor locus of at least one allele of the cell.
62. The cell of claim 61, wherein the tolerogenic factors inhibit immune rejection.
63. The cell of claim 61, wherein the tolerogenic factors are selected from the group consisting of HLA-C, HLA-E, HLA-G, PD-L1, CTLA-4-Ig, CD47, C1-inhibitor, and IL-35.
64. The cell of claim 61, wherein the safe harbor locus comprises an AAVS1 locus.

65. The cell of claim 61, wherein the cell does not express one or more of NLRC5, CIITA and B2M.
66. The cell of claim 61, wherein the cell does not express one or more of HLA-A, HLA-B and HLA-C.
67. The cell of claim 61, wherein the cell has reduced expression of one or more of HLA-A, HLA-B and HLA-C relative to a wild-type human stem cell.
68. A method of preparing a hypoinmunogenic stem cell, the method comprising modulating expression of one or more MHC-I and MHC-II human leukocyte antigens by the stem cell and thereby preparing the hypoinmunogenic stem cell.
69. A method of modulating expression of one or more MHC-I and MHC-II human leukocyte antigens by a stem cell, comprising deleting one or more genes encoding one or more transcriptional regulators of MHC-I or MHC-II from at least one allele of the cell and thereby modulating expression of the one or more MHC-I and MHC-II human leukocyte antigens.
70. The method of claims 68-69, wherein the modulating expression of the one or more MHC-I and MHC-II human leukocyte antigens comprises reducing expression of the one or more MHC-I and MHC-II human leukocyte antigens.
71. The method of claims 68-69, wherein the modulating expression of the one or more MHC-I and MHC-II human leukocyte antigens comprises inhibiting expression of the one or more MHC-I and MHC-II human leukocyte antigens.
72. The method of claims 68-69, wherein the modulating expression of the one or more MHC-I and MHC-II human leukocyte antigens comprises interfering

with expression of the one or more MHC-I and MHC-II human leukocyte antigens.

73. The method of claim 68, wherein the modulating expression of the one or more MHC-I and MHC-II human leukocyte antigens comprises deleting one or more genes encoding one or more transcriptional regulators of MHC-I or MHC-II from at least one allele of the cell.
74. The method of claim 73, wherein the transcriptional regulators of MHC-I or MHC-II are selected from the group consisting of NLRC5, CIITA and B2M.
75. The method of claim 73, wherein the transcriptional regulator of MHC-I or MHC-II comprises NLRC5.
76. The method of claim 73, wherein the transcriptional regulator of MHC-I or MHC-II comprises CIITA.
77. The method of claim 73, wherein the transcriptional regulator of MHC-I or MHC-II comprises B2M.
78. The method of claim 68, further comprising modulating expression of one or more tolerogenic factors by the stem cell.
79. The method of claim 78, wherein the modulating expression of the tolerogenic factors comprises increasing the expression of the tolerogenic factors.
80. The method of claim 78, wherein the tolerogenic factors are inserted into a safe harbor locus of at least one allele of the cell.
81. The method of claim 78, wherein the safe harbor locus comprises an AAVS1 locus.

82. The method of claim 78, wherein the tolerogenic factors inhibit immune rejection.
83. The method of claim 78, wherein the tolerogenic factors are selected from the group consisting of HLA-C, HLA-E, HLA-G, PD-L1, CTLA-4-Ig, CD47, C1-inhibitor, and IL-35.
84. A method of preparing a hypoimmunogenic stem cell, the method comprising modulating expression of one or more tolerogenic factors by the stem cell and thereby preparing the hypoimmunogenic stem cell.
85. The method of claim 84, wherein the modulating expression of the tolerogenic factors comprises increasing the expression of the tolerogenic factors.
86. The method of claim 84, wherein the tolerogenic factors are inserted into a safe harbor locus of at least one allele of the cell.
87. The method of claim 86, wherein the safe harbor locus comprises an AAVS1 locus.
88. The method of claim 84, wherein the tolerogenic factors inhibit immune rejection.
89. The method of claim 84, wherein the tolerogenic factors are selected from the group consisting of HLA-C, HLA-E, HLA-G, PD-L1, CTLA-4-Ig, CD47, C1-inhibitor, and IL-35.
90. The method of claim 84, further comprising modulating expression of one or more MHC-I and MHC-II human leukocyte antigens by the cell.
91. The method of claim 90, wherein the modulating expression of the one or more MHC-I and MHC-II human leukocyte antigens comprises deleting one

or more genes encoding one or more transcriptional regulators of MHC-I or MHC-II from at least one allele of the cell.

92. The method of claim 84, further comprising deleting one or more genes encoding one or more transcriptional regulators of MHC-I or MHC-II from at least one allele of the cell.
93. The method of claims 91-92, wherein the transcriptional regulators of MHC-I or MHC-II from are selected from the group consisting of NLRC5, CIITA and B2M.
94. The method of claims 91-92, wherein the transcriptional regulators of MHC-I or MHC-II from comprise NLRC5.
95. The method of claims 91-92, wherein the transcriptional regulators of MHC-I or MHC-II from comprise CIITA.
96. The method of claims 91-92, wherein the transcriptional regulators of MHC-I or MHC-II from comprise B2M.
97. A hypoimmunogenic stem cell comprising a modified genome comprising a first genomic modification in which the NLRC5 gene has been edited to reduce or eliminate NLRC5 surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 36353-81239.
98. A hypoimmunogenic stem cell comprising a modified genome comprising a first genomic modification in which the CIITA gene has been edited to reduce or eliminate CIITA surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a

ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 5184-36352.

99. A hypoimmunogenic stem cell comprising a modified genome comprising a first genomic modification in which the B2M gene has been edited to reduce or eliminate B2M surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 81240-85644.
100. A hypoimmunogenic stem cell comprising a modified genome comprising:
 - (a) a first genomic modification in which the NLRC5 gene has been edited to reduce or eliminate NLRC5 surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 36353-81239;
 - (b) a second genomic modification in which the CIITA gene has been edited to reduce or eliminate CIITA surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 5184-36352; and/or
 - (c) a third genomic modification in which the B2M gene has been edited to reduce or eliminate B2M surface expression and/or activity in the cell by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 81240-85644.
101. A hypoimmunogenic stem cell comprising a modified genome comprising a first genomic modification in which the NLRC5 gene has been edited to delete a first contiguous stretch of genomic DNA, thereby reducing or eliminating NLRC5 surface expression and/or activity in the cell, wherein the first contiguous stretch of genomic DNA has been deleted by contacting the cell

with a Cas protein or a nucleic acid encoding a Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 36353-81239.

102. A hypoimmunogenic stem cell comprising a modified genome comprising a first genomic modification in which the CIITA gene has been edited to delete a first contiguous stretch of genomic DNA, thereby reducing or eliminating CIITA surface expression and/or activity in the cell, wherein the first contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 5184-36352.
103. A hypoimmunogenic stem cell comprising a modified genome comprising a first genomic modification in which the B2M gene has been edited to delete a first contiguous stretch of genomic DNA, thereby reducing or eliminating B2M surface expression and/or activity in the cell, wherein the first contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 81240-85644.
104. A hypoimmunogenic stem cell comprising a modified genome comprising:
 - (a) a first genomic modification in which the NLRC5 gene has been edited to delete a first contiguous stretch of genomic DNA, thereby reducing or eliminating NLRC5 surface expression and/or activity in the cell, wherein the first contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 36353-81239;
 - (b) a second genomic modification in which the CIITA gene has been edited to delete a first contiguous stretch of genomic DNA, thereby reducing

or eliminating CIITA surface expression and/or activity in the cell, wherein the first contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 5184-36352; and/or

(c) a third genomic modification in which the B2M gene has been edited to delete a first contiguous stretch of genomic DNA, thereby reducing or eliminating B2M surface expression and/or activity in the cell, wherein the first contiguous stretch of genomic DNA has been deleted by contacting the cell with a Cas protein or a nucleic acid encoding a Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 81240-85644.

105. A method for producing a hypoinmunogenic stem cell, the method comprising contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 36353-81239, thereby editing the NLRC5 gene to reduce or eliminate NLRC5 surface expression and/or activity in the cell.
106. A method for producing a hypoinmunogenic stem cell, the method comprising contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 5184-36352, thereby editing the CIITA gene to reduce or eliminate CIITA surface expression and/or activity in the cell.
107. A method for producing a hypoinmunogenic stem cell, the method comprising contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 81240-85644,

thereby editing the B2M gene to reduce or eliminate B2M surface expression and/or activity in the cell.

108. A method for producing a hypoinmunogenic stem cell, the method comprising:
 - (a) contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a first pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 36353-81239, thereby editing the NLRC5 gene to reduce or eliminate NLRC5 surface expression and/or activity in the cell;
 - (b) contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a second pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 5184-36352, thereby editing the CIITA gene to reduce or eliminate CIITA surface expression and/or activity in the cell; and/or
 - (c) contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a third pair of ribonucleic acids having sequences selected from the group consisting of SEQ ID NOs: 81240-85644, thereby editing the B2M gene to reduce or eliminate B2M surface expression and/or activity in the cell
109. A method for producing a hypoinmunogenic stem cell, the method comprising contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a first ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 36353-81239, thereby editing the NLRC5 gene to reduce or eliminate NLRC5 surface expression and/or activity in the cell.
110. A method for producing a hypoinmunogenic stem cell, the method comprising contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a first ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 5184-36352,

thereby editing the CIITA gene to reduce or eliminate CIITA surface expression and/or activity in the cell.

111. A method for producing a hypoinmunogenic stem cell, the method comprising contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a first ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 81240-85644, thereby editing the B2M gene to reduce or eliminate B2M surface expression and/or activity in the cell.
112. A method for producing a hypoinmunogenic stem cell, the method comprising:
 - (a) contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a first ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 36353-81239, thereby editing the NLRC5 gene to reduce or eliminate NLRC5 surface expression and/or activity in the cell;
 - (b) contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a second ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 5184-36352, thereby editing the CIITA gene to reduce or eliminate CIITA surface expression and/or activity in the cell; and/or
 - (c) contacting a stem cell with a Cas protein or a nucleic acid sequence encoding the Cas protein and a third ribonucleic acid having a sequence selected from the group consisting of SEQ ID NOs: 81240-85644, thereby editing the B2M gene to reduce or eliminate B2M surface expression and/or activity in the cell.

The Promise of Regenerative Medicine

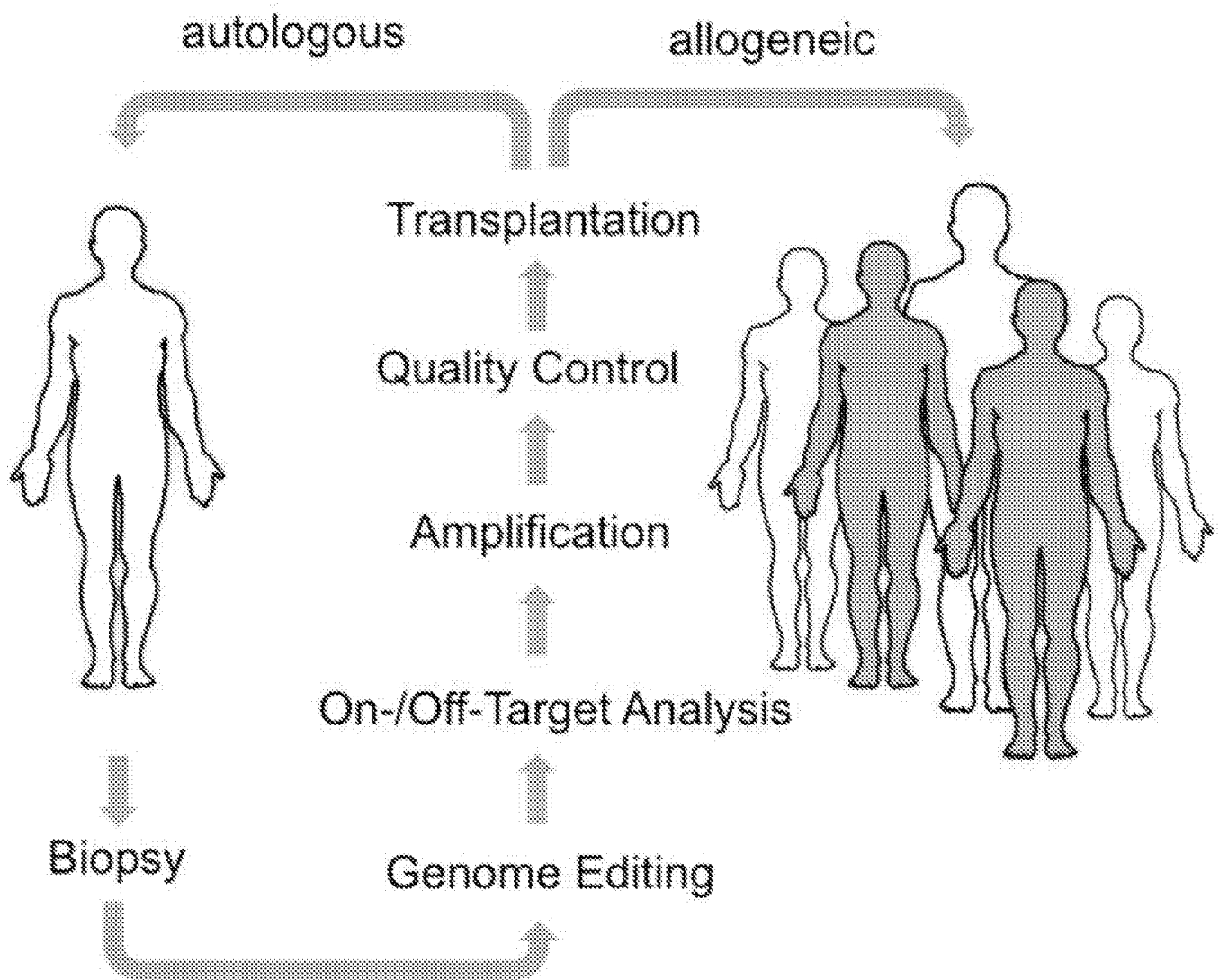
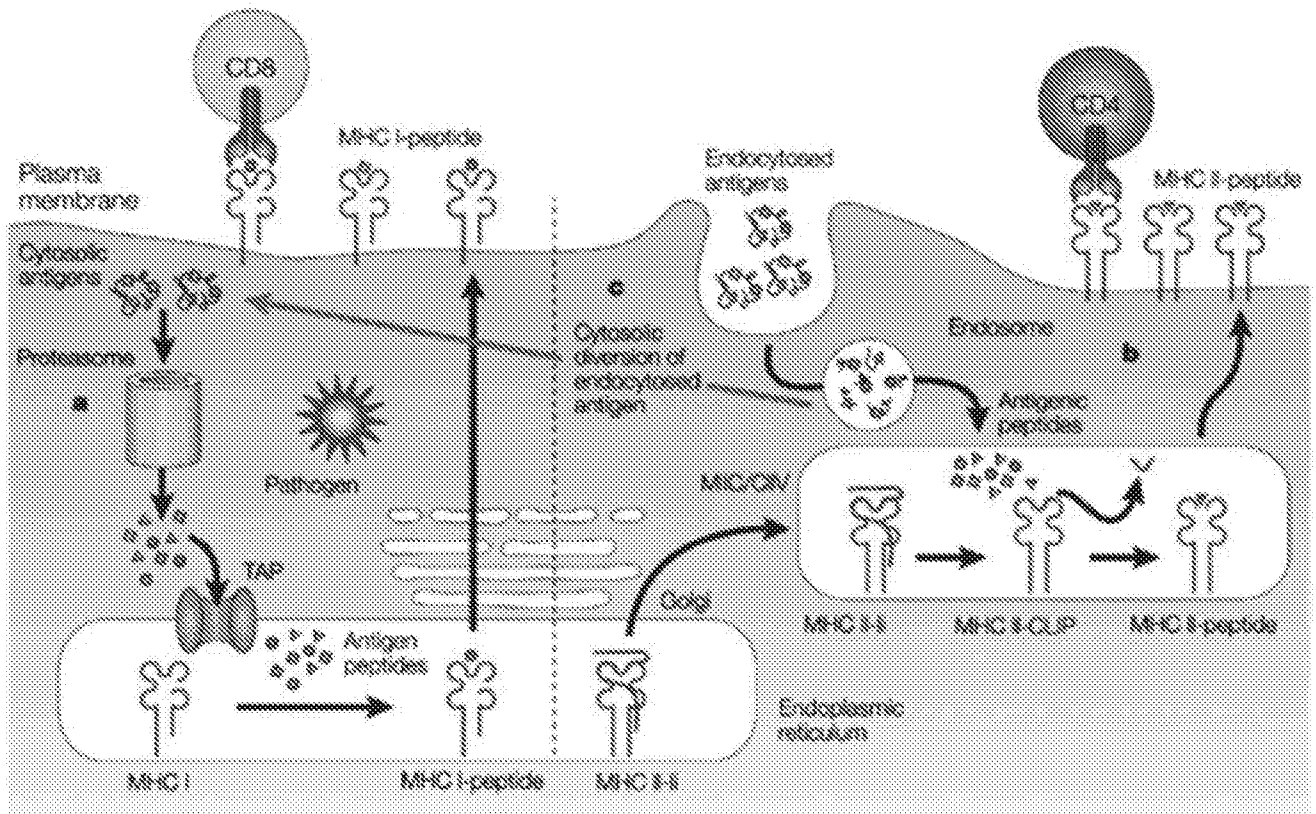


FIG. 1

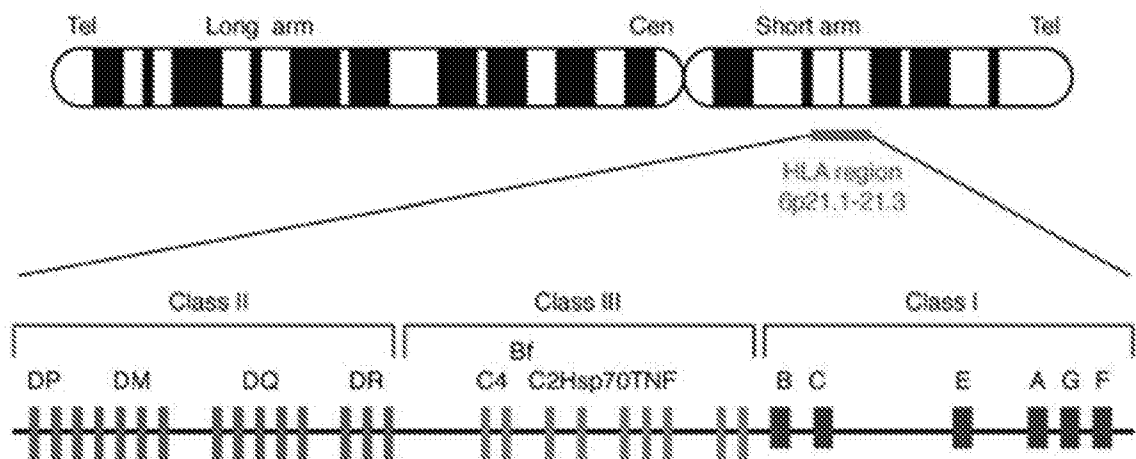
The HLA Barrier in Transplantation

2 **A**



Heath & Carbone, 2011 Nature Reviews Immunology

2 **B**

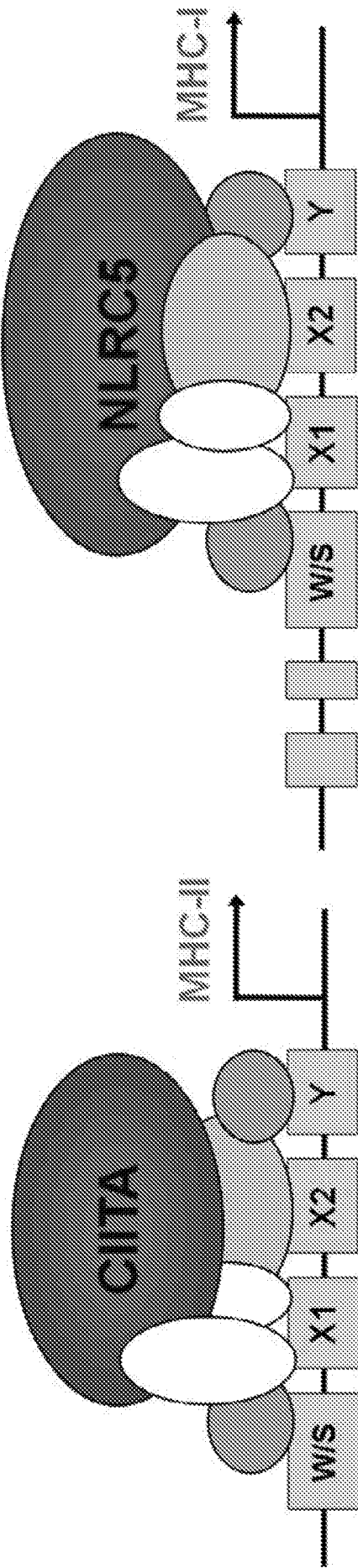


Expert Reviews in Molecular Medicine 2003, Cambridge University press

FIGS. 2A-2B

3 A

3 B



Steimle et al., 1993 Cell

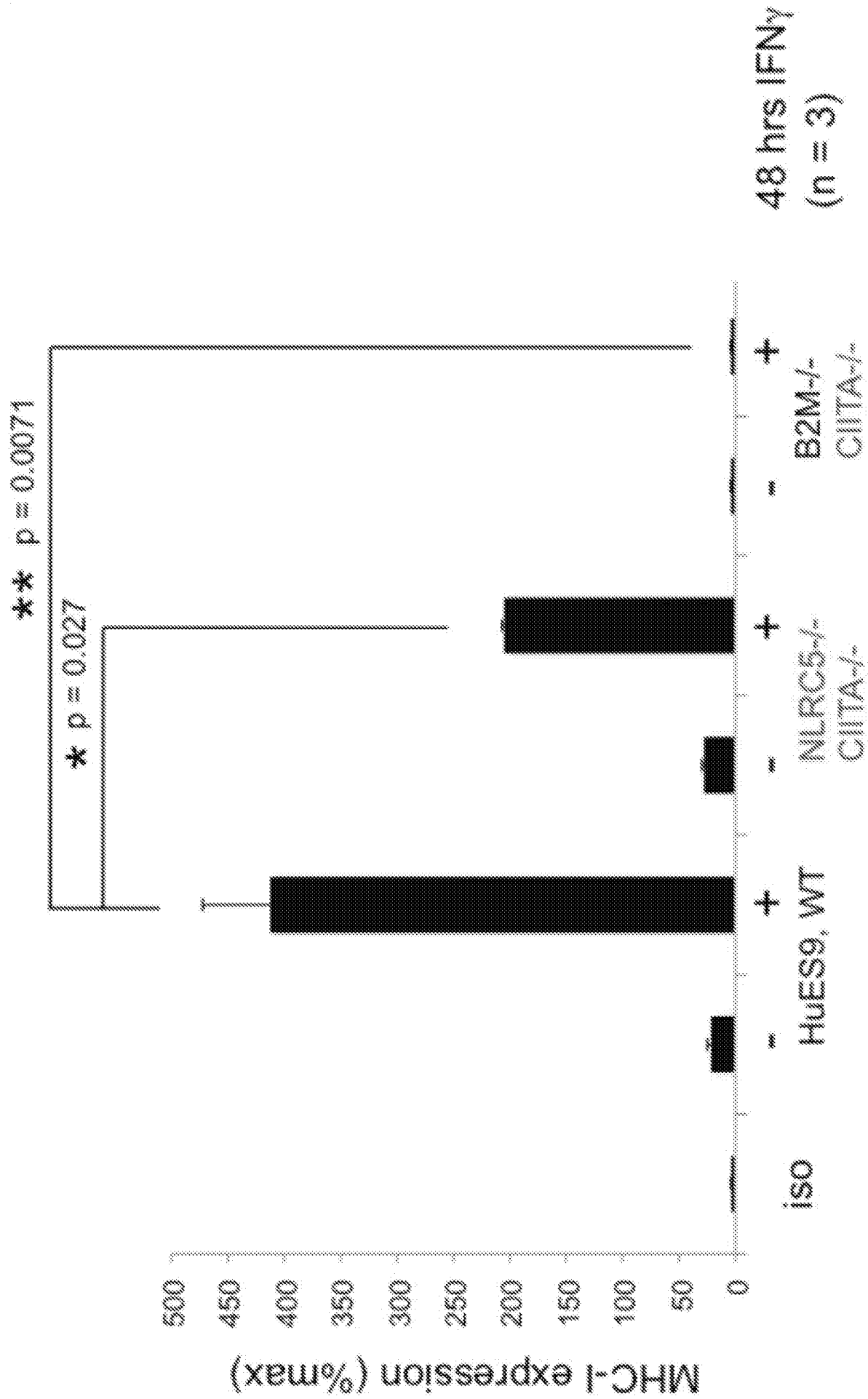
Meissner et al., 2012 J Immunology

Biswas and Meissner et al., 2012 J Immunology

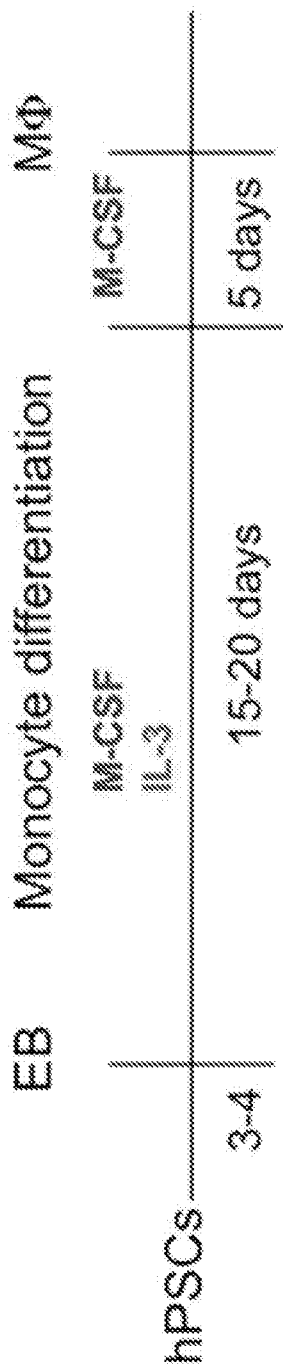
Meissner et al., 2012 Microbes&Infection

Meissner et al., 2010 PNAS

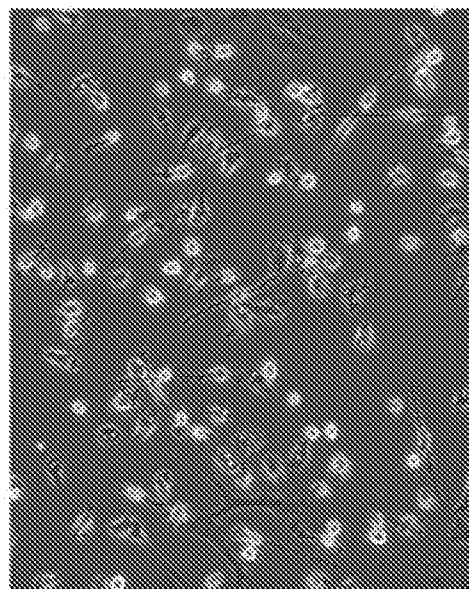
FIGS. 3A-3B

**FIG. 4**

5 A

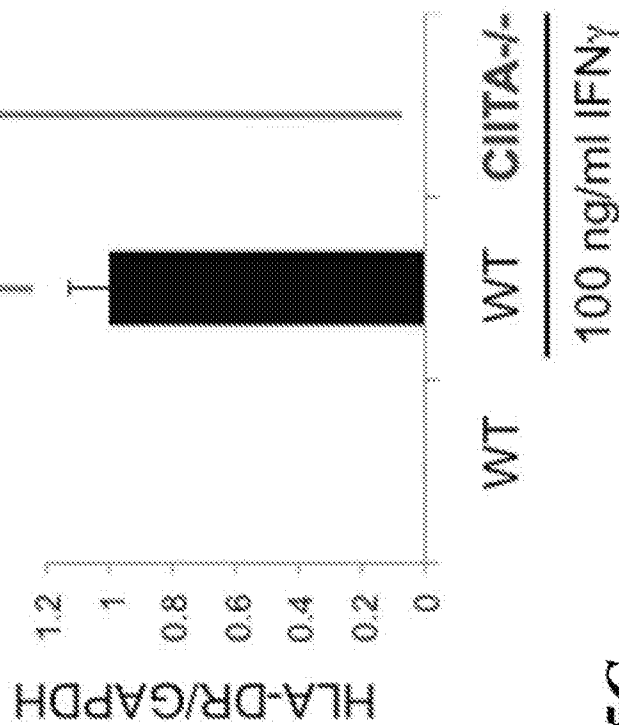


5 B

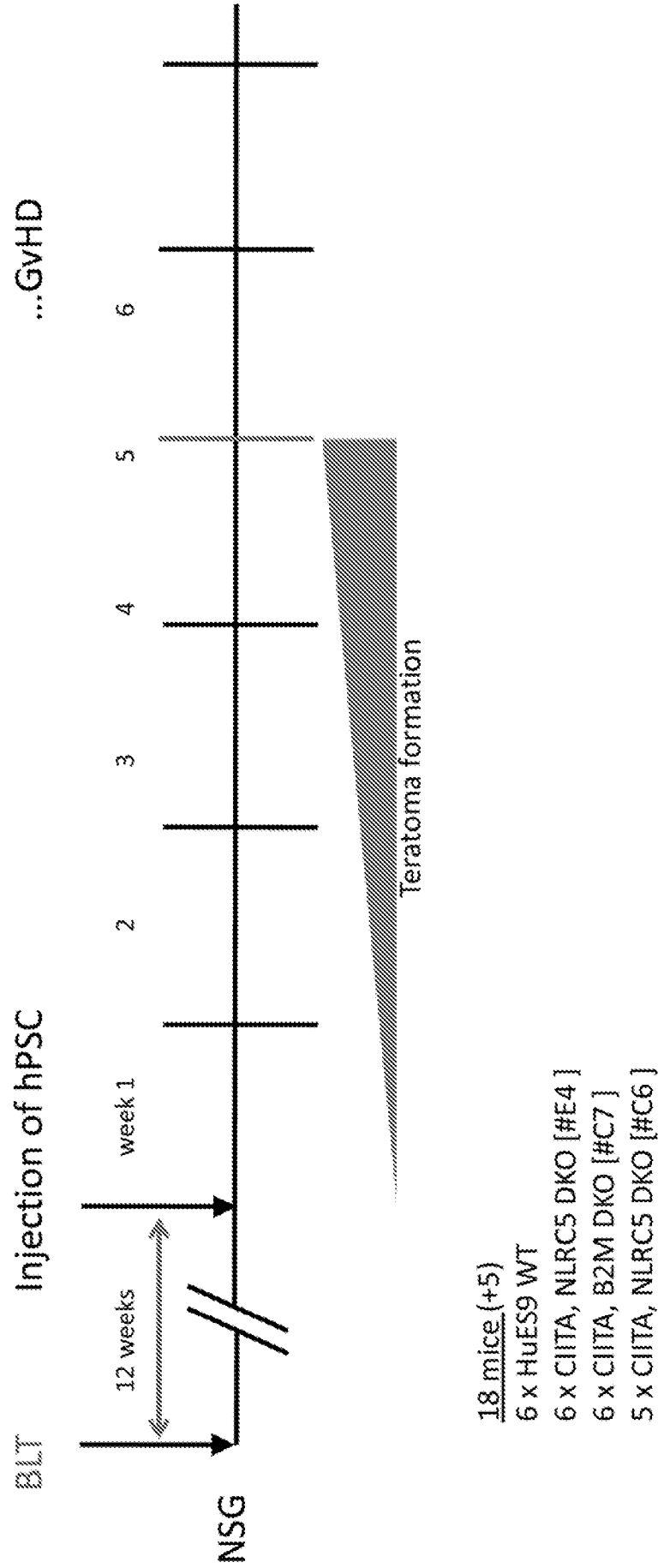


65% CD11b+ CD14+

5 C

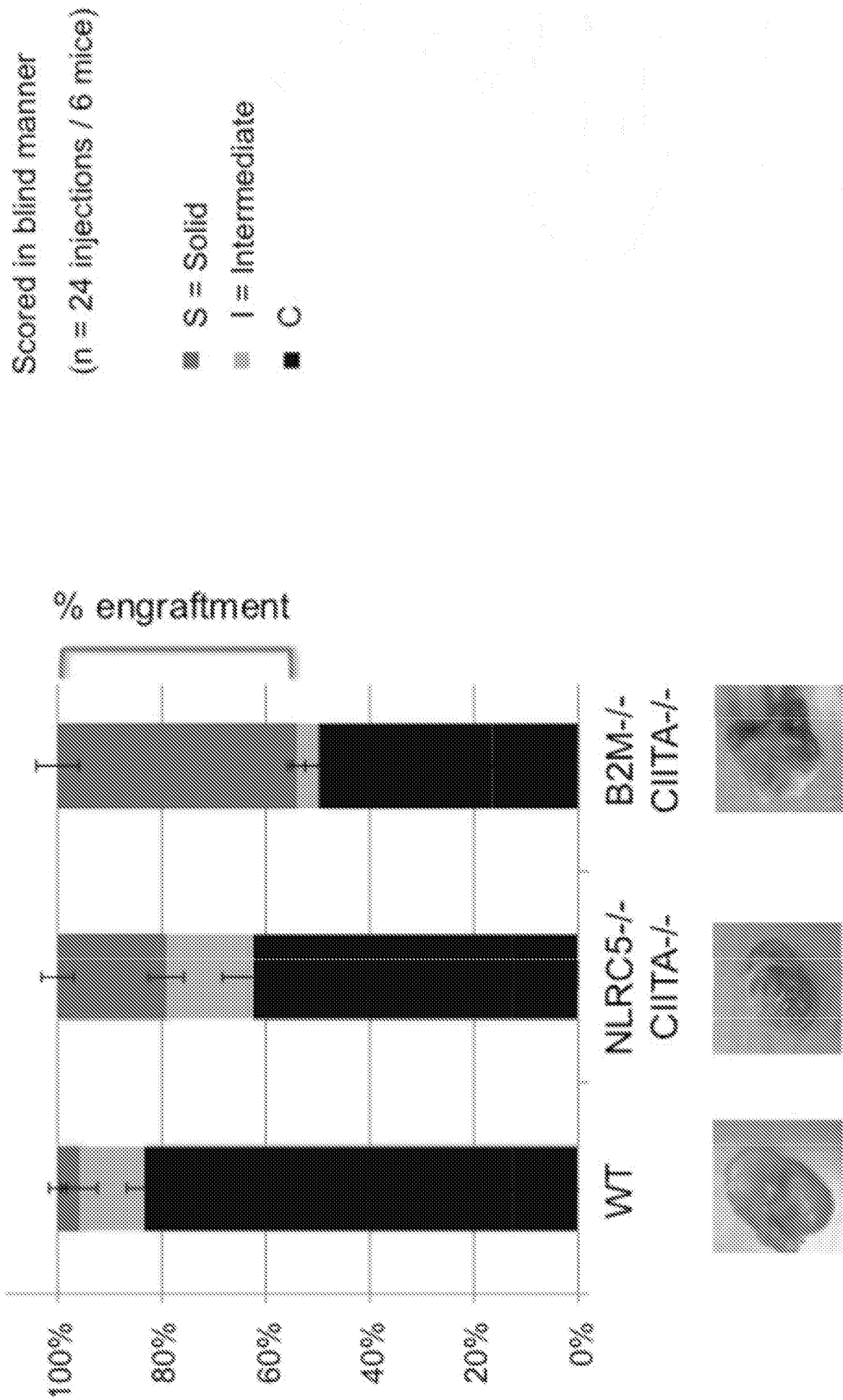


FIGS. 5A-5C

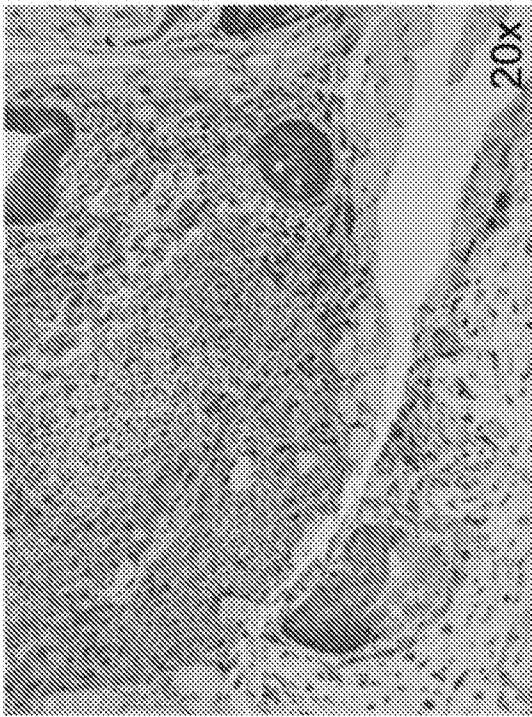


SubQ injection
0.5-1 x 10⁶ cells in Matrigel /injection
4 x /mouse => 24 teratomas /group

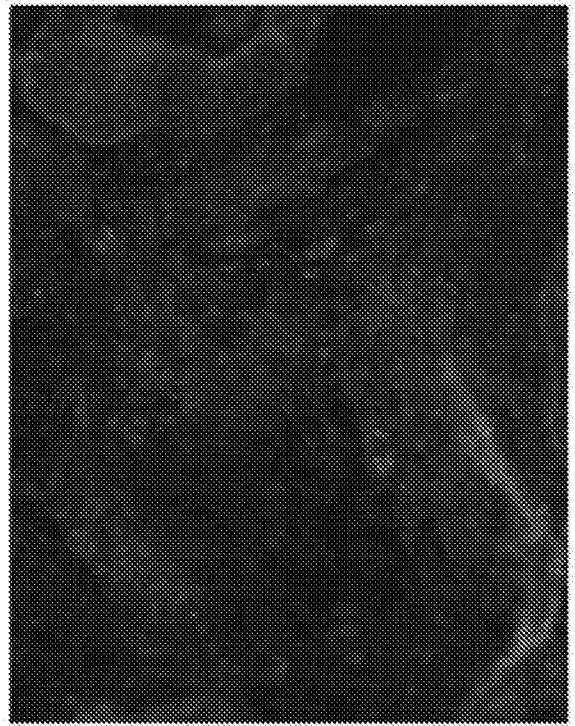
FIG. 6

**FIG. 7**

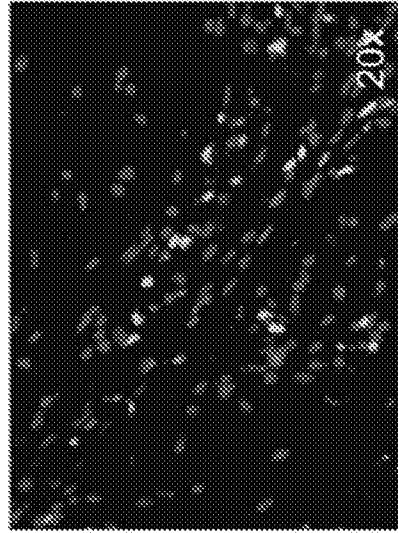
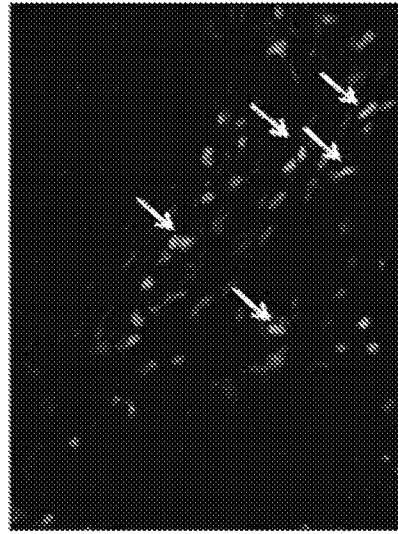
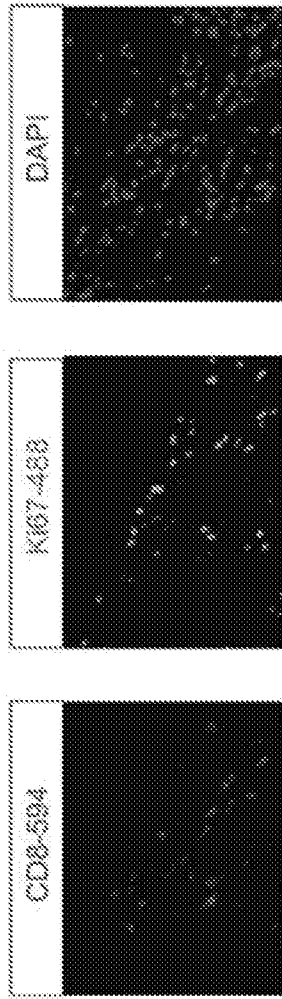
8A
 α -CD3-HRP



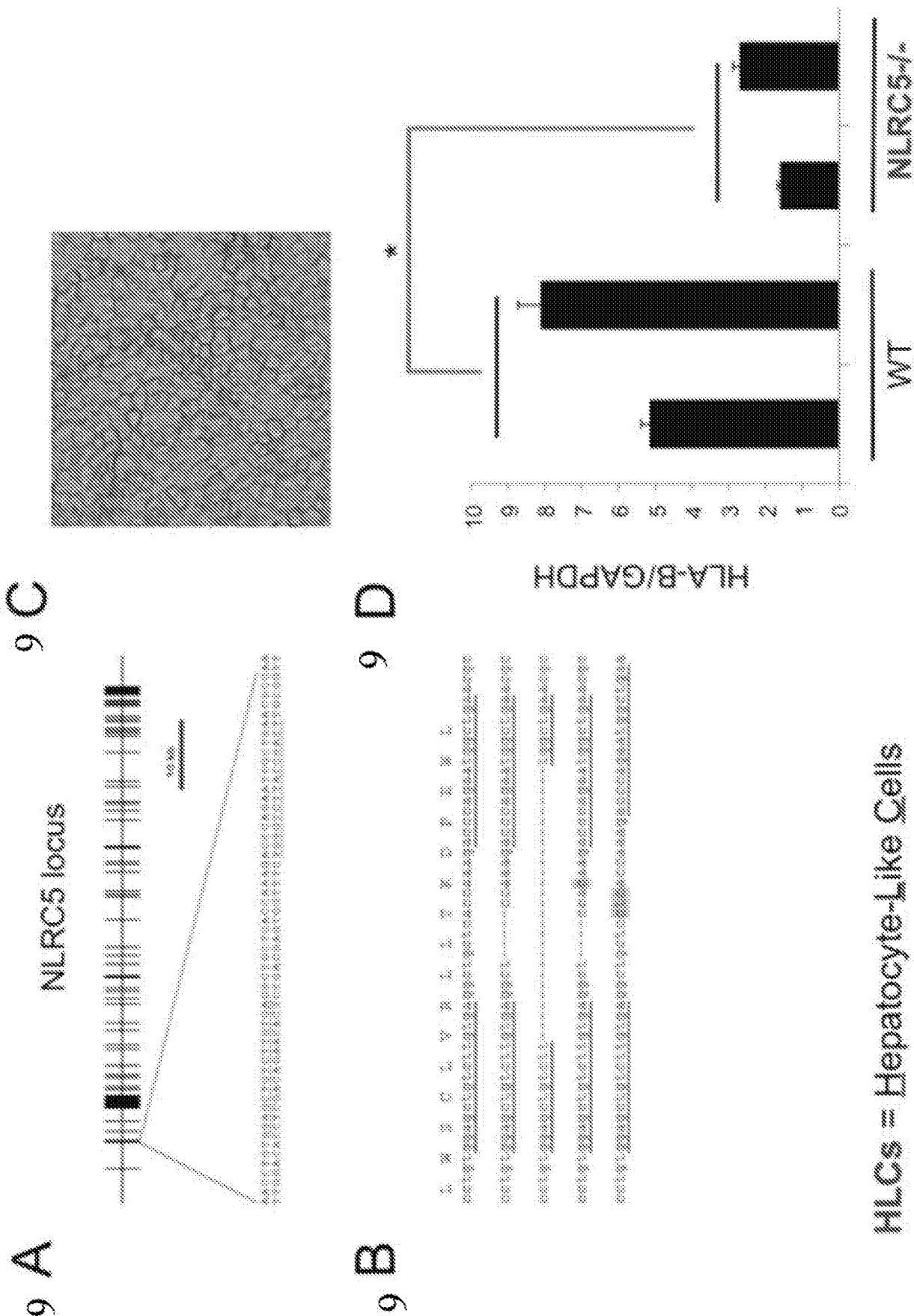
8B
 α -CD3-488



8C



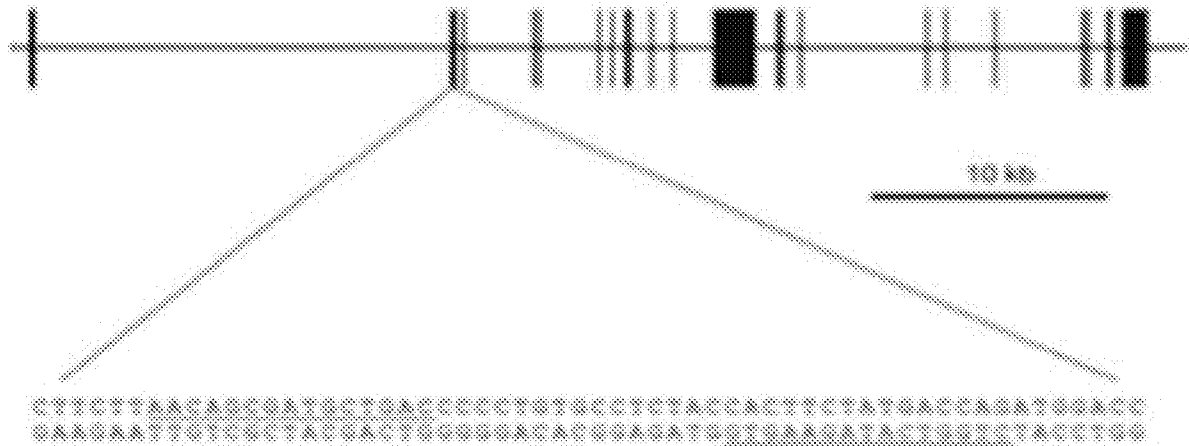
FIGS. 8A-8C



HLCs = Hepatocyte-Like Cells
derived from BJ-RIPSCs,
day 7 of final hepatocyte differentiation

FIGS. 9A-9D

CIITA locus

[illegible]

FIGS. 10A-10B

1 MDKKYSIGLD IGTNSVGWAV ITDEYKVPSK KFKVLGNTDR HSIKKNLIGA LLFDSGETAE
 61 ATRLKERTARR RYTRRKNRIC YLQEIFSNEK AKVDDSFHHR LEESFLVEED KKHHRHPHFG
 121 NIVDEVAYHE KYPTIYHLRK KLYVSTDKAD LRLIYLALAH MIKFRGHFLI EGDLPDNDSD
 181 VDKLFIQLVQ TYNQLFEENP INASGVDAKA ILSARLSKSR RLENLIAQLP GEKKNGLFGN
 241 LIALSLGLTP NFKSNFDLAE DAKLQLSKDT YDDDLNLLA QIGDQYADLF LAAKNLSDAI
 301 LLSDLRVNT EITKAPLSAS MIKRYDEHHQ DLTLLKALVR QQLPEKYKEI PFDQSKNOYA
 361 GYIDOGASQE EFYKFIKPIL EKMDOTEELL VKLNREDLLR KQRTFDNGSI PHQIHLGELH
 421 AILRRQEDFY PFLKDNREKI EKILTRIPY YVGPLARGNS RFAWMTRKSE ETITPWNFEE
 481 VVDKGASAQ S FIERMTNFDK NLPNEKVLPK HSLLEYFTV YNELTKVKYV TEGMRKPAFL
 541 SGEQKKAIVD LLFKNRNVK VKQLKEDYFK KIECFDSVEI SGVEDRFNAS LGTYHDLKI
 601 IKDKDFLDNE ENEDILEDIV LTLTLFEDRE MIEERLKYA HLFDDKVMKQ LKRRRYTGWO
 661 RLSRKLINGI RDKQSGKITL DFLKSDGFAN RNFMQLIHDD SLTFKEDIQK AQVSGQGDSL
 721 HEHIANLAGS PAIKKGILQT VKVVDLVKV MGRHKPENIV IEMARENOTT QKGQKNSRER
 781 MKRIEEGIKE LGSQILKEHP VENTOLONEK LYL YYLONGR DMYVDOELDI NRLSDYDVH
 841 IVPOSFLKDD SIDNKVLT RS DKNRGKSDNV PSEEVVKKMK NYWRQLLNAK LITQRKFDNL
 901 TKAERGGLSE LDKAGFIKQ LVETRQITKH VAQILDSRMN TKYDENDKLI REVKVITLKS
 961 KLVSDFRKDF QFYKVRINN YHHHARDAYLN AVVGITALIKK YPKLESEFVY GDYKVYDVRK
 1021 MIAKSEQEIG KATAKYFFYS NIMNFFKTEI TLANGEIRKR PLIETNOETG EIVWDKGRDF
 1081 ATVRKVL SMP QVNIVKKTEV QTGGFSKESI LPKRNSDKLI ARKKDWDPKK YGGFDSPTVA
 1141 YSVLVVAKVE KGSKKLKS SV KELLGITIME RSSFEKNPID FLEAKGYKEV KKDIIKLKPK
 1201 YSLFELENGR KRMLASAGEL QKGNELALPS KYVNFLYLAS HYEKLKGSPE DNEQKQLFVE
 1261 QHKHYLDEII EQISEFSKRV ILADANLDKV LSAYNKHRDK PIREQAENII HLFTLTNLGA
 1321 PAAFKYFDTT IDRKYRSTK EVLDATLIHQ SITGLYETRI DLSQLGGD (SEQ ID NO: 1)

FIG. 12

Comparison of the MHC-II and MHC-I Enhanceosomes

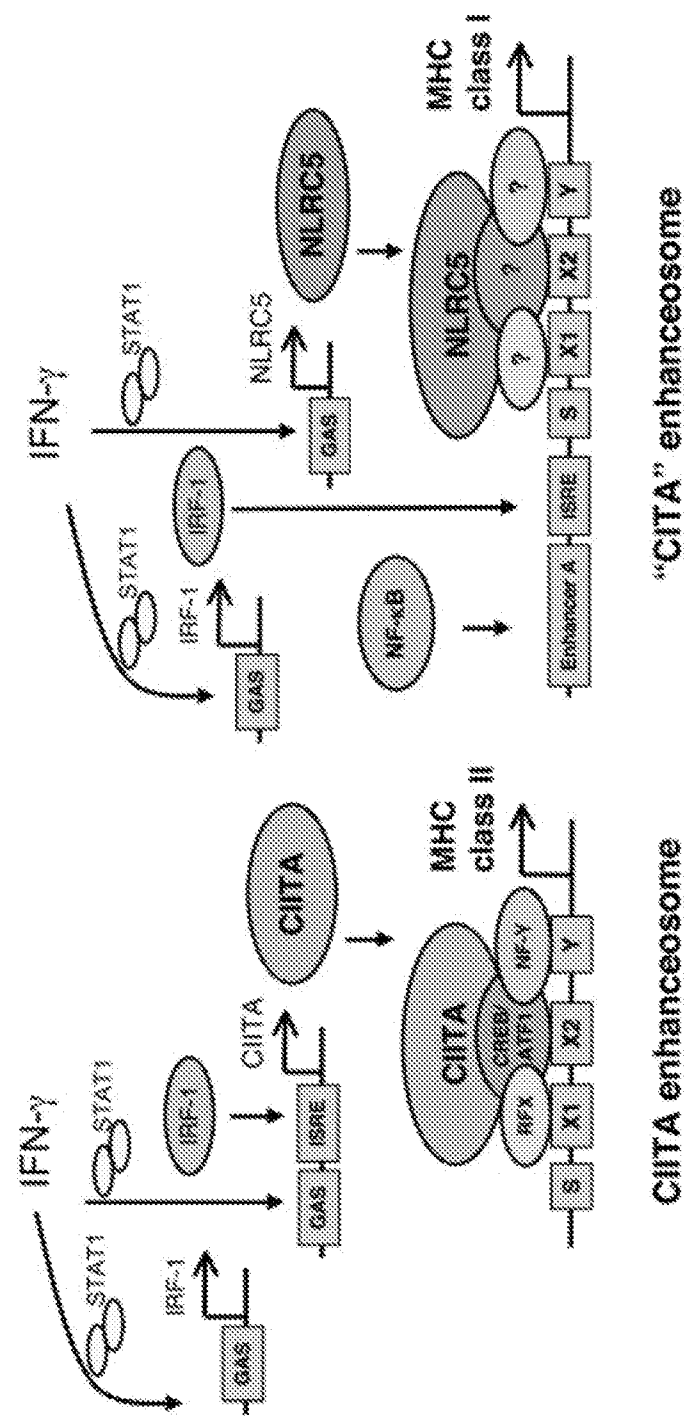
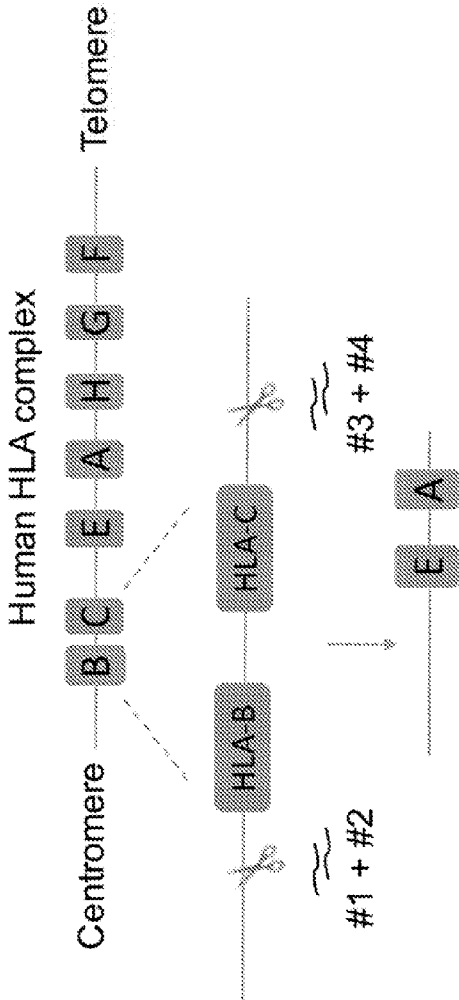


FIG. 13

Meissner et al., 2011 Microbes&Infection

HLA-B and HLA-C knock-out strategy



CRISPR sgRNA sequences:

- sgRNA #1: ATCCCTAAATATGGTGCCC
- sgRNA #2: TCCCTAAATATGGTGCCCT
- sgRNA #3: GTGATCCGGGTATGGGCAGT
- sgRNA #4: TGATCCGGGTATGGGCAGTG

FIG. 14A

PCR screening confirms clone 1D as a homozygous knock-out clone

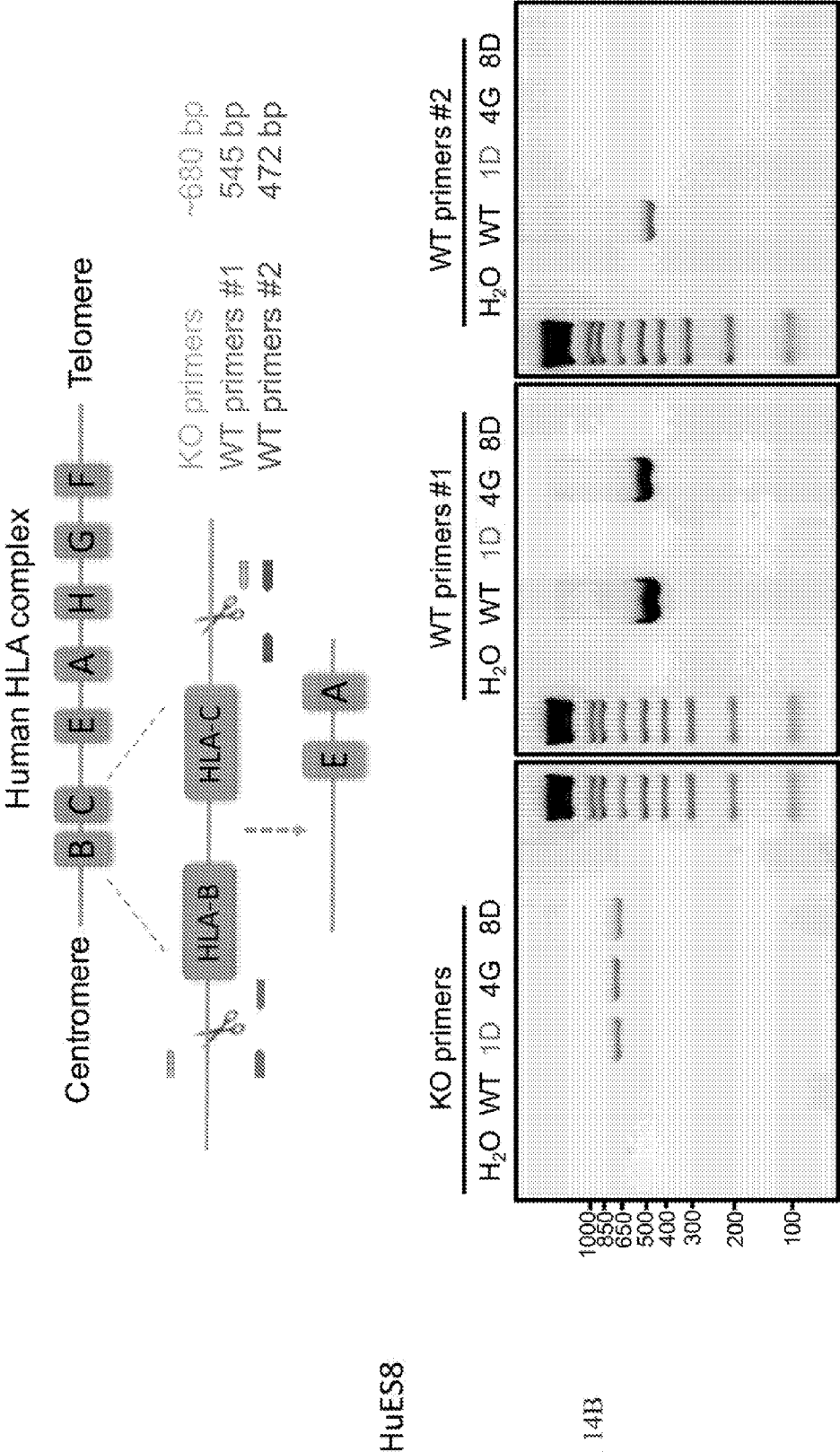
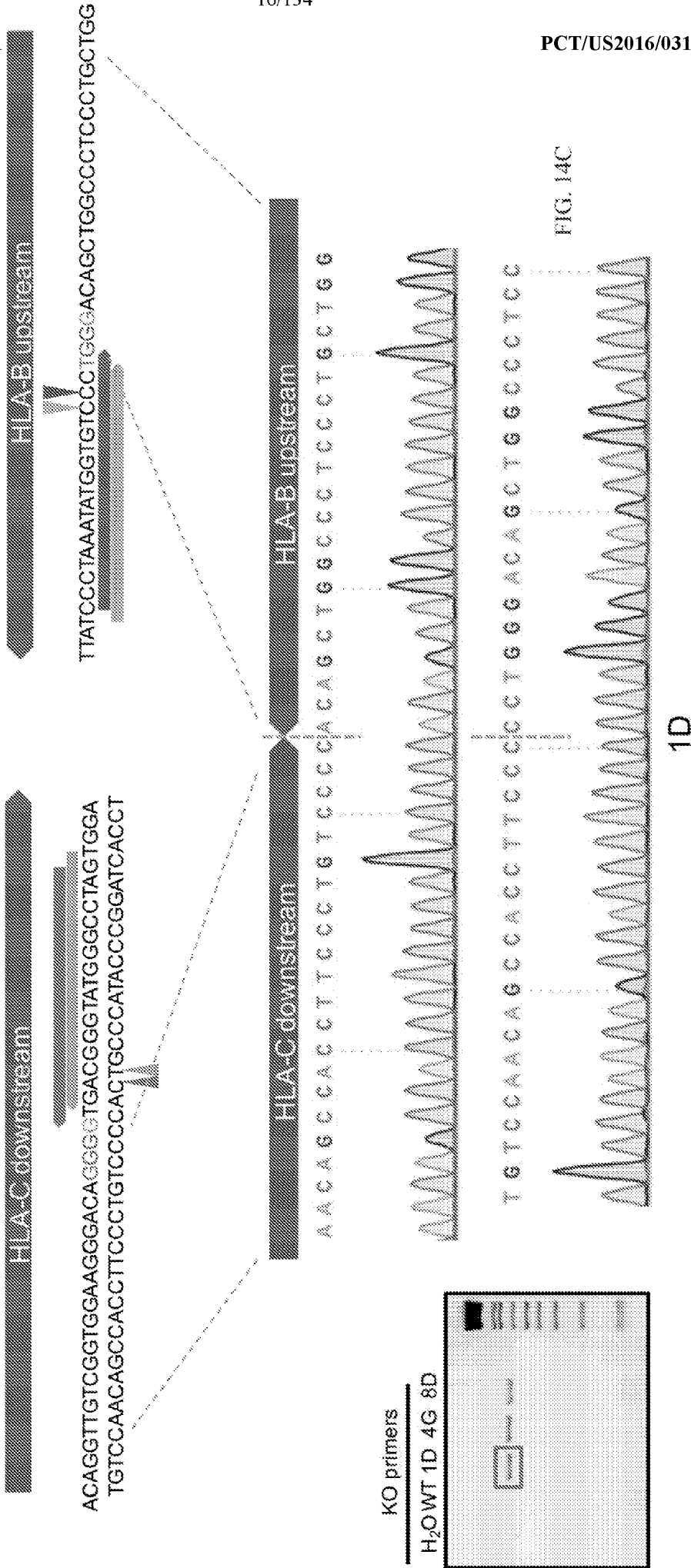


FIG. 14B

Sequence confirmation of HLA-B, -C deletion in 1D KO clone



RT-PCR confirms loss of HLA-B and HLA-C mRNA expression in HuES8

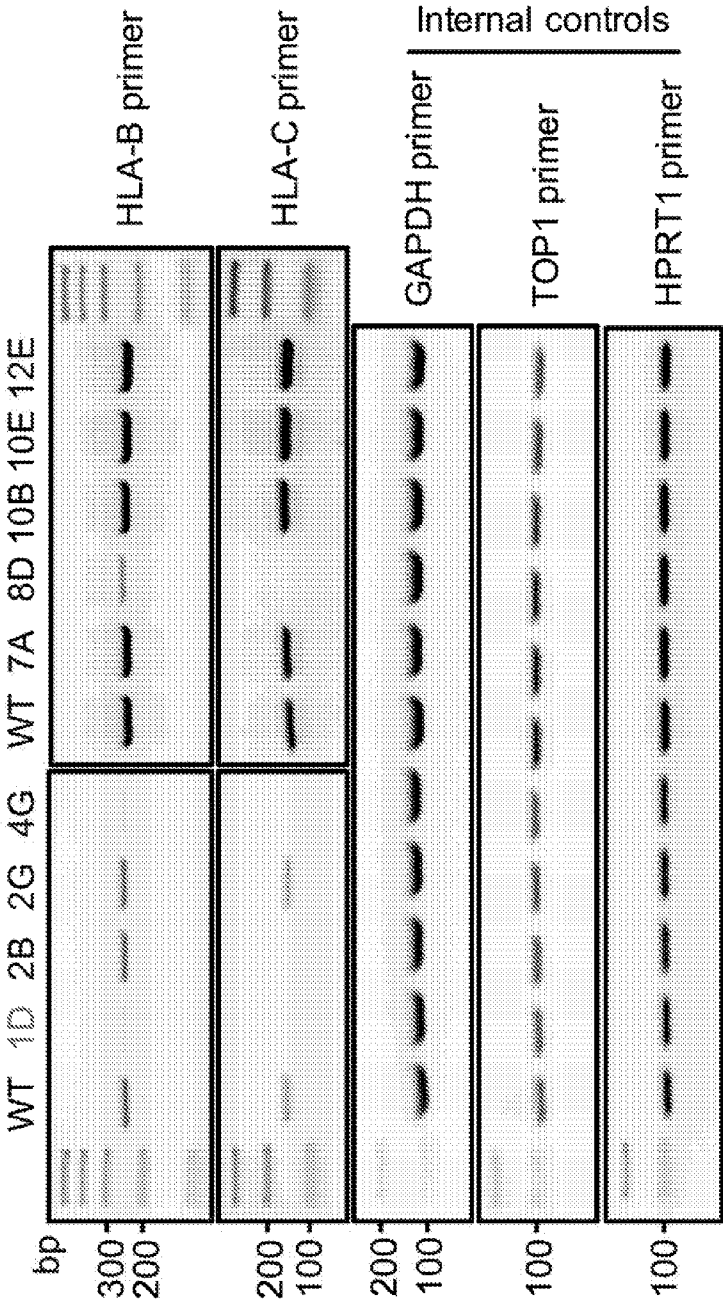


FIG. 14D

Non-specific amplification

Karyotyping of HuES8 clone 1D by NanoString nCounter

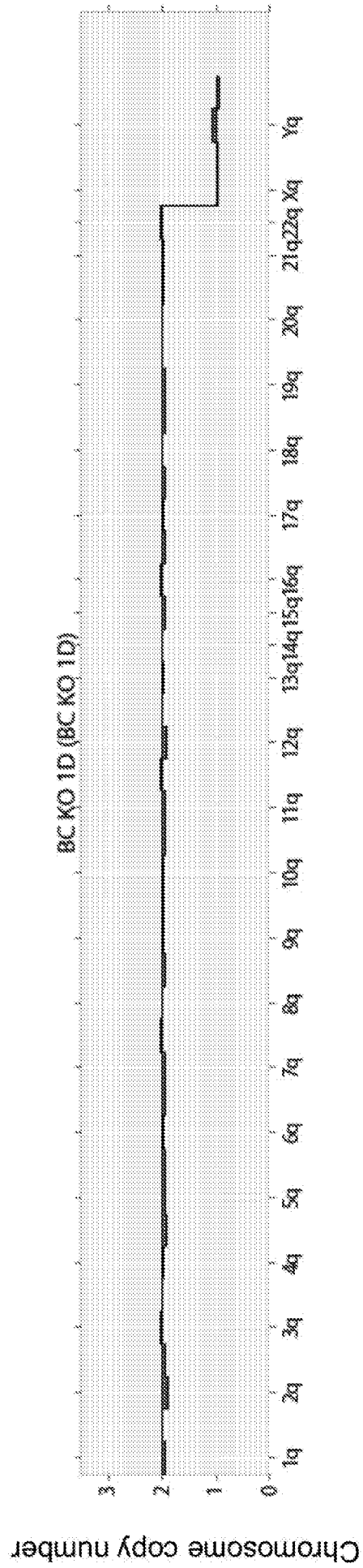
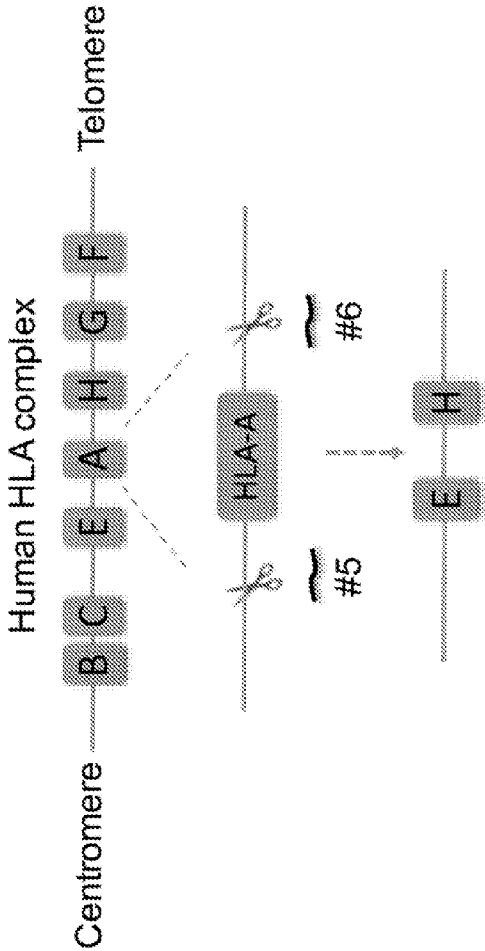


FIG. 14F

HLA-A knockout strategy using the dual sgRNA approach

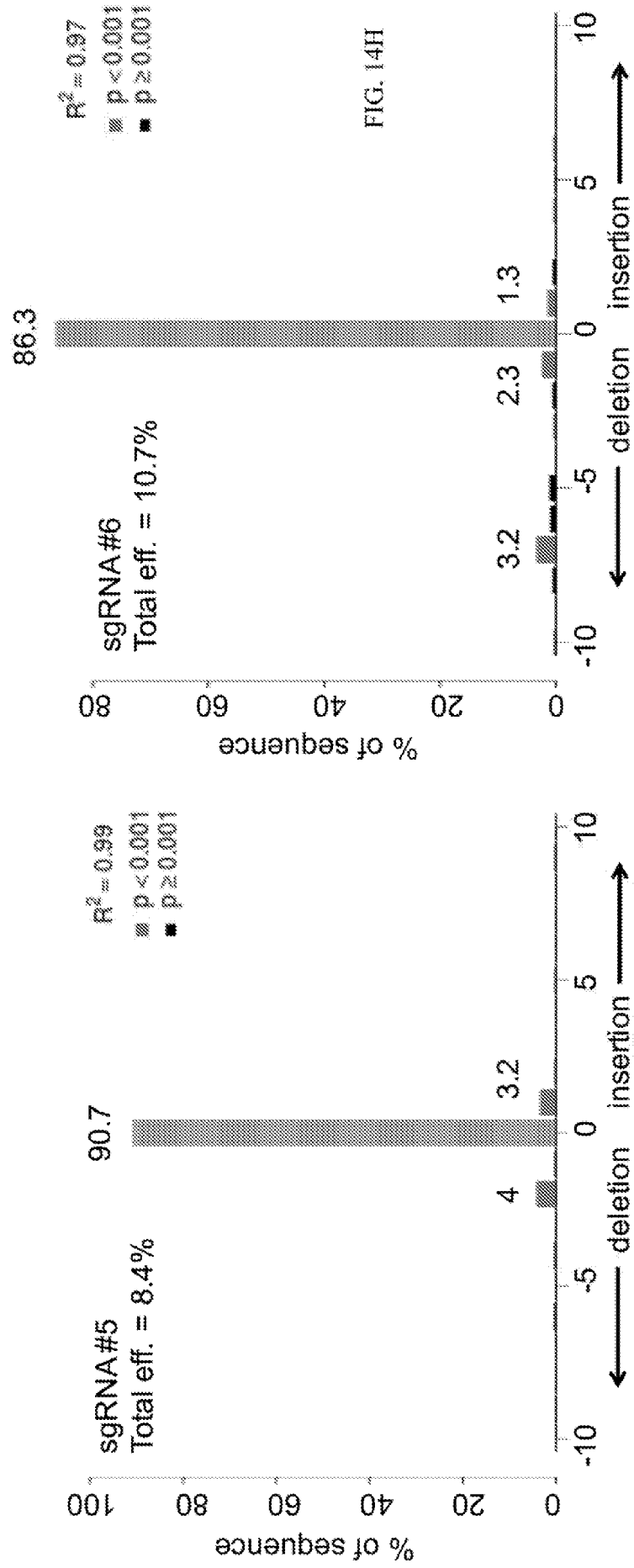


CRISPR sgRNA sequences:

sgRNA #5: AGCGCAAGTGGGAGGCGGC
sgRNA #6: CGGCTCGTGGGCTGCATGTG

FIG. 14G

On-target cutting efficiency of HLA-A sgRNAs using TIDE



KO primer ~220 bp
WT Primers #1 589 bp
WT Primers #2 571 bp

Sequencing confirms successful deletion of HLA-A in HuES8

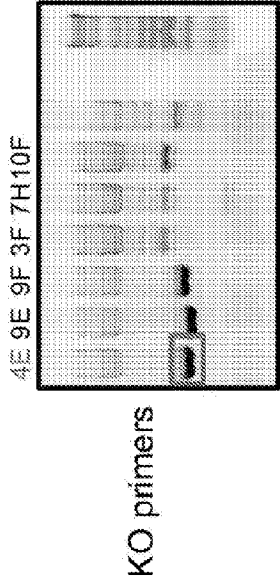
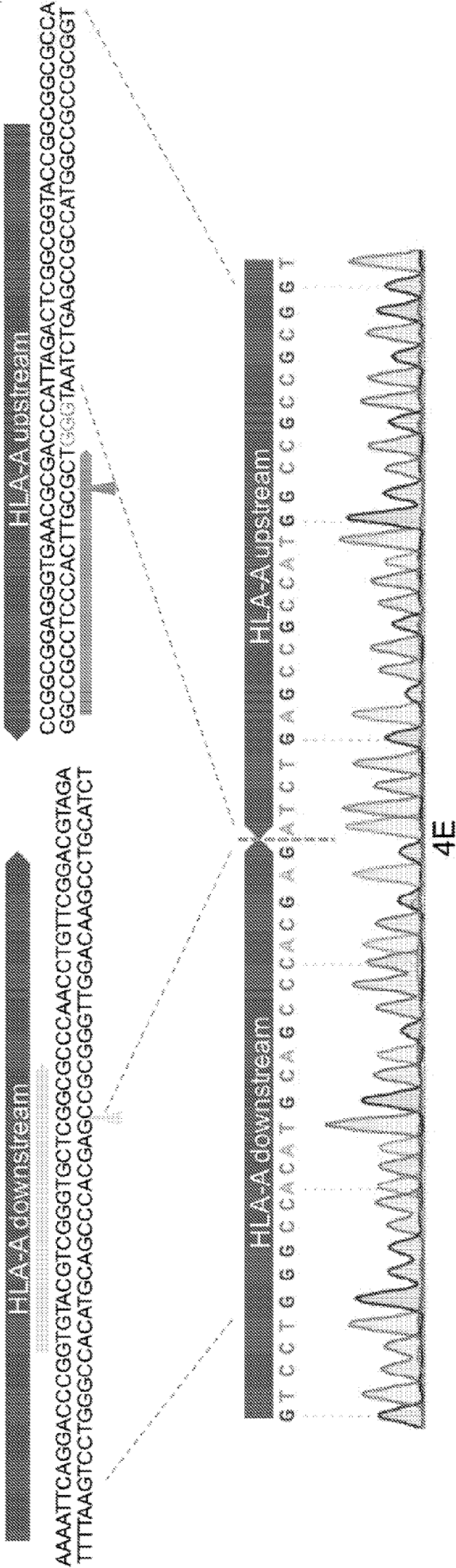


FIG. 14J

NLRC5 mutations, BJ-RIPSCs

	W S C L V R L L T K D P E W L
3D6 A6	<u>GGAGCTGTCTTGTGAGGCTGCTCA</u> -----ACCCAGATGGCTGA
3F7 A4	<u>GGAGCTGTCTTGTGAGGCTGCTCA</u> -----ACACCCAGATGGCTGA
3C6 A24	<u>GGAGCTGTCTTGTGAGGCTG</u> -----A
2B10 1*	<u>GGAGCTGTCTTGTGAGGCTG</u> CCACCAAGACCCAGATGGCTGA
	<u>CCCTGTCTTGTGAGGCTGCTCA</u> CCCAAGACCCAGATGGCTGA
2A6 A15	<u>GGAGCTGTCTT</u> -----AAAGACCCAGATGGCTGA
4H11 2*	<u>GGAGCTGTCTT</u> TGAGGCTGCTCACCAGAGACCCAGATGGCTGA
A24	<u>GGAGCTGTCTTGTGAGGCTG</u> -----A
	W S C L V R L L T K D P E W L
A17	<u>GGAGCTGTC</u> -----AAAGACCCAGATGGCTGA
5F2 A18	<u>GGAGCT</u> -----CCAGACCCAGATGGCTGA
4H9 in4	<u>GGAGCTGTCTTGTGAGGCTGCTC</u> CCCAAGACCCAGATGGCTGA
1*	<u>GGAGCTGTCTTGTGAG</u> CTGCTCACCAGAGACCCAGATGGCTGA
2D8 A23	<u>GGAGCTGT</u> -----CCAGATGGCTGA
A14	<u>GGAGCTGTCTTGTGAGG</u> -----CCAGATGGCTGA
4C9 A20	<u>GGAGCTGTCT</u> -----ACCCAGATGGCTGA

FIG. 1B

Targeting of HuES9

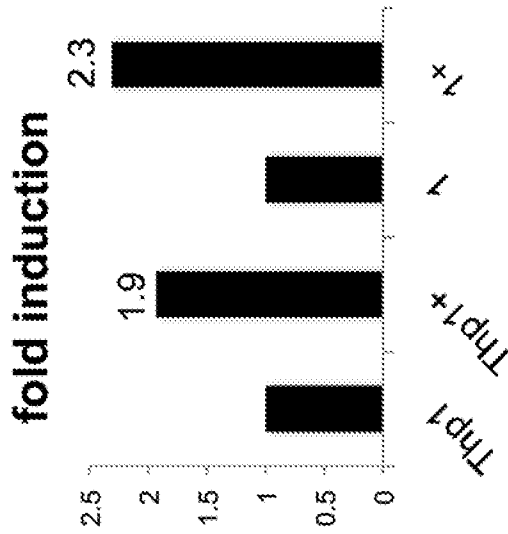
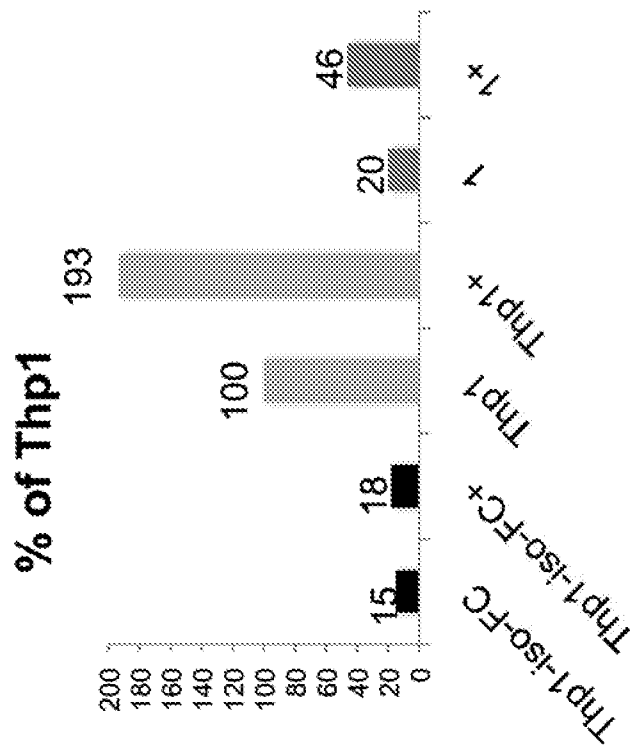
NLRC5 mutations, HuES-9

1FS A4 GGAGCTGTCTGTGAGGCTG-----CCAAAGACCCACAGAAATGGCTGA
2G7 A8 GGAGCTGTCTGTGAGGCTG-----AAAGACCCACAGAAATGGCTGA
3E7 A26 GGAG-----ACCCAGAAATGGCTGA
3F7 1n4 GGAGCTGTCTGTGAGGCTGTCTCAG#####CAAAGACCCACAGAAATGGCTGA

FIG. 15C

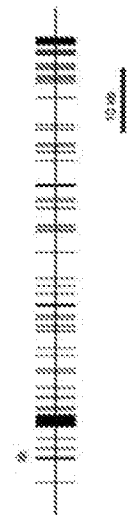
FIG. 15D

Reduced MHC-I expression in NLRC5^{-/-} Thp1 cells



NLRC5 Targeting Strategy in Thp1

NLRC5 CRISPR



WT CCGAGACGCGAGATGGCTGAAACGCGCAAGATTAAGTCTTCTCCGCGACACGCGAGCTGG
#1 Δ2 CCGAGACGCGAGATGGCTGAAACGCGCAAGATTAAGTCTTCTCCGCGACACGCGAGCTGG

% Reduction

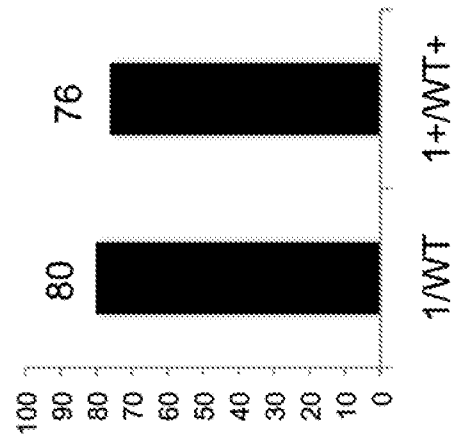


FIG. 16A

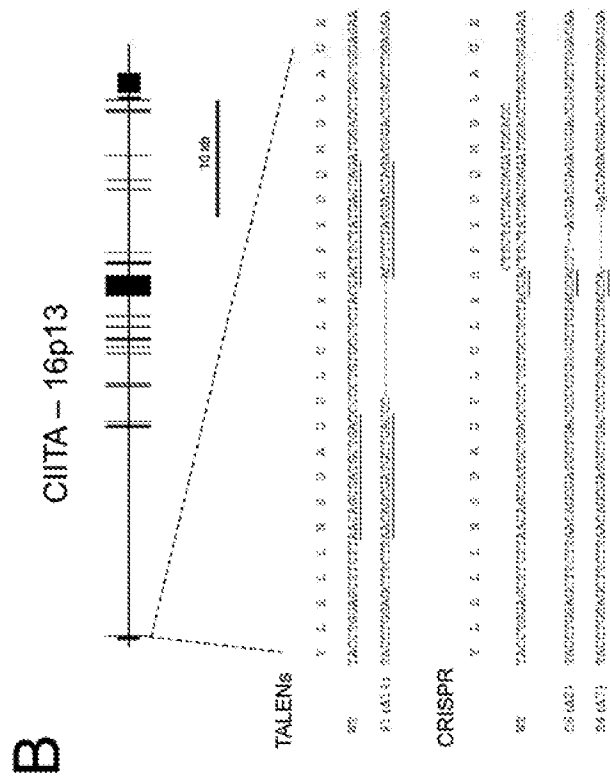
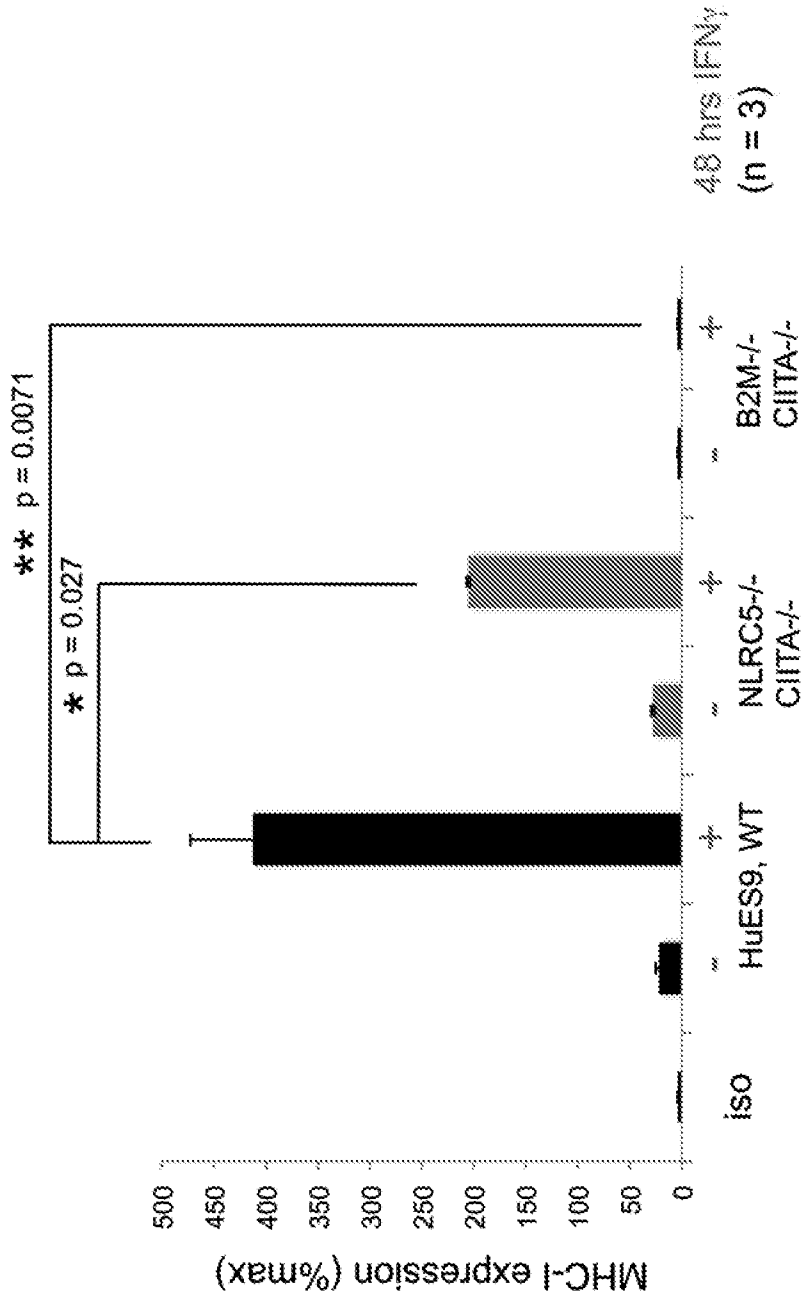


FIG. 16B

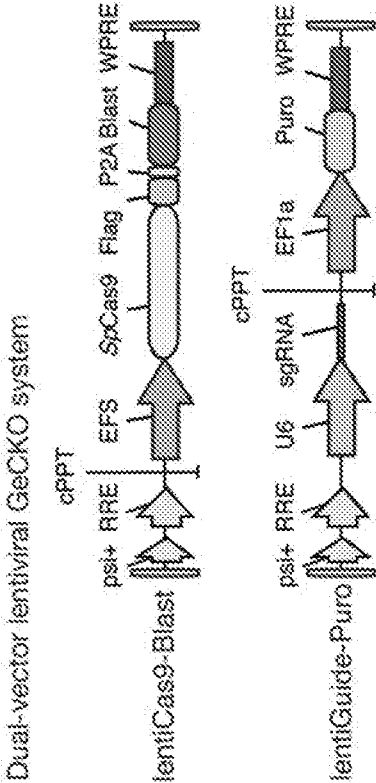
Reduced MHC class I expression in HuES9 following targeting with
NLRC5 or B2M CRISPRs



- Low basal MHC-I expression in stem cells
- Can be increased by IFN γ stimulation
- ~50% reduction in IFN γ -treated NLRC5-/- cells
- Complete loss of MHC-I surface expression in B2M-/- cells

FIG. 16C

Lentiviral Transduction of Thp-1



2 component system

Lenti-Cas9-Blasticidin [establish stable Thp-1 Cas9 cell line]

Lenti-Guide-puro [bring in guide]

FIG. 16D

CRISPRs used for Lentiviral Transduction of Thp-1

CHTA	GGTCCATCTGGTCATAGAAG(TGG)
NLRCS	
CR1	GATGTCCAGGGTTCGGACACCG(TGG)
CR2	GATGAGGCCCTCCAGCCTAT(GGG)
IRF1	
CR1	GATGCCCTGTTTGTCCGGAGC
CR2	GAGATGATCTTCCAGATCCCA
CR3	GCTCGGATGGGCATGAGACCC

FIG. 16E

CIITA and NLRC5 act independently on MHC-II and MHC-I, respectively

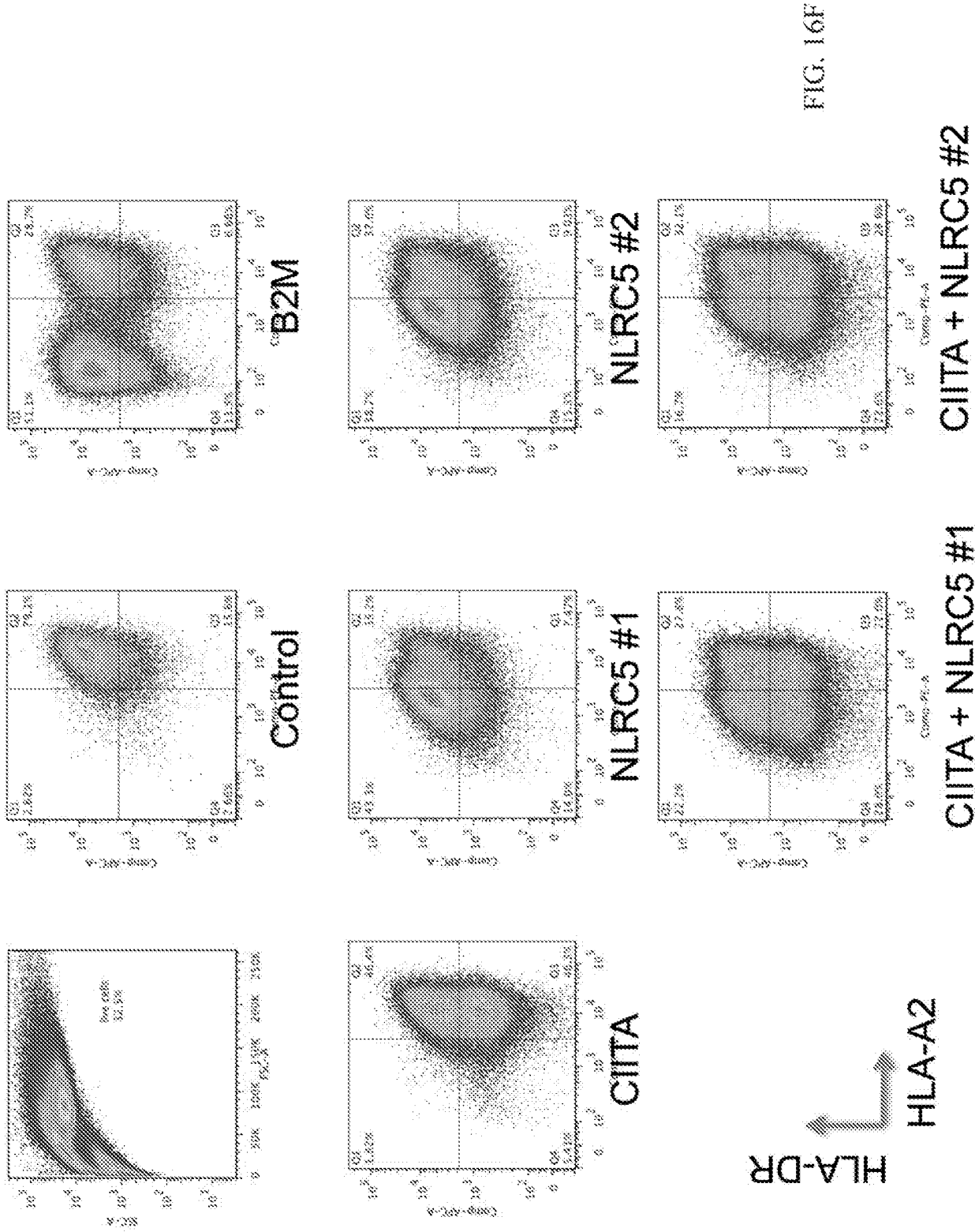


FIG. 16F

Targeting IRF1 results in Loss of MHC-II expression

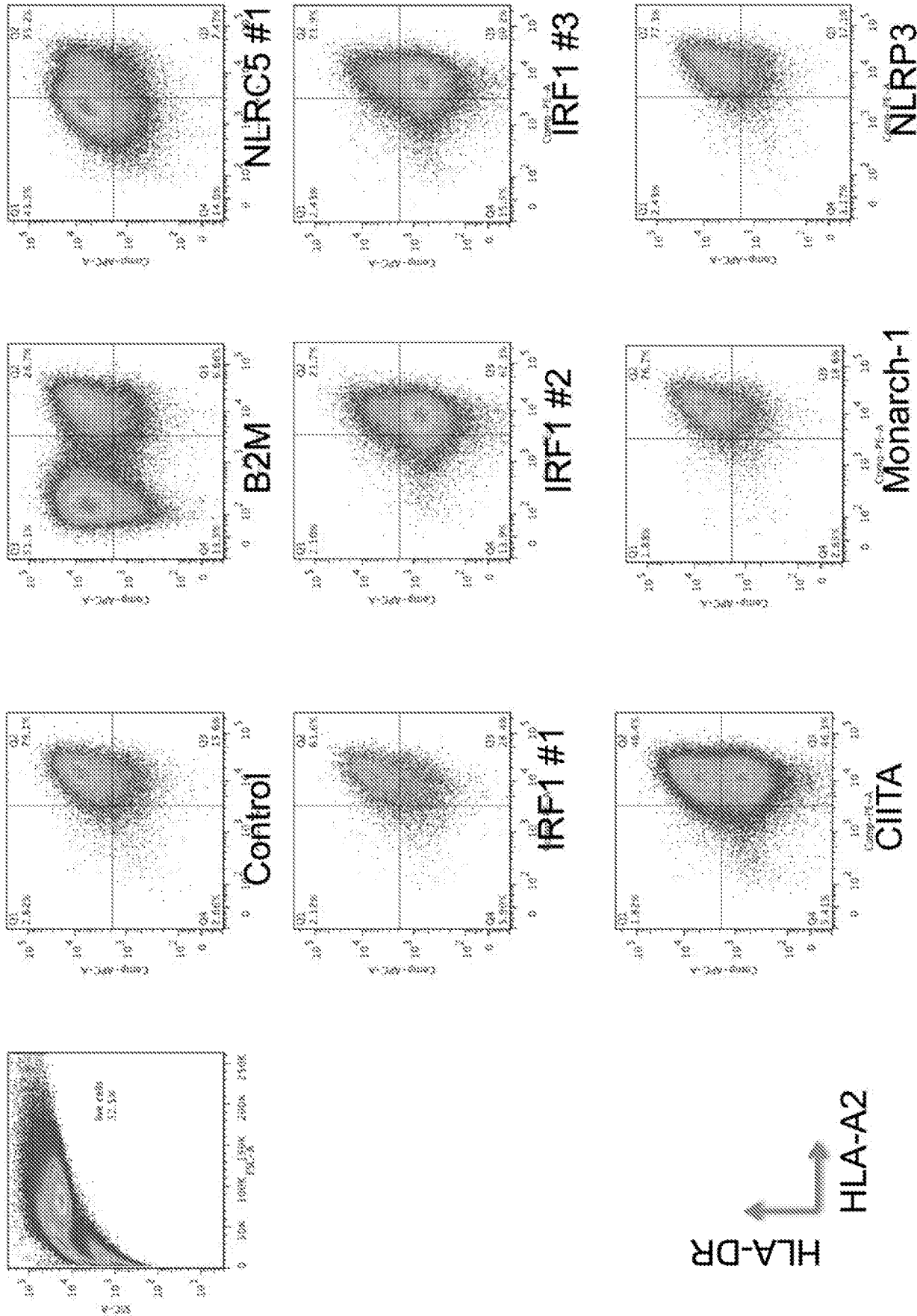


FIG. 16G

Dual CRISPR Strategy targeting the *IRF1* locus

IRF1 gene locus – Chr. 5q31.1

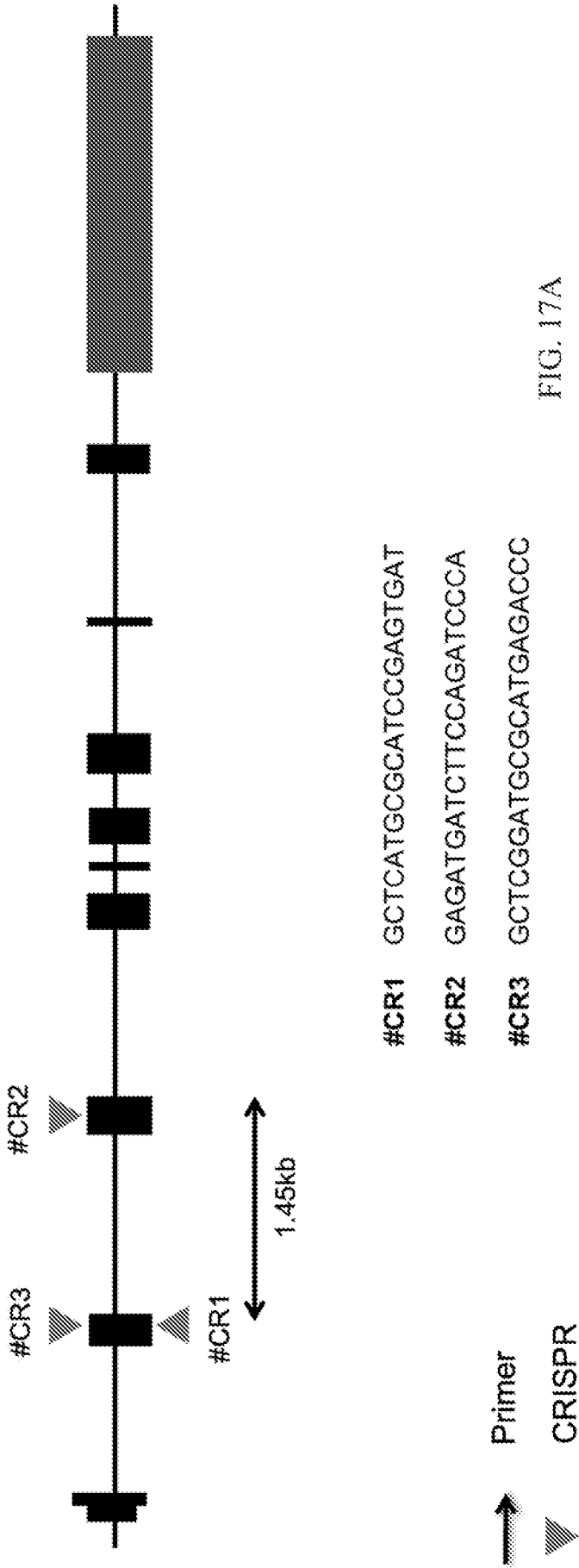
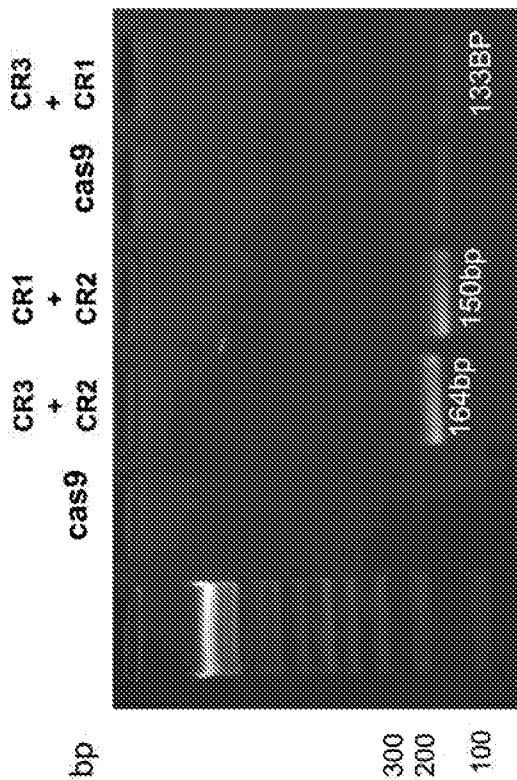
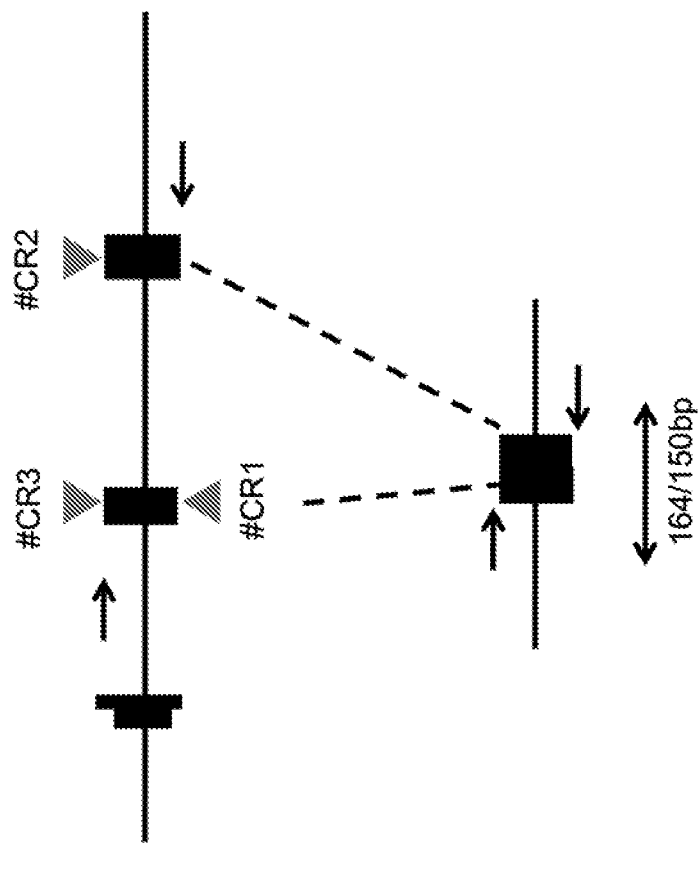


FIG. 17A

Testing of Different *RF1* Guide Combinations

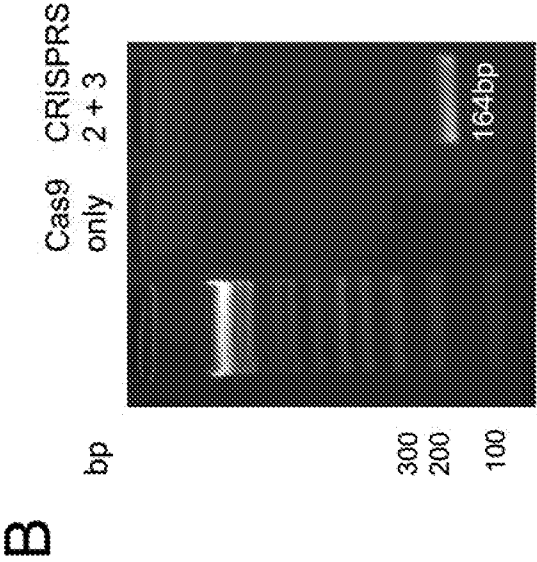
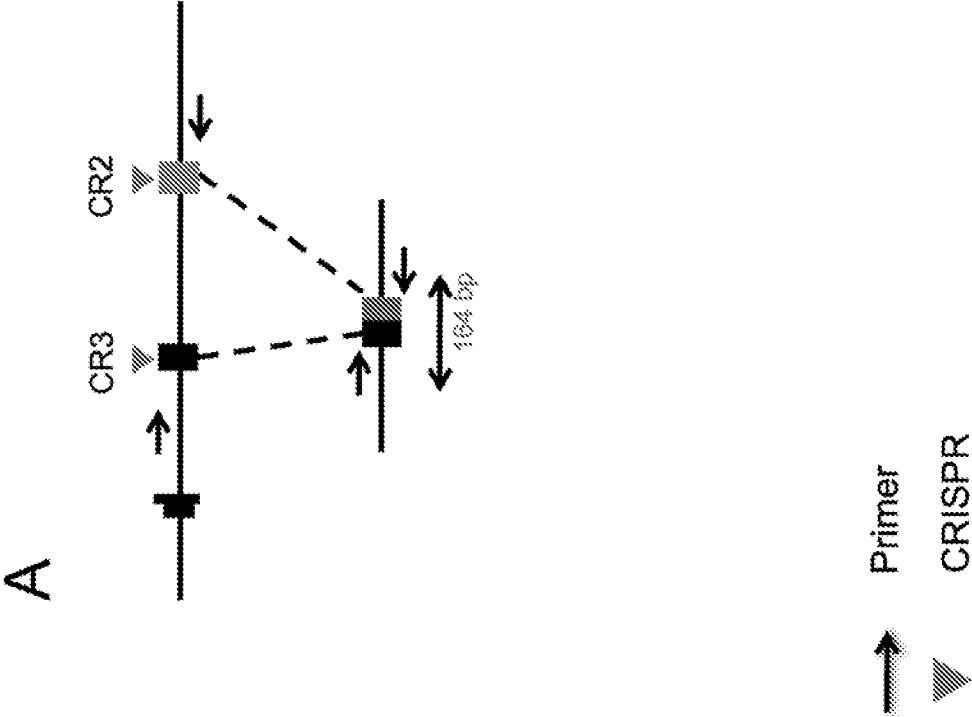


 Primer
 CRISPR

FIG. 17B

293T

‘Dual guide strategy’ for the targeted deletion of *IRF1*



293T cells

FIG. 17C

SEQUENCE CONFIRMATION OF IRF-1 CRISPR INDUCED DELETION

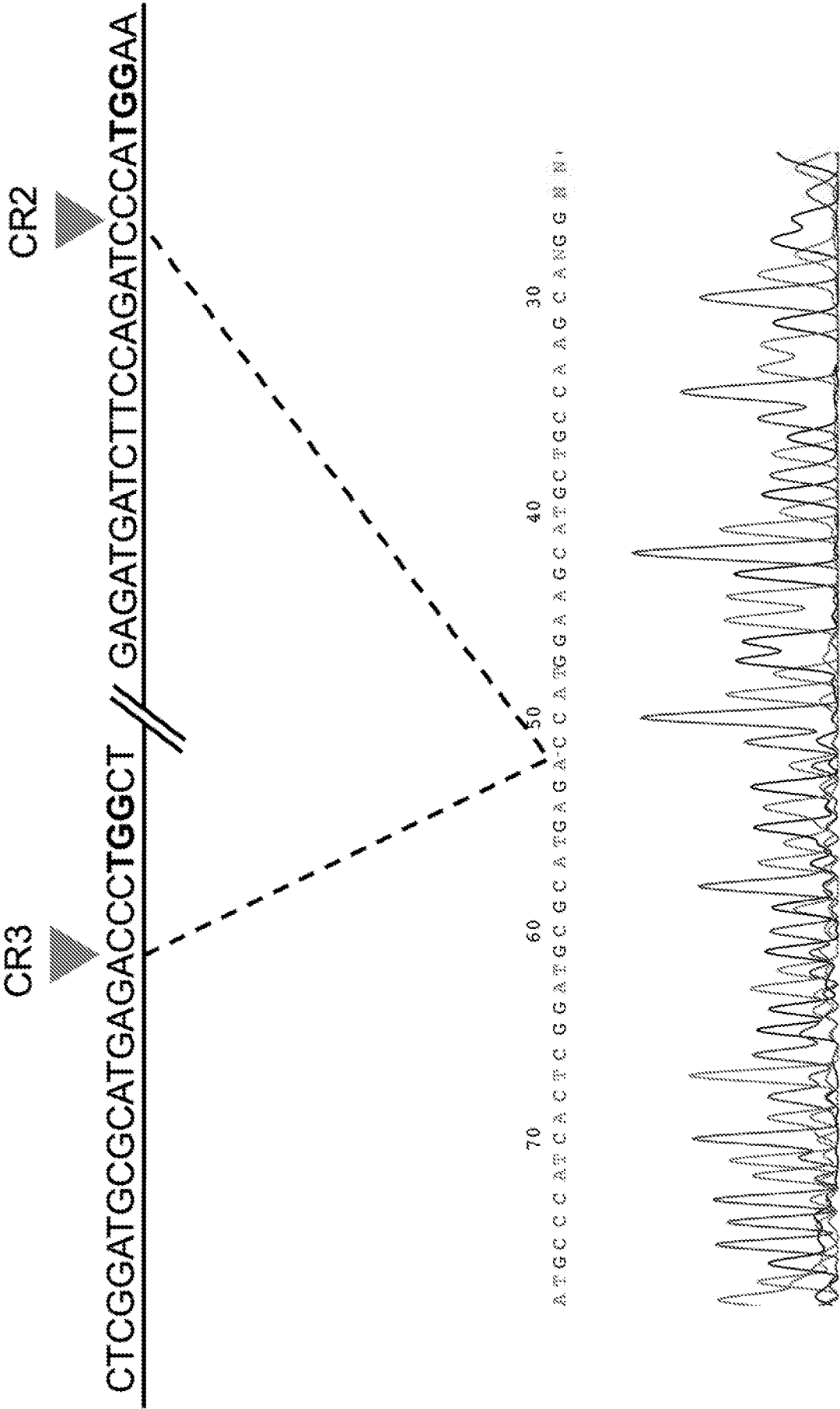


FIG. 17D

293T cells

Screening of *IRF1*-targeted HuES9

Dual CRISPR strategy using CRISPRs #2 and #3

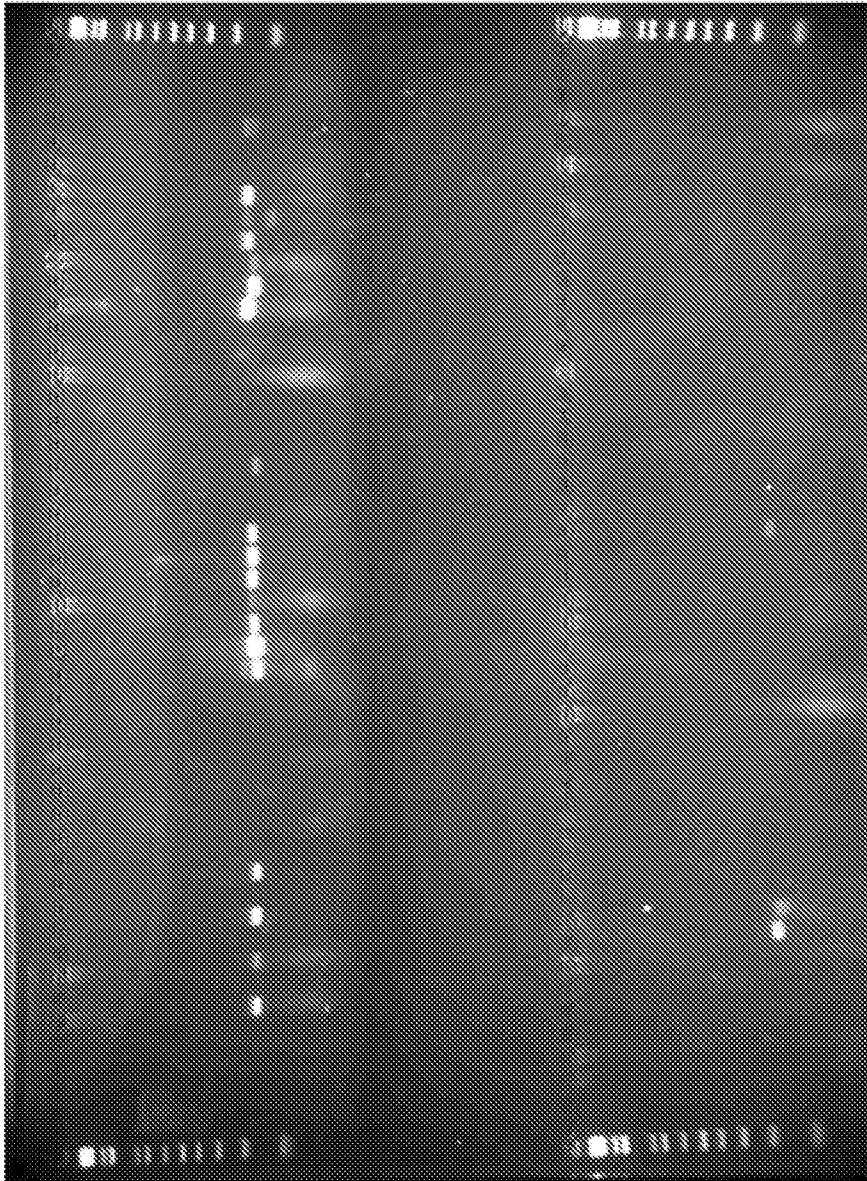
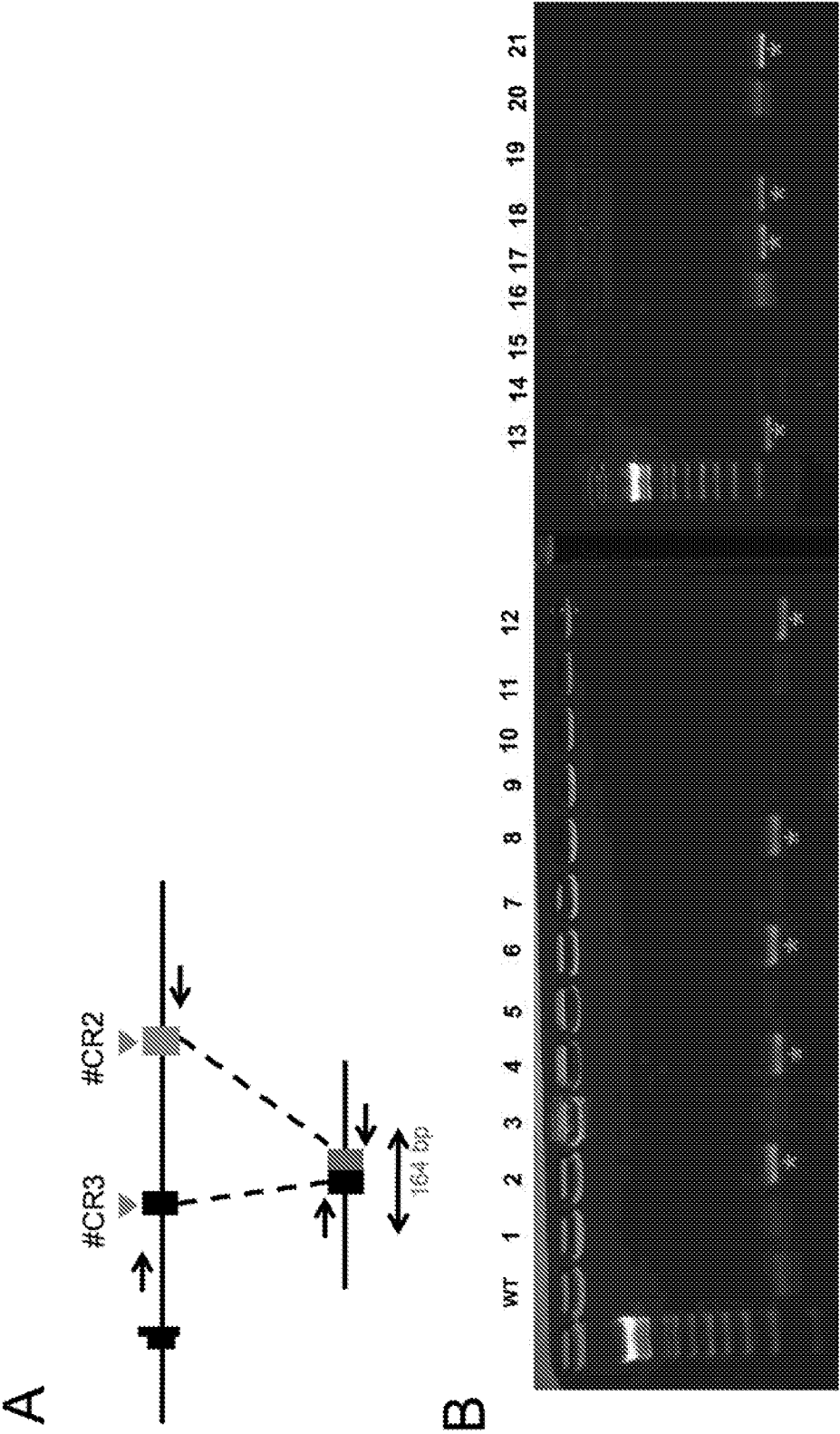


FIG. 17E

RECONFIRMATION OF IRF-1 CLONES

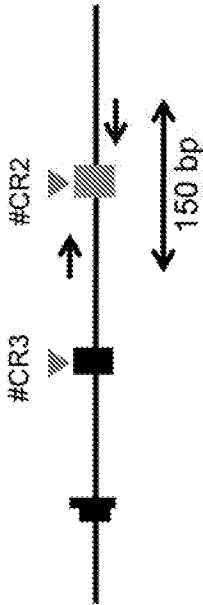


PRIMERS: KYM07 and TM377

FIG. 17F

Genotyping of IRF-1 Clones

A



B

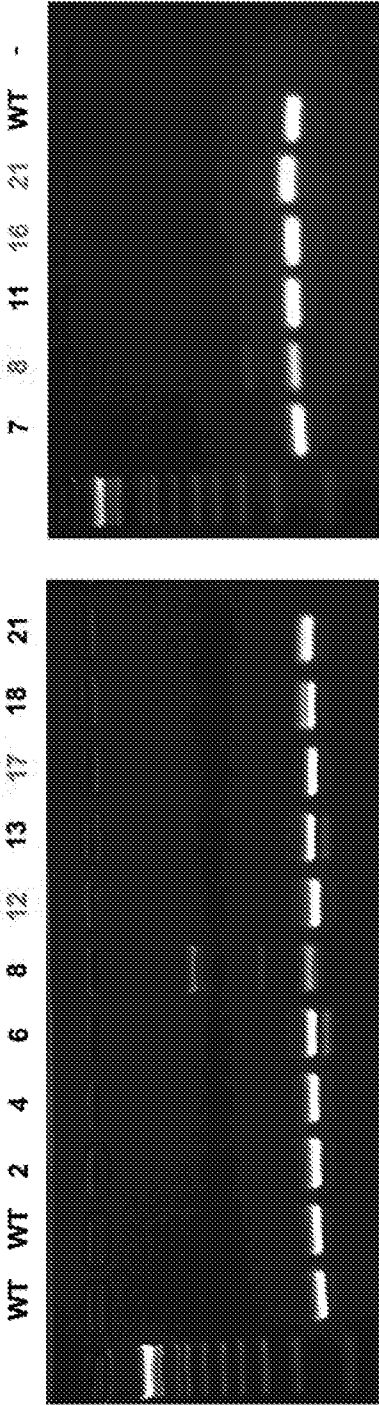
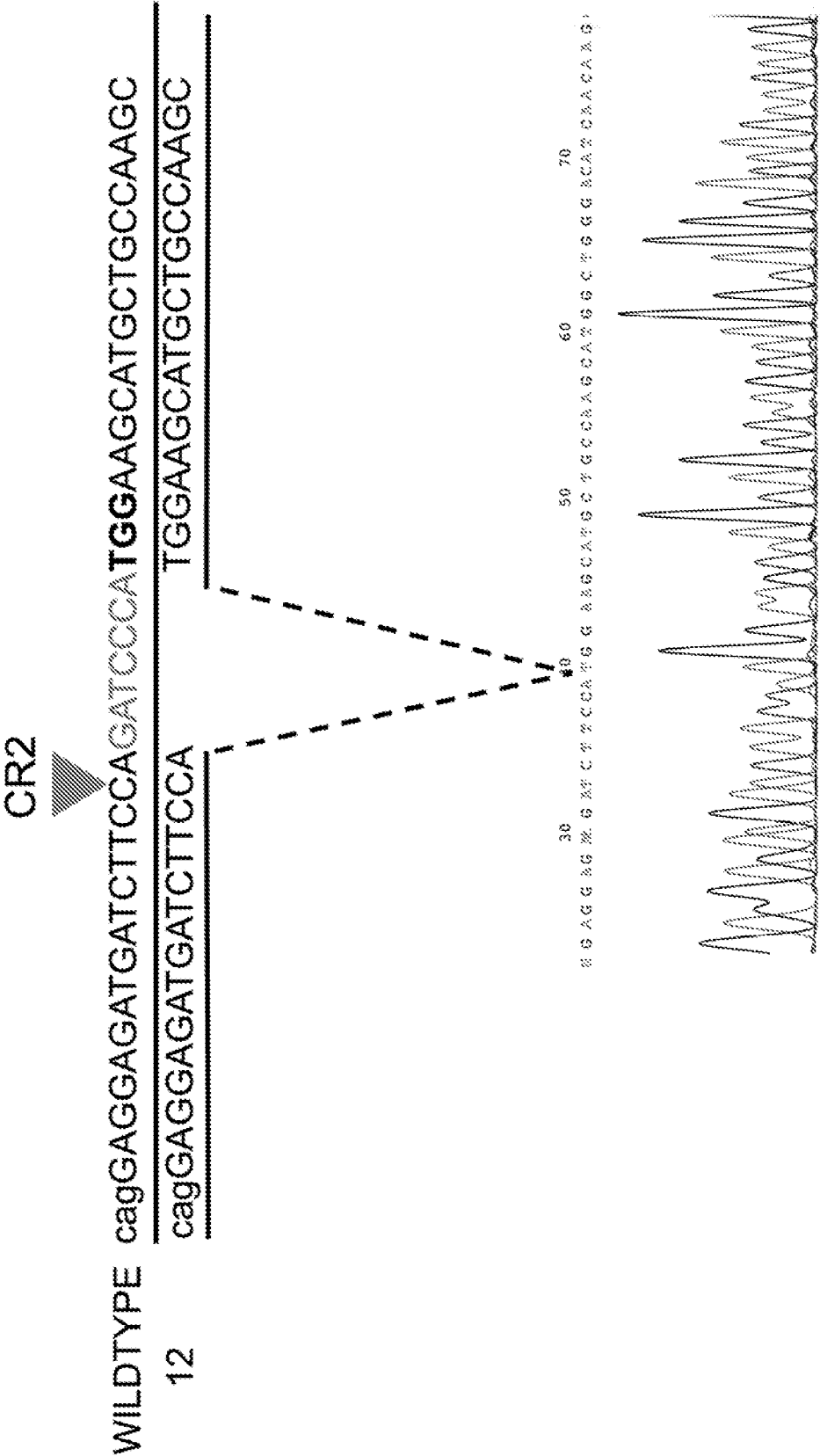


FIG. 17G

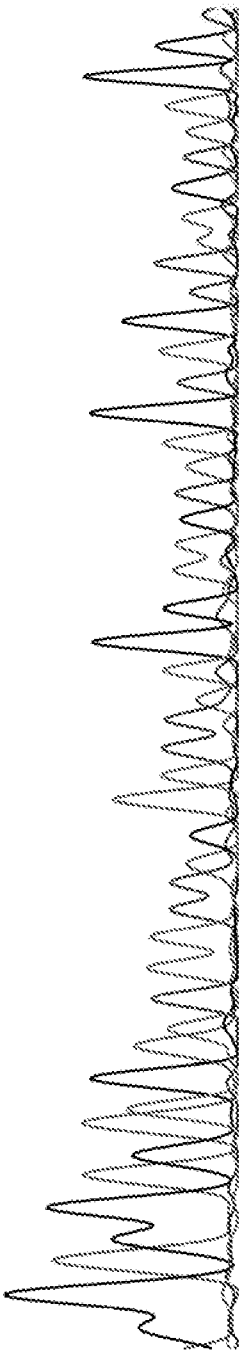
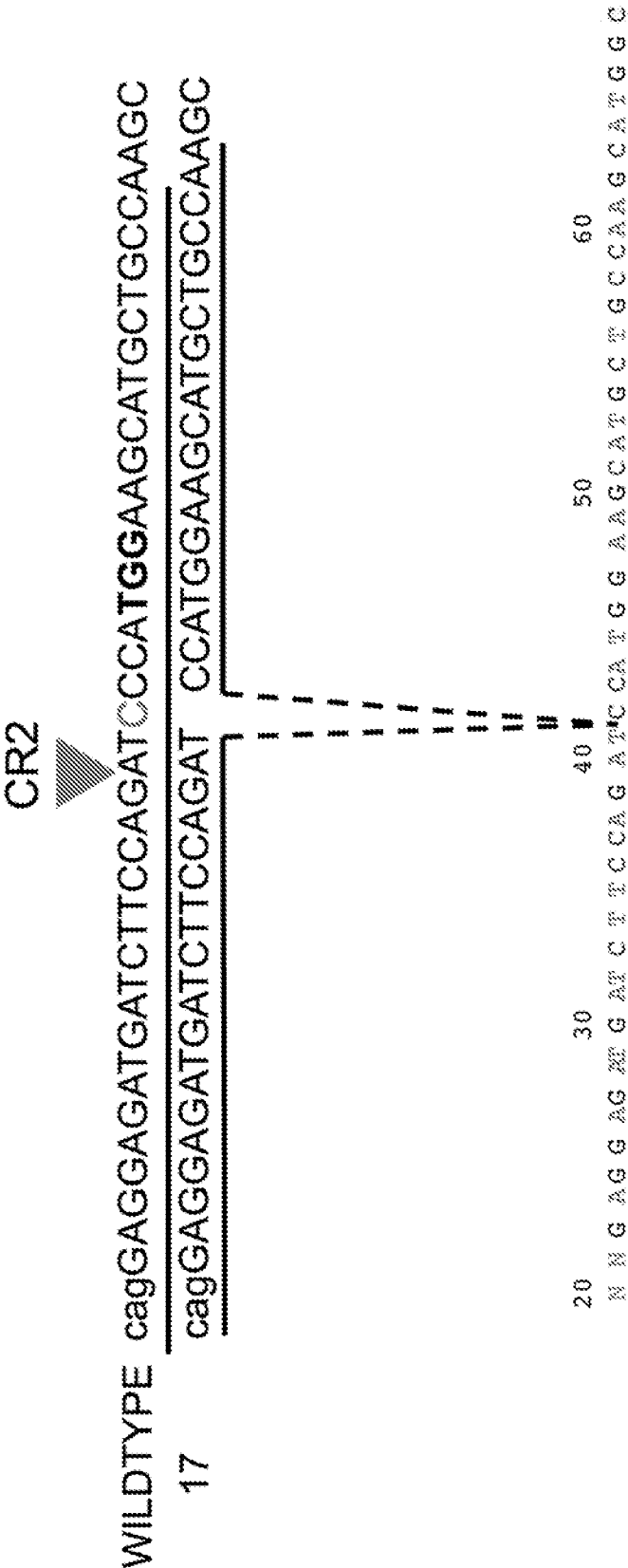
SEQUENCE CONFIRMATION OF IRF-1 CRISPR INDUCED DELETION
IN CLONE 12



HuES9

FIG. 17H

SEQUENCE CONFIRMATION OF IRF-1 CRISPR INDUCED DELETION
IN CLONE 17



HuES9

FIG. 17I

SEQUENCE CONFIRMATION OF IRF-1 CRISPR INDUCED INSERTION IN CLONE 21

CR2



WILDTYPE cagGAGGAGATGATCTTCCAGATC-----CCAT**GGA**GCATGCTGCCAAGC

21 cagGAGGAGATGATCTTCCAGATC**ATGCTGCC**ATGGAAGCATGCTGCCAAGC

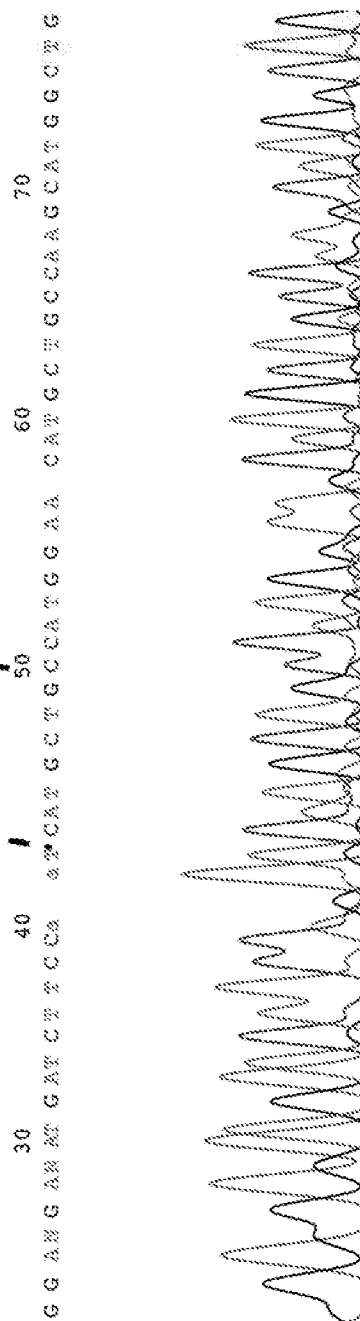


FIG. 171

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Impaired MHC class I Induction in IRF1^{-/-} HuES9 clones
following IFN γ treatment

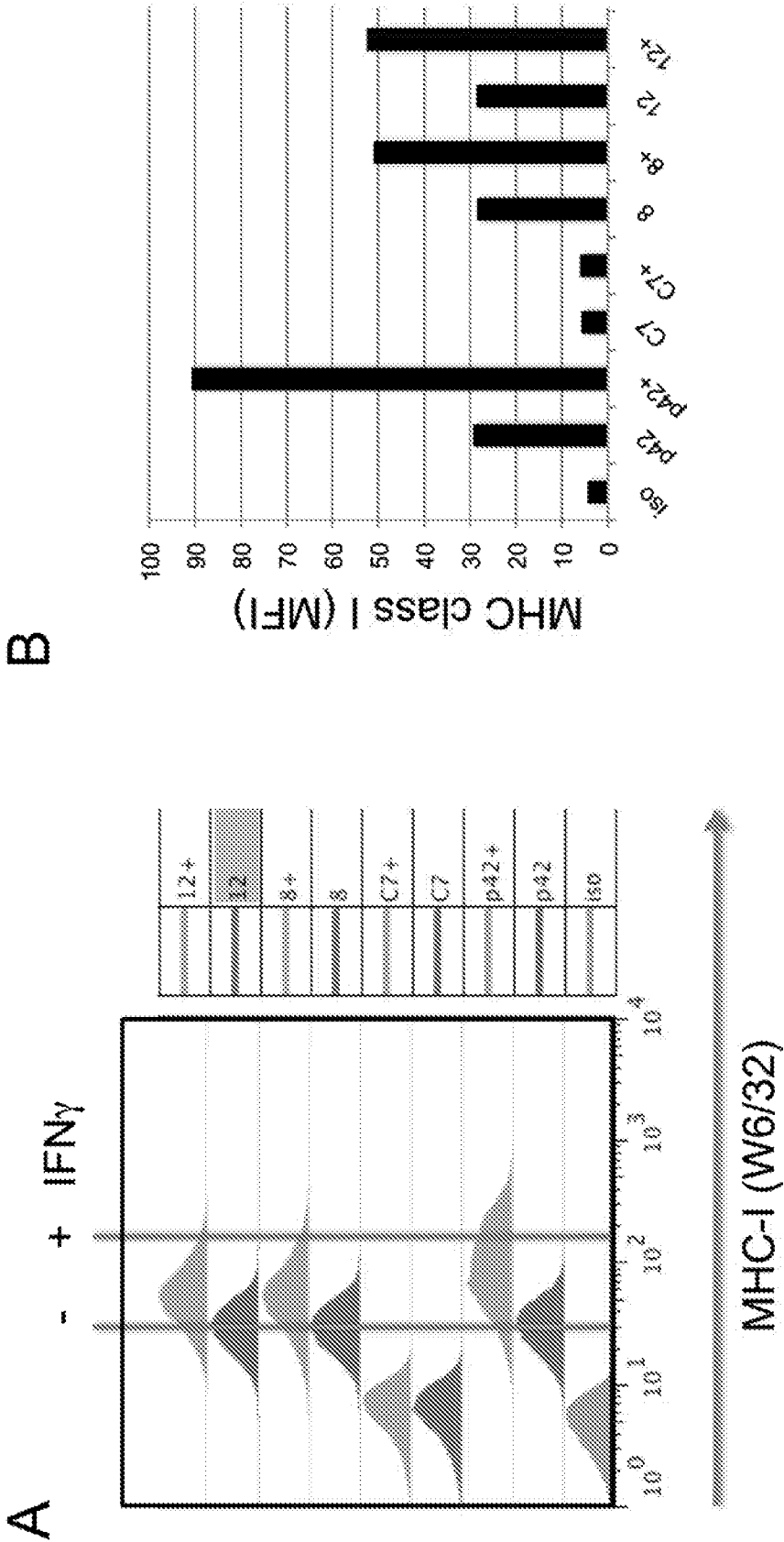


FIG. 17K

Dual Guide Targeting of RFX5 in 293T Cells

CRISPR Pair #1: GTCITGGGGCTCTTAGDTC
CRISPR Pair #2: ACCCTTCTCAGAGGCTCCG
CRISPR Pair #3: GGGCTAGAATTGAGAGGGAC
CRISPR Pair #4: GGAGTGCCCTGGGGCTTCT

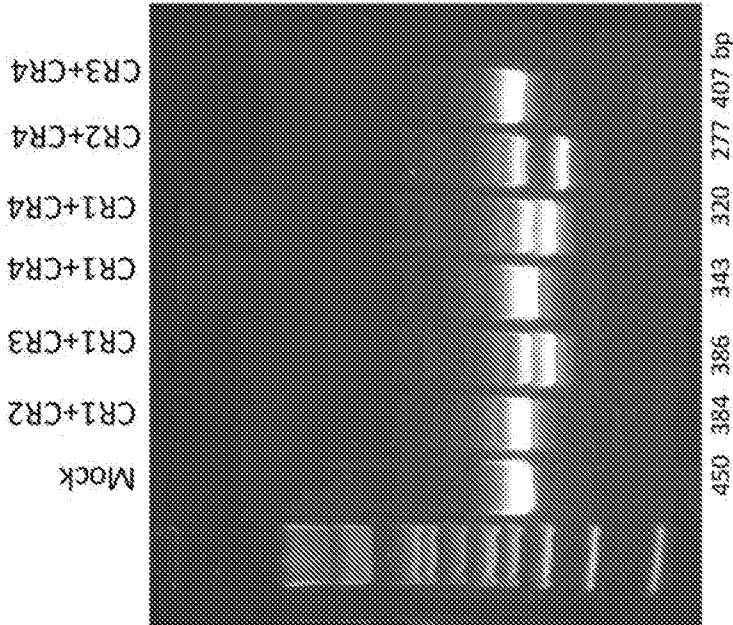


FIG. 18A

Targeting of RFX5 results in reduced MHC class I expression

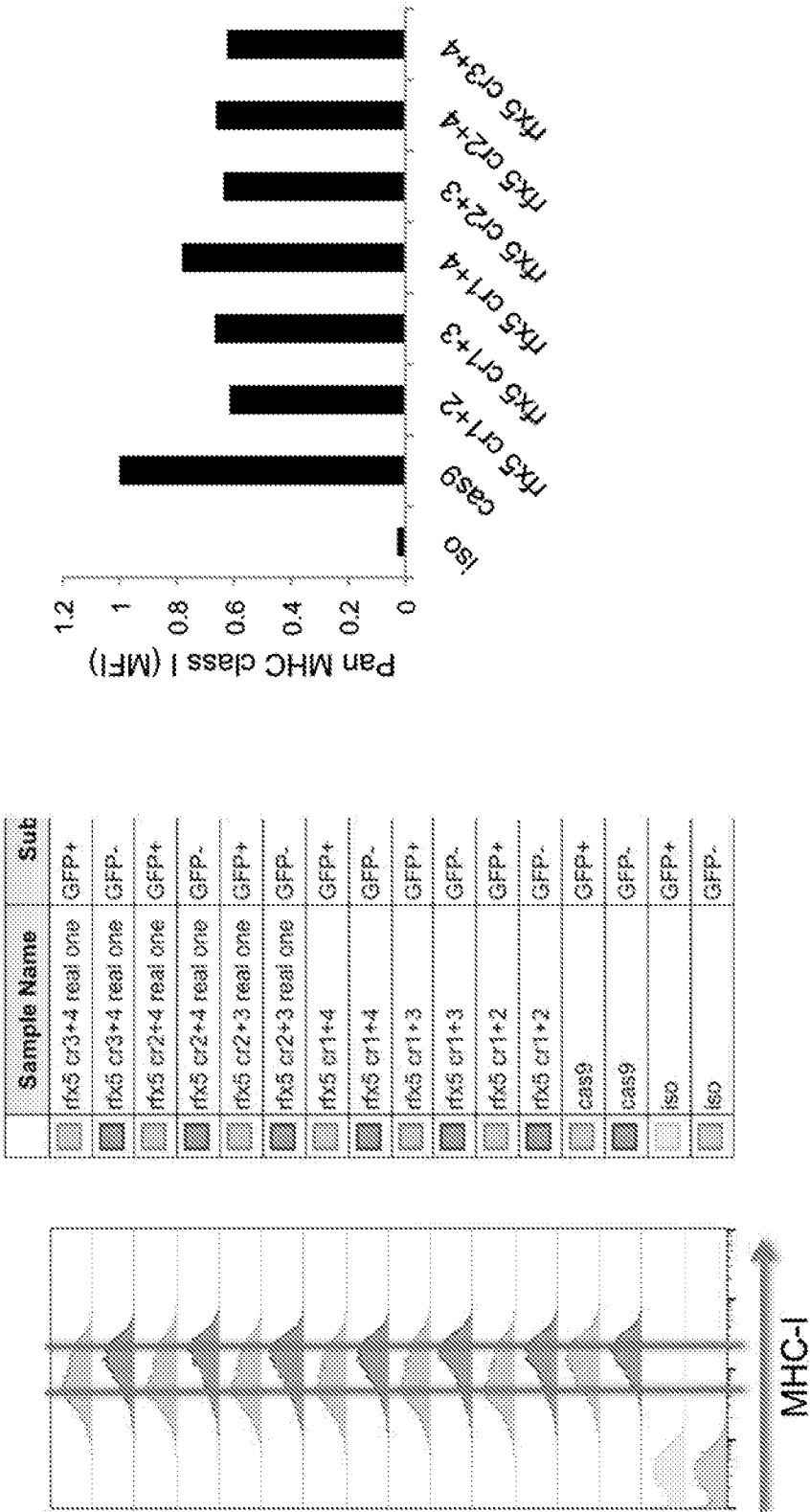


FIG. 18B

Dual Guide Targeting of RFX-ANK in 293T Cells

CRISPR Pair #1: GCAGGCTGGGTAAGCTCCAT
CRISPR Pair #2: TGCAAGGCTAGGTAIGCAGT
CRISPR Pair #3: GACCCCTGGCTCAGAACTTG
CRISPR Pair #4: CTGTGAGGGTGGGTAAACTG

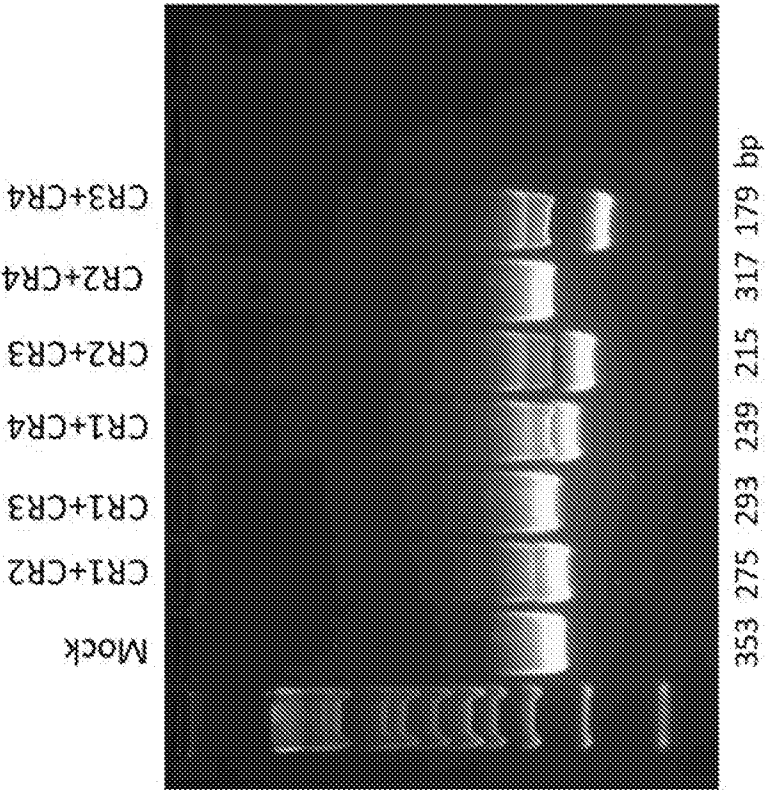


FIG. 18C

Targeting of RFX-ANK results in reduced MHC class I expression

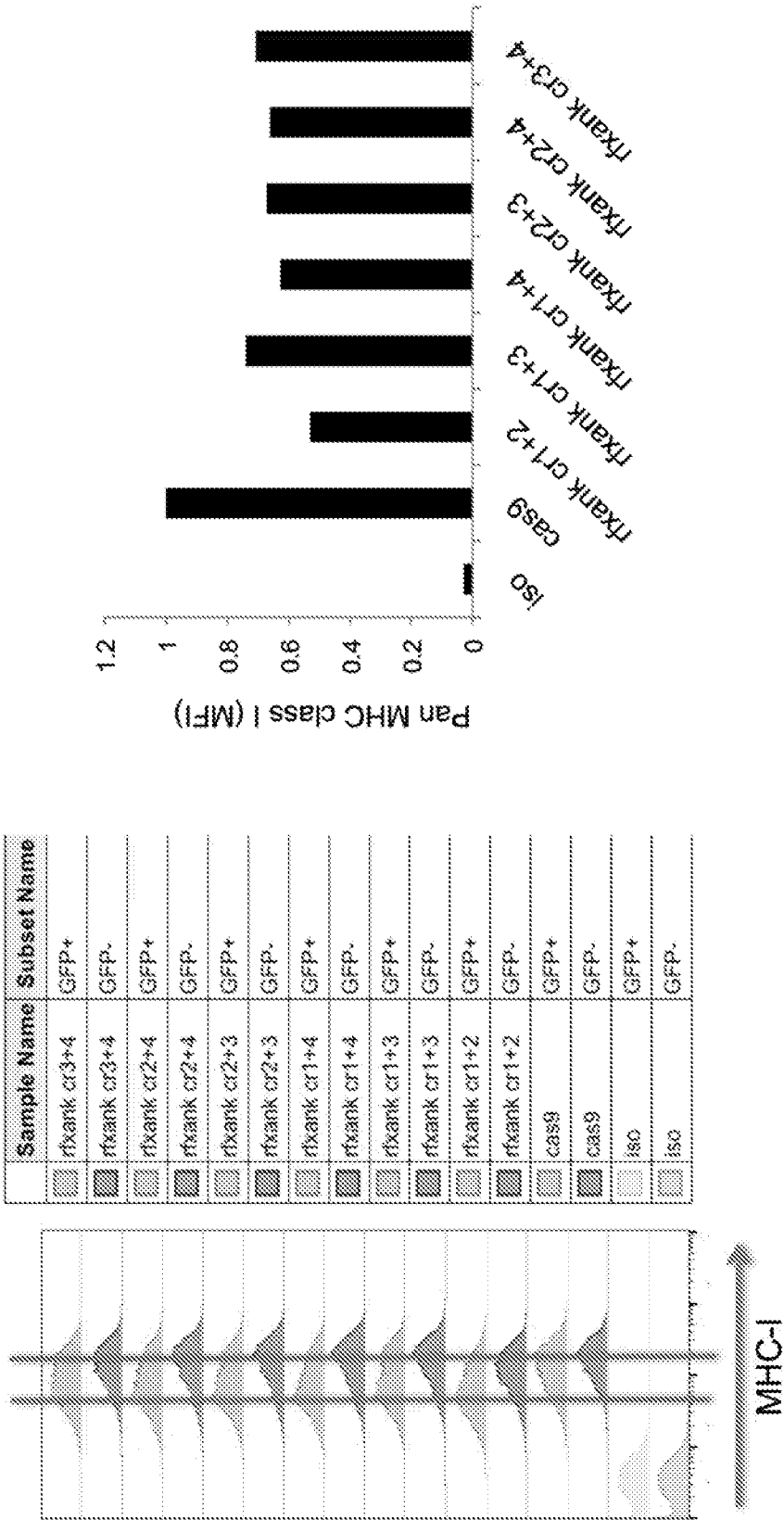


FIG. 18D

Targeting RFX5 and RFX-ANK Results in Reduced MHC class I Expression

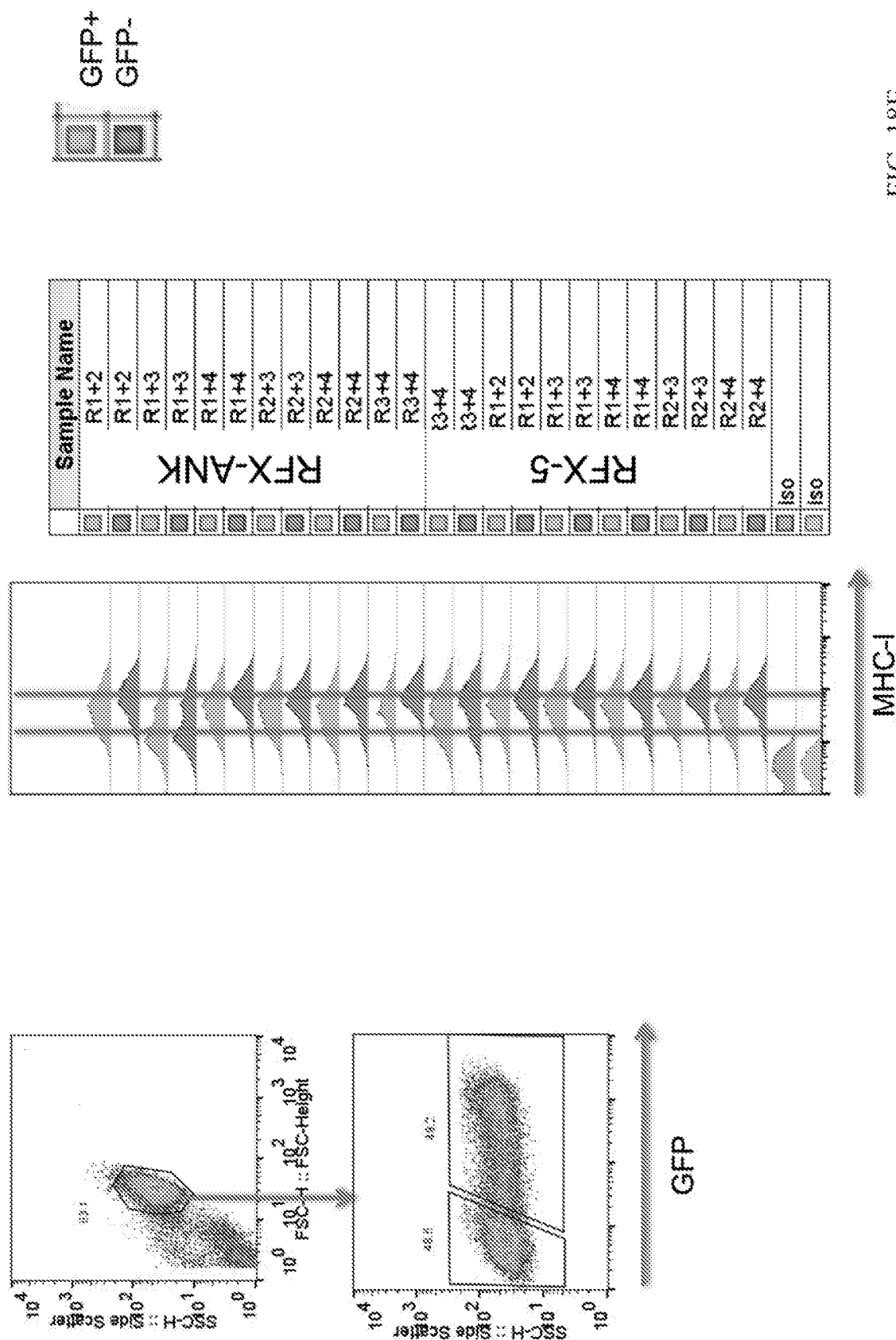


FIG. 18E

Targeting RFX5 and RFX-ANK Results in Reduced MHC class I Expression

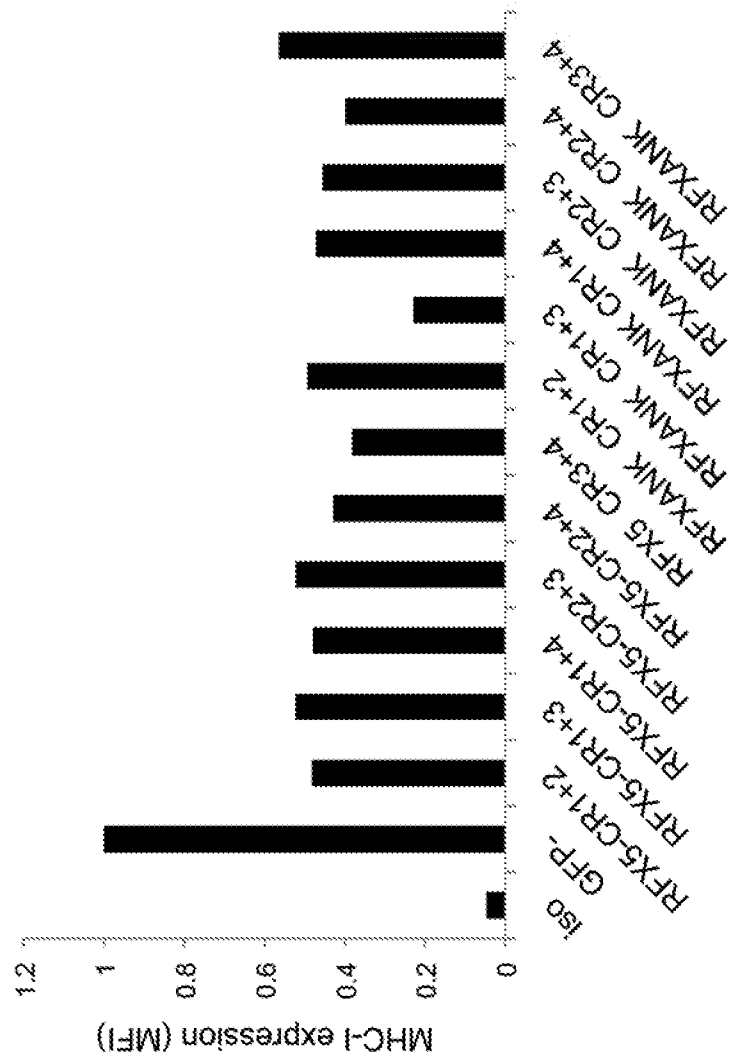


FIG. 18F

Dual Guide Targeting of RFX-AP in 293T Cells

CRISPR Pair #1: TTGGTTGCGAAGTGCCGTT
CRISPR Pair #2: ACTTCGCGAACCAGAAAGACTC
CRISPR Pair #3: CGCGGGGTGGGGCACGCCGC
CRISPR Pair #4: ACCGAGGCTGGCGCCAAAGGT

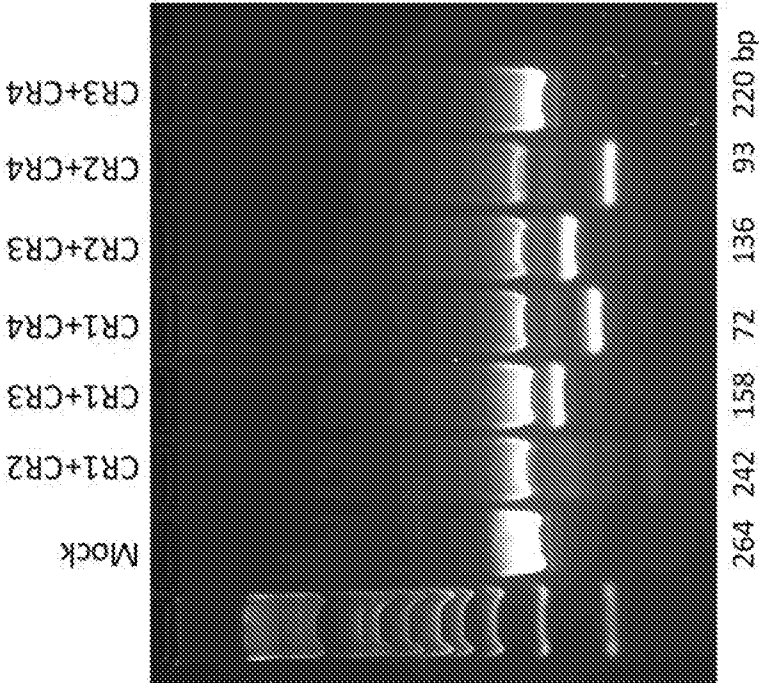


FIG. 18G

Targeting of RFX-AP results in reduced MHC class I expression

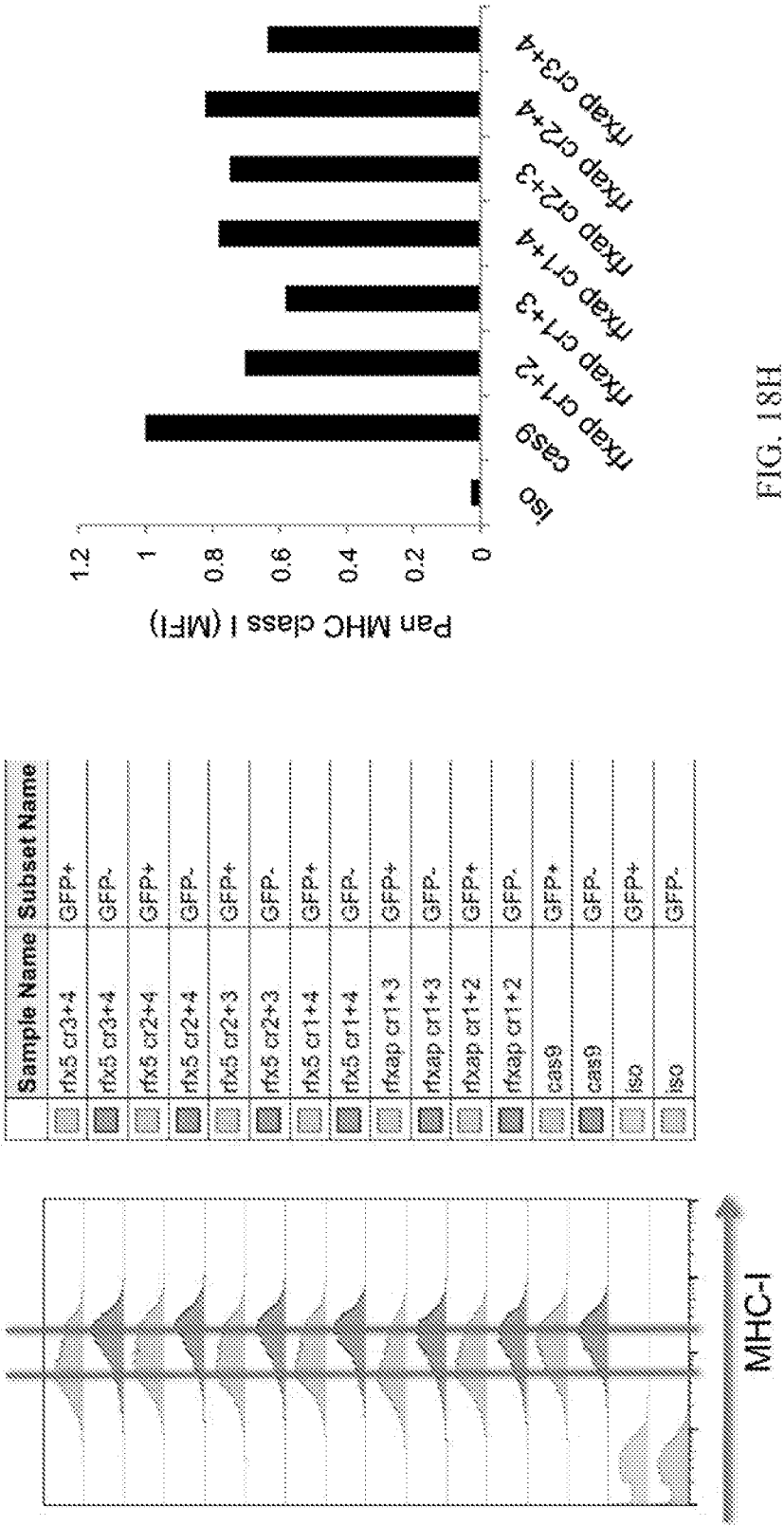


FIG. 18H

Dual Guide Targeting of NFY-A in 293T Cells

CRISPR Pair #1: AGTGTACCTCAGCCCTTCT
CRISPR Pair #2: GACAGAGCAGATTGTTGTCC

CRISPR Pair #3: AGTGAGATTCTGTCCACTC
CRISPR Pair #4: GACAGATTCAGCAGCAGGTA

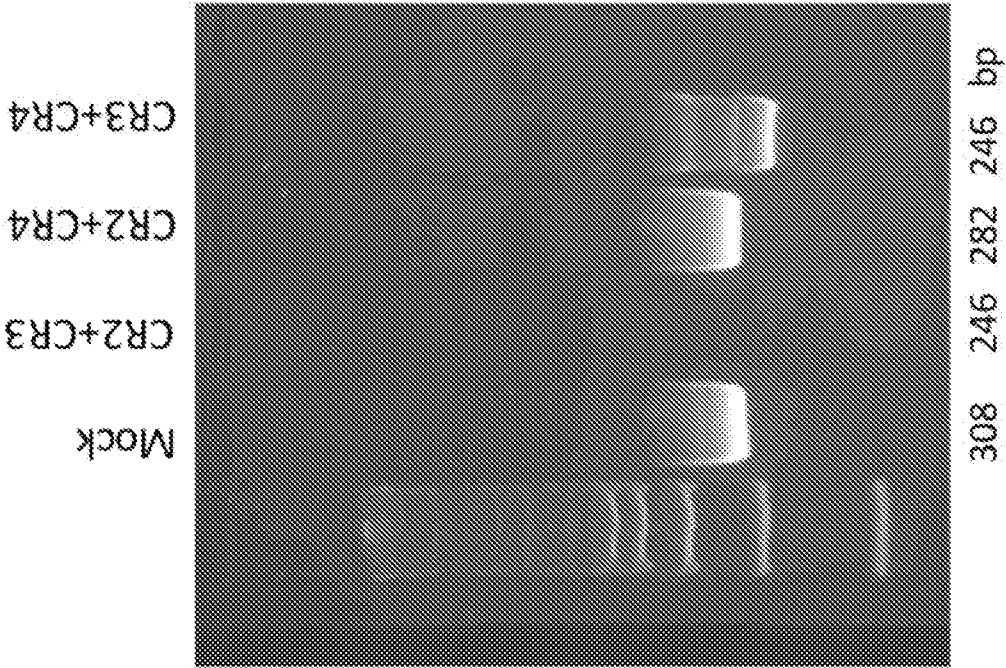


FIG. 19A

Dual Guide Targeting of NFY-C in 293T Cells

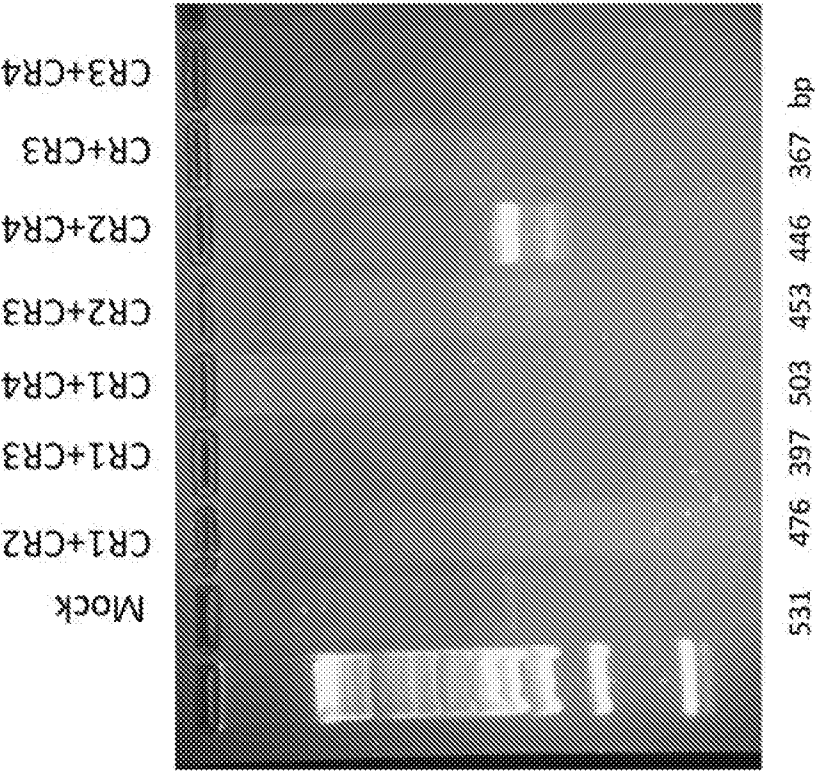


FIG. 19B

Targeting NFY-C and NFY-A Results in Reduced MHC class I Expression

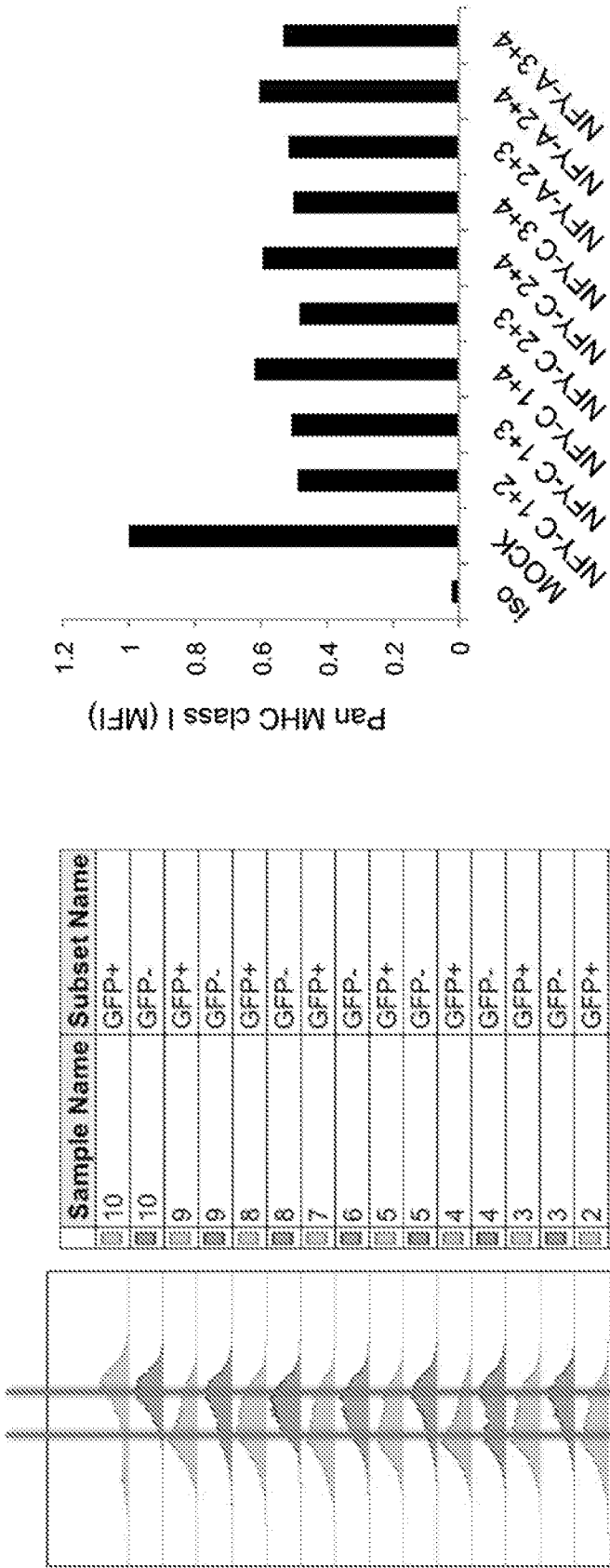
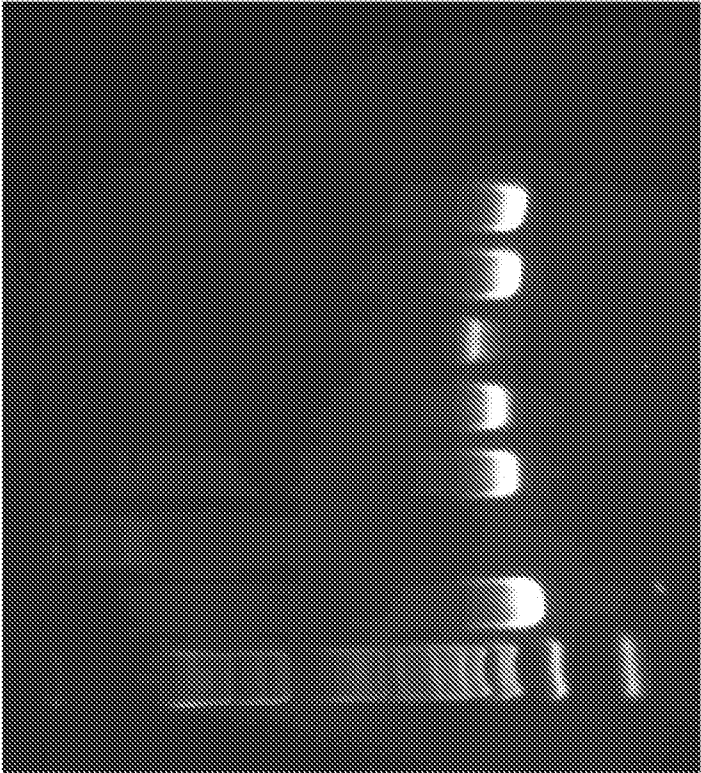


FIG. 19C

Dual Guide Targeting of NFY-B in 293T Cells

CR1+CR2
CR1+CR3
CR1+CR4
CR2+CR3
CR2+CR4
CR3+CR4



334 299 272 317 295 322 307 bp

CRISPR Pair #1: GTGAGCGCTTAGTATTACC
CRISPR Pair #2: ACCAGCACATAGCATGAACC
CRISPR Pair #3: GTAGCTGTCAACAACAGACA
CRISPR Pair #4: ACCAGGTTTCATGCTATGTGC

FIG. 19D

Targeting NFY-B Results in Reduced MHC class I Expression

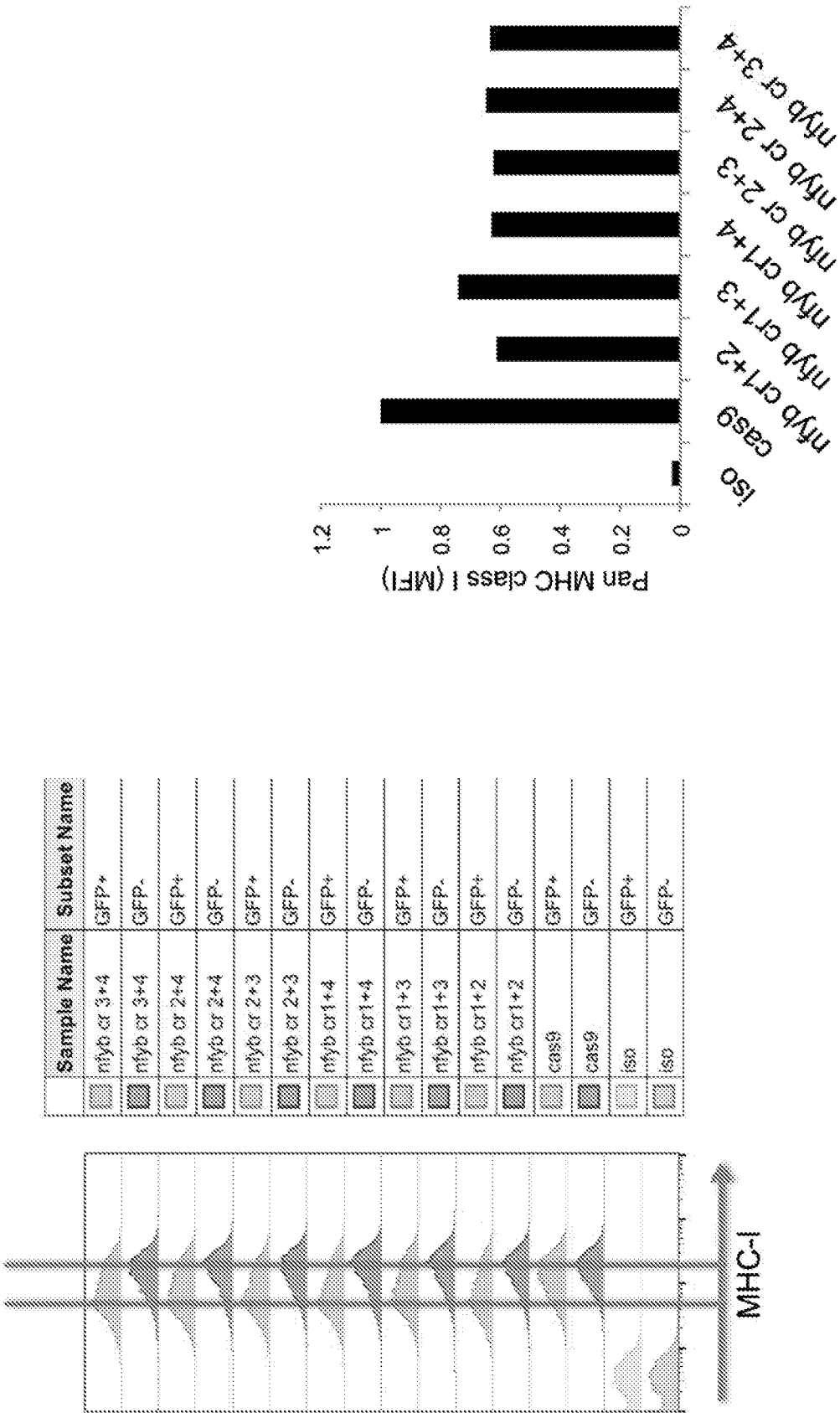
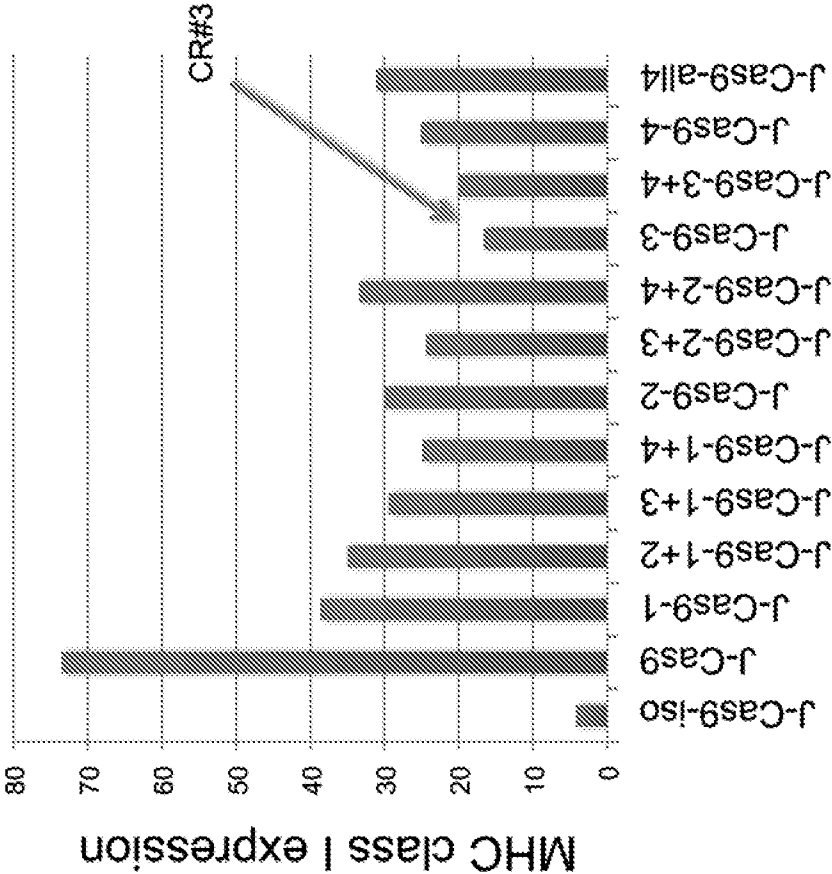


FIG. 19E

TAP1 CRISPR expression reduces MHC-I surface expression in Jurkat T cells

TAP1	
CR#1	TTGGCACTCGGACGCCGTCC(CGG)
CR#2	TCGGGGTACCCGGAGCTTC(AGG)
CR#3	CCGGTCCGGGATAGCACCC(AGG)
CR#4	TGGTGCTATCCGGGACCCG(GGG)



48 hrs IFNg, W6/32 1:200

FIG. 20A

TAP1 CRISPR expression reduces MHC-I surface expression in Jurkat T cells

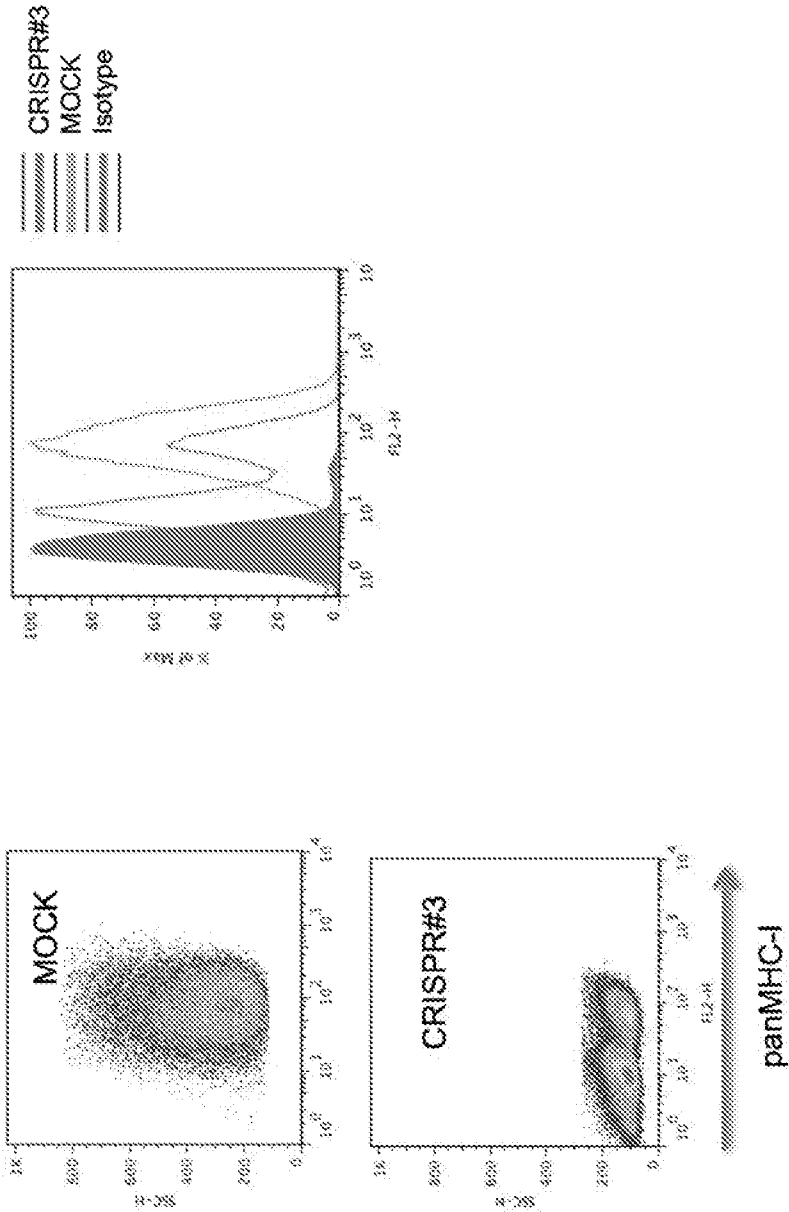


FIG. 20B

48 hrs IFNg, W6/32 1:200

Eliminating HLA surface expression in Jurkat (Cas9) T cells

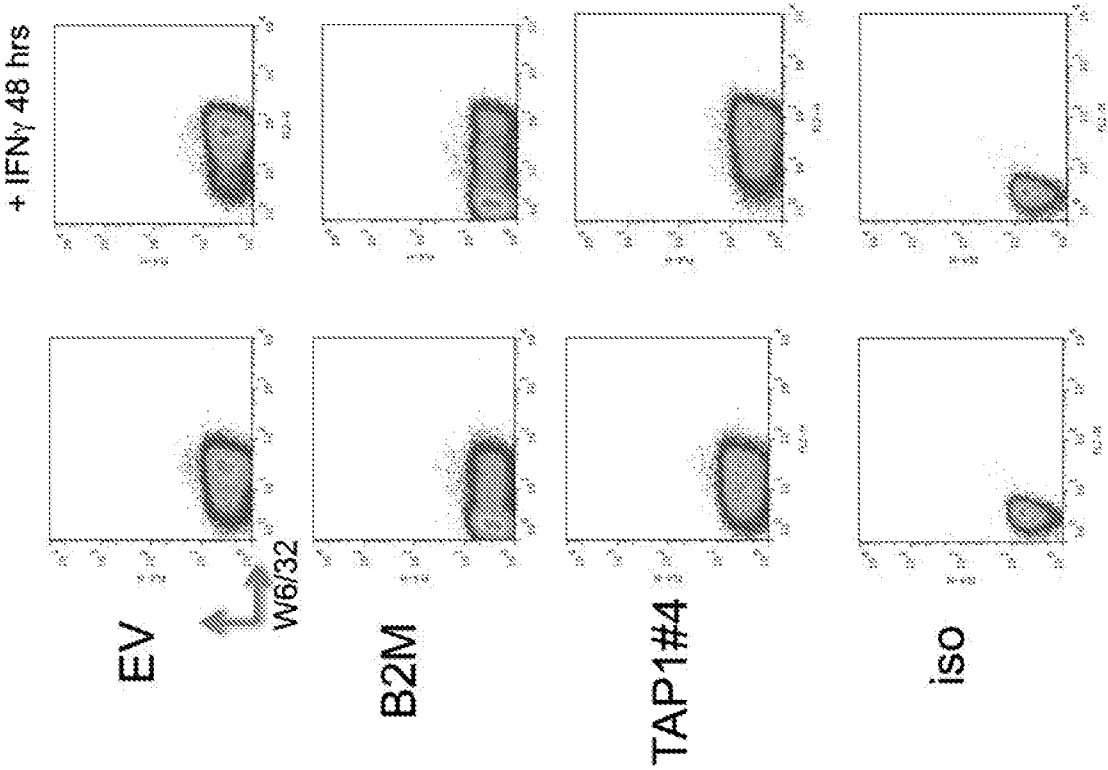


FIG. 20C

Eliminating HLA surface expression in Jurkat (Cas9) T cells

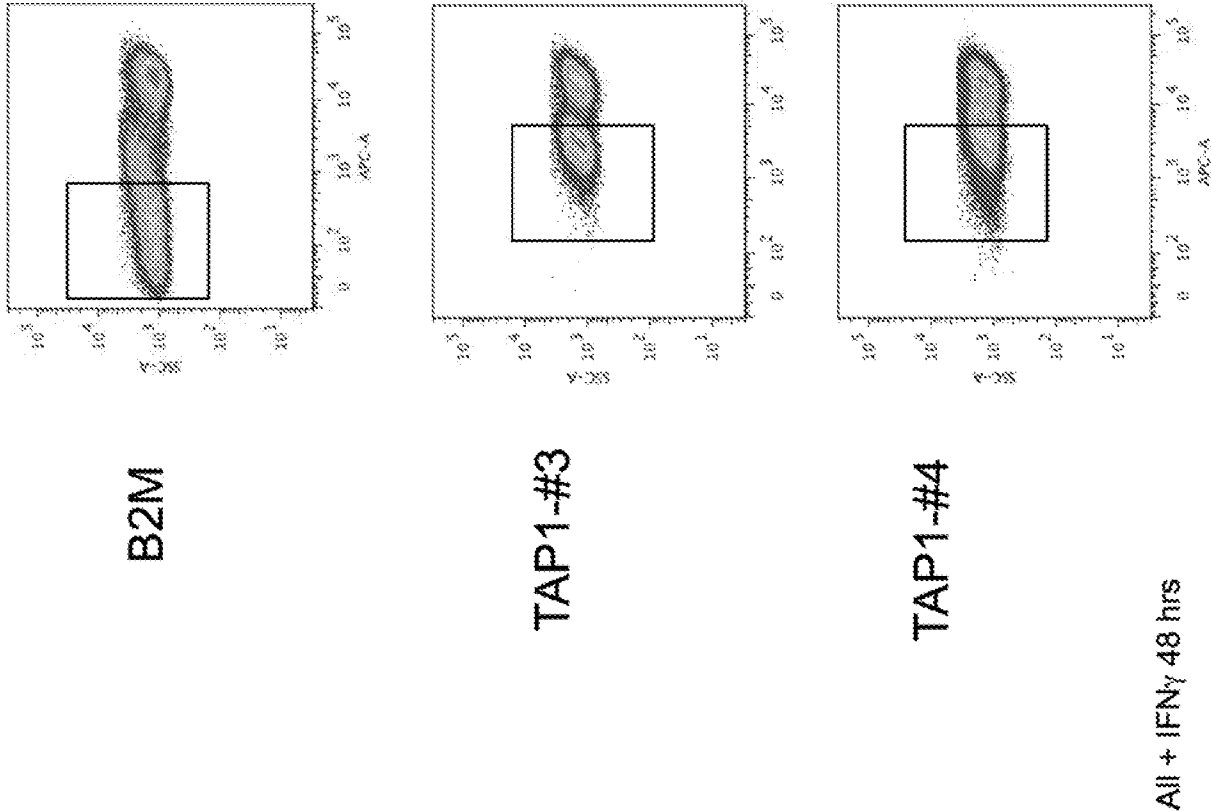


FIG. 20D

Expression of pan-HLA-TALENs in 293T and HuES9

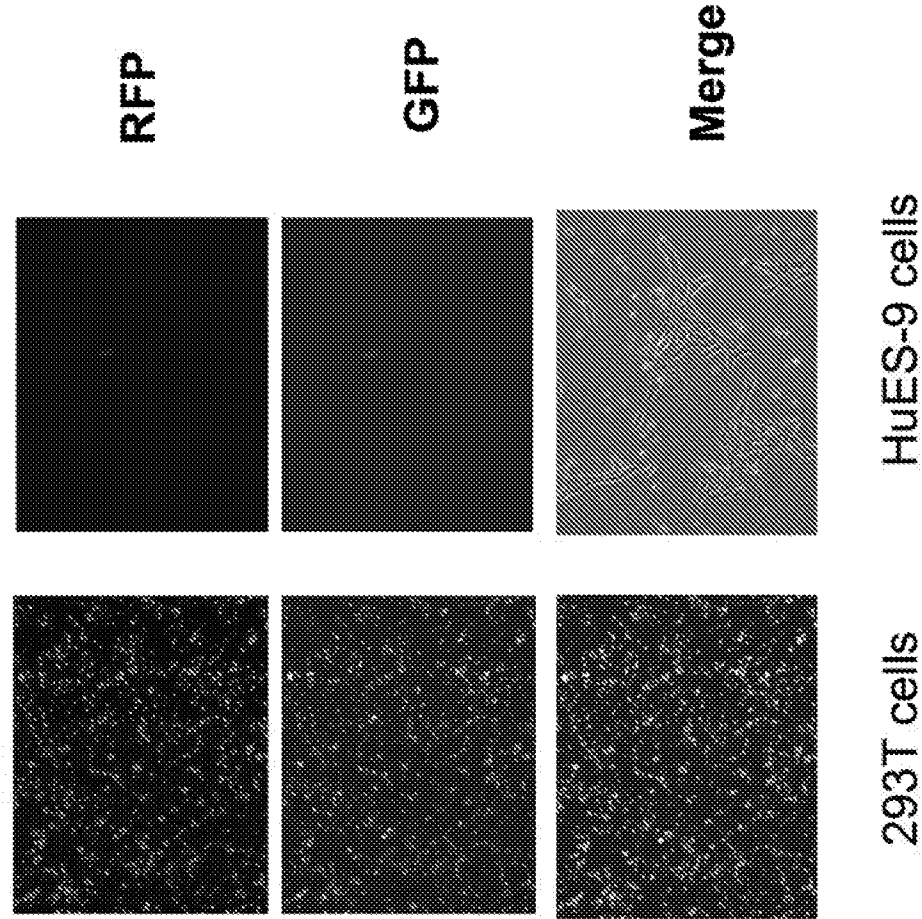
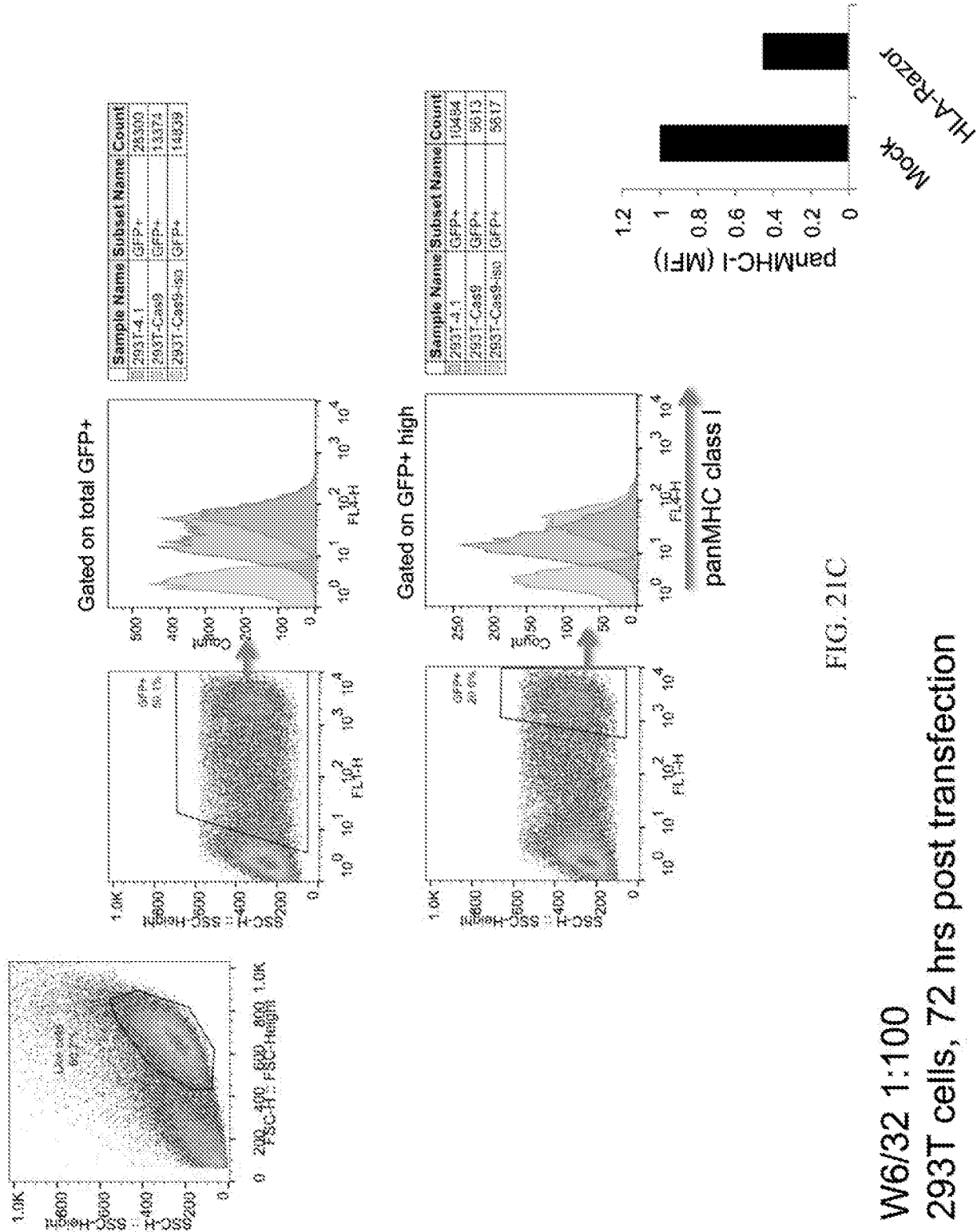
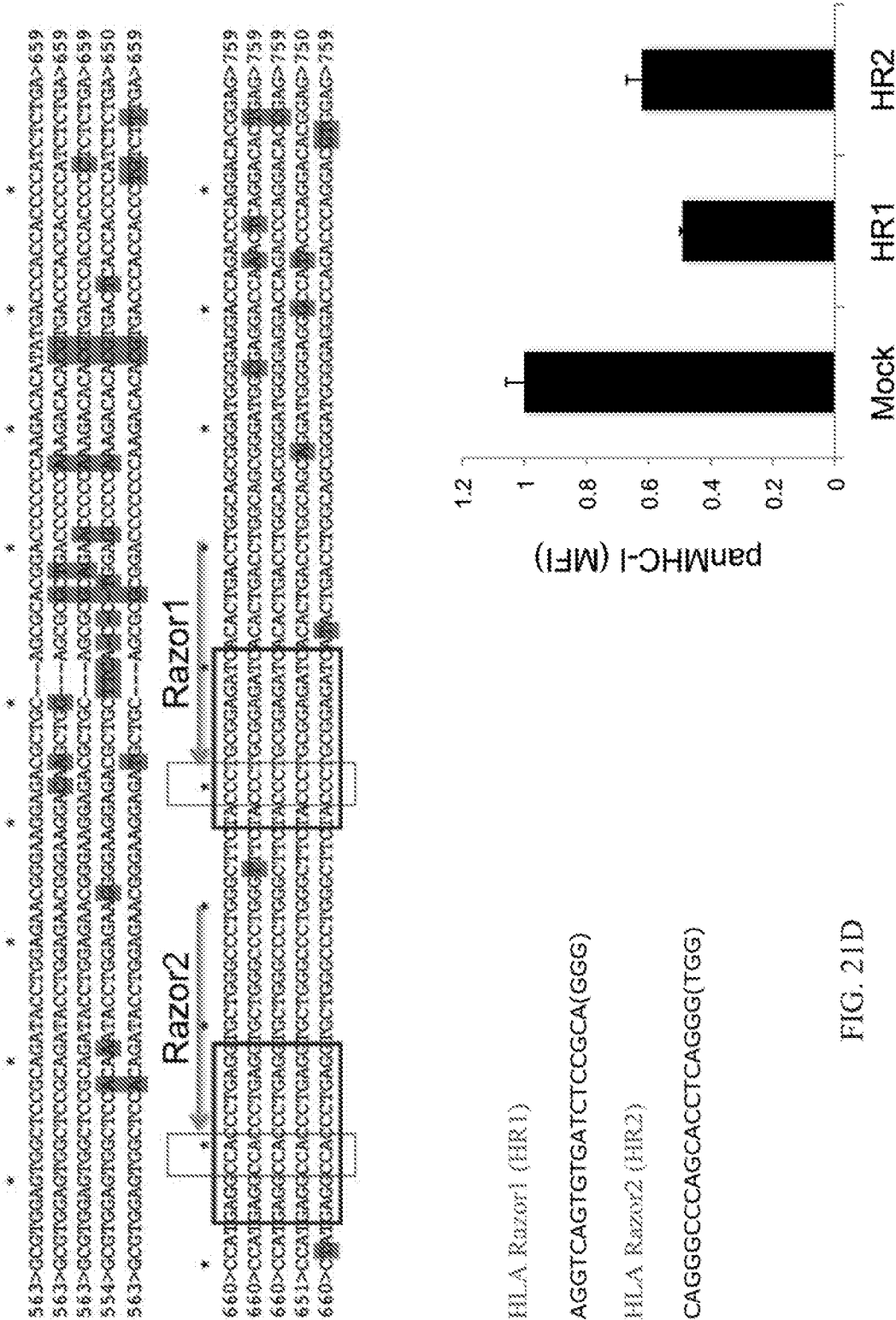


FIG. 21B

HLA-Razor CRISPR blunts MHC class I expression



Comparison of the Activity of two different HLA Razors



Schematic of PD-L1 and HLA-G knock-in strategy

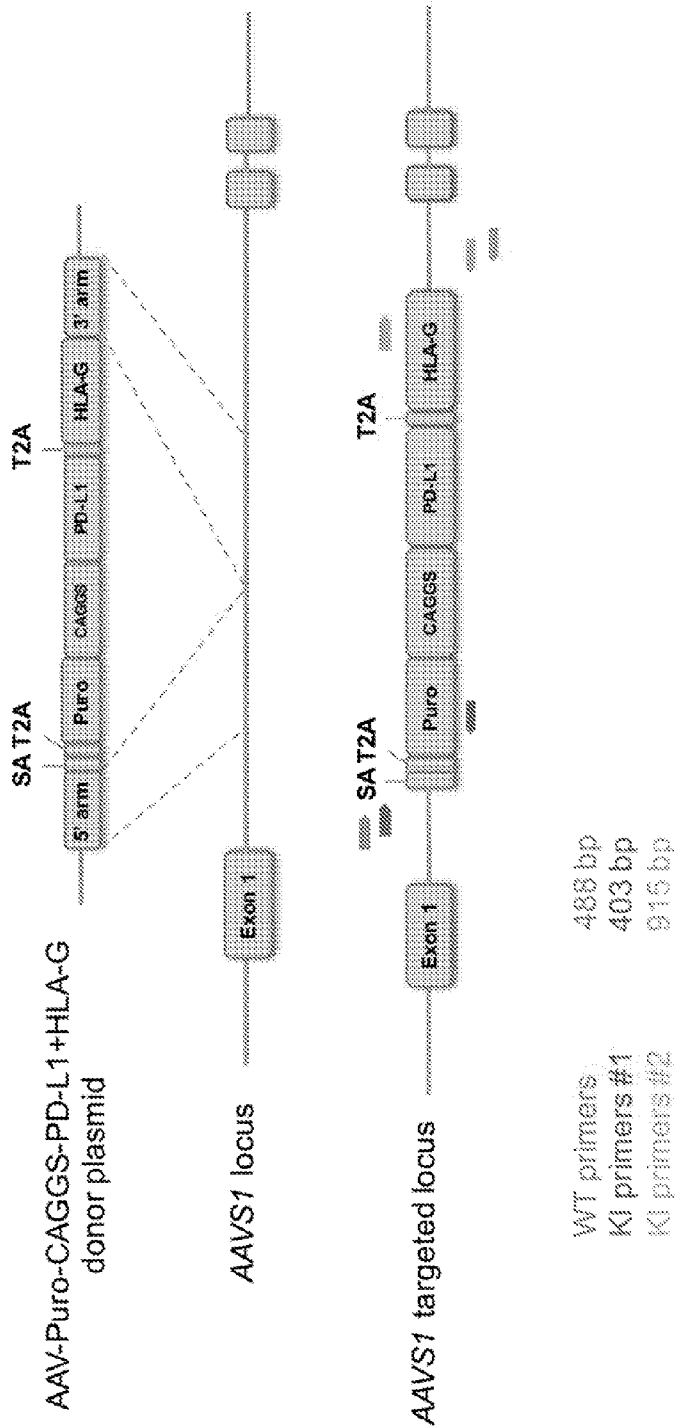


FIG. 22A

Design of knock-in donor plasmid

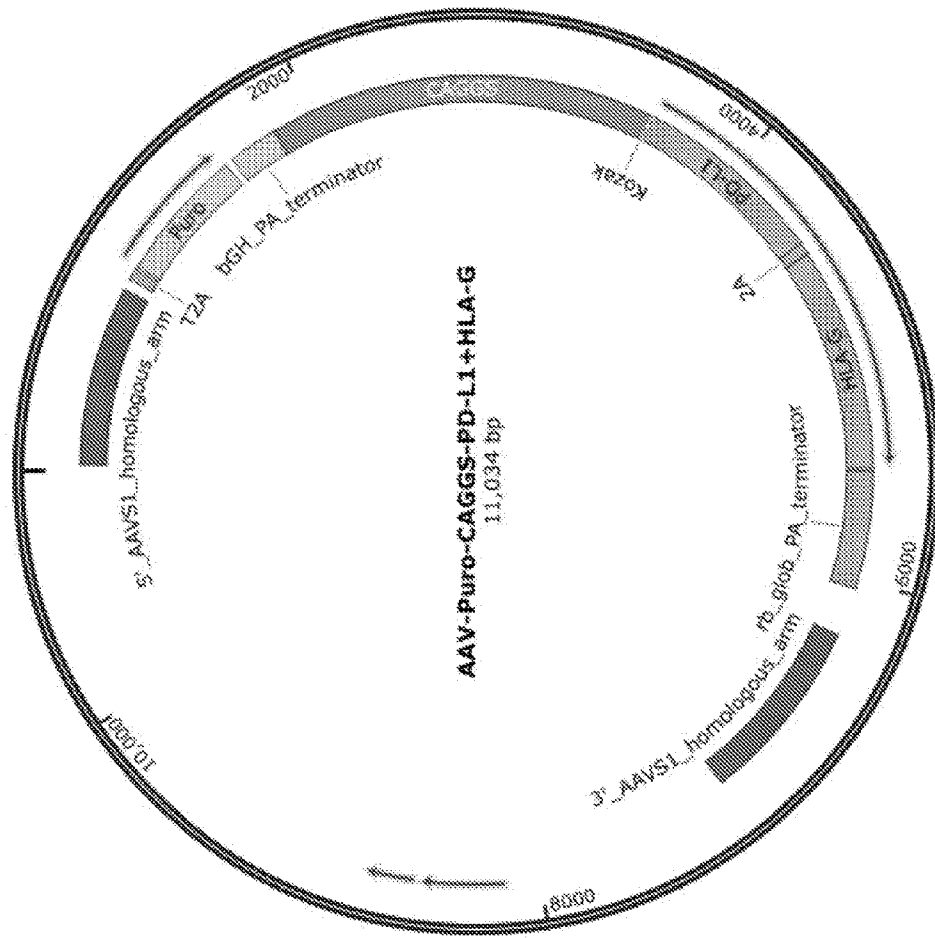


FIG. 22B

Ectopic PD-L1 and HLA-G expression in 293T cells

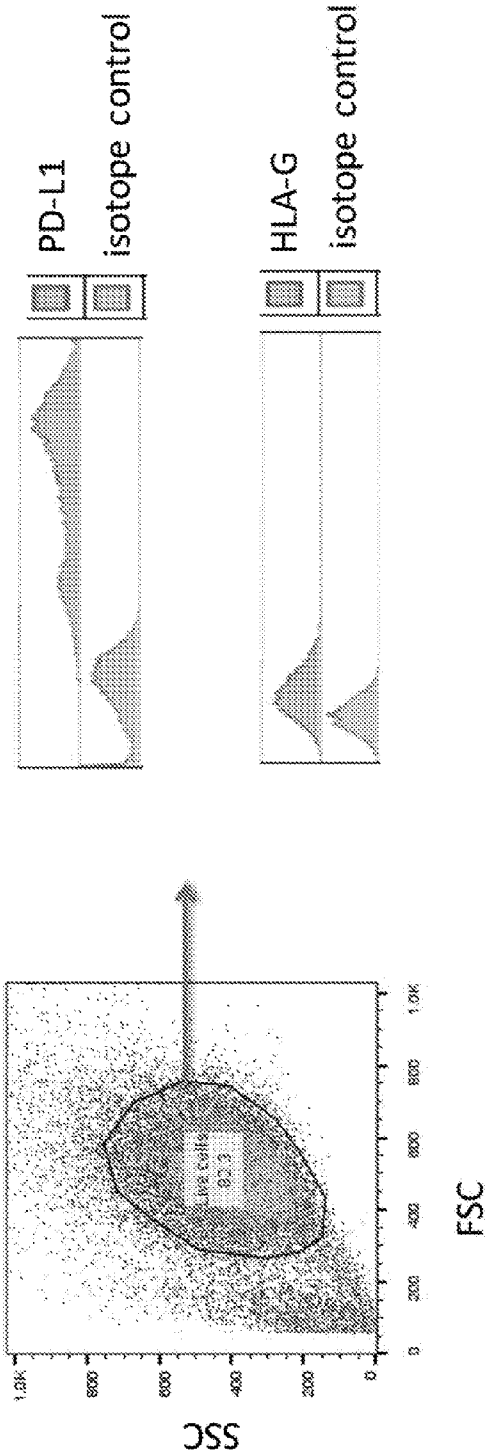


FIG. 22C

Ectopic HLA-G expression in JEG-3 cells

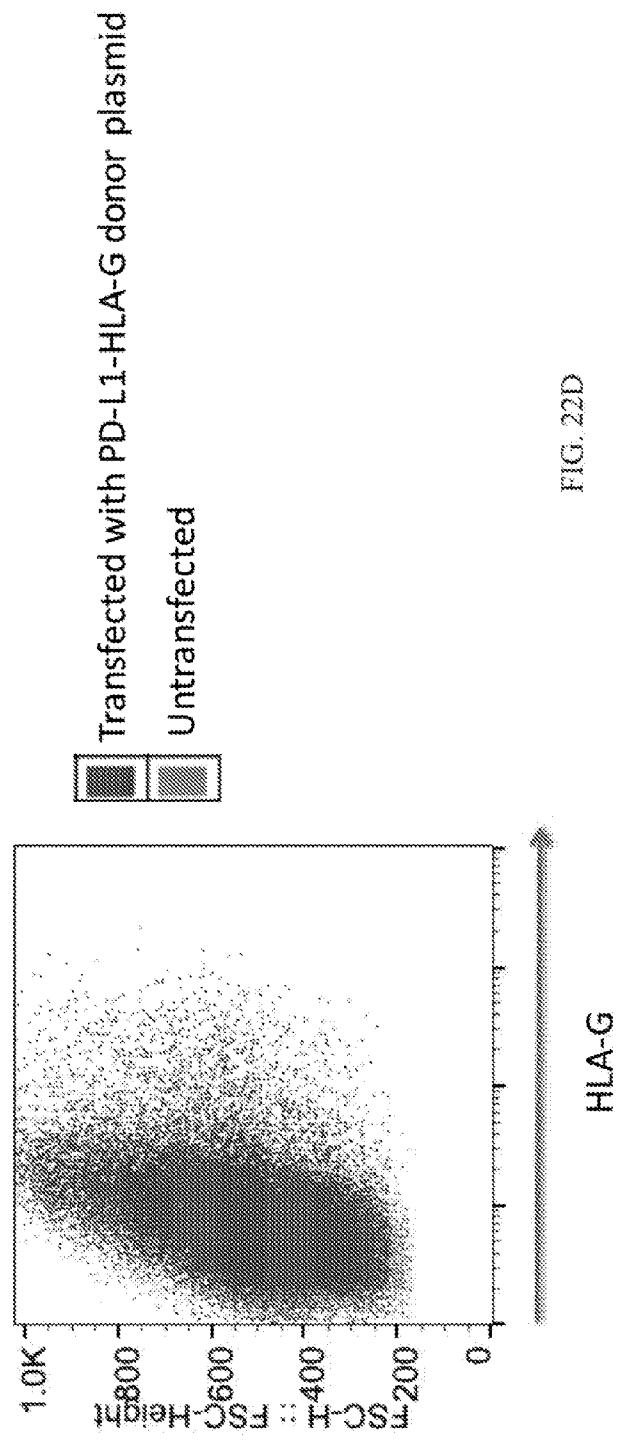
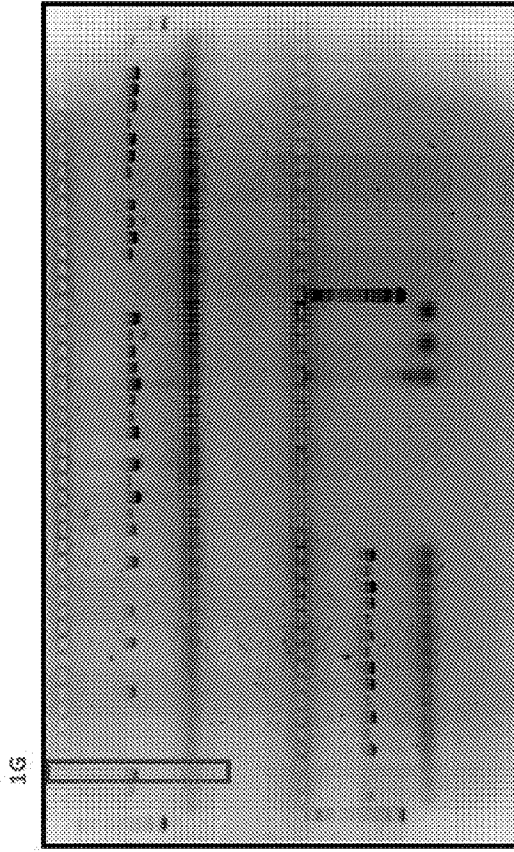


FIG. 22D

KI primers #1

PCR screening confirms 1G as a heterozygous KI clone for PD-L1/HLA-G

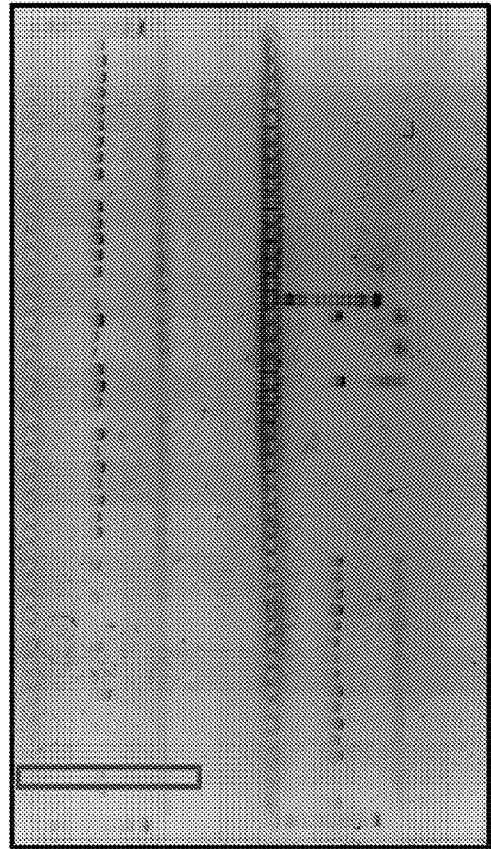


HuES8

FIG. 22E

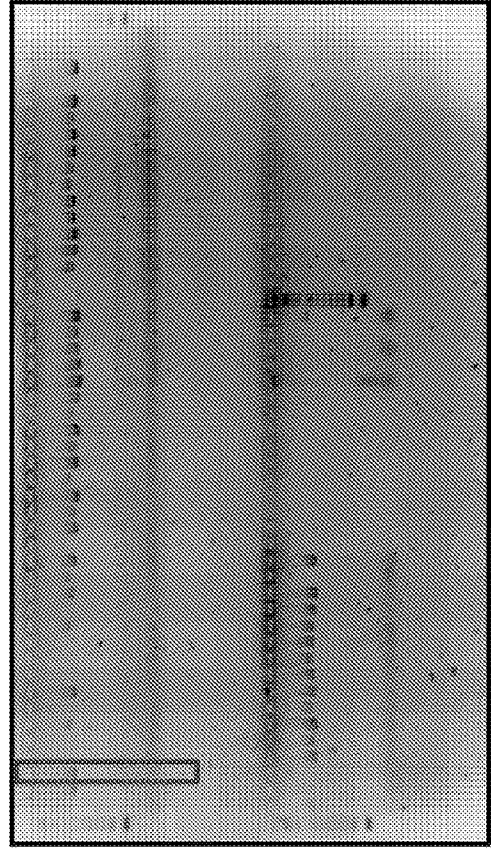
WT primers

1G



KI primers #2

1G



Stable PD-L1 and HLA-G expression from safe harbor locus in HuES8

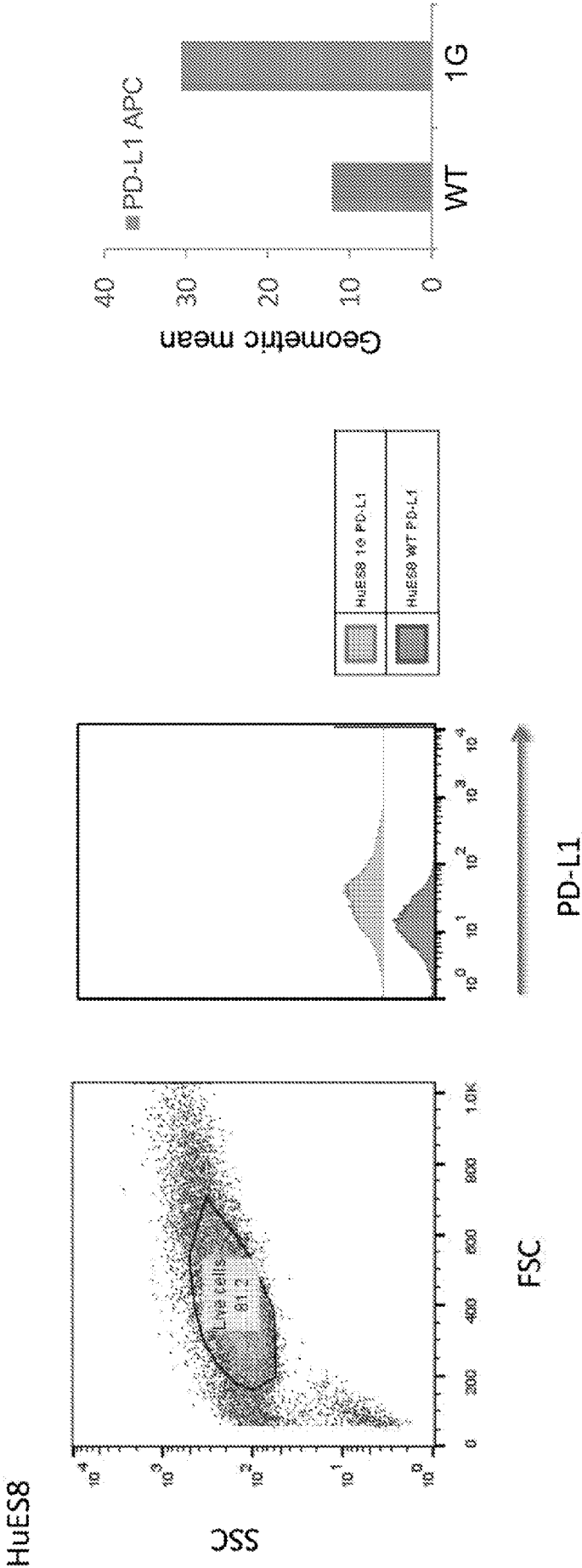
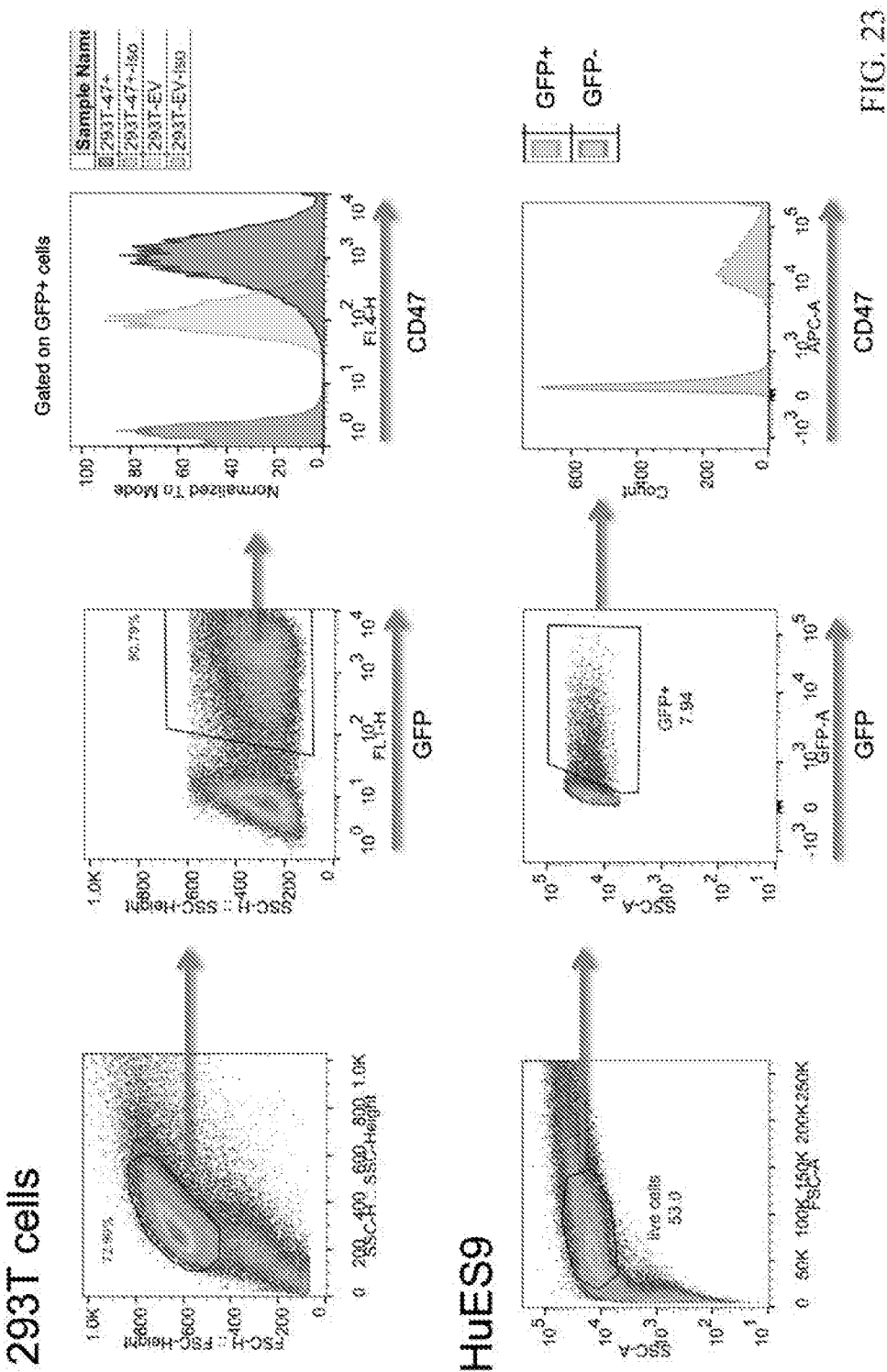
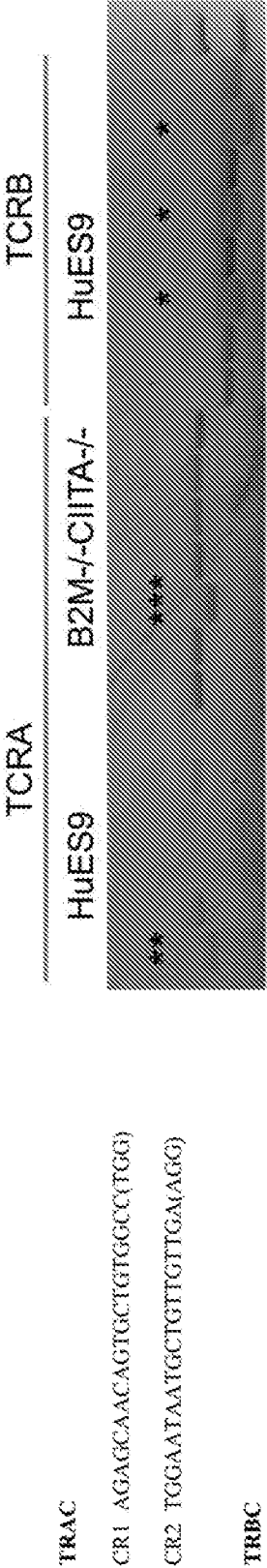


FIG. 22F

Ectopic CD47 Expression in 293T and hPSCs



Deletion of TRAC and TRBC in HuES9 to disrupt TCR Expression



**TCRA KO in HuES9

*TCRB KO in HUES9

***TCRA KO in HuES9 B2M-/CIITA-/- . In fact this is now a triple knock-out stem cell line for B2M-/-, CIITA-/-, TCR-/-, which upon differentiation into T cells will be devoid of MHC-I and -II and no TCR surface expression; the perfect blank canvas for introducing a Chimeric Antigen Receptor (CAR). Additional modifications such as deletion of the inhibitory receptors PD-1 and CTLA4, will make this cells powerful tools for cancer immunotherapy.

FIG. 24

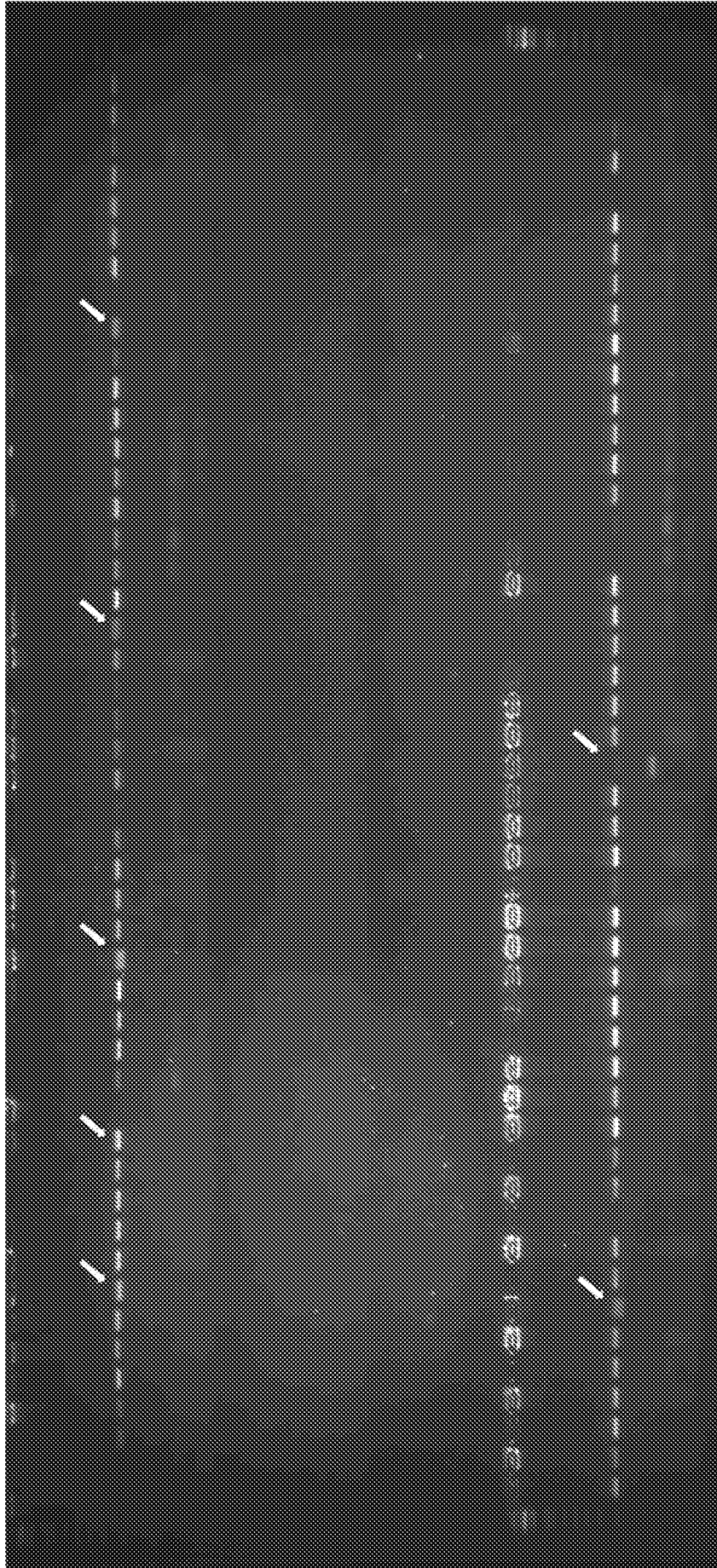
CD274/B7-H1/PD-L1

CRISPR gGTAGAAAACAATTAGACC(TGG)

KO in JEG-3, a choriocarcinoma cell line and in 2 melanoma cell lines, 501 and MalMe.
CRISPRs targeting PD-L1 are very useful in breaking tolerance in cancer immunotherapy!

FIG. 25A

Screening of targeted B7-H1 colonies



CRISPR Cutting Efficiency: 22/265 => 8.3%
JEG-3 cells

FIG. 25B

Reconfirmation of 501 Melanoma KO

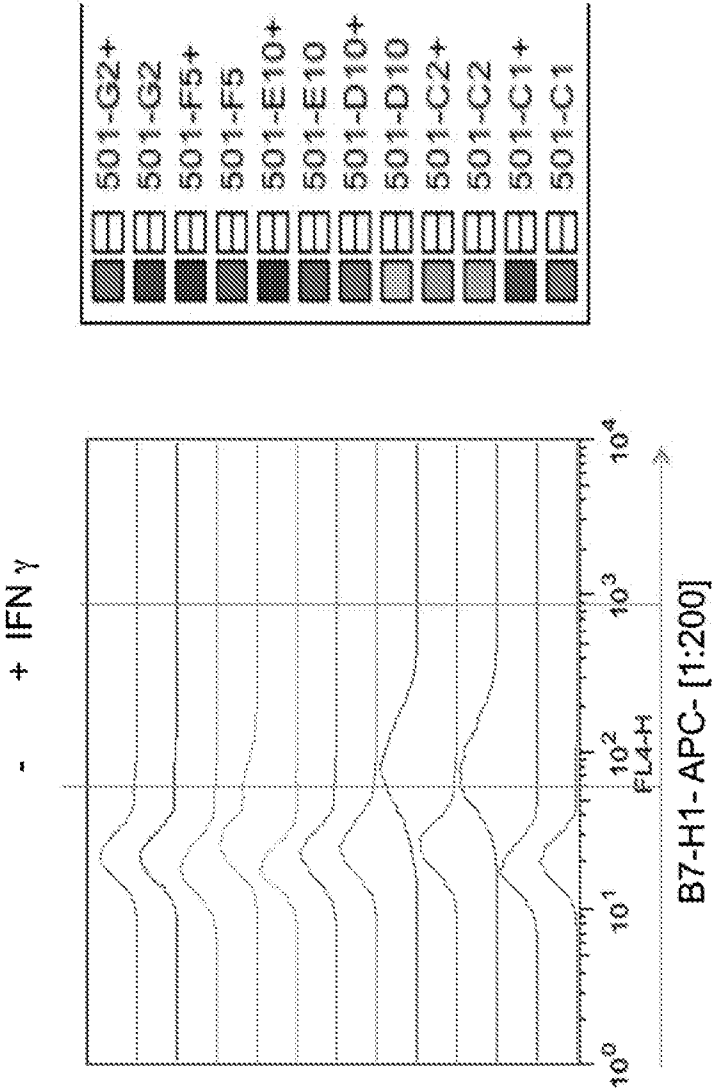


FIG. 25C

Reconfirmation of MalMe melanoma KO clones

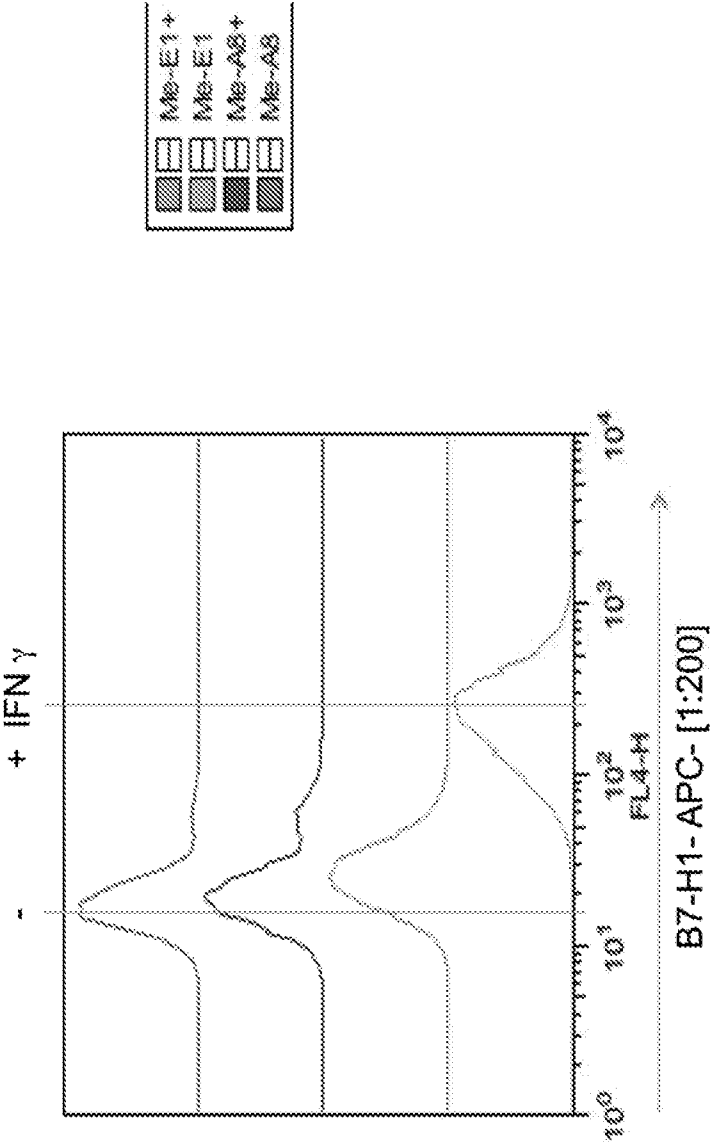
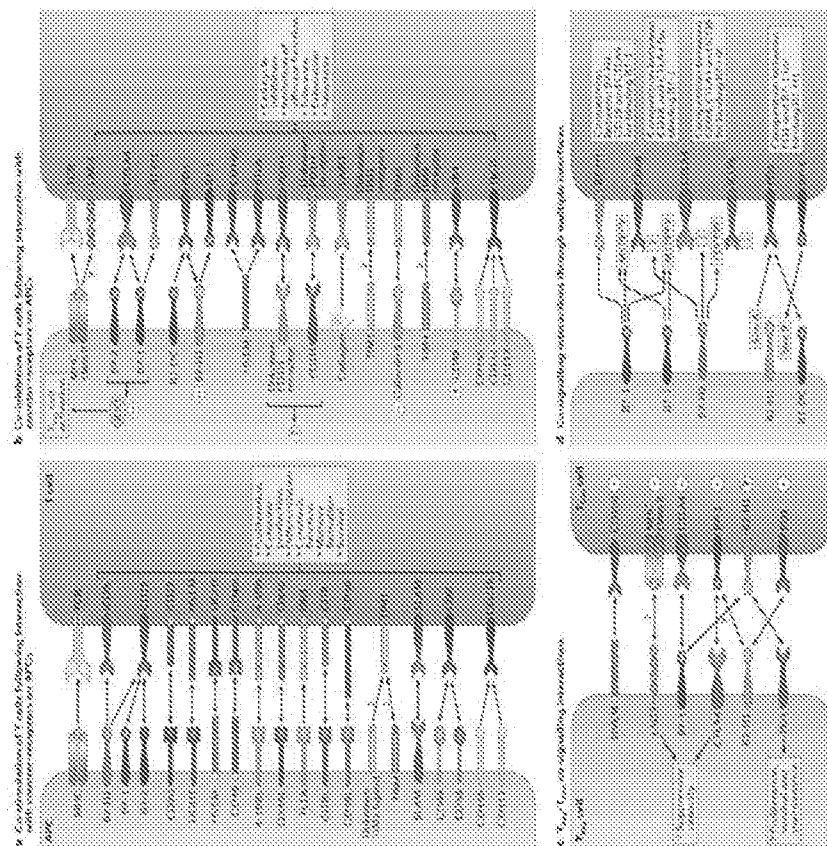


FIG. 25D

Co-Stimulatory/Inhibitory Molecules and their Receptors on T cells



Staphylococcus aureus

Chen and Flies, Nat Immunol 2013

FIG. 26A

Dual Guide Targeting of TIGIT in 293T Cells

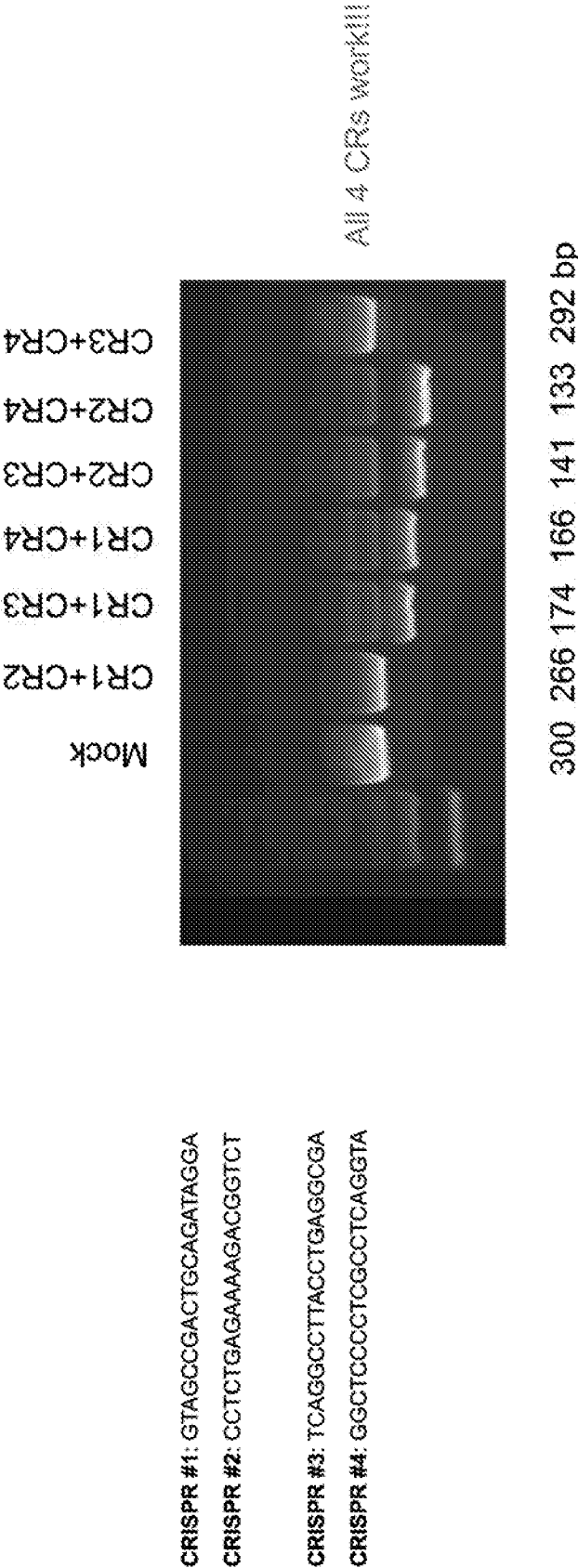


FIG. 26B

Dual Guide Targeting of TIM3 in 293T Cells

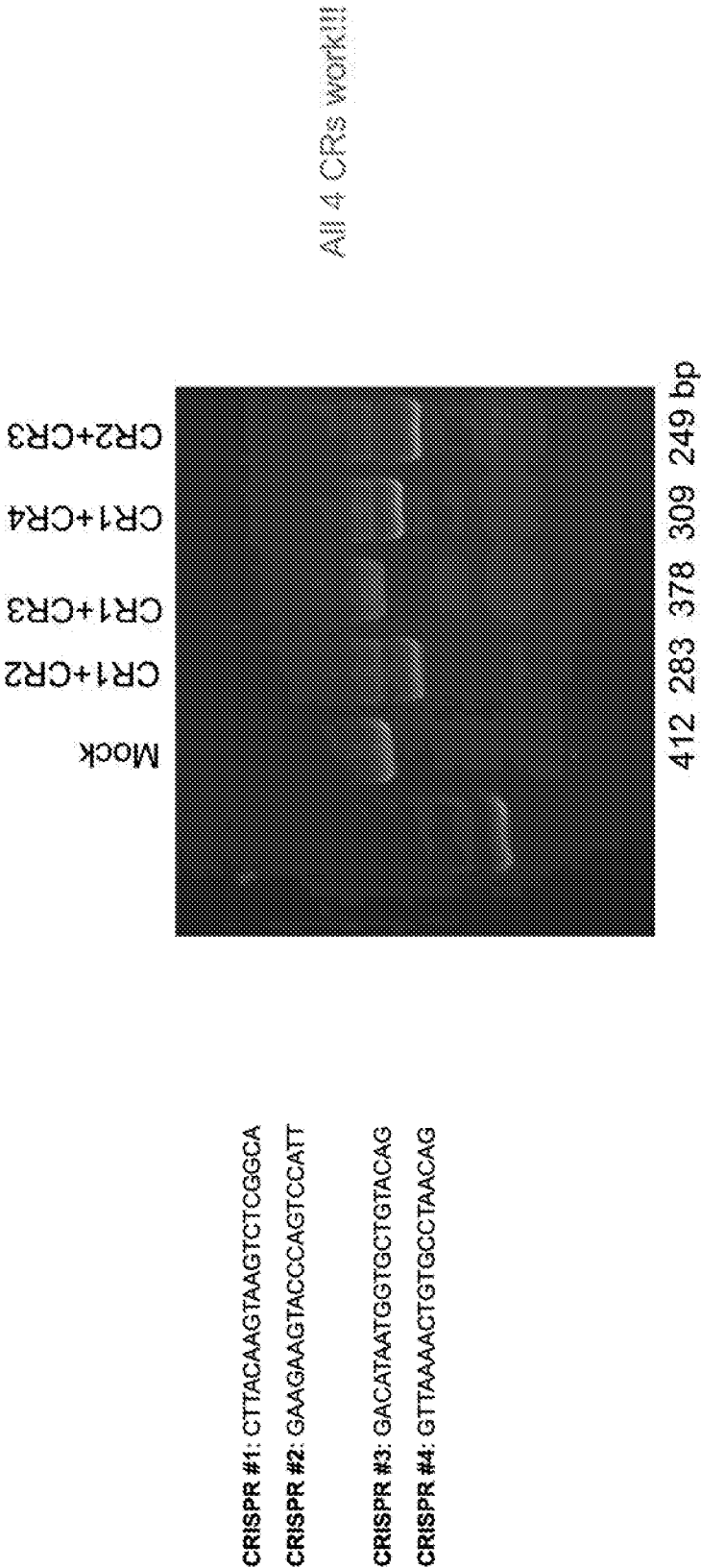


FIG. 26C

Dual Guide Targeting of HVEM in 293T Cells

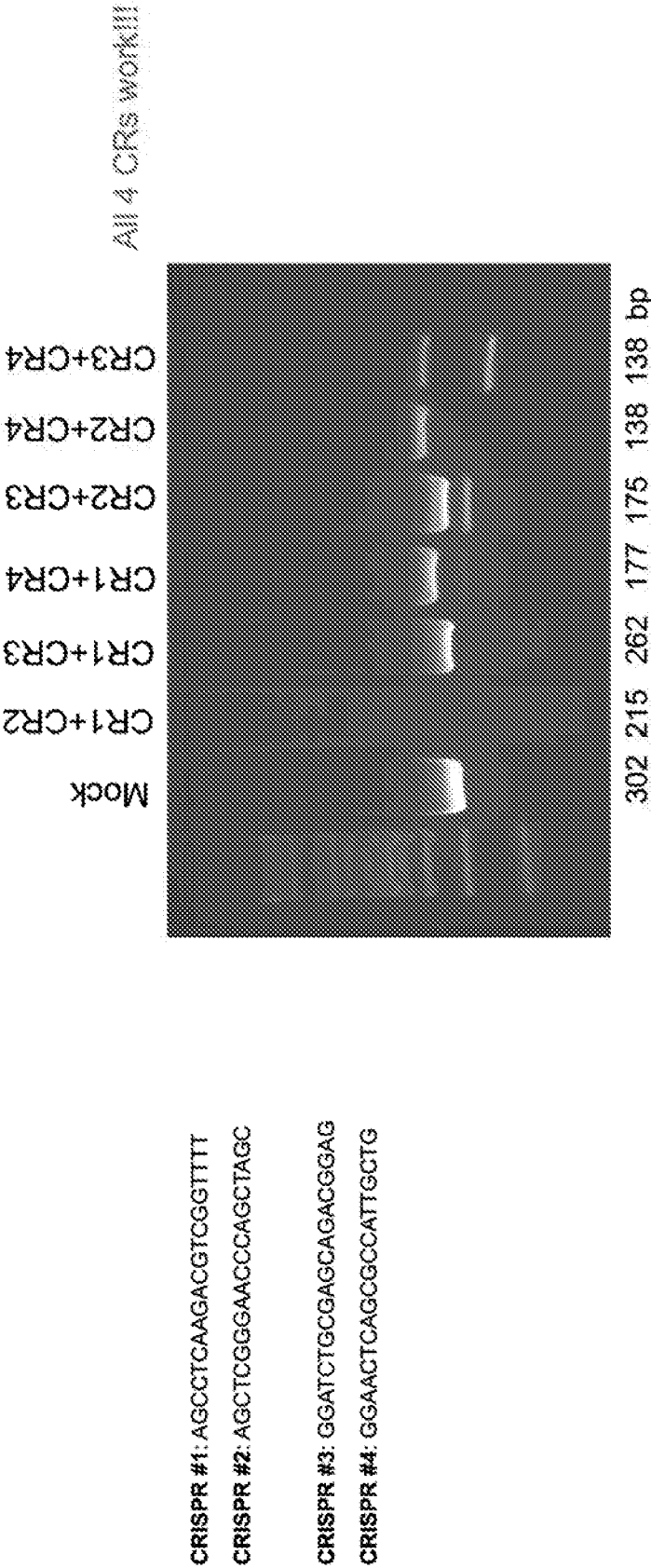
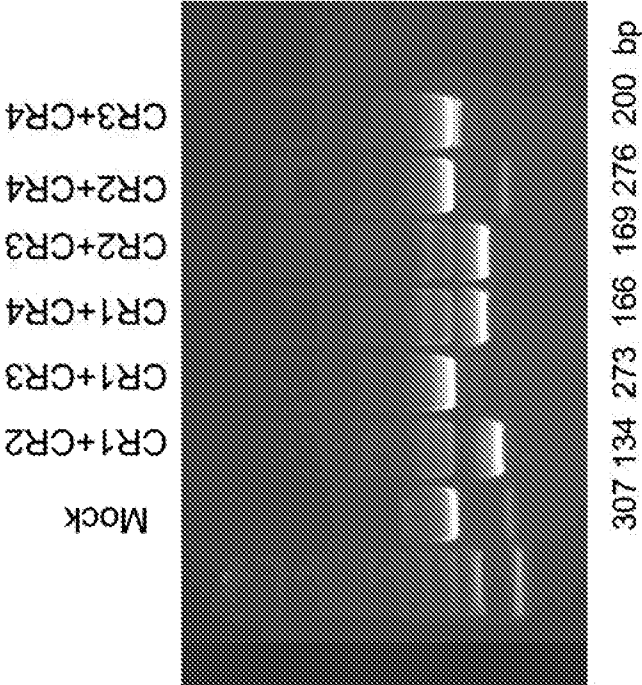


FIG. 26D

Dual Guide Targeting of 2B4/CD244 in 293T Cells



All 4 CRs work!!!

FIG. 26E

Dual Guide Targeting of CD28 in 293T Cells

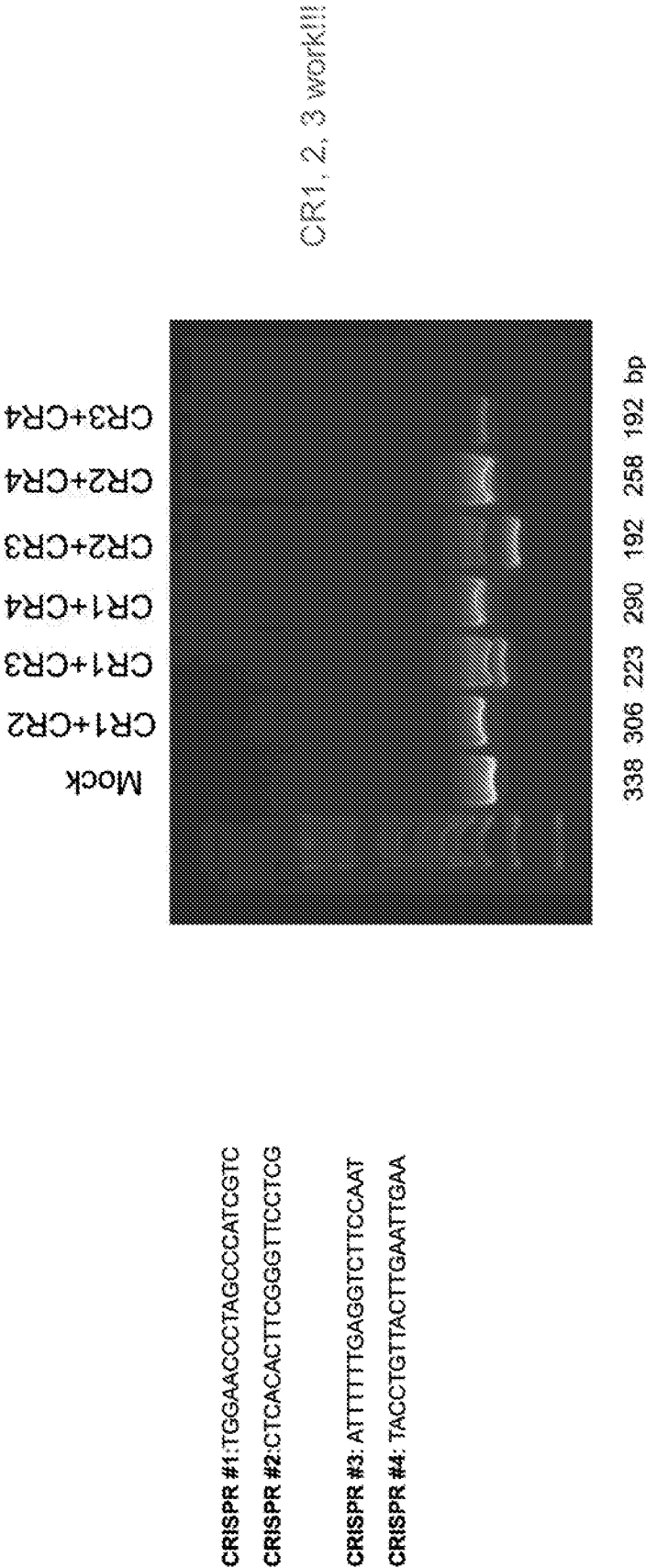


FIG. 26F

Dual Guide Targeting of OX40 in 293T Cells

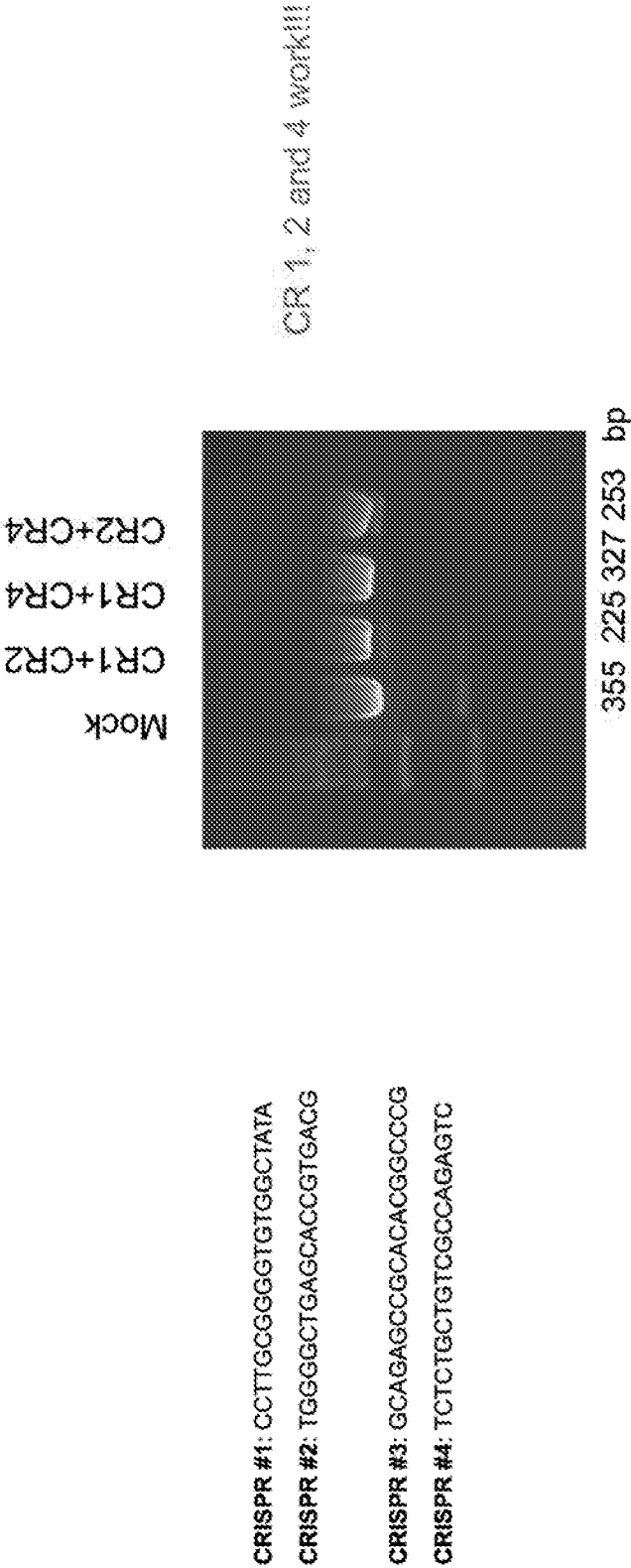


FIG. 26G

Dual Guide Targeting of B71 in 293T Cells

CRISPR #1: ATGGTCCGGTTC TTGTACTC
CRISPR #2: TGGCACAAACTCGCATCTAC
CRISPR #3: TGCTGGGGACATGAATATA
CRISPR #4: GGTCACGTGGATAACACCTA

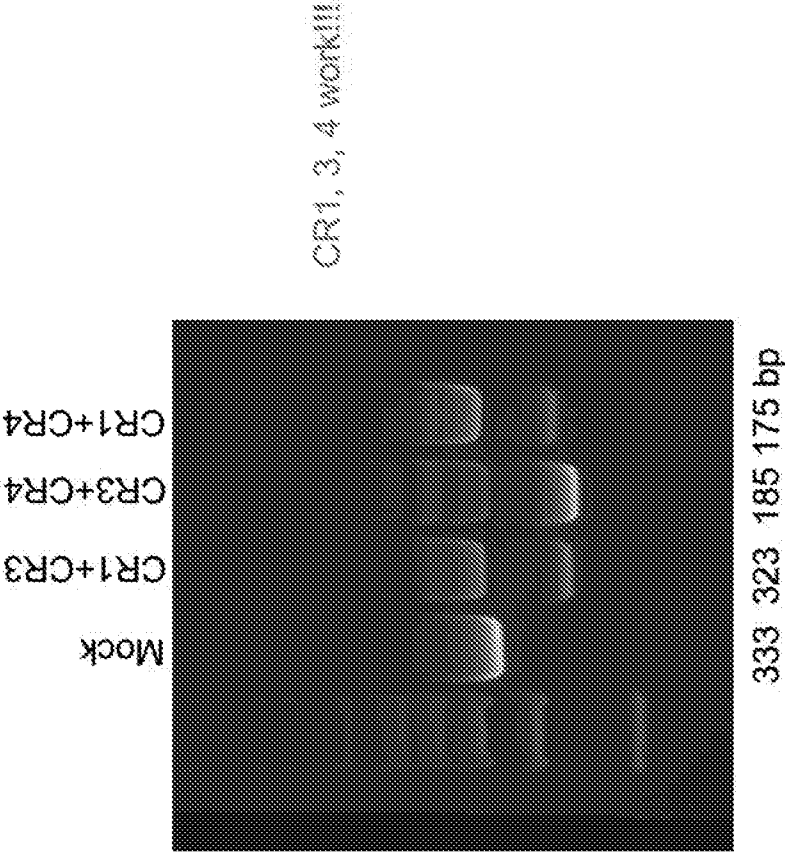


FIG. H

Dual Guide Targeting of CD226 in 293T Cells

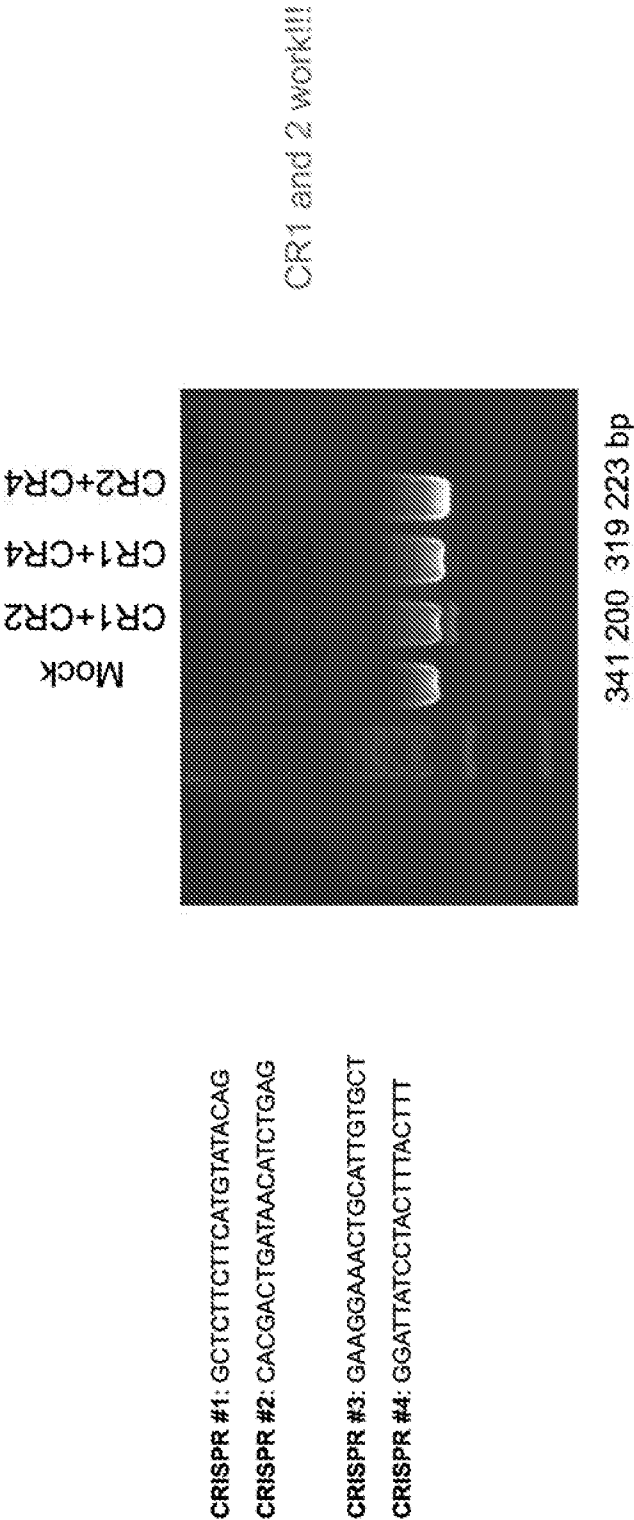


FIG. 26I

Dual Guide Targeting of CD2 in 293T Cells

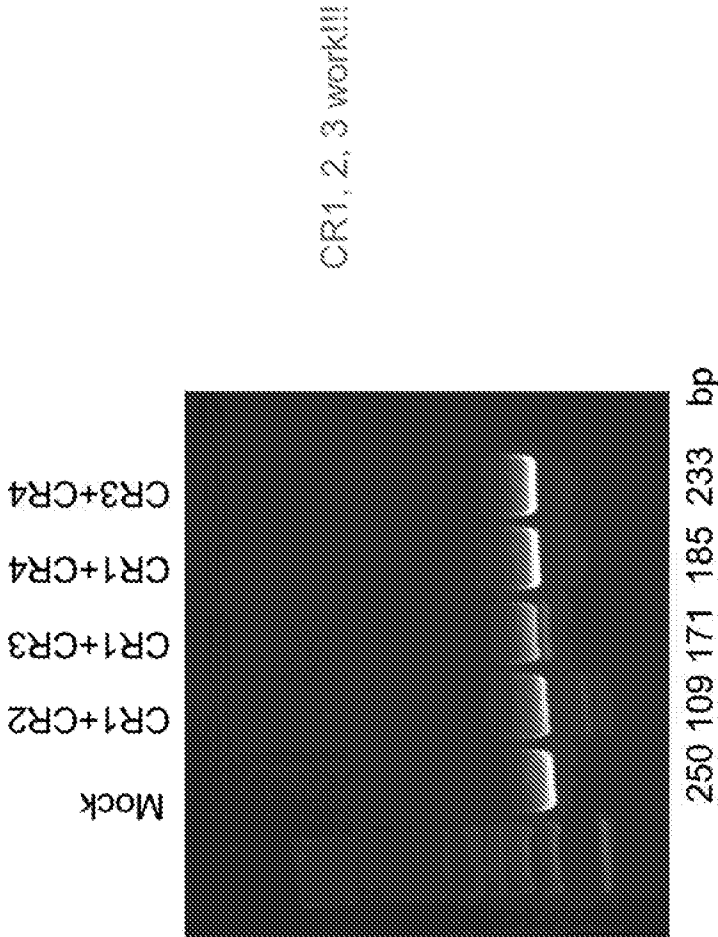


FIG. 26J

Dual Guide Targeting of LAG3 in 293T Cells

CRISPR #1: CCTTTGGAGGGCTCAGCGC
CRISPR #2: GACCATAGGAGAGATGTGGG
CRISPR #3: GGGTGGCTCCAGgtaaaacg
CRISPR #4: CCGCCATCCCCGTTTACC

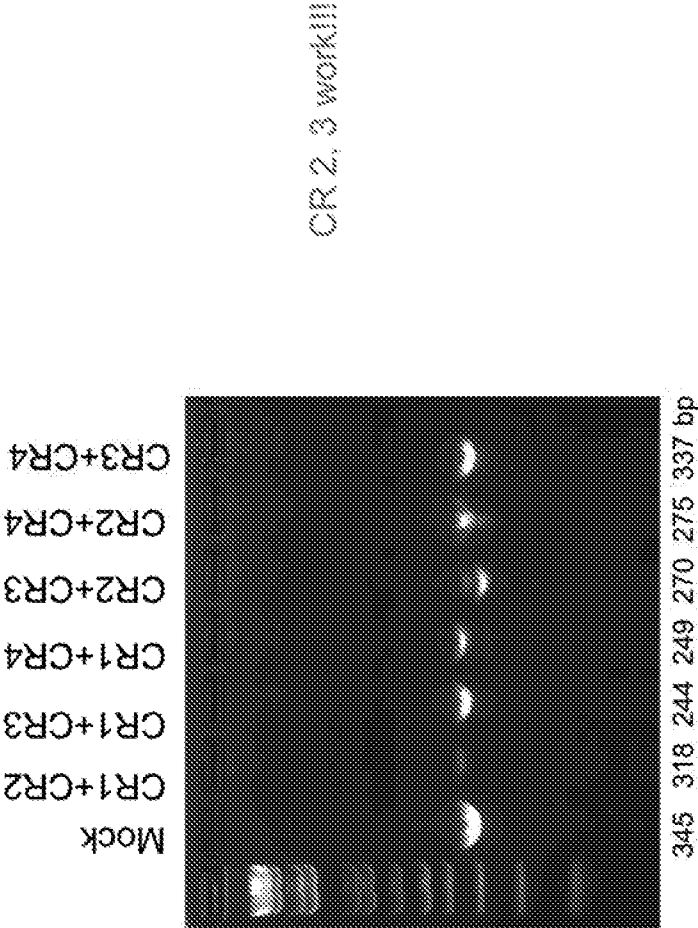


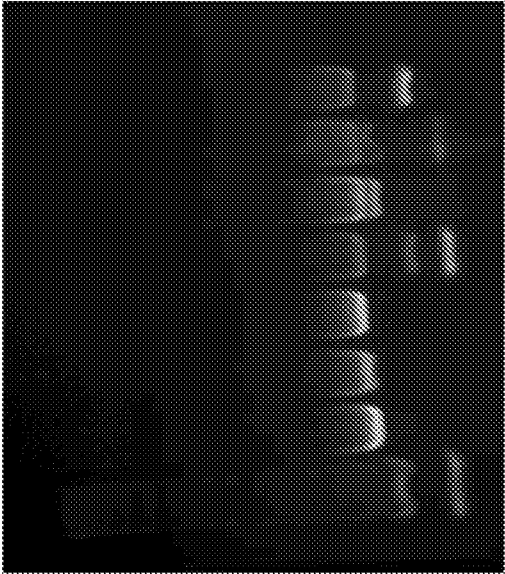
FIG. 26K

Dual Guide Targeting of **BTLA** in 293T Cells

CRISPR #1: GGTCAGTTTACCTACCCGAG
CRISPR #2: TTCCATCACTGATATGTC

CRISPR #3: CCTAAGCAGGTCCTTACCA
CRISPR #4: TAATCCATATCTGGACATC

Mock
CR1+CR2
CR1+CR3
CR1+CR4
CR2+CR3
CR2+CR4
CR3+CR4



All 4 CRs work!!!

FIG. 26L

Dual Guide Targeting of ICOS in 293T Cells

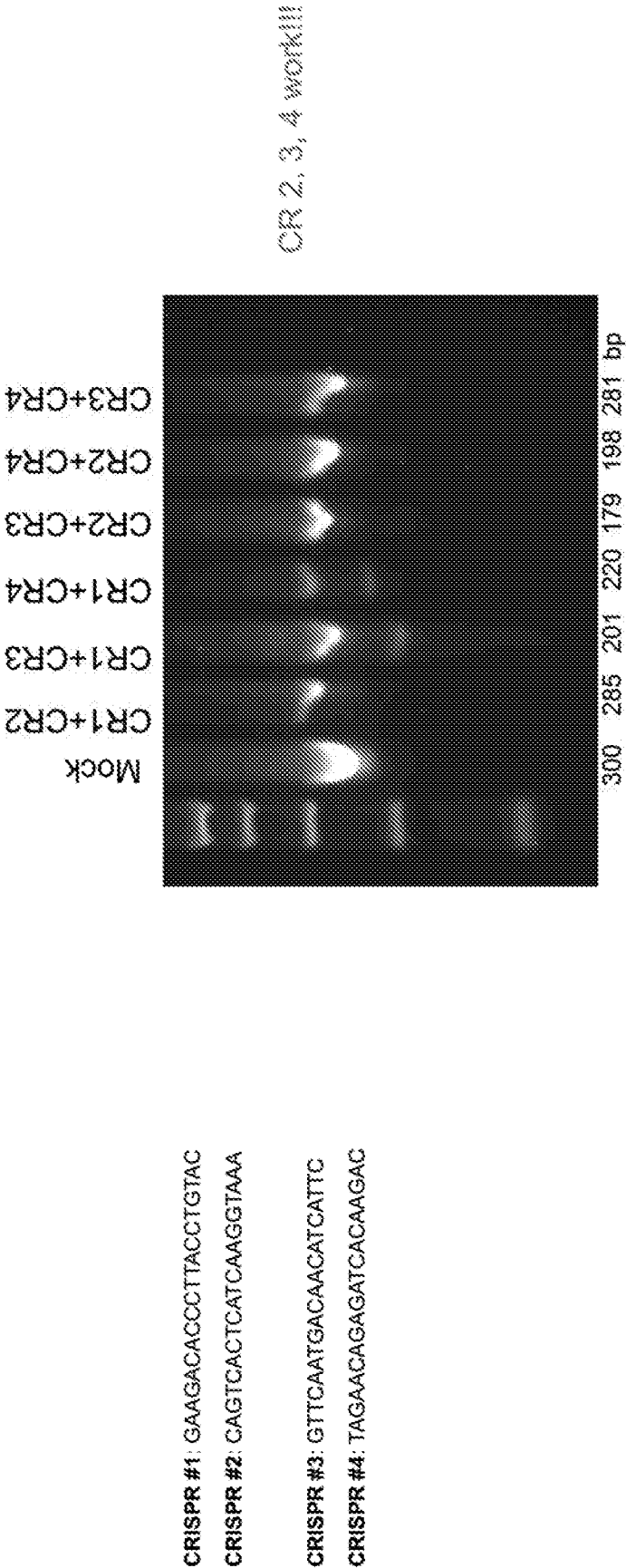


FIG. 26M

Dual Guide Targeting of CD27in 293T Cells

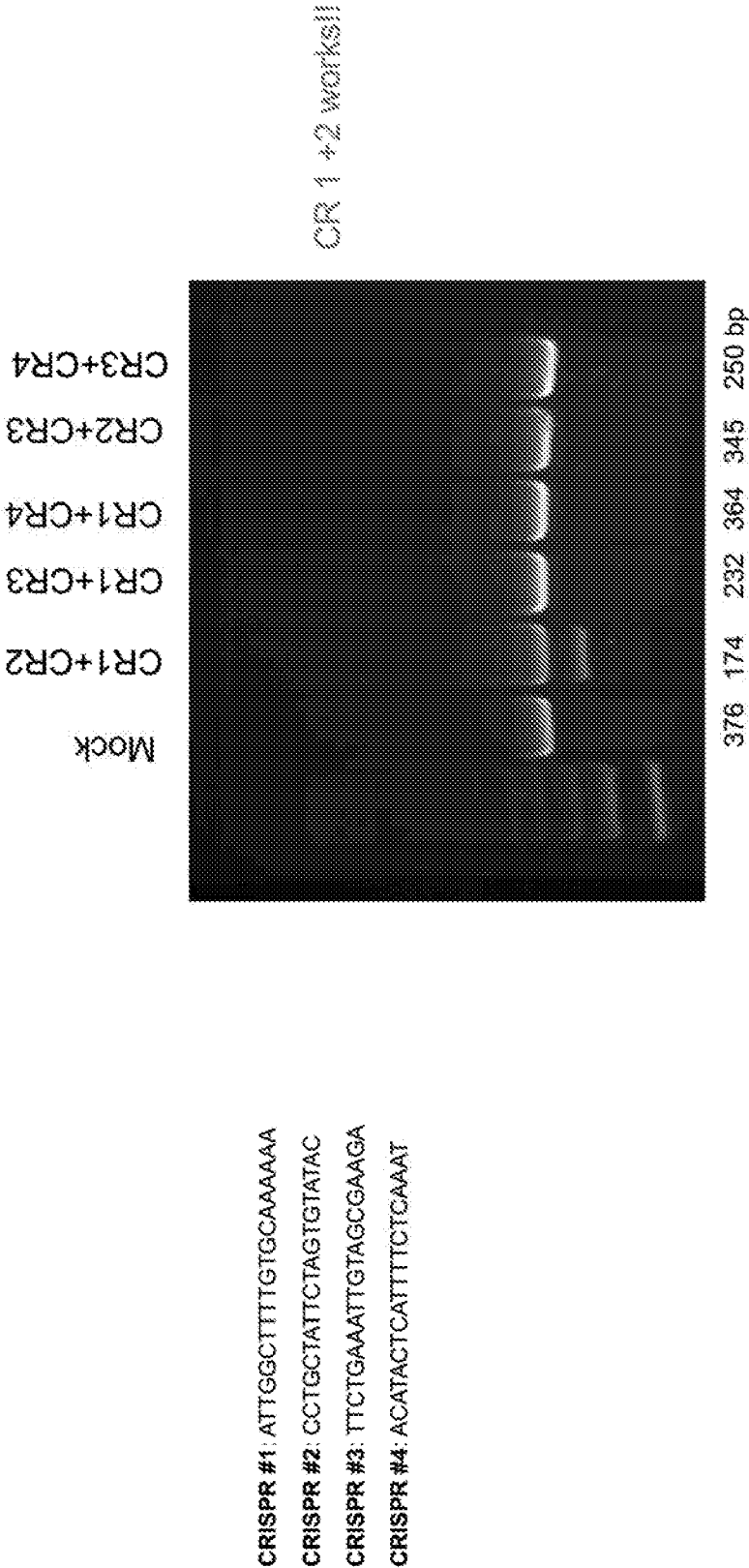


FIG. 26N

Dual Guide Targeting of ST2 in 293T Cells

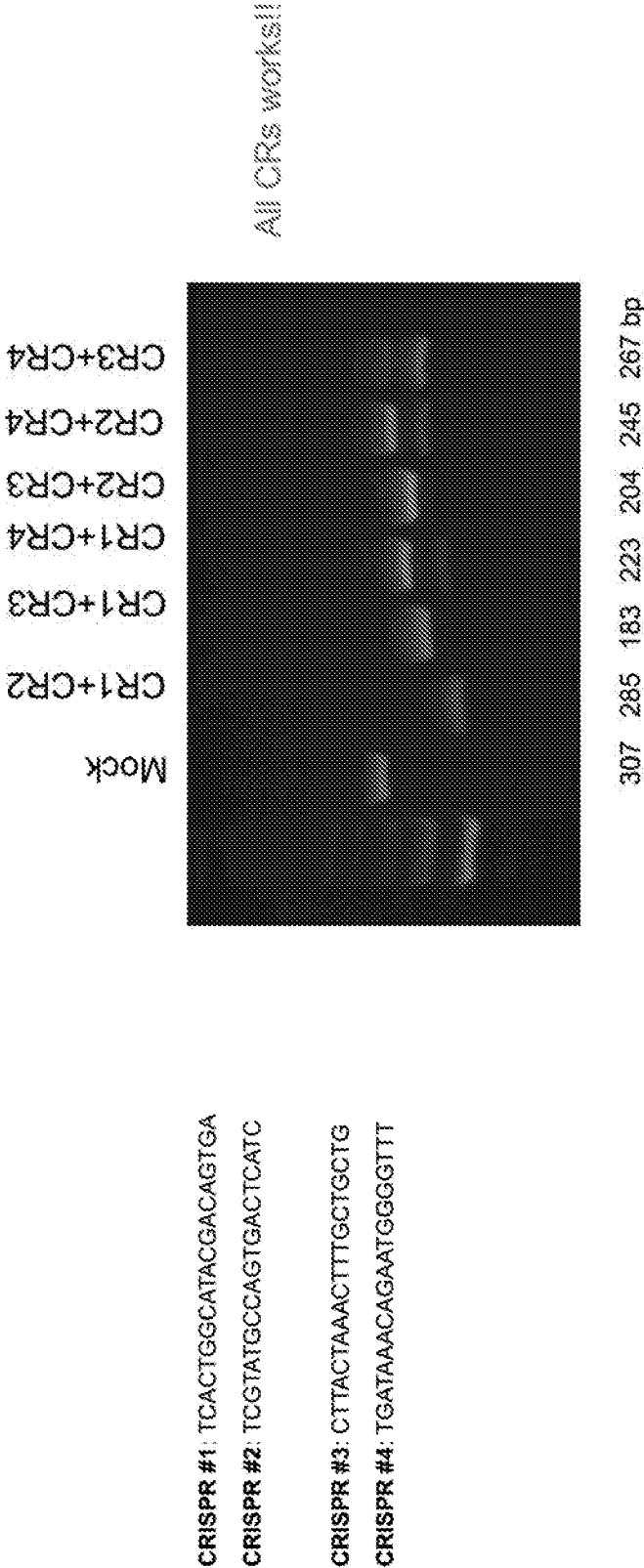


FIG. 260

Dual Guide Targeting of *GLTR* in 293T Cells

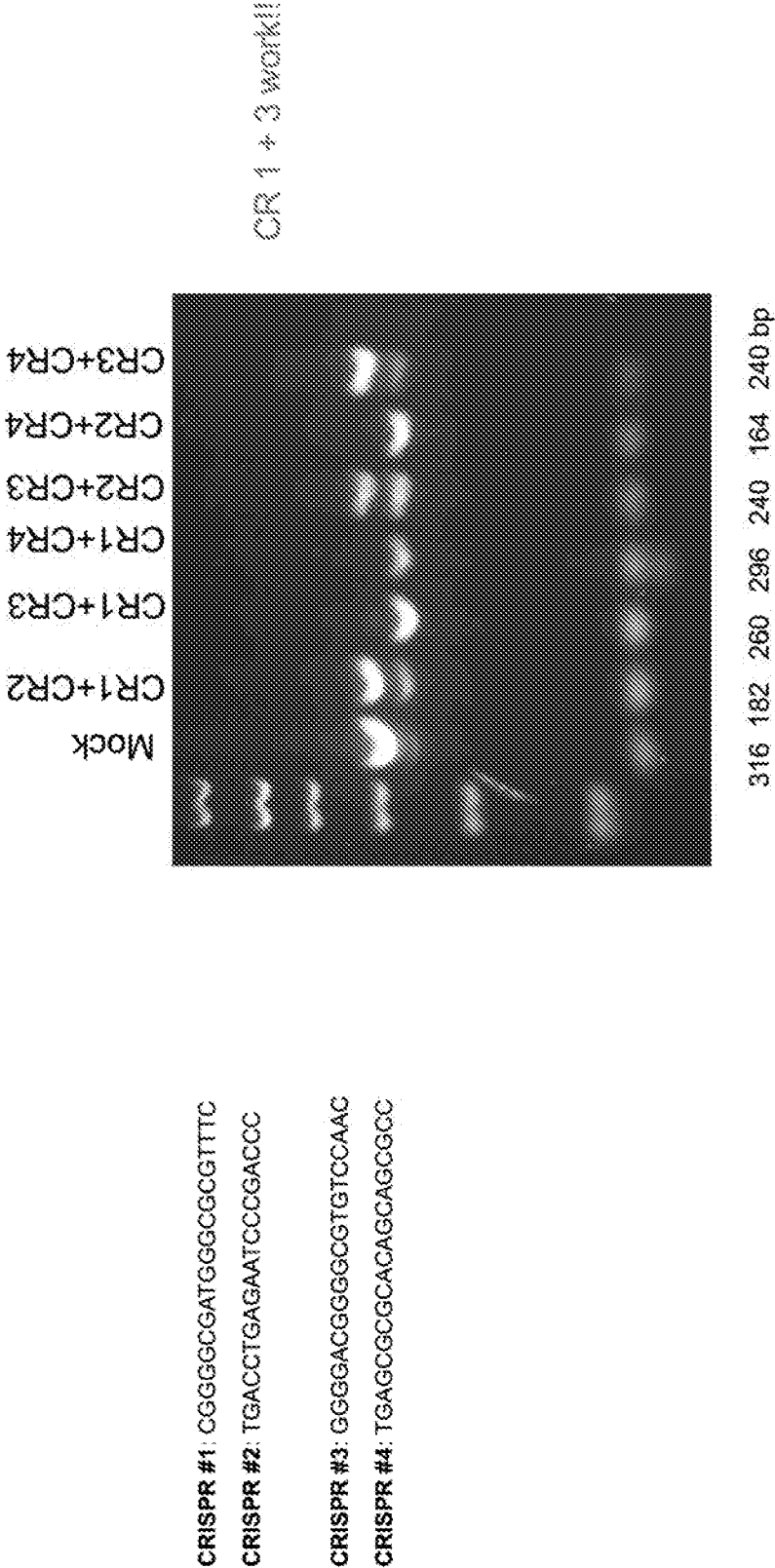


FIG. 26P

Various Cell Lines Tested

	HLA-A	HLA-B/C	NLRP5	CIITA	B2M	IRF1
HUES8	+	+				
HUES9			+	+	+	+
BJ-RiPSCs			+	+		
Thp1			+	+	+	+
Jurkat					+	+
Primary T cells					+	
HEK293T	+	+	+	+	+	+

HUES8 and HUES9 are human ES cell lines
BJ-RiPSCs is an iPSC line

All other enhanceosome components (RFX and NFY) were only tested in HEK293T cells at this point

FIG. 27

Modified ES cells can be differentiated into various different
Cell types with reduced or absent HLA expression

MPCs = Mesenchymal Progenitor Cells [Mesoderm]

ECs = Endothelial cells [Mesoderm]

Macrophages [Mesoderm]

Hepatocytes [Endoderm]

Beta-Cells [Endoderm]

NPCs = Neural progenitor cells [Ectoderm]

Representatives of all three germ layers

FIG. 28A

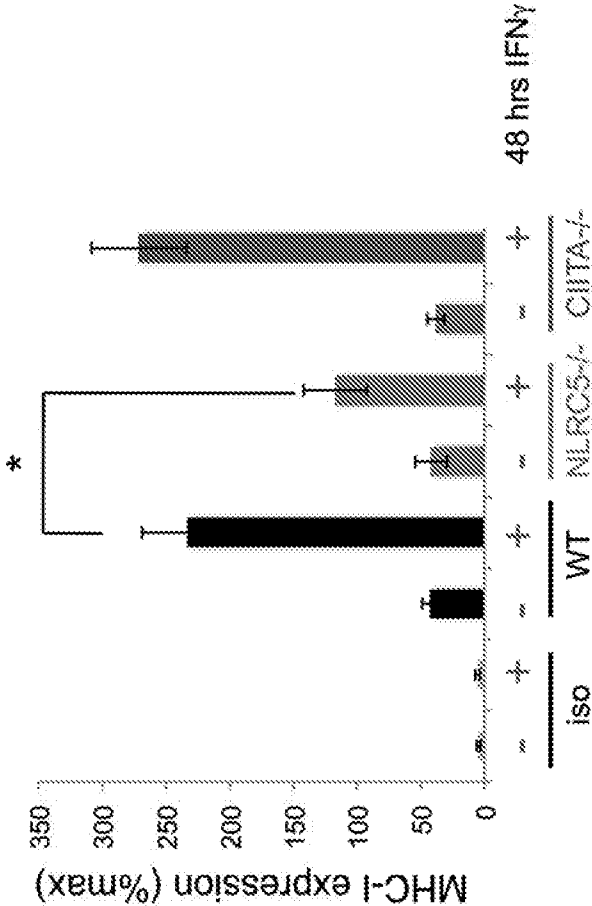
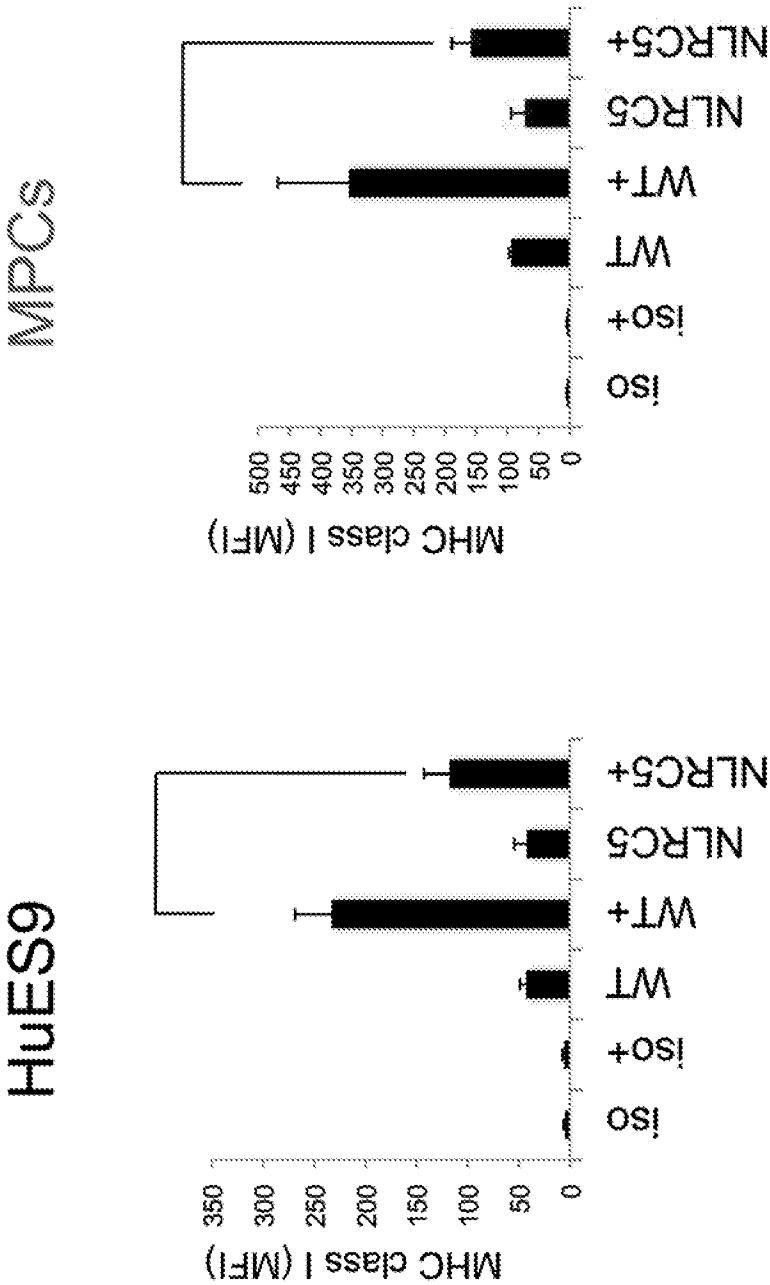


FIG. 28B

- Low basal MHC-I expression in stem cells
- Can be increased by IFN γ stimulation
- ~50% reduction in IFN γ -treated NLRC5-/- cells

Reduced MHC-I Expression in NLRC5-/- Human MPCs



Data combined:
two independent experiments using 3x WT, 4x NLRC5-/-

FIG. 28C

Reduced MHC-I expression in stem cell-derived NLRC5-/- ECs

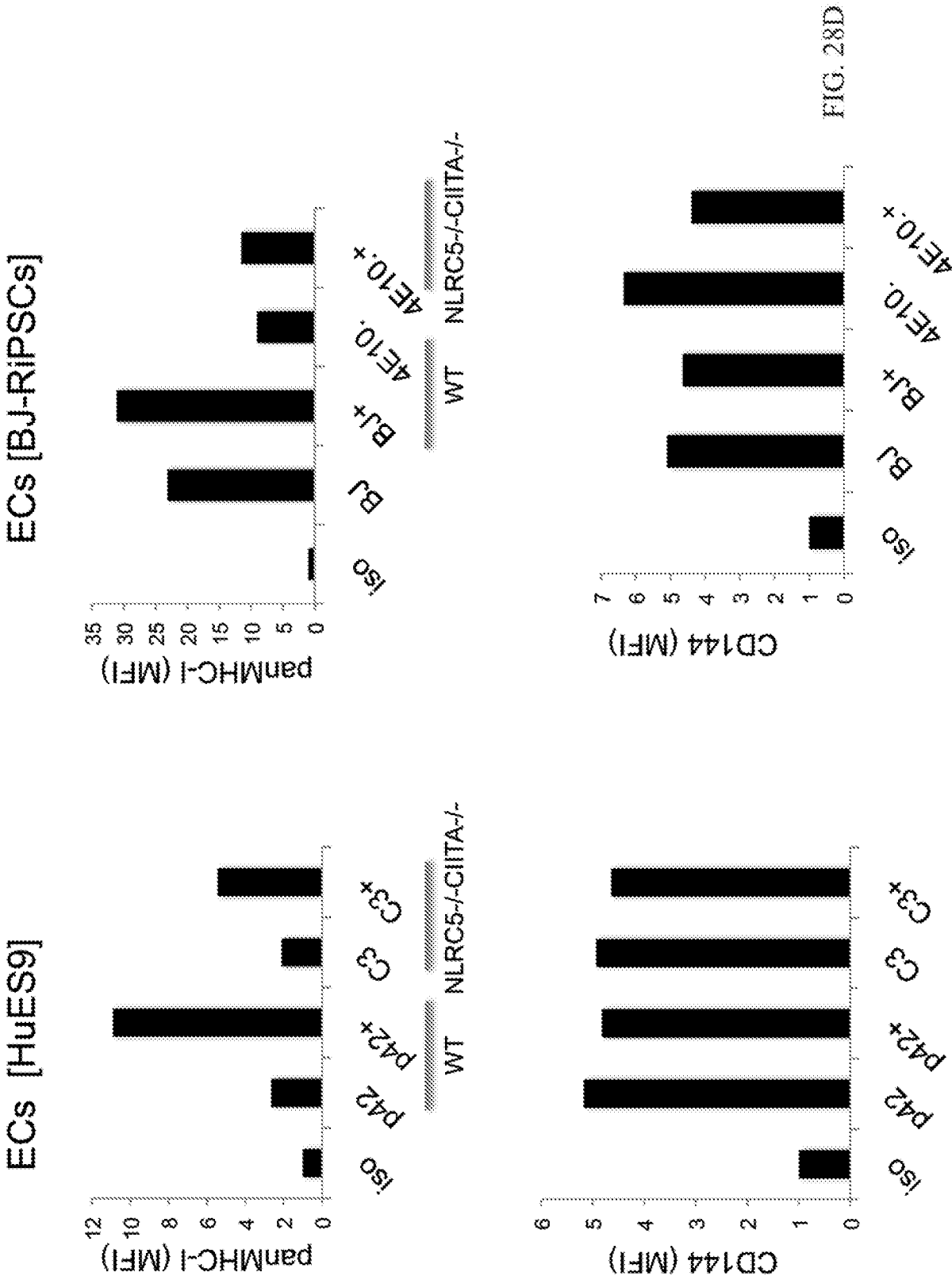


FIG. 28D

ECs – Similar Differentiation Efficiency

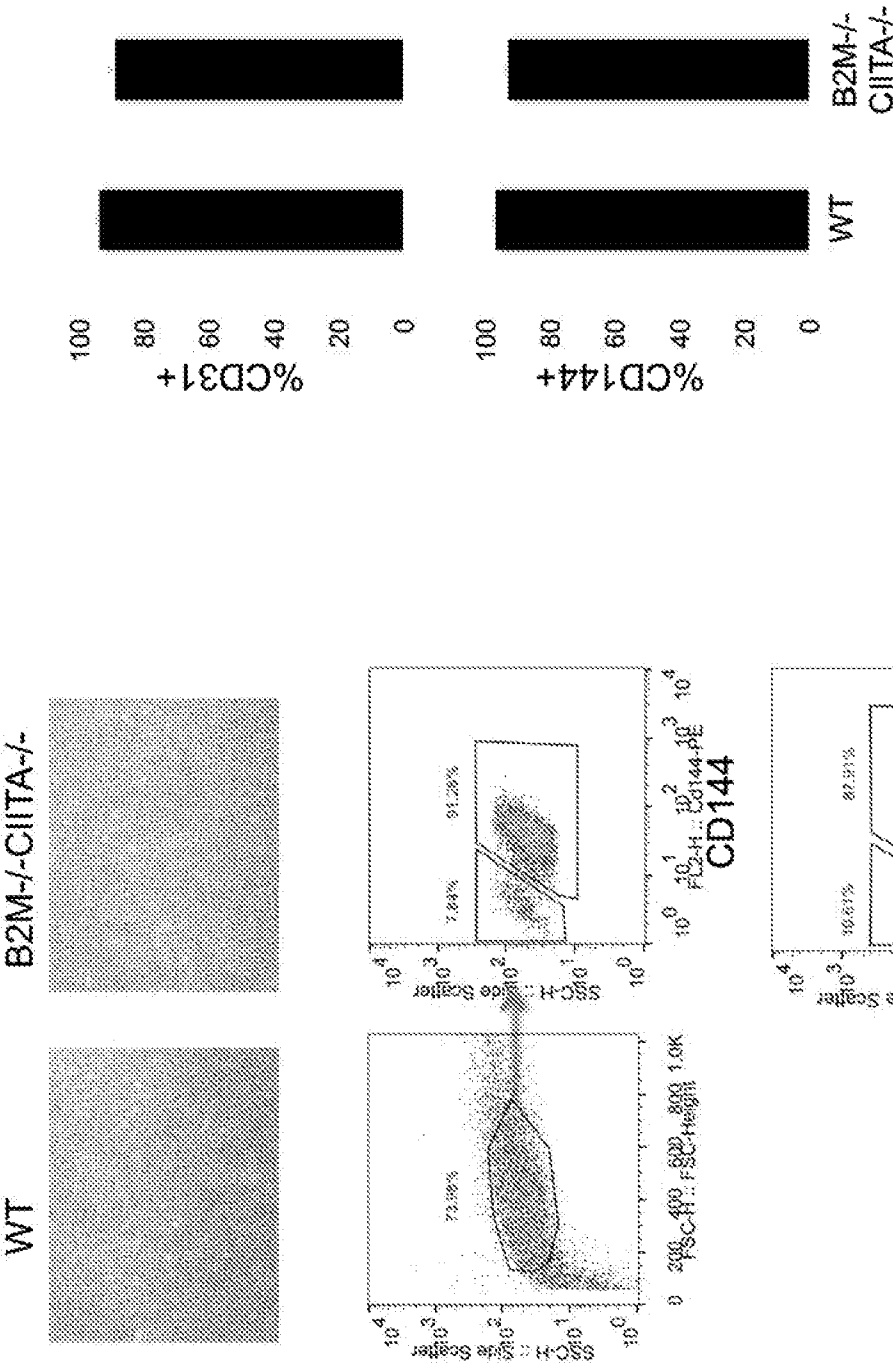
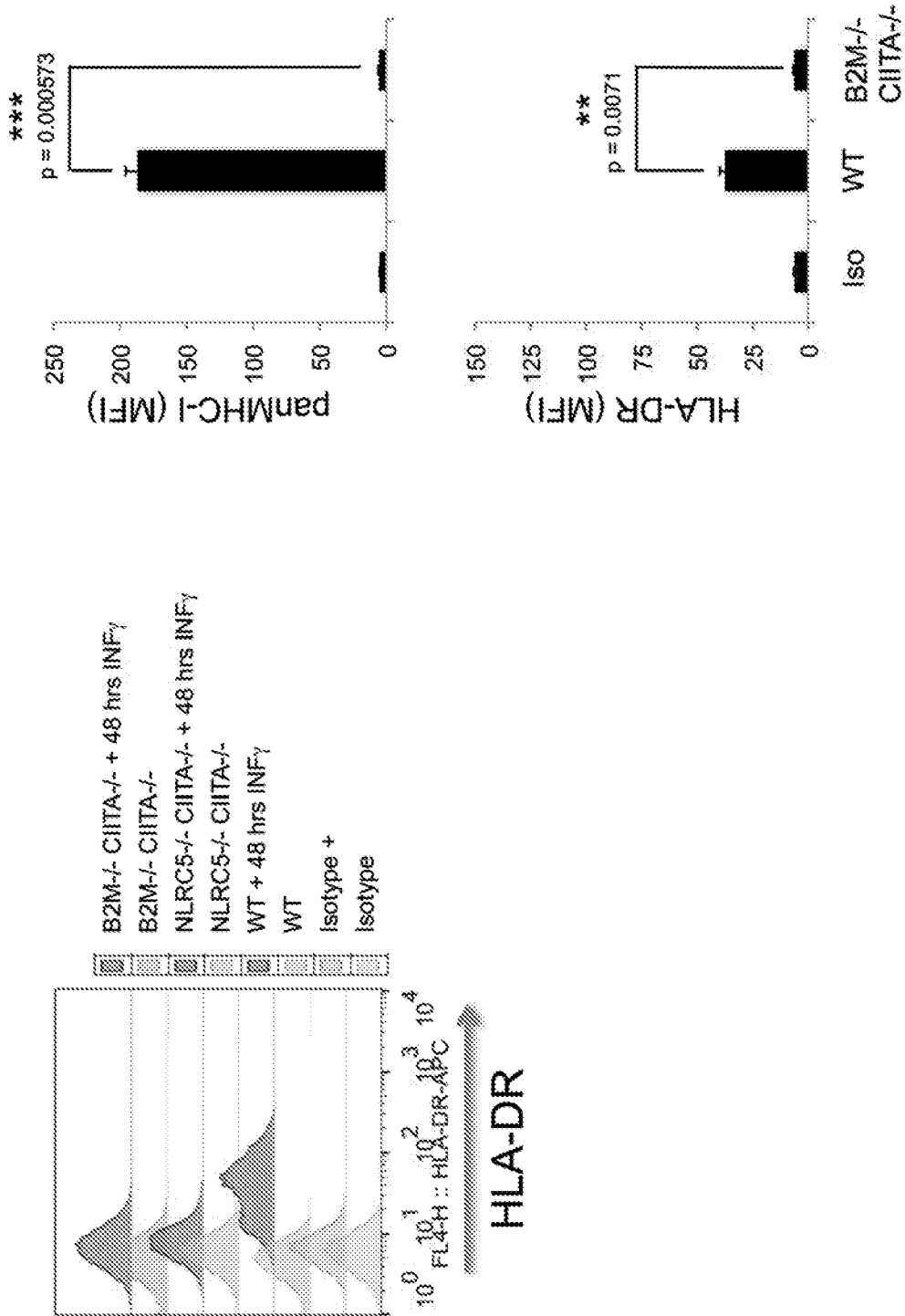


FIG. 28E

Loss of HLA expression in B2M^{-/-}-CIITA^{-/-} ECs



HuES9-derived ECs

FIG. 28F

Neural Progenitor Cell (NPC) Differentiation

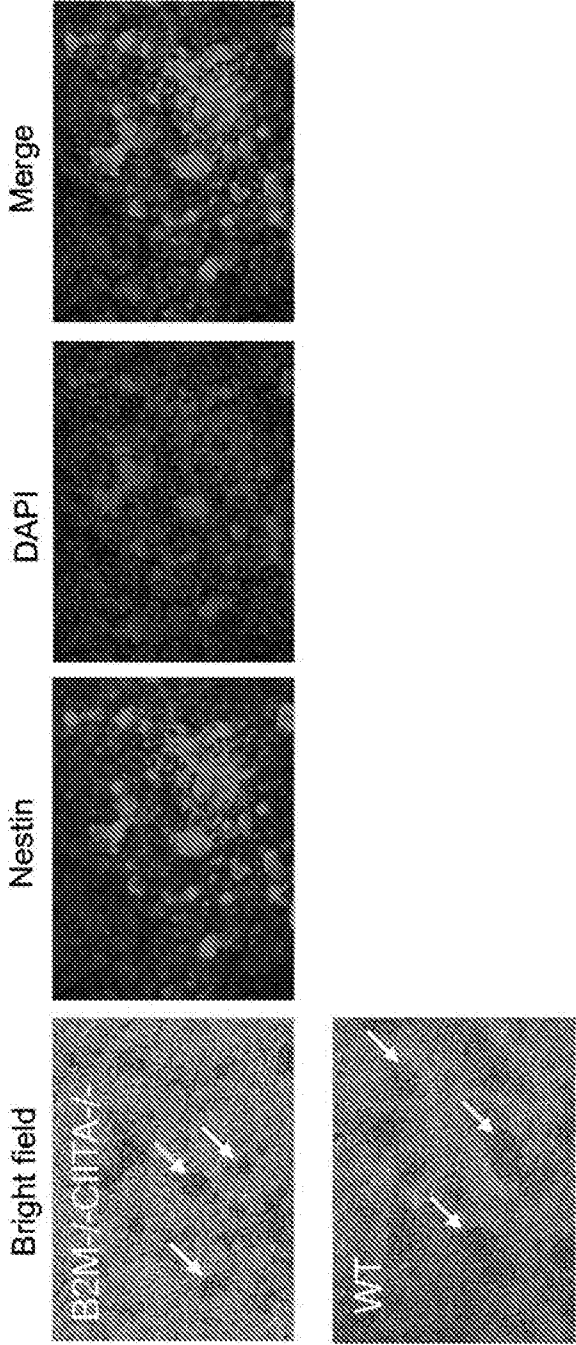


FIG. 28I

Adaptation to Spin Culture for beta-Cell Differentiation

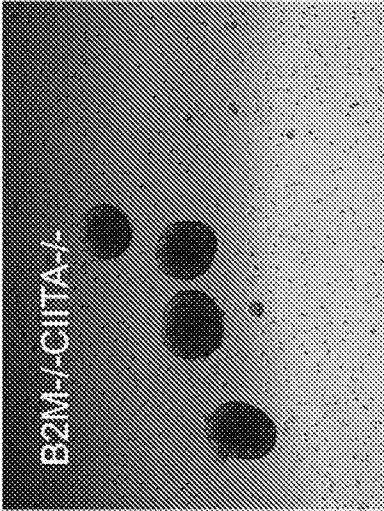
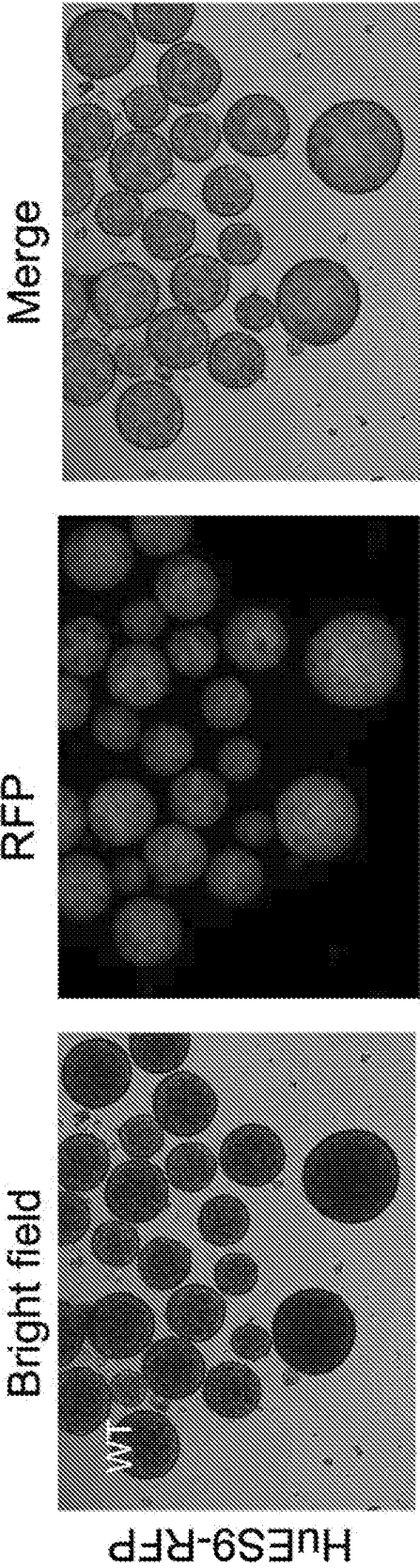


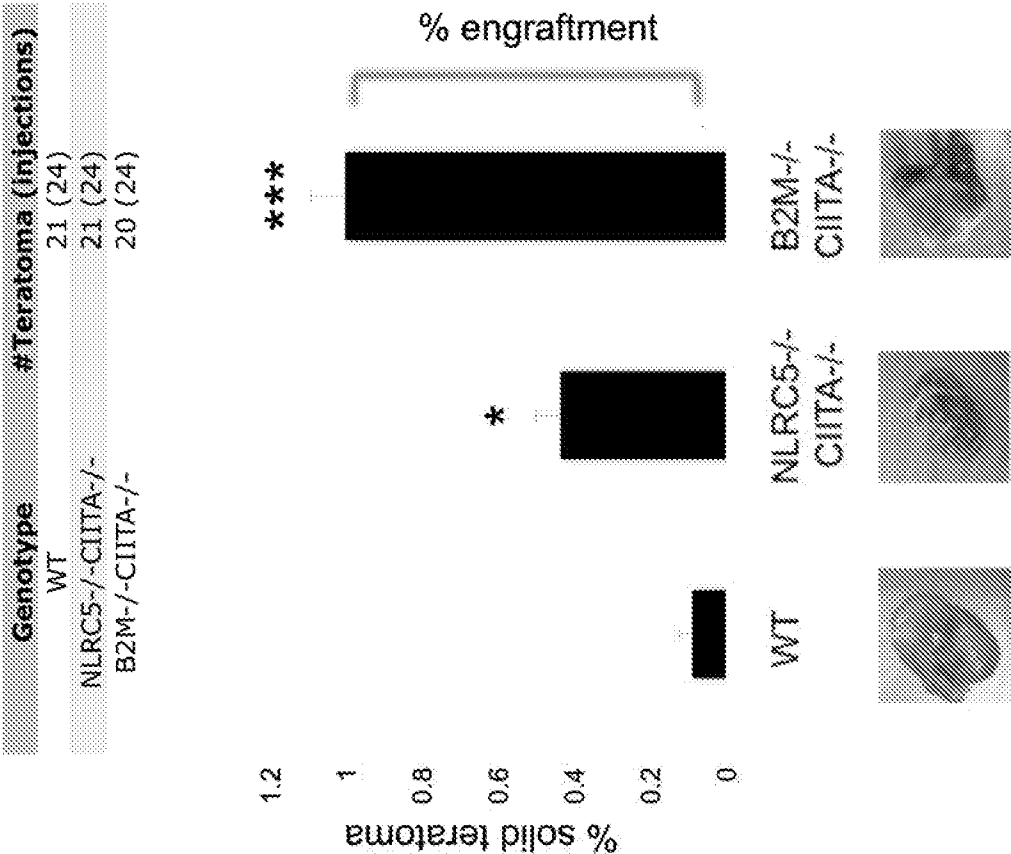
FIG. 28J

‘Hypoimmunogenic’ DKO Cell Lines Generated

HUES9	MHC-I	MHC-II
WT	yes	yes
NLRC5-/- C2TA-/-	reduced	no
B2M-/- C2TA-/-	no	no

FIG. 29A

Improved Engraftment of Genome-Edited Stem Cells
in Humanized Mice

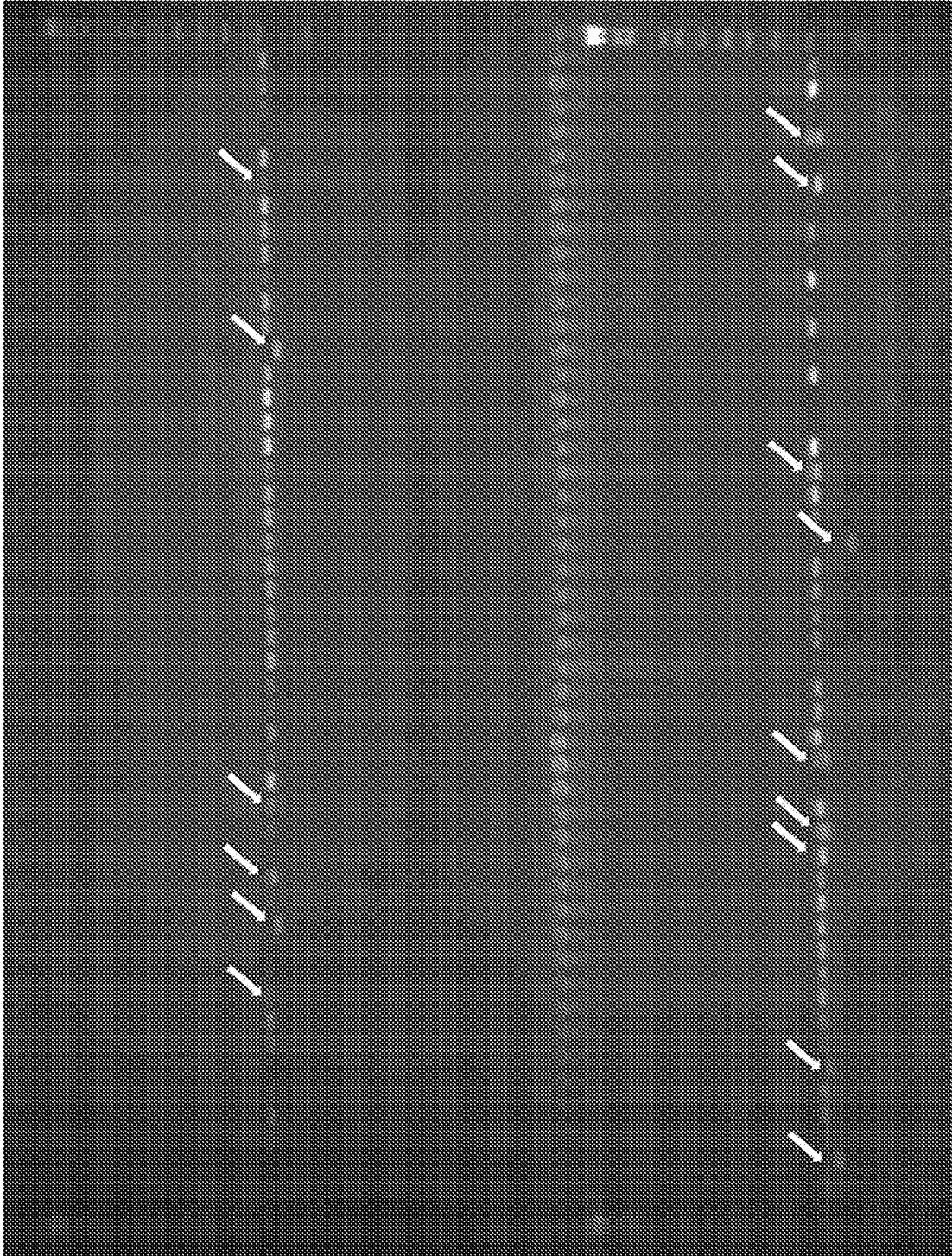


CRISPR Targeting of B7-H3 in JEG-3 cells

GCTGACAGATACCAACAGC (TGG)

FIG. 30A

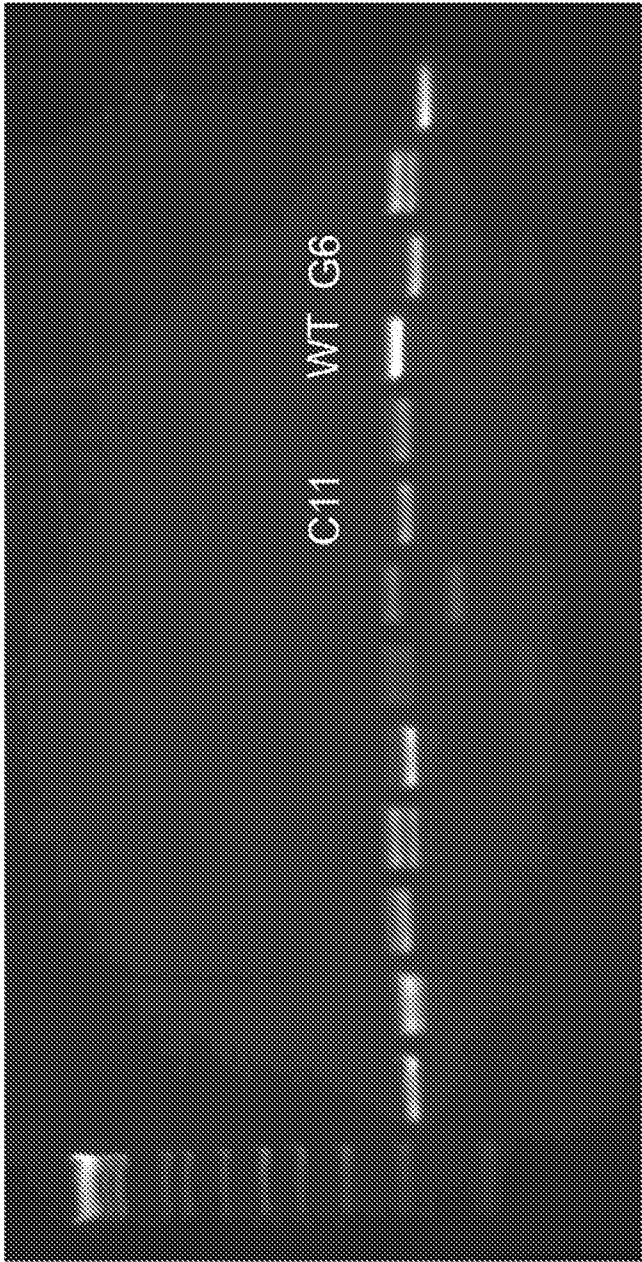
Screening of targeted B7-H3 colonies



CRISPR Cutting Efficiency: 15/80 => 18.7%
In JEG-3 cells

FIG. 30B

Confirmation of B7-H3 Knock-Outs through Sequencing



WT	CACAGCTCAACCTCATCTGGCAGCTGACAGATACCAACAGCTGGTGCACAGCCTTT
C11 Δ16	CACAGCTCAACCTNATCTGGCAG-----AGCTGGTGCACAGCCTTT
G6 Δ26	CACAGCTCAACCTCATCTGG---TG-C-----ACAG-----TTT

FIG. 30C

Loss of B7-H3 surface expression in targeted Jeg3 clones

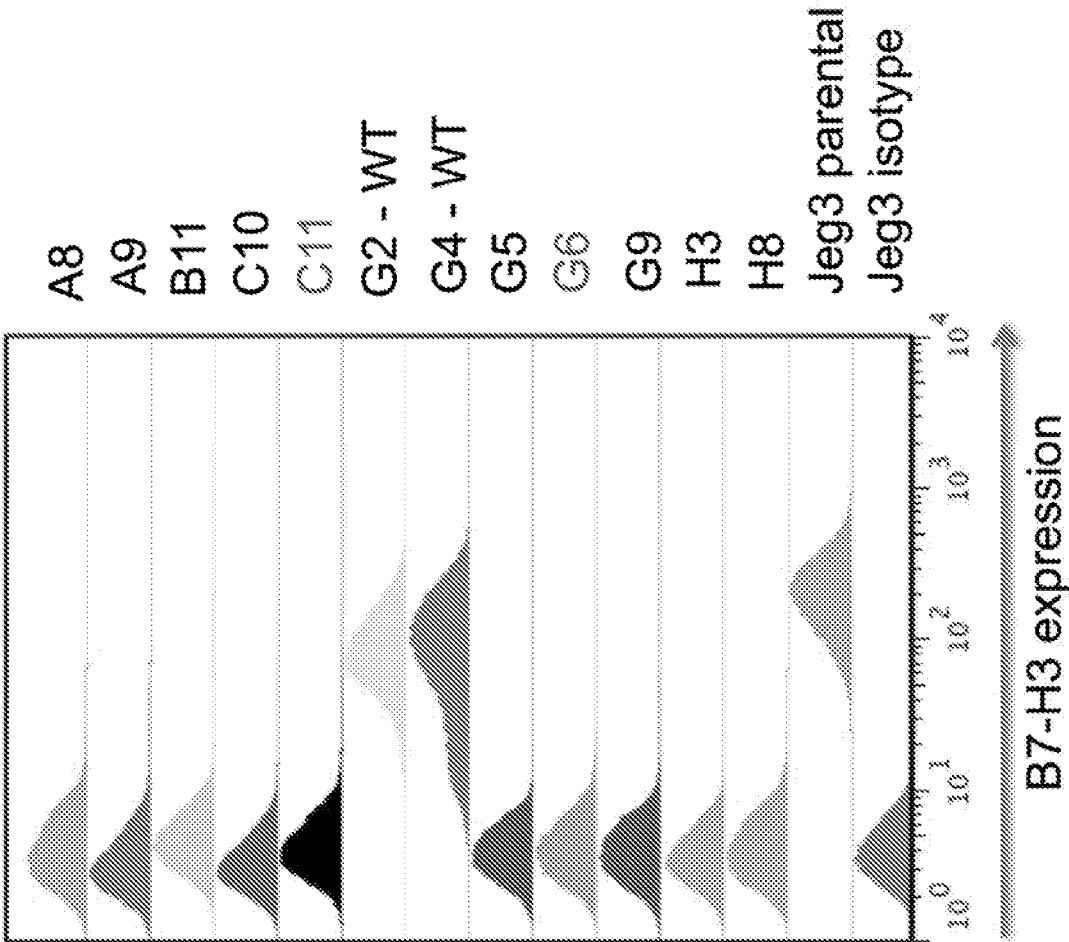


FIG. 30D

Loss of MHC class I surface expression in B2M^{-/-} Jurkat Cas9 T cells

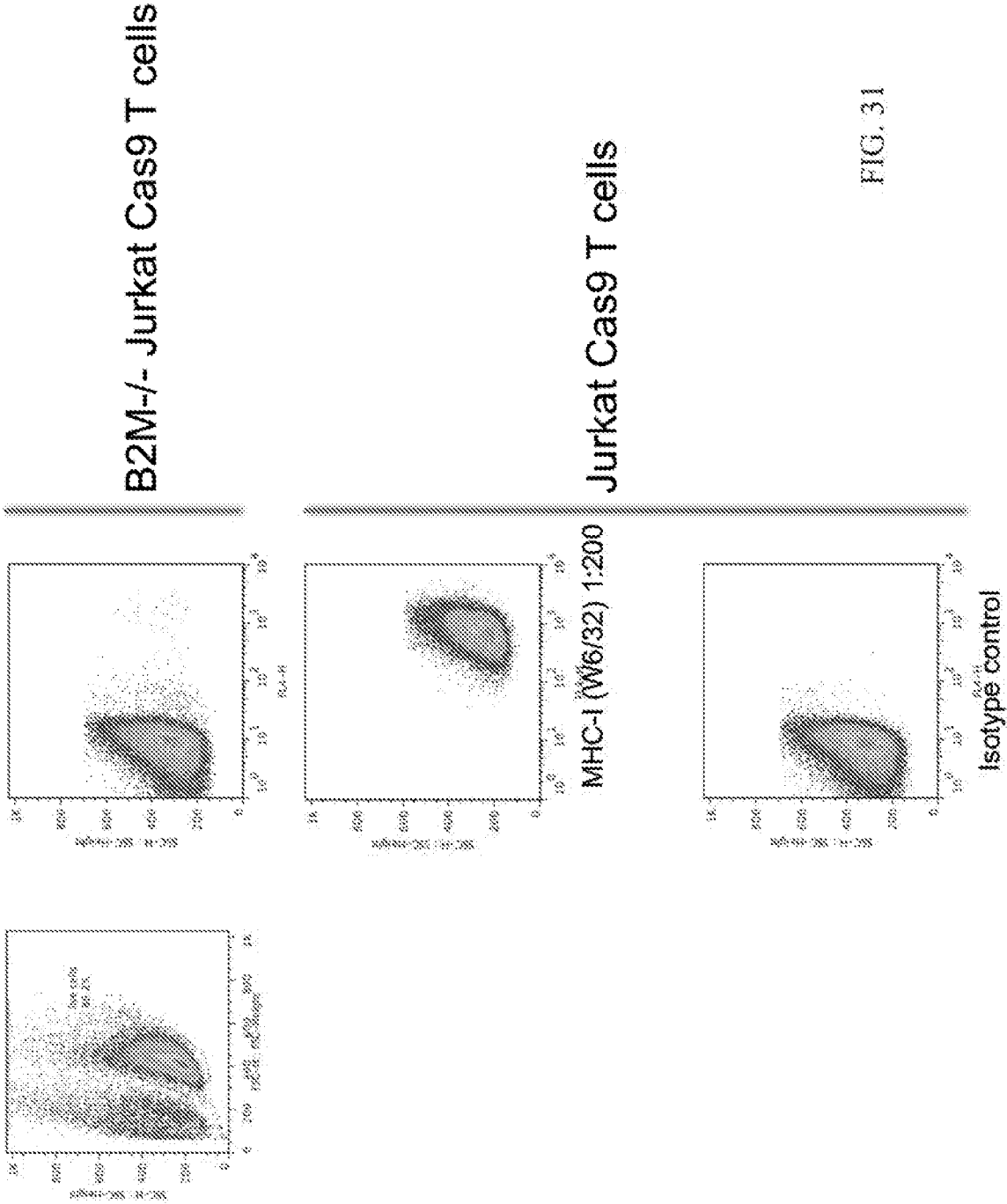
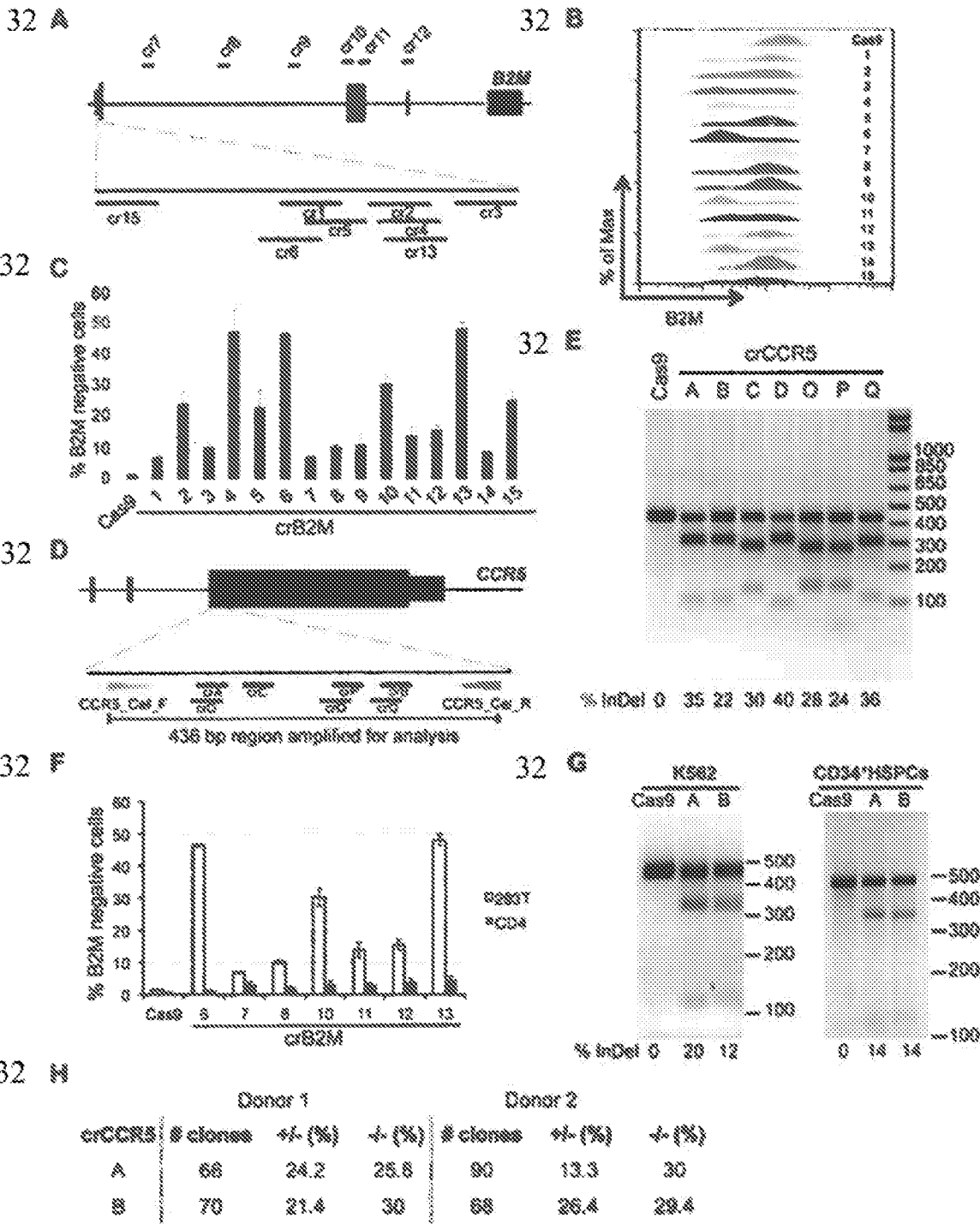
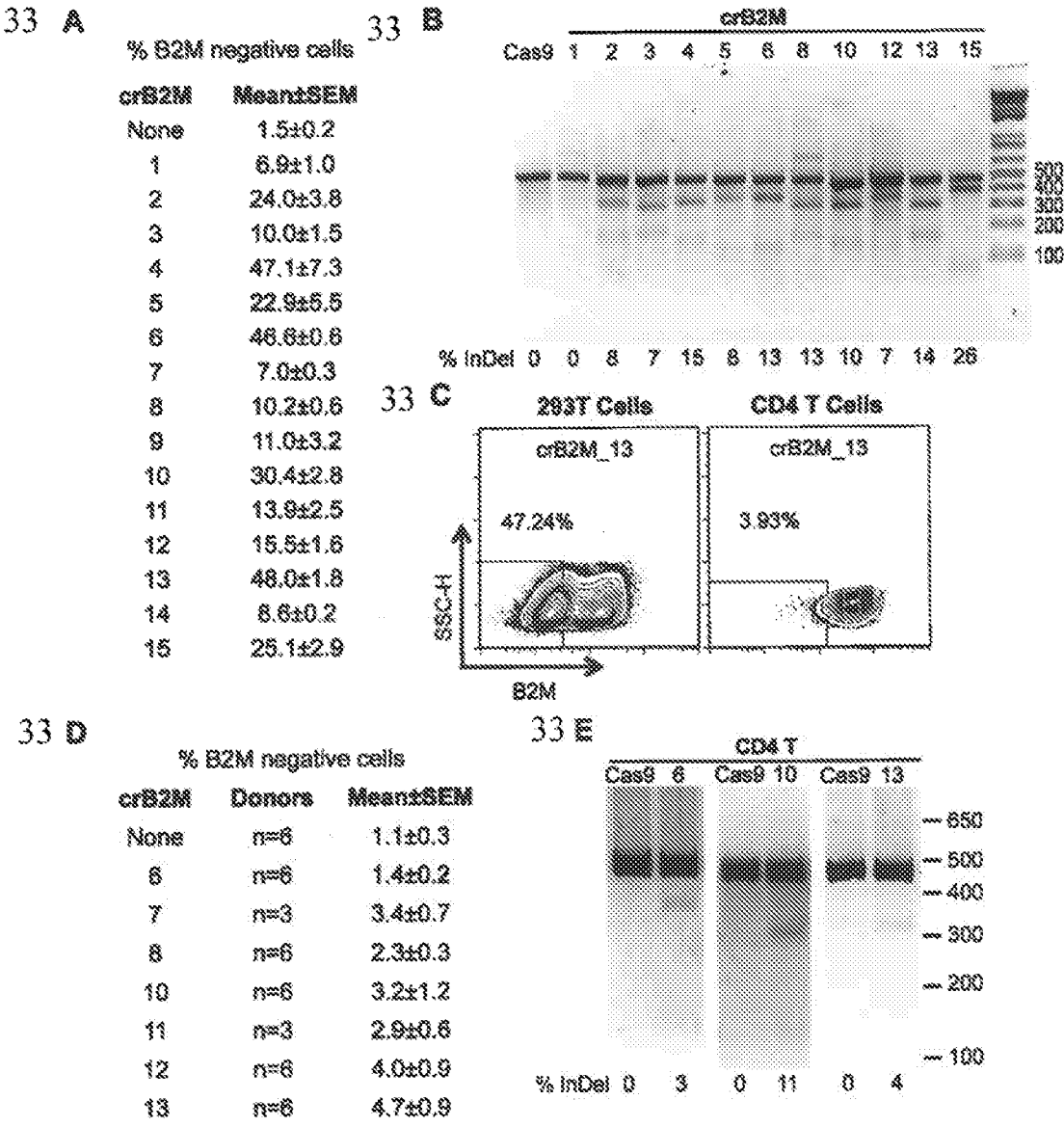


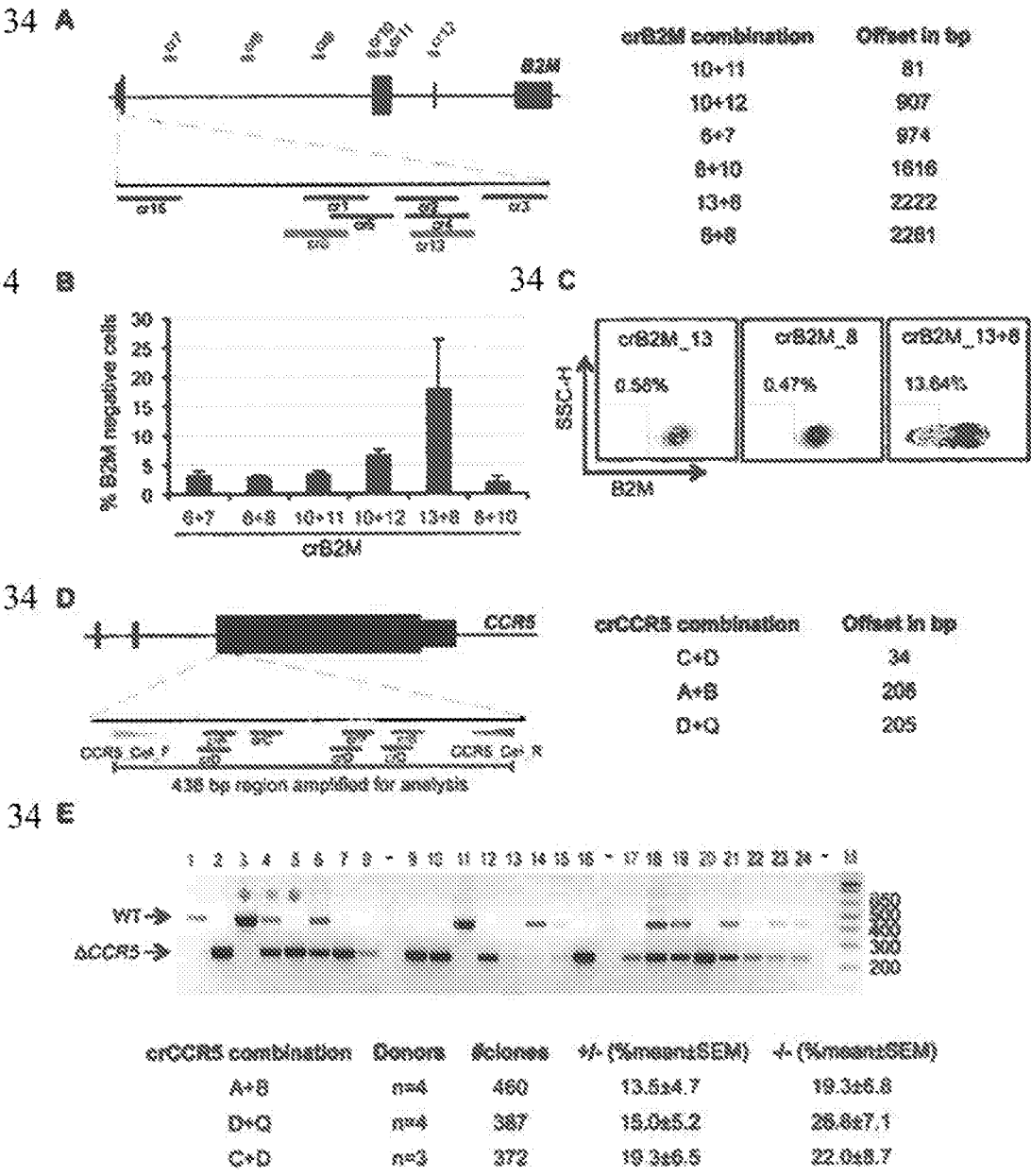
FIG. 31



FIGS. 32A-32H



FIGS. 33A-33E



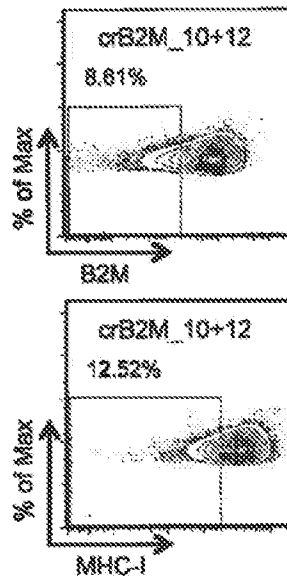
FIGS. 34A-34E

35 A

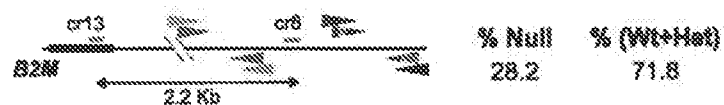
% B2M negative cells

crB2M	Donor 1	Donor 2	Donor 3	Mean±SEM
6+7	2.14	4.47	2.99	3.2±0.66
6+8	2.80	3.31	3.25	3.05±0.23
10+11	2.81	4.01	3.96	3.59±0.39
10+12	8.61	5.89	5.82	6.71±0.95
13+8	34.15	6.22	13.64	18.0±8.35
8+10	0.09	3.34	2.95	2.13±1.02

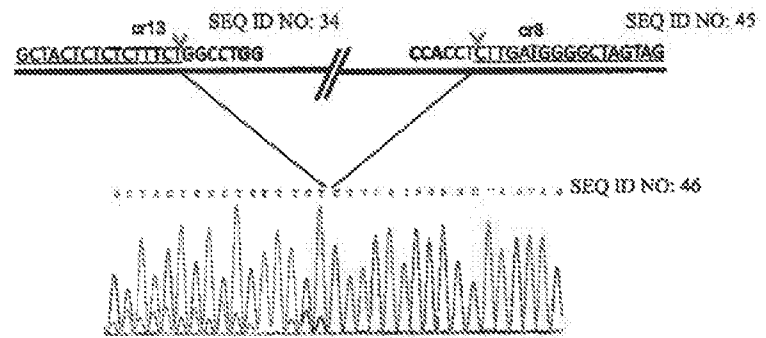
35 B



35 C



35 D



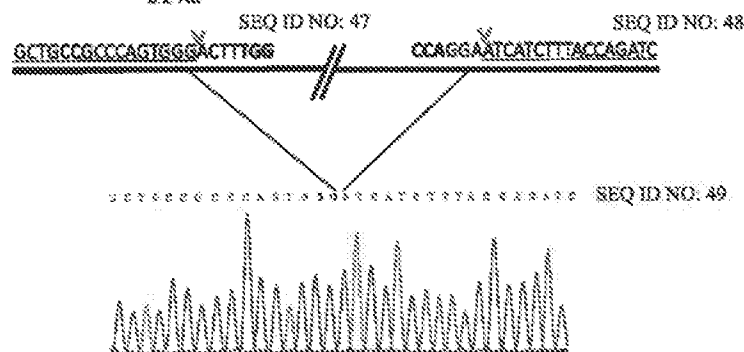
35 E

	Donor 1			Donor 2			Donor 3			Donor 4		
crCCR3	# clones	+/- (%)	-/- (%)	# clones	+/- (%)	-/- (%)	# clones	+/- (%)	-/- (%)	# clones	+/- (%)	-/- (%)
A+B	83	11.5	9	96	27	8	169	10	23	92	5.4	37
D+Q	88	8.8	9	84	25	42	154	5.8	33	81	23	23
C+D	87	12.6	4.6	NA	-	-	169	13	29	96	32.3	32.3

35 F



35 G



FIGS. 35A-35E

293T cells, 12-wells, 48 h post-transfection

Cpf1 cuts - Surveyor

AsCpf1 only B2M C1 B2M C2 B2M C3



Blue arrows indicate Surveyor nuclease cleavage bands

B2M C1 and C2 Cpf1 crRNAs bind to first exon
B2M C3 binds to first intron

(bp)

C1 sequence: [TTTA]ATAAAGTGGAGGCGTCGCG
(SEQ ID NO: 42543)
C2 sequence: [TTTC]TGGCCTGGAGGCTATCCAGC
(SEQ ID NO: 42544)
C3 sequence: [TTTA]ATGTTATGAAAAAATCAGG
(SEQ ID NO: 42545)

Surveyor assay:

C1 expected bands: 50 and 450 bp
C2 expected bands: 150 and 350 bp
C3 expected bands: 125 and 375 bp

FIG. 36

293T cells, 12-wells, 48 h post-transfection

AsCpf1 cuts - FACS

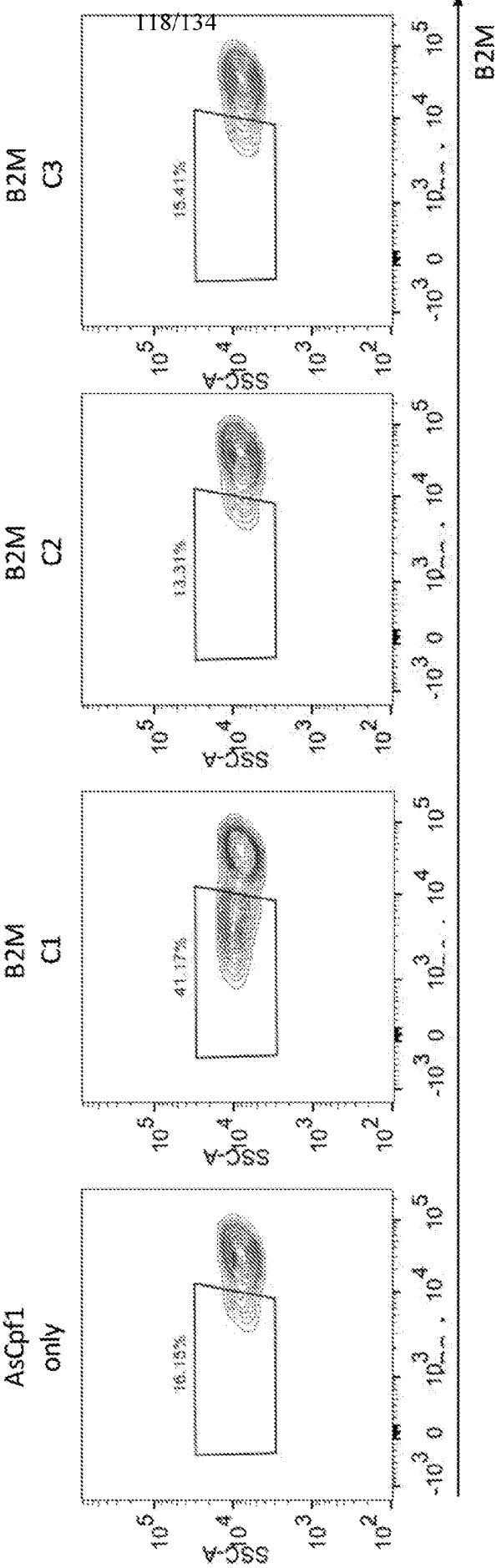


FIG. 37

293T cells, 12-wells, 48 h post-transfection

LbCpf1 cuts - FACS

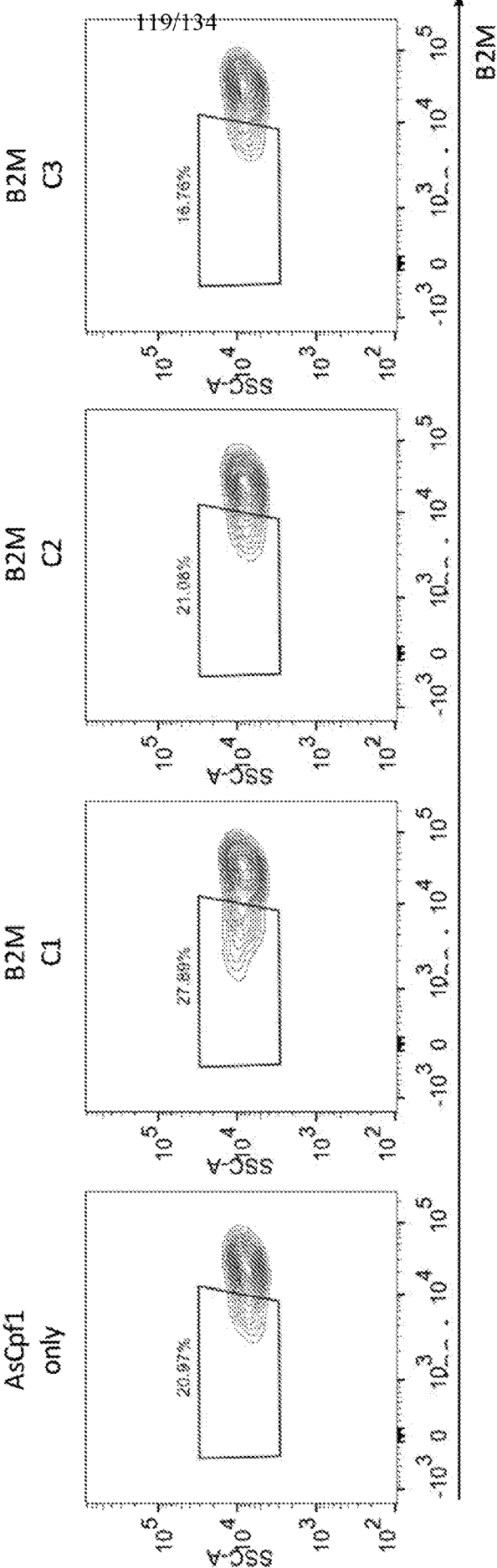


FIG. 38

Cpf1 crRNA design and cloning

Express guides (crRNAs) as U6 promoter-direct repeat seq -- 20 nt guide PCR product!

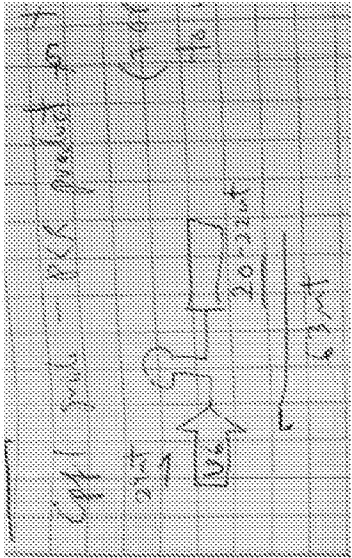
Fw primer (binding U6 promoter)

GAGGGCCTATTCCCATGATTCCT (24 nt) (SEQ ID NO: 42546)

Rev primers: rev comp target seq (20 nt)-rev comp direct repeat seq-rev comp end U6 p

Rev primer example: AsCpf1 DNMT1 GUIDE 4 (63 nt)

CCTTTATTTTAGCTGAAGGGGAAAATCTACAAGAGTAGAAAATTACGGTGTTTCGTCCTTCCACAAG
(SEQ ID NO: 42547)



Cells transfected with Cpf1 DNA (either As or Lb) and crRNA PCR product generated using
Lentiguide-puro plasmid as template (for hU6 promoter) and guide specific reverse primers

FIG. 39

Design of B2M TALEN and induced mutations

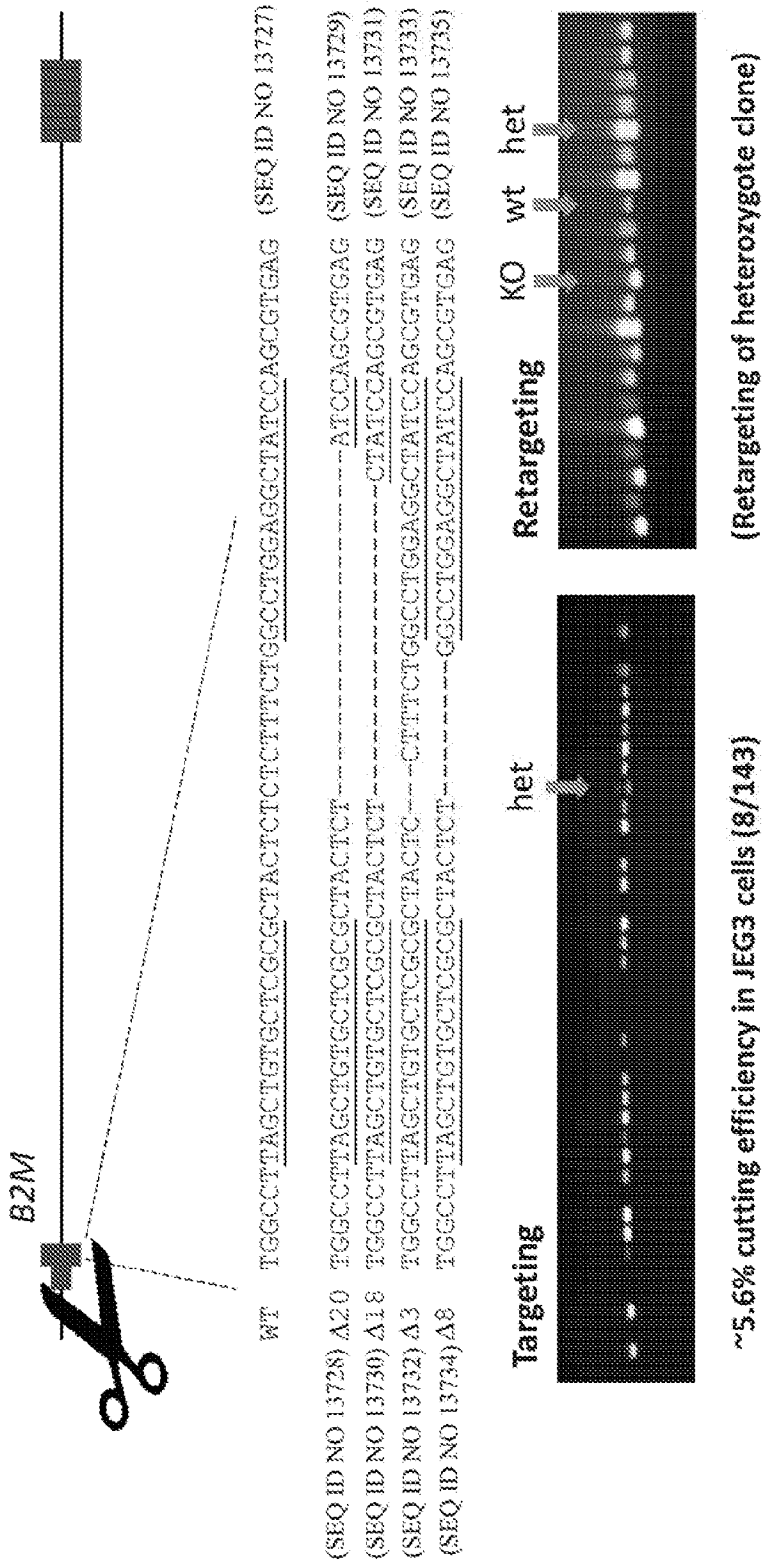


FIG. 40A

Analysis of B2M at the transcript and protein levels

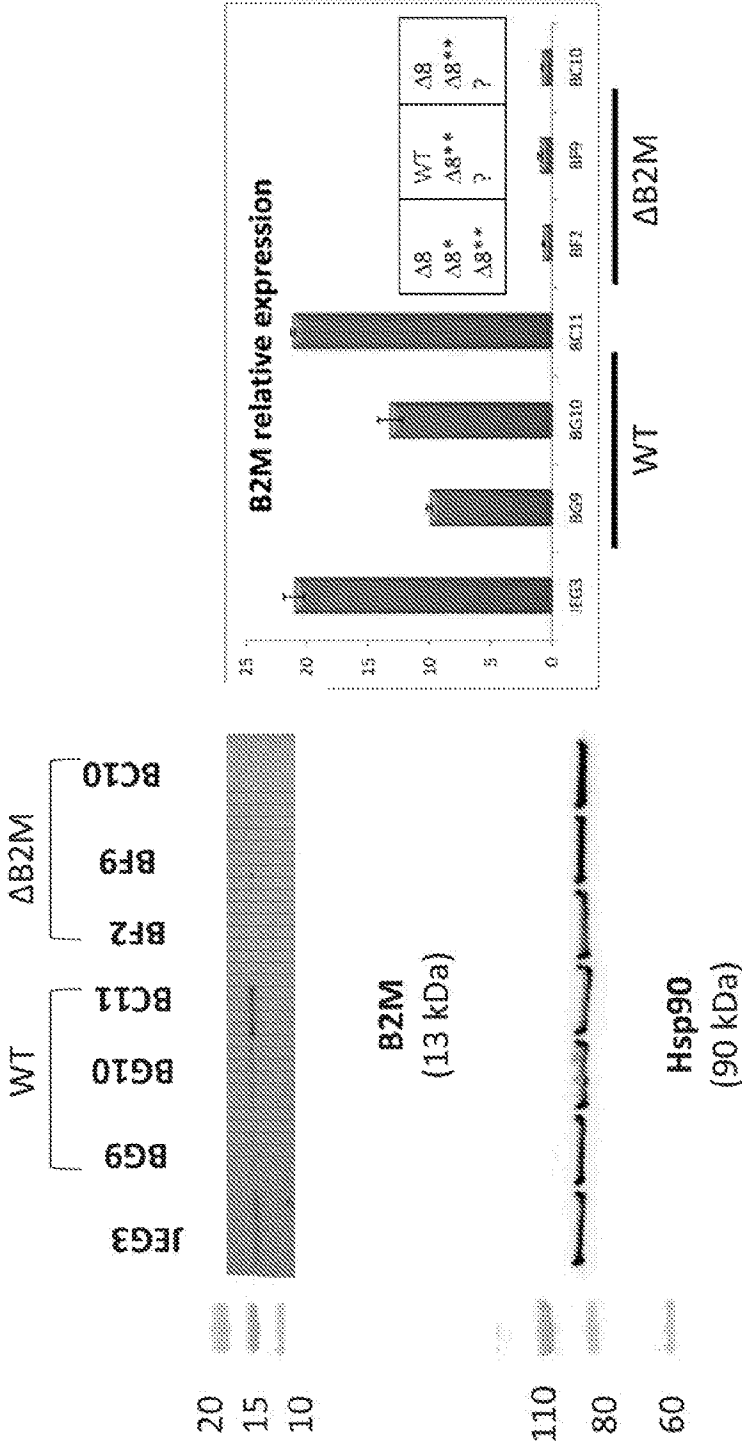


FIG. 40B

Analysis of B2M at the surface expression level

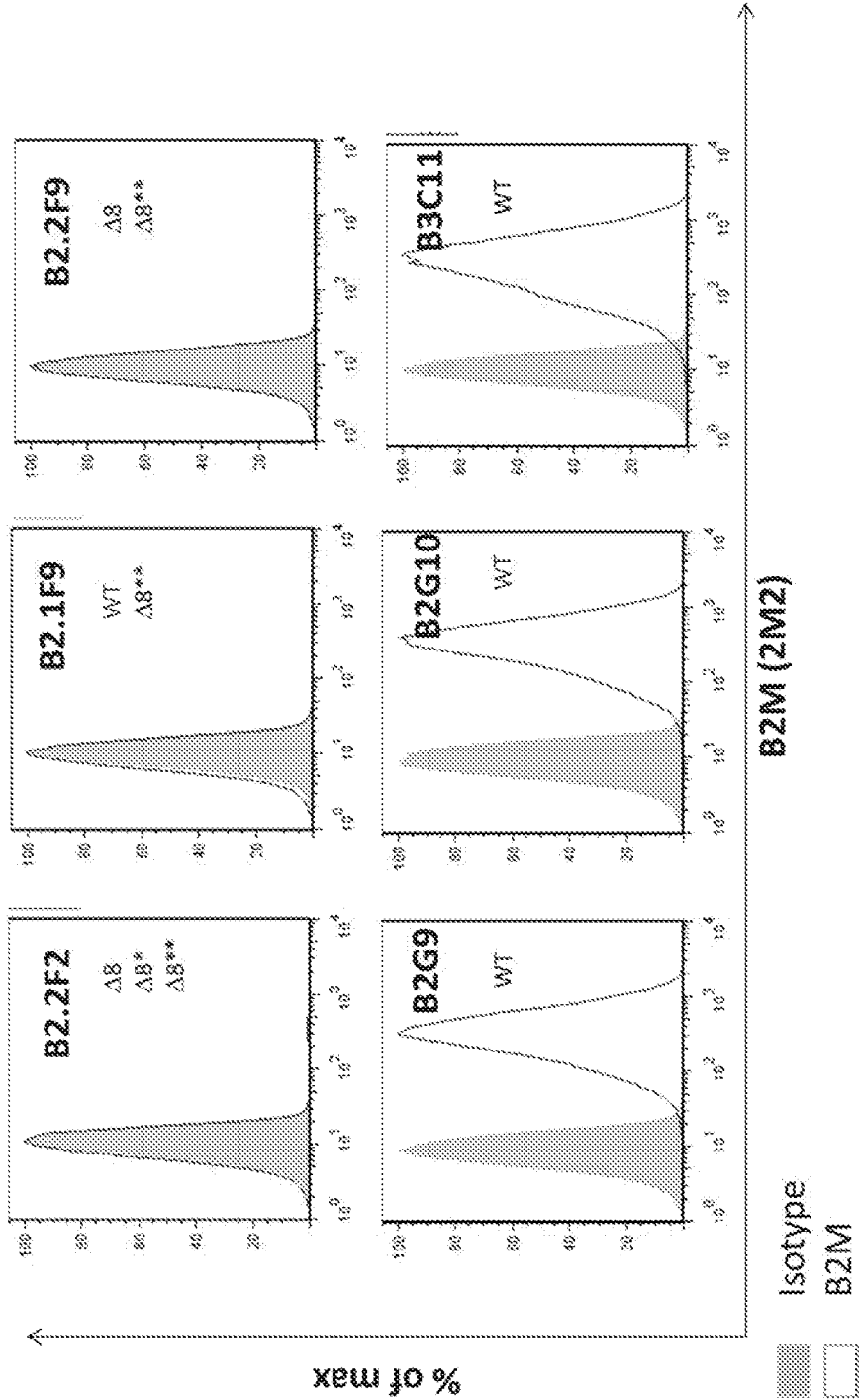


FIG. 40C

Δ B2M clones are devoid of
MHC-I surface expression

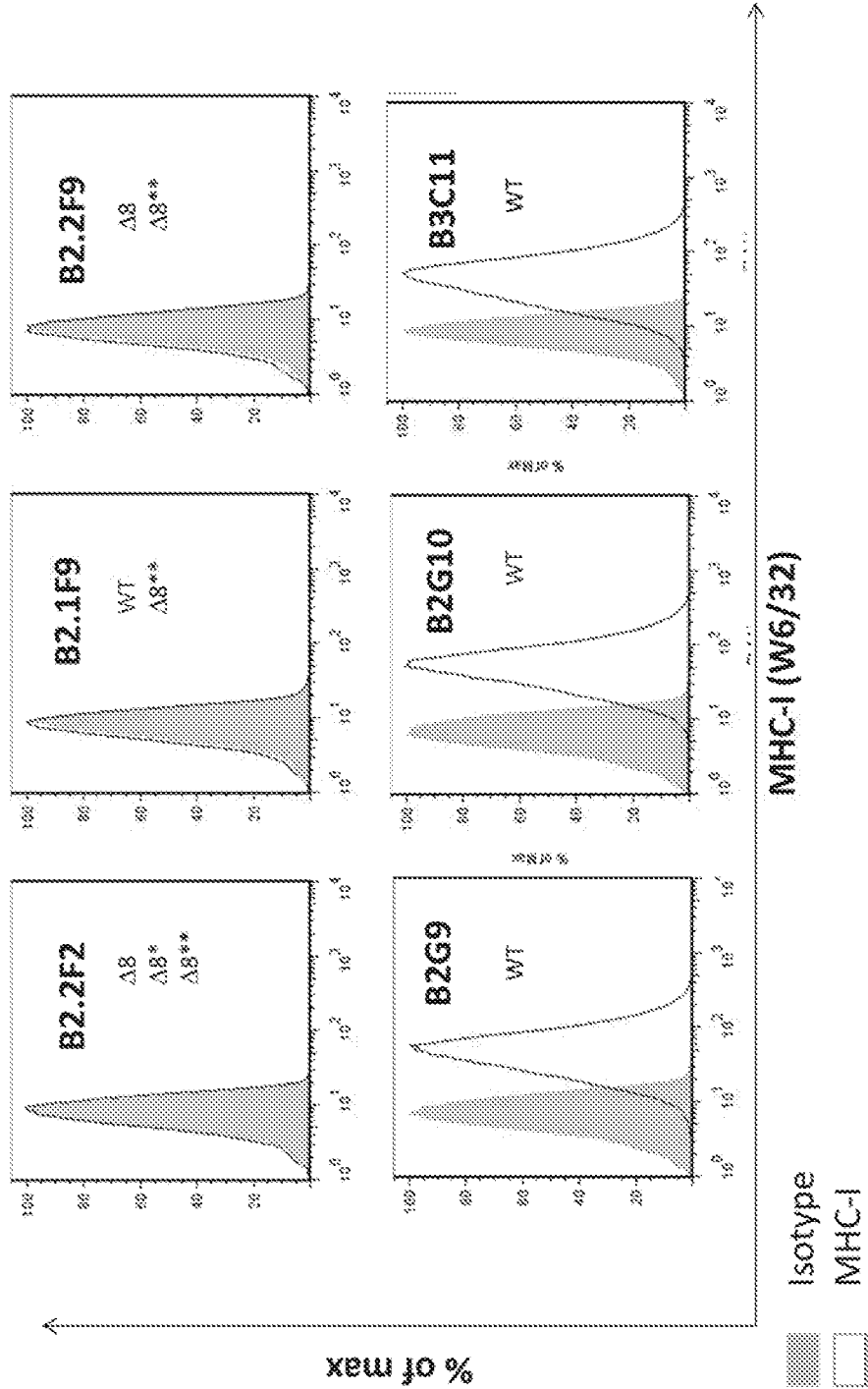


FIG. 40D

Δ B2M clones are devoid of HLA-G surface expression

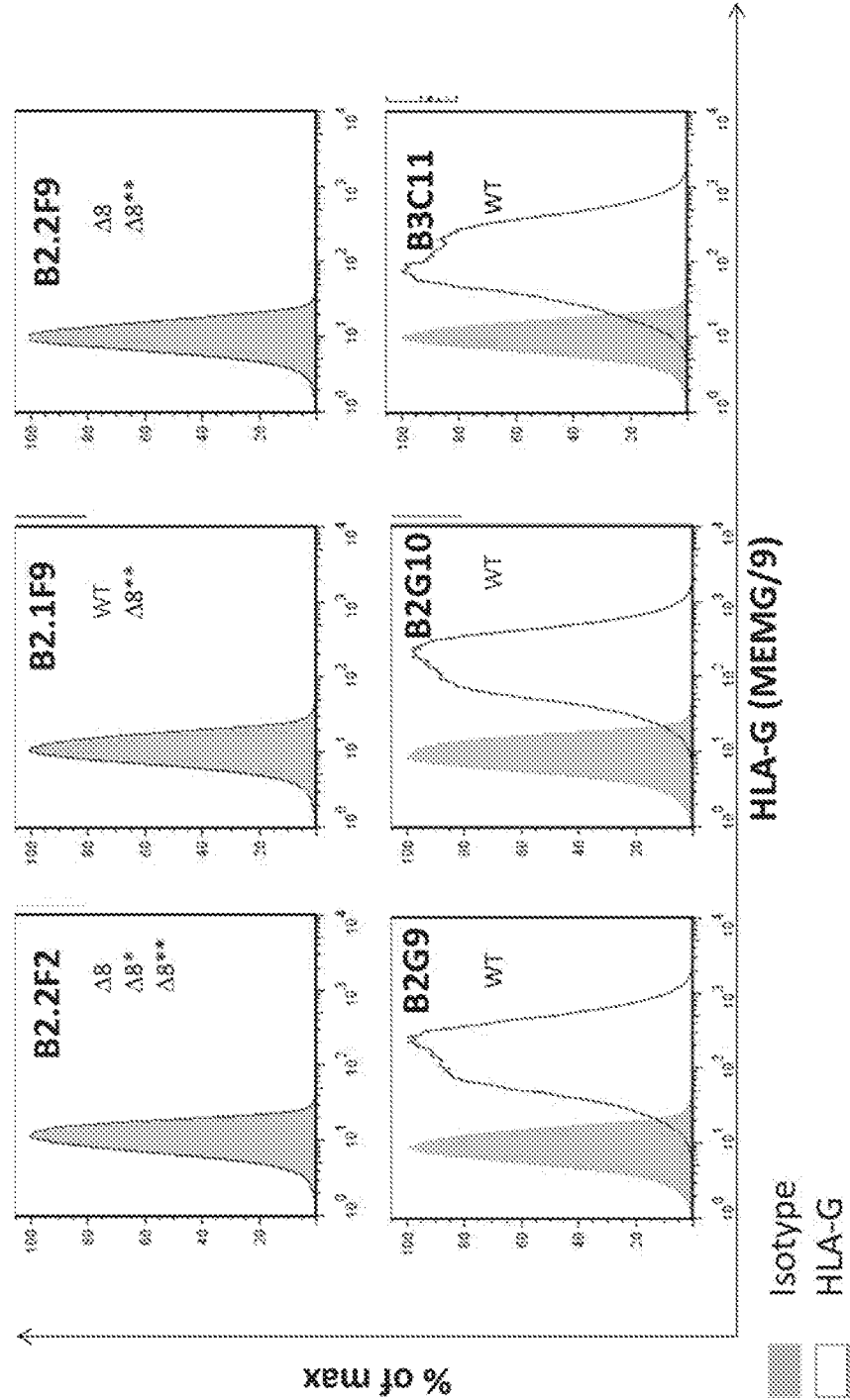


FIG. 40E

Δ B2M clones are devoid of
HLA-C surface expression

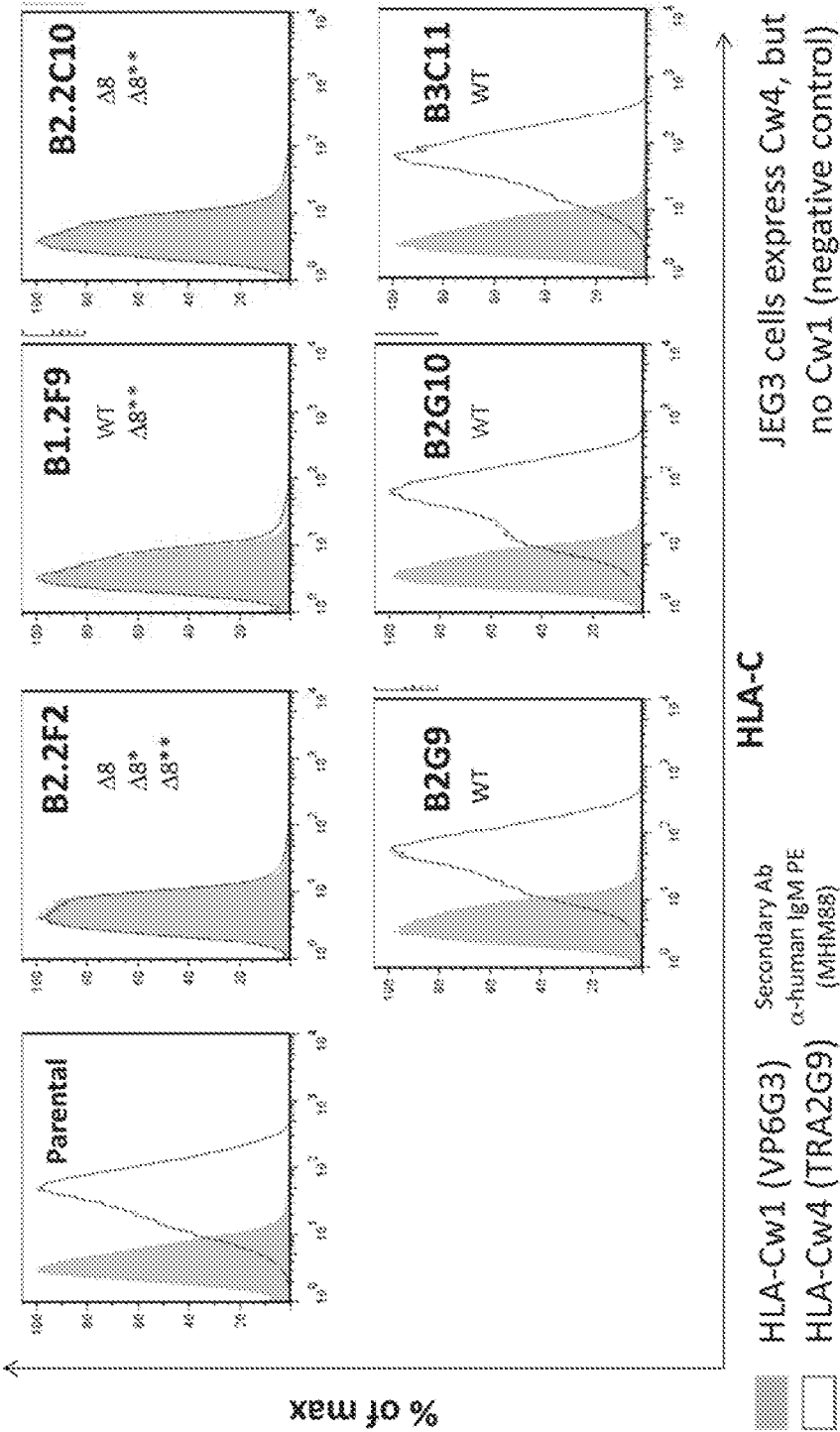


FIG. 40F

Δ B2M clones are devoid of HLA-E surface expression

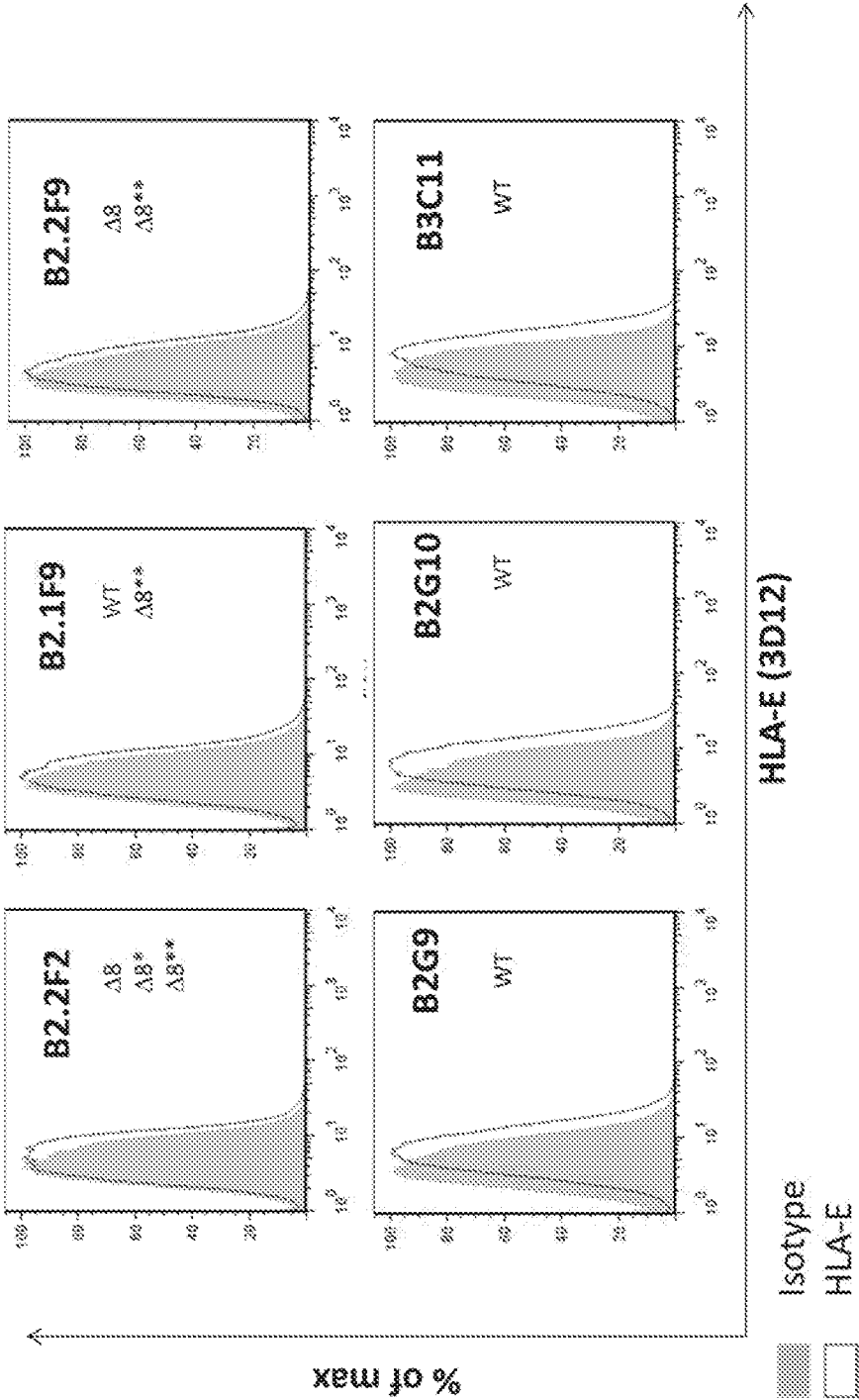


FIG. 40G

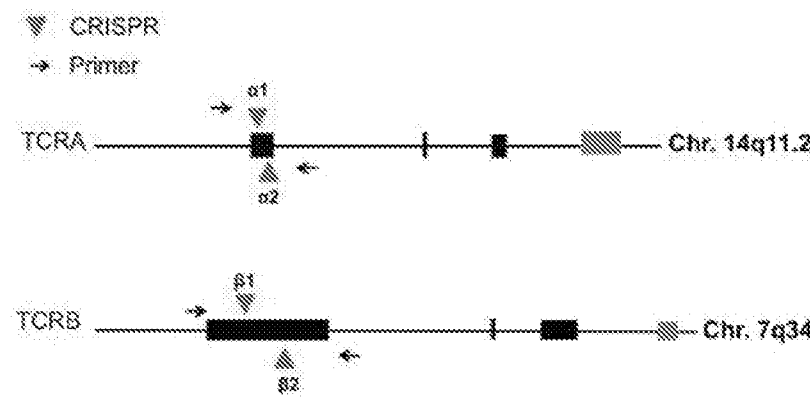
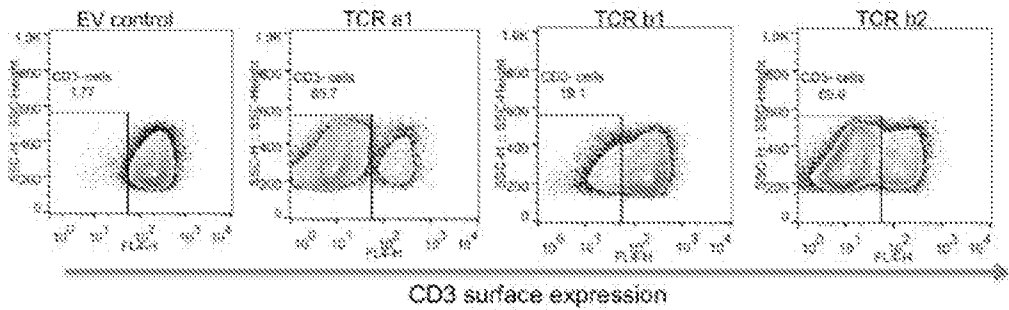
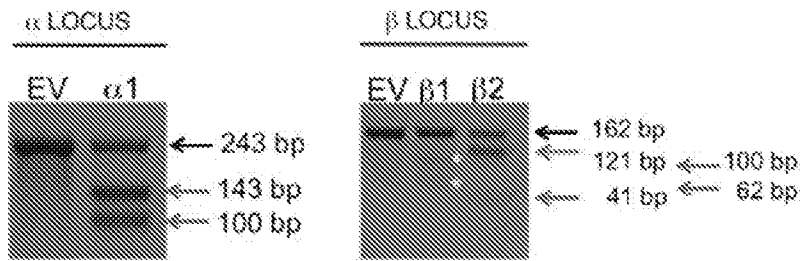


FIG. 41

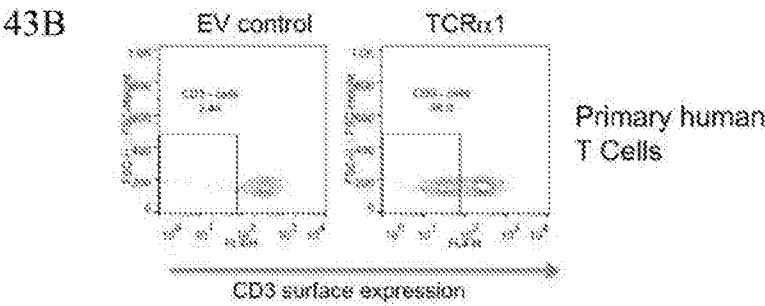
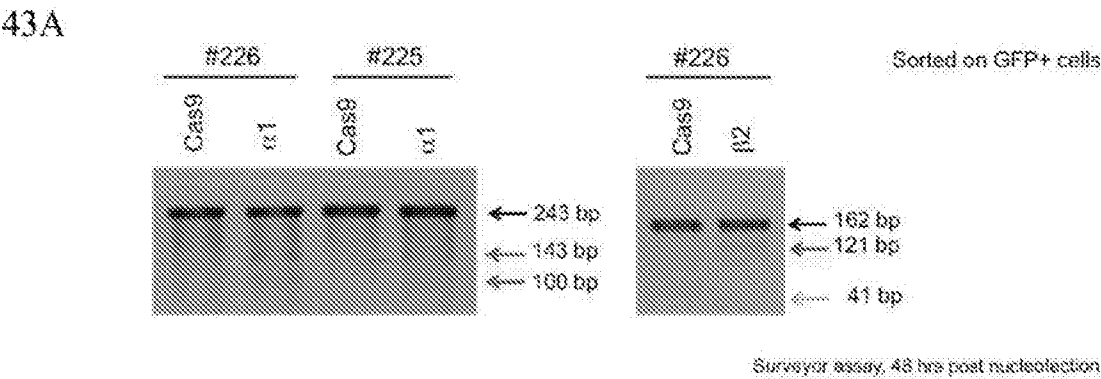
42A



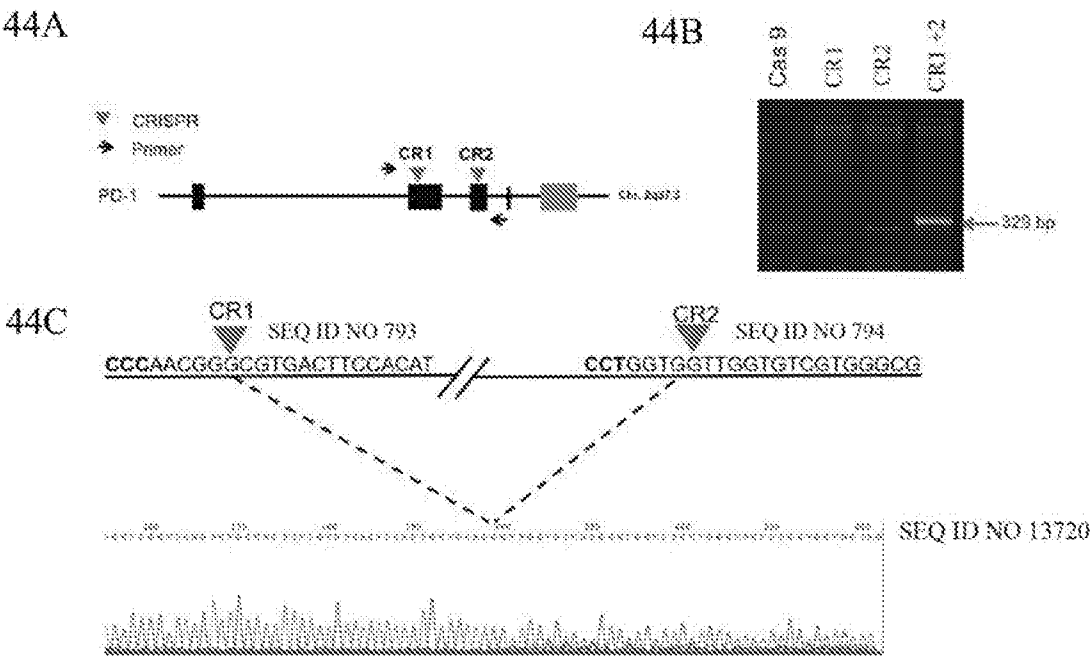
42B



FIGS. 42A-42B

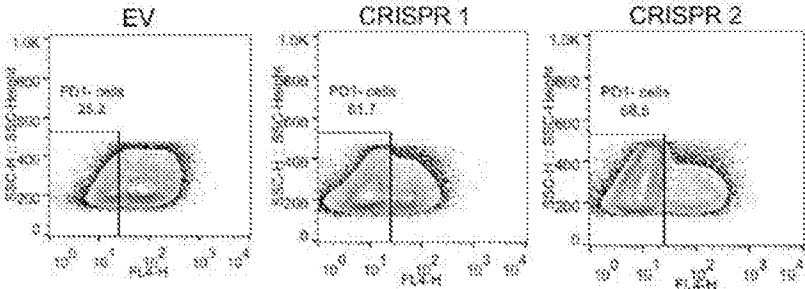


FIGS. 43A-43B

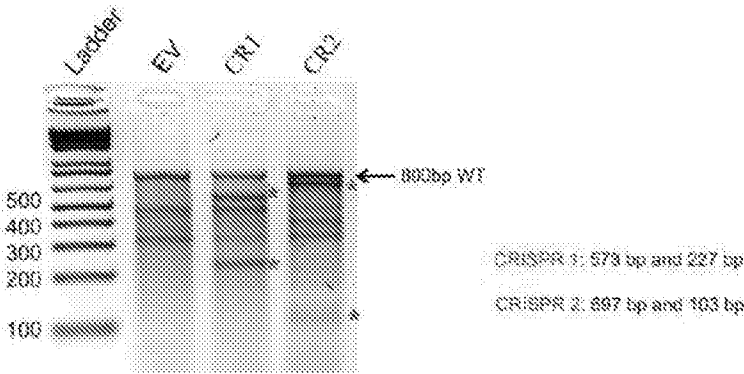


FIGS. 44A-44C

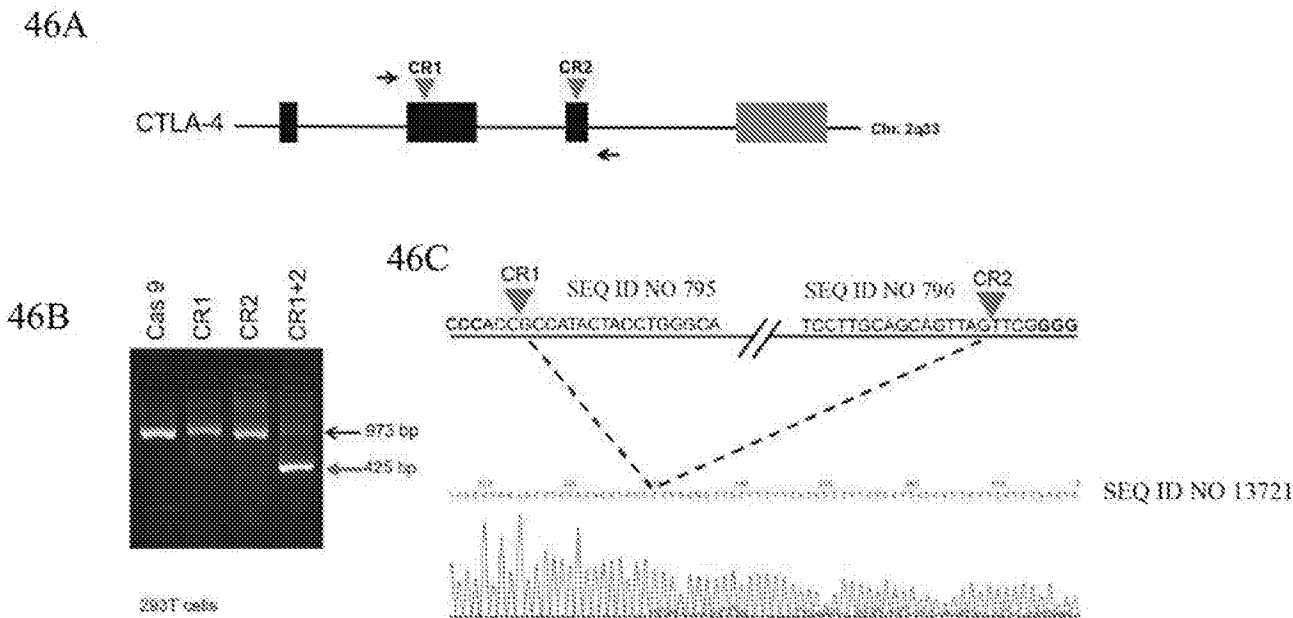
45A



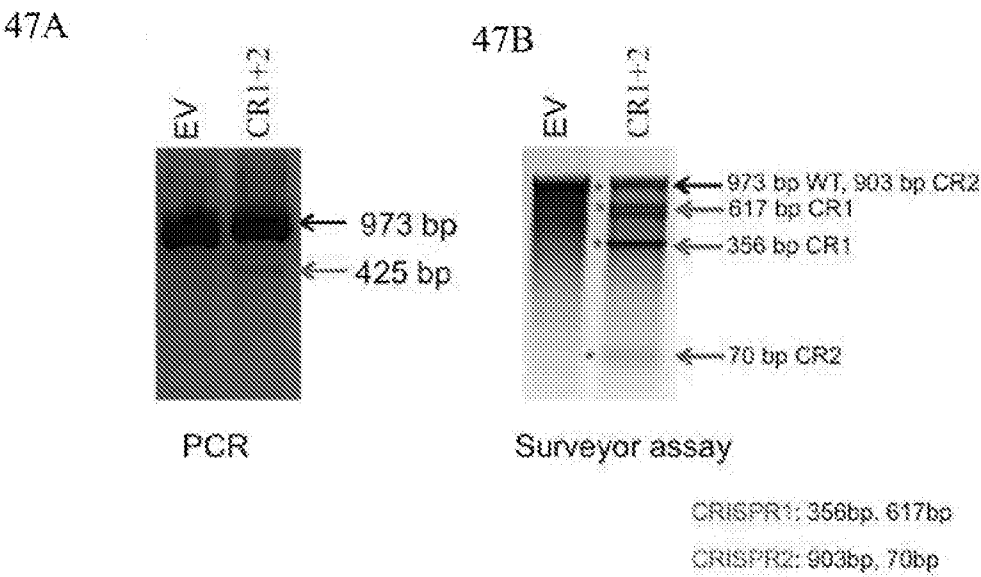
45B



FIGS. 45A-45B



FIGS. 46A-46C



FIGS. 47A-47B