

SAFE HARBOR LOCI**CROSS REFERENCE TO RELATED APPLICATIONS**

[0001] This application claims priority to and the benefit of U.S. Provisional Patent Application No. 63/179,143, filed on April 23, 2021, U.S. Provisional Patent Application No. 63/141,926, filed on January 26, 2021, and U.S. Provisional Patent Application No. 63/105,834, filed on October 26, 2020, the entire contents of which are incorporated by reference herein for all purposes.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which will be submitted via EFS-Web and is hereby incorporated by reference in its entirety. Said ASCII copy, created on October 15, 2021, is named ANB-203WO_SequenceListing and is 623,177 bytes in size.

BACKGROUND

[0003] Cancer continues to present a significant clinical burden despite the substantial research efforts and scientific advances in cancer therapies. Blood and bone marrow cancers are frequently diagnosed cancer types, including multiple myelomas, leukemia, and lymphomas. Current treatment options for these cancers are not effective for all patients and/or can have substantial adverse side effects. Other types of cancer also remain challenging to treat using existing therapeutic options. Cancer immunotherapies are a promising solution because they can be highly specific, allowing for increased therapeutic effectiveness and the mitigation of side effects.

[0004] Genetically engineered immune cell therapy is a growing field with promising applications for the treatment of diseases including, but not limited to, cancer. Through the alteration of coding and/or non-coding genomic regions, researchers are identifying transgenes and insertion sites within cells that facilitate, for example, enhanced cell function, arrest cell growth, induced cell death, and tumor size/volume reduction. The identification of safe harbor sites (SHS) has improved outcomes of genome-engineering therapies. Well known SHS include the AAVS1 adeno-associated virus insertion site on chromosome 19, the human homolog of the murine Rosa26 locus, and the CCR5 chemokine receptor gene—the absence of which confers HIV resistance. (See, for example, Pellenz *et al.*, 2018, the relevant disclosures of which are herein incorporated by reference). However, there is still a need for improved guidelines for gene editing therapies and additional SHS to address challenges such

as poor knock-in (KI) efficiency, insertional oncogenesis, unstable and/or anomalous expression of transgenes and/or adjacent genes, *etc.*.

SUMMARY

[0005] The present disclosure is directed, *inter alia*, to safe harbor loci that exhibit high knock-in efficiency and stable expression of their transgenes. These safe harbor loci can be used to alter T cells for immunotherapy. These safe harbor loci are useful for the treatment of various diseases, including cancer.

[0006] In one aspect, the present disclosure provides an engineered cell, comprising at least one sequence encoding a transgene, wherein the at least one sequence is inserted within a safe harbor locus, the safe harbor locus is at any one or more of the sgRNA target loci provided in Table 4; and wherein expression of the at least one sequence encoding the transgene is operatively linked to an endogenous promoter. In another aspect, the present disclosure provides an engineered cell, comprising at least one sequence encoding a transgene, wherein the at least one sequence is inserted within a safe harbor locus, the safe harbor locus is at any one or more of the sgRNA target loci provided in Table 4; and wherein expression of the at least one sequence encoding the transgene is operatively linked to an exogenous promoter.

[0007] In some embodiments, the target locus is selected from: chr10:33130000-33140000, chr10:72290000-72300000, chr11:128340000-128350000, chr11:65425000-65427000 (NEAT1), chr15:92830000-92840000, chr16:11220000-11230000, chr2:87460000-87470000, chr3:186510000-186520000, chr3:59450000-59460000, chr8:127980000-128000000, and chr9:7970000-7980000. In some embodiments, the target locus is selected from: chr10:72290000-72300000, chr11:128340000-128350000, chr15:92830000-92840000, and chr16:11220000-11230000. In some embodiments, the target locus is chr11:128340000-128350000. In some embodiments, the target locus is chr15:92830000-92840000. In some embodiments, the target locus is a gene selected from: *APRT*, *B2M*, *CAPNS1*, *CBLB*, *CD2*, *CD3E*, *CD3G*, *CD5*, *EDF1*, *FTL*, *PTEN*, *PTPN2*, *PTPN6*, *PTPRC*, *PTPRCAP*, *RPS23*, *RTRAF*, *SERF2*, *SLC38A1*, *SMAD2*, *SOCS1*, *SRP14*, *SRSF9*, *SUB1*, *TET2*, *TIGIT*, *TRAC*, and *TRIM28*.

[0008] In some embodiments, the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS88, GS89, GS90, GS91, GS92, GS93, GS94, GS95, GS96, GS97, GS98, GS99, GS100, GS101, GS102, GS103, GS104, GS105, GS106, GS107, GS108, GS109, GS110, GS111, GS112, GS113, GS114, GS115, GS116, GS117, GS118, GS119, GS120. In some embodiments, the safe harbor locus is selected from any one

of the integration sites in Table 4 designated: GS91, GS92, GS93, GS94, GS95, GS96, GS100, GS101, GS102, GS103, GS104, and GS105. In some embodiments, the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS103, GS104, and GS105. In some embodiments, the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS94, GS95, and GS96. In some embodiments, the safe harbor locus is the GS94 integration site in Table 4. In some embodiments, the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS100, GS101, and GS102. In some embodiments, the safe harbor locus is the GS102 integration site in Table 4. In some embodiments, the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS91, GS92, and GS93.

[0009] In some embodiments, the exogenous promoter is an EF1a promoter. In some embodiments, the engineered cell is a stem cell, a human cell, a primary cell, an hematopoietic cell, an adaptive immune cell, an innate immune cell, a T cell or a T cell progenitor. In some embodiments, the transgene encodes a recombinant protein, optionally a therapeutic agent. In some embodiments, the transgene encodes a chimeric antigen receptor (CAR).

[0010] In another aspect, the present disclosure provides a composition comprising the engineered cell as described herein and a pharmaceutical excipient.

[0011] In another aspect, the present disclosure provides a guide ribonucleic acids (gRNA) for editing a cell at a safe harbor locus, wherein gRNA comprises any one of the sgRNA sequences in Table 4.

[0012] In some embodiments, the gRNA comprises any one of SEQ ID NOS:1-120. In some embodiments, the gRNA comprises any one of SEQ ID NOS: 91-96 and 100-105. In some embodiments, the gRNA comprises SEQ ID NO:94 or SEQ ID NO:102. In some embodiments, the gRNA comprises SEQ ID NO:94. In some embodiments, the gRNA comprises SEQ ID NO:102. In some embodiments, the cell is a stem cell, a human cell, a primary cell, an hematopoietic cell, an adaptive immune cell, an innate immune cell, a T cell or a T cell progenitor.

[0013] In another aspect, the present disclosure provides a method of editing a cell having chromosomal DNA, comprising inserting at least one sequence encoding a transgene within a safe harbor locus in the chromosomal DNA of the cell, wherein the safe harbor locus is any one or more of the sgRNA target loci provided in Table 4.

[0014] In some embodiments, the target locus is selected from: chr10:33130000-33140000, chr10:72290000-72300000, chr11:128340000-128350000, chr11:65425000-65427000 (NEAT1), chr15:92830000-92840000, chr16:11220000-11230000, chr2:87460000-87470000, chr3:186510000-186520000, chr3:59450000-59460000, chr8:127980000-128000000, and chr9:7970000-7980000. In some embodiments, the target locus is selected from: chr10:72290000-72300000, chr11:128340000-128350000, chr15:92830000-92840000, and chr16:11220000-11230000. In some embodiments, the target locus is chr11:128340000-128350000. In some embodiments, the target locus is chr15:92830000-92840000. In some embodiments, the target locus is a gene selected from: *APRT*, *B2M*, *CAPNS1*, *CBLB*, *CD2*, *CD3E*, *CD3G*, *CD5*, *EDF1*, *FTL*, *PTEN*, *PTPN2*, *PTPN6*, *PTPRC*, *PTPRCAP*, *RPS23*, *RTRAF*, *SERF2*, *SLC38A1*, *SMAD2*, *SOCS1*, *SRP14*, *SRSF9*, *SUB1*, *TET2*, *TIGIT*, *TRAC*, and *TRIM28*.

[0015] In some embodiments, the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS88, GS89, GS90, GS91, GS92, GS93, GS94, GS95, GS96, GS97, GS98, GS99, GS100, GS101, GS102, GS103, GS104, GS105, GS106, GS107, GS108, GS109, GS110, GS111, GS112, GS113, GS114, GS115, GS116, GS117, GS118, GS119, GS120. In some embodiments, the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS91, GS92, GS93, GS94, GS95, GS96, GS100, GS101, GS102, GS103, GS104, and GS105. In some embodiments, the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS103, GS104, and GS105. In some embodiments, the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS94, GS95, and GS96. In some embodiments, the safe harbor locus is the GS94 integration site in Table 4. In some embodiments, the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS100, GS101, and GS102. In some embodiments, the safe harbor locus is the GS102 integration site in Table 4. In some embodiments, the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS91, GS92, and GS93.

[0016] In some embodiments, the transgene encodes a recombinant protein, optionally a therapeutic agent. In some embodiments, the transgene encodes a chimeric antigen receptor (CAR). In some embodiments, the at least one sequence comprises an exogenous promoter and the exogenous promoter is operably linked to the transgene. In some embodiments, the exogenous promoter is an EF1a promoter. In some embodiments, the cell is a stem cell, a human cell, a primary cell, an hematopoietic cell, an adaptive immune cell, an innate immune

cell, a T cell or T cell progenitor. In some embodiments, the at least one sequence is inserted using a homology-directed repair. In some embodiments, the at least one sequence is inserted using a homology independent targeted insertion. In some embodiments, the at least one sequence is inserted using one or more guide ribonucleic acids (gRNAs) and one or more Cas9 endonucleases.

[0017] In some embodiments, the one or more gRNAs comprises any one of SEQ ID NOS: 1-120. In some embodiments, the one or more gRNAs comprises any one of SEQ ID NOS: 91-96 and 100-105. In some embodiments, the gRNA comprises SEQ ID NO:94 or SEQ ID NO:102. In some embodiments, the gRNA comprises SEQ ID NO:94. In some embodiments, the gRNA comprises SEQ ID NO:102.

[0018] In another aspect, the present disclosure provides a method of editing a T cell, comprising contacting a T cell with one or more guide ribonucleic acids (gRNAs), at least one sequence encoding a transgene, and one or more Cas9 endonucleases, wherein the one or more gRNAs and Cas9 endonucleases facilitate the insertion of the at least one sequence into chromosomal DNA within a safe harbor locus, wherein the safe harbor locus is selected from any one or more of the sgRNA target loci in Table 4.

[0019] In some embodiments, the one or more gRNAs comprises a sequence selected from any one of the sgRNA sequences in Table 4. In some embodiments, the one or more gRNAs comprises any one of SEQ ID NOS: 1-120. In some embodiments, the one or more gRNAs comprises any one of SEQ ID NOS: 91-96 and 100-105. In some embodiments, the gRNA comprises SEQ ID NO:94 or SEQ ID NO:102. In some embodiments, the gRNA comprises SEQ ID NO:94. In some embodiments, the gRNA comprises SEQ ID NO:102.

[0020] In some embodiments, the target locus is selected from: chr10:33130000-33140000, chr10:72290000-72300000, chr11:128340000-128350000, chr11:65425000-65427000 (NEAT1), chr15:92830000-92840000, chr16:11220000-11230000, chr2:87460000-87470000, chr3:186510000-186520000, chr3:59450000-59460000, chr8:127980000-128000000, and chr9:7970000-7980000. In some embodiments, the target locus is selected from: chr10:72290000-72300000, chr11:128340000-128350000, chr15:92830000-92840000, and chr16:11220000-11230000. In some embodiments, the target locus is chr11:128340000-128350000. In some embodiments, the target locus is chr15:92830000-92840000. In some embodiments, the target locus is a gene selected from: *APRT*, *B2M*, *CAPNS1*, *CBLB*, *CD2*, *CD3E*, *CD3G*, *CD5*, *EDF1*, *FTL*, *PTEN*, *PTPN2*, *PTPN6*, *PTPRC*, *PTPRCAP*, *RPS23*,

RTRAF, *SERF2*, *SLC38A1*, *SMAD2*, *SOCS1*, *SRP14*, *SRSF9*, *SUB1*, *TET2*, *TIGIT*, *TRAC*, and *TRIM28*.

[0021] In some embodiments, the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS88, GS89, GS90, GS91, GS92, GS93, GS94, GS95, GS96, GS97, GS98, GS99, GS100, GS101, GS102, GS103, GS104, GS105, GS106, GS107, GS108, GS109, GS110, GS111, GS112, GS113, GS114, GS115, GS116, GS117, GS118, GS119, GS120. In some embodiments, the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS91, GS92, GS93, GS94, GS95, GS96, GS100, GS101, GS102, GS103, GS104, and GS105. In some embodiments, the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS103, GS104, and GS105. In some embodiments, the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS94, GS95, and GS96. In some embodiments, the safe harbor locus is the GS94 integration site in Table 4. In some embodiments, the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS100, GS101, and GS102. In some embodiments, the safe harbor locus is the GS102 integration site in Table 4. In some embodiments, the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS91, GS92, and GS93

[0022] In another aspect, the present disclosure provides an *ex vivo* method of obtaining an engineered cell or population thereof, comprising (a) obtaining a cell; and (b) genetically modifying the cell by inserting at least one sequence encoding a transgene within a safe harbor locus, wherein the safe harbor locus is selected from any one of the sgRNA target loci in Table 4.

[0023] In some embodiments, obtaining the cell comprises: (i) collecting a tissue sample from a subject, (ii) isolating the cells from the tissue samples, and (iii) culturing the cells in vitro. In some embodiments, the tissue sample is a blood sample. In some embodiments, the cell is a stem cell, a human cell, a primary cell, an hematopoietic cell, an adaptive immune cell, an innate immune cell, a T cell or T cell precursor (T cell progenitor). In some embodiments, the at least one sequence is inserted using a homology-directed repair. In some embodiments, the at least one sequence is inserted using a homology independent targeted insertion.

[0024] In some embodiments, the genetically modifying in step (b) comprises contacting the cell with one or more guide ribonucleic acids (gRNAs), the at least one sequence, and one or more Cas9 endonucleases, wherein the one or more gRNAs and Cas9 endonucleases facilitate

the insertion of the at least one sequence into chromosomal DNA within the safe harbor locus. In some embodiments, the one or more gRNAs comprises a sequence selected from any one of the sgRNA sequences in Table 4.

[0025] In some embodiments, the transgene encodes a recombinant protein, optionally a therapeutic agent. In some embodiments, the transgene encodes a chimeric antigen receptor (CAR). In some embodiments, the at least one sequence comprises an exogenous promoter and the exogenous promoter is operably linked to the transgene. In some embodiments, the exogenous promoter is an EF1a promoter.

[0026] In yet another aspect, the present disclosure provides a method of treating a subject having or at risk of having a disease, comprising administering to the subject an effective amount of an engineered cell as described herein, a population thereof, or a composition as described herein. In some embodiments, the cell, the population thereof, or the composition is administered to the subject by infusion.

[0027] In yet another aspect, the present disclosure provides a method of treating a subject having or at risk of having a disease, comprising (a) conducting any one of the methods described *supra*; and (b) administering to the subject an effective amount of a composition comprising the cell or a population thereof. In some embodiments, the composition is administered to the subject by infusion. In some embodiments, the disease is cancer. In some embodiments, the disease is blood cancer.

[0028] In another aspect, the present disclosure provides a method of identifying a safe harbor locus, comprising: (a) identifying genes or non-coding regions in a chromosome that are above a threshold level for expression across developmental cell states and/or a threshold level for accessibility of chromatin; (b) generating a linear model that correlates the gene or non-coding region from step (a) with knock-in (KI) efficiency and estimates the KI efficiency of any gene or coding region on the chromosome; and (c) selecting the safe harbor locus based on threshold parameters; wherein the safe harbor locus is selected for insertion of at least one sequence encoding a transgene within a cell.

[0029] In some embodiments, the threshold parameters include one or more of: stable expression of a transgene, knockout of the gene confers benefit to the function of the cell, no known function within the cell, stable transgene expression *in vitro* with or without CD3/CD28 stimulation, negligible off-target cleavage as detected by iGuide-Seq or CRISPR-Seq, less off-target cleavage relative to other loci as detected by iGuide-Seq or CRISPR-Seq, negligible transgene-independent cytotoxicity, negligible transgene-independent cytokine

expression, negligible transgene-independent chimeric antigen receptor expression, negligible deregulation or silencing of nearby genes, and positioned outside of a cancer-related gene. In some embodiments, the stable expression of a transgene at the safe harbor locus is less than or equal to 2-fold expression change over the course of at least 1, 2, 3, 4, 5, 6, or 7 days, and wherein expression change is measured by mean fluorescence intensity of a reporter gene encoded by the at least one sequence. In some embodiments, the accessibility of chromatin is measured using an assay for transposase-accessible chromatin using sequencing (ATAC-seq). In some embodiments, the level of expression across developmental cell states is measured using RNA sequencing (RNA-seq).

[0030] In some embodiments, the cell is a stem cell, a human cell, a primary cell, an hematopoietic cell, an adaptive immune cell, an innate immune cell, a T cell or T cell progenitor. In some embodiments, the linear model has a coefficient of determination (R^2 value) of at least 30%.

[0031] In yet another aspect, the present disclosure provides an engineered cell, composition, gRNA or method as described herein, wherein insertion within the safe harbor locus increase cell cytotoxicity of diseased cells.

[0032] In yet another aspect, the present disclosure provides an engineered cell, composition, gRNA or method as described herein, wherein knock-in efficiency at the safe harbor locus is increased relative to other locations along the chromosome.

BRIEF DESCRIPTION OF THE DRAWINGS

[0033] These and other features, aspects, and advantages of the present invention will become better understood with regard to the following description, and accompanying drawings, where:

[0034] FIG. 1 includes a schematic depicting the methodology used to identify safe harbor loci in the present disclosure, in some embodiments.

[0035] FIGS. 2A-2C include schematic depicting 3 top safe harbor loci known in the art: AAVS1 (**FIG. 2A**), CCR5 (**FIG. 2B**), and Rosa26 (**FIG. 2C**). The figures were retrieved from Sadelain, M., et al. (2012). Safe harbours for the integration of new DNA in the human genome. *Nature reviews Cancer*, 12(1), 51-58, the relevant disclosures of which are herein incorporated by reference in their entirety.

[0036] FIG. 3 includes a schematic outlining the data provided in Roth, T. L., et al. 2019. Rapid discovery of synthetic DNA sequences to rewrite endogenous T cell circuits. *bioRxiv*,

604561, the relevant disclosures of which are herein incorporated by reference in their entirety.

[0037] **FIGS. 4A-4B** include heatmaps with samples clustered based on activation status and cell type, generated with processed RNA-seq data. **FIG. 4A** includes a heatmap of samples generated with processed RNA-seq data. **FIG. 4B** includes a heatmap sample generated with processed RNA-seq data, showing the clustering of ~20k genes.

[0038] **FIGS. 5A-5B** include plots generated using processed RNA-seq data. **FIG. 5A** includes a plot showing direct correlation between transcript expression data from Roth, T.L., et al. 2019 and transcript expression data generated by the inventors of the present disclosure. **FIG. 5B** includes a heatmap showing clusters of the top 10% expressed genes.

[0039] **FIG. 6** includes a heatmap of samples generated with processed ATAC-seq data.

[0040] **FIGS. 7A-7B** includes plots depicting the signal enrichment at transcription start sites (TSS) (**FIG. 7A**) and peak size distribution (**FIG. 7B**), generated with processed ATAC-seq data for coding regions.

[0041] **FIG. 8** includes a plot depicting the open chromatin regions around the TRAC locus.

[0042] **FIG. 9** includes a plot depicting KI (knock-in) efficiency for coding regions/genes with GFP as a reporter.

[0043] **FIG. 10** includes a plot depicting KI efficiency for coding regions/genes with tNGFR as a reporter.

[0044] **FIG. 11** includes plots showing scaled KI efficiency for 90 genes vs d2 (day-2) RNA-seq data, d4 (day-4) RNA-seq data and ATAC-seq data, utilized for the predictive linear model.

[0045] **FIG. 12** includes a plot showing chromatin accessibility for a top candidate non-coding region, measured using ATAC sequencing.

[0046] **FIG. 13A** includes plots showing the cell counts for GFP controls used for the evaluation of candidate KI loci. **FIG. 13B** includes pmax (GFP_high) readings for GFP controls used for the evaluation of candidate KI loci.

[0047] **FIG. 14A** includes plots showing the maximum episomal GFP expression (GFP_high) readings for non-targeting controls. **FIG. 14B** includes the cell count for non-targeting controls from donors 1, 2, and 3.

[0048] **FIG. 15** includes the cell count and maximum GFP expression (GFP_high) readings for WT controls.

[0049] **FIG. 16** includes plots showing the cell count and maximum GFP expression (GFP_high) readings when using sgRNA5, which targets a B2M safe harbor locus, and the construct expression was driven by an endogenous promoter.

[0050] **FIG. 17** includes plots showing the cell count and maximum GFP expression (GFP_high) readings when using sgRNA5, which targets a B2M safe harbor locus, and the construct expression was driven by an EF1a promoter.

[0051] **FIG. 18** includes plots showing the cell count and maximum GFP expression (GFP_high) readings when using sgRNA79 to target a TRAC safe harbor locus, and the construct expression was driven by an endogenous promoter.

[0052] **FIG. 19** includes plots showing the cell count and maximum GFP expression (GFP_high) readings when using sgRNA79, which targets a TRAC safe harbor locus, and the construct expression was driven by an exogenous promoter.

[0053] **FIG. 20** includes plots showing TCR (T cell receptor) vs. GFP among all donors and time points when using sgRNA79, and the construct is driven by an endogenous promoter.

[0054] **FIG. 21** includes plots showing TCR vs. GFP among all donors and time points when using sgRNA79 and the construct is driven by an exogenous promoter.

[0055] **FIG. 22** includes plots showing the cell count and maximum GFP expression (GFP_high) readings when using sgRNA83, which targets a TRAC safe harbor locus, and the construct expression was driven by an endogenous promoter.

[0056] **FIG. 23** includes plots showing the cell count and maximum GFP expression (GFP_high) readings when using sgRNA83, which targets a TRAC safe harbor locus, and the construct expression was driven by an exogenous promoter.

[0057] **FIG. 24** includes plots showing TCR vs. GFP among all donors and time points when using sgRNA83 and the construct is driven by an endogenous promoter.

[0058] **FIG. 25** includes plots showing TCR vs. GFP among all donors and time points when using sgRNA83 and the construct is driven by an exogenous promoter.

[0059] **FIG. 26** includes plots illustrating potential sources of variation (e.g., edge effects and electroporation errors) observed between replicates and donors.

[0060] **FIG. 27** includes plots illustrating potential sources of variation observed between replicates and donors, e.g., relating to inherent differences between donors.

[0061] **FIG. 28** includes plots illustrating potential sources of variation observed between replicates and donors, e.g., relating to gating errors.

[0062] **FIG. 29** includes plots showing the GFP mean fluorescence intensity (GFP MFI) and KI efficiency for top KI loci evaluated with endogenous promoters.

[0063] **FIG. 30** includes plots showing the GFP mean fluorescence intensity (GFP MFI) and KI efficiency for top KI loci evaluated with the EF1a promoter.

[0064] **FIGS. 31A-31C** include plots showing all the significant KI loci (top KI loci) as evaluated with endogenous and EF1a promoters. **FIG. 31A** includes a plot showing that the expression from the EF1a promoter was approximately 10 times higher than expression from an endogenous promoter. **FIG. 31B** shows the top KI loci ranked by GFP MFI at week 3.

FIG. 31C shows the top integration loci ranked by GFP MFI (at weeks 3 and 4; donors 1-3).

[0065] **FIG. 32A** includes a plot showing some target loci and their measured transgene expression levels. **FIG. 32B** includes plots showing the transgene (Prime Receptor (PrimeR)) and TCR expression for the control and insertion at GS94, GS102 and TRAC loci.

[0066] **FIG. 33A** includes a plot showing the PrimeR levels measured for the indicated integration sites. **FIG. 33B** includes a schematic showing the GS94 integration site on Chromosome 11.

[0067] **FIG. 34A** includes plots showing CAR induction and primeR expression of engineered T cells after 48 hours of coculturing with K562-CD19 cells. **FIG. 34B** includes plots showing the cytotoxicity and cytokine secretion levels for engineered T cells 48 hours of coculturing with K562-CD19/MSLN cells.

[0068] **FIG. 35A** includes a schematic showing the experimental overview for evaluating the effect of integration site on cytotoxicity. **FIG. 35B** includes plots showing the measured cytotoxicity for engineered T cells cocultured for 48 hours with the K562 CD19+/MSLN+ or K562 CD19-/MSLN+ cells.

[0069] **FIG. 36A** includes a schematic showing the experimental overview for evaluating the effect of integration site on cytokine secretion. **FIG. 36B** includes plots showing the measured cytokine levels for engineered T cells cocultured for 48 hours with K562 CD19+/MSLN+ cells.

[0070] **FIG. 37** includes a schematic showing the *in vitro* experiment conducted to determine the effect of integration site on primeR-independent CAR expression. “Flow” refers to flow cytometry and “restim” refers to repetitive CD3/CD28 stimulation of the engineered T cells. “EP” refers to electroporation.

[0071] **FIGS. 38A and 38B** include plots showing the stability of PrimeR expression over time when using the indicated integration sites. “Flow” refers to flow cytometry and “restim”

refers to repetitive CD3/CD28 stimulation of the engineered T cells. “EP” refers to electroporation. In **FIG. 38B**, the PrimeR expression is normalized to the expression from using the TRAC integration site.

[0072] **FIG. 39A** includes a schematic showing the iGuide-Seq assay technique. **FIG. 39B** includes a plot showing the on-target efficiency, using iGuide Seq assay, for the indicated integration sites. **FIG. 39C** includes schematics from the iGuide-Seq analysis showing that GS94 had no reproducible putative off-targets across two donors.

[0073] **FIG. 40** includes a schematic showing the iGuide-Seq workflow and data.

[0074] **FIG. 41** includes a plot showing rhAmp-seq analysis of putative off-target sites identified by iGUIDE-seq and Elevation prediction.

[0075] **FIG. 42** includes plots showing RNA-seq analysis of cells with GS94, GS102 and TRAC knock-in of CD19/MSLN circuits. Scatterplot of gene expression in cells with integration at the GS94 locus (y-axis) vs cells with integration at either the TRAC or the GS102 locus (x-axis) in two donors. The yellow dots correspond to ETS1 and FLI1. In blue are the genes that were found to be differentially expressed using edgeR (fold-change > 0, FDR-corrected p-value < 0.01, average counts-per-million across compared conditions at least 2).

[0076] **FIG. 43** includes plots showing the absence of cytokine-independent growth in cells with CD19/MSLN circuit KI at GS94.

[0077] **FIG. 44** shows a diagram of a 8.3 kb cassette that was inserted into the GS94 safe harbor locus.

[0078] **FIG. 45** shows the expression of a 8.3 kb transgene circuit comprising a priming receptor and CAR in K562 cells.

[0079] **FIG. 46** shows that non-viral editing generated less differentiated T cells.

DETAILED DESCRIPTION

[0080] The present disclosure provides safe harbor loci and methods for identifying safe harbor loci that exhibit high integration efficiency (*e.g.*, high knock-in (KI) efficiency), high and constant levels of transgene expression, and such benefits independent of T cell activation/differentiation state. In some embodiments, the safe harbor loci also exhibit minimal to no disruption to T cell function and/or capacity for product manufacturing. In some embodiments, these loci are useful for effective and safe integration and expression of transgenes in T cells (*e.g.* in CAR T therapies). In some embodiments, the methods described

herein can be used for the identification of safe harbor loci for insertion of transgenes in other types of cells.

[0081] FIG. 1 illustrates the overall approach that the inventors of the present disclosure used to identify safe harbor loci. In some embodiments, the present disclosure provides a method comprising the identification of genes within a genome and non-coding regions with sustained expression in a treatment cell (e.g. T cell) and using a predictive model of KI efficiency as a function of T cell chromatic state and computational analysis to predict candidate integration sites. The method further comprises evaluating the candidate integration sites for actual KI efficiency, sustained levels of transgene expression of a transgene, and minimal disruption to the treatment cell phenotype (e.g., T cell function and/or capacity for treatment product expansion and manufacturing). In some embodiments, the safe harbor loci allow for integration of a transgene driven by an endogenous promoter. In some embodiments, the safe harbor loci allow for integration of a transgene driven by an exogenous promoter (e.g. EF1a promoter).

[0082] To facilitate an understanding of the present disclosure, a number of terms and phrases are defined below. Unless otherwise defined herein, scientific and technical terms used in this application shall have the meanings that are commonly understood by those of ordinary skill in the art. Generally, nomenclature used in connection with, and techniques of pharmacology, cell and tissue culture, molecular biology, cell and cancer biology, neurobiology, neurochemistry, virology, immunology, microbiology, genetics and protein and nucleic acid chemistry, described herein, are those well-known and commonly used in the art. In case of conflict, the present specification, including definitions, will control.

[0083] Unless otherwise defined, all terms of art, notations and other scientific terminology used herein are intended to have the meanings commonly understood by those of skill in the art. In some cases, terms with commonly understood meanings are defined herein for clarity and/or for ready reference, and the inclusion of such definitions herein should not necessarily be construed to represent a difference over what is generally understood in the art. The techniques and procedures described or referenced herein are generally well understood and commonly employed using conventional methodologies by those skilled in the art, such as, for example, the widely utilized molecular cloning methodologies described in Sambrook et al., *Molecular Cloning: A Laboratory Manual* 4th ed. (2012) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY. As appropriate, procedures involving the use of

commercially available kits and reagents are generally carried out in accordance with manufacturer-defined protocols and conditions unless otherwise noted.

[0084] As used herein, the singular forms “a,” “an,” and “the” include the plural referents unless the context clearly indicates otherwise. The terms “include,” “such as,” and the like are intended to convey inclusion without limitation, unless otherwise specifically indicated.

[0085] As used herein, the term “comprising” also specifically includes embodiments “consisting of” and “consisting essentially of” the recited elements, unless specifically indicated otherwise.

[0086] The term “about” indicates and encompasses an indicated value and a range above and below that value. In certain embodiments, the term “about” indicates the designated value $\pm 10\%$, $\pm 5\%$, or $\pm 1\%$. In certain embodiments, where applicable, the term “about” indicates the designated value(s) $\pm$ one standard deviation of that value(s).

[0087] As used herein, the term “gene” refers to the basic unit of heredity, consisting of a segment of DNA arranged along a chromosome, which codes for a specific protein or segment of protein. A gene typically includes a promoter, a 5' untranslated region, one or more coding sequences (exons), optionally introns, a 3' untranslated region. The gene may further comprise a terminator, enhancers and/or silencers.

[0088] As used herein, the term “locus” refers to a specific, fixed physical location on a chromosome where a gene or genetic marker is located.

[0089] As used herein, the term “target locus” refers to a locus on a chromosome within which a safe harbor locus can be used for the insertion of a sequence. A target locus can consist of multiple potential safe harbor loci (integration sites). Examples of target loci are provided in Table 4, as sgRNA target loci. The notation used for the sgRNA target loci in Table 4 refers to the genomic region of the target locus, defined by the chromosome of the target locus and the coordinate range for that target locus. For example, chr10:33130000-33140000 refers to a target locus on Chr10 (chromosome 10) starting from coordinate 33130000 and ending with coordinate 33140000.

[0090] The term “safe harbor locus” refers to a locus at which genes or genetic elements can be incorporated without disruption to expression or regulation of adjacent genes. These safe harbor loci are also referred to as safe harbor sites (SHS). As used herein, a safe harbor locus refers to an “integration site” or “knock-in site” at which a sequence encoding a transgene, as defined herein, can be inserted. In some embodiments the insertion occurs with replacement of a sequence that is located at the integration site. In some embodiments, the insertion occurs

without replacement of a sequence at the integration site. Examples of integration sites contemplated are provided in Table 4.

[0091] As used herein, the term “insert” refers to a nucleotide sequence that is integrated (inserted) at a safe harbor site. The insert can be used to refer to the genes or genetic elements that are incorporated at the safe harbor site using, for example, homology-directed repair (HDR) CRISPR/Cas9 genome-editing or other methods for inserting nucleotide sequences into a genomic region known to those of ordinary skill in the art.

[0092] The “CRISPR/Cas” system refers to a widespread class of bacterial systems for defense against foreign nucleic acid. CRISPR/Cas systems are found in a wide range of eubacterial and archaeal organisms. CRISPR/Cas systems include type I, II, and III subtypes. Wild-type type II CRISPR/Cas systems utilize an RNA-mediated nuclease, Cas9 in complex with guide and activating RNA to recognize and cleave foreign nucleic acid. Guide RNAs having the activity of both a guide RNA and an activating RNA are also known in the art. In some cases, such dual activity guide RNAs are referred to as a small guide RNA (sgRNA).

[0093] Cas9 homologs are found in a wide variety of eubacteria, including, but not limited to bacteria of the following taxonomic groups: *Actinobacteria*, *Aquificae*, *Bacteroidetes-Chlorobi*, *Chlamydiae-Verrucomicrobia*, *Chloroflexi*, *Cyanobacteria*, *Firmicutes*, *Proteobacteria*, *Spirochaetes*, and *Thermotogae*. An exemplary Cas9 protein is the *Streptococcus pyogenes* Cas9 protein. Additional Cas9 proteins and homologs thereof are described in, e.g., Chylinski, *et al.*, RNA Biol. 2013 May 1; 10(5): 726–737; Nat. Rev. Microbiol. 2011 June; 9(6): 467-477; Hou, *et al.*, Proc Natl Acad Sci U S A. 2013 Sep 24; 110(39):15644-9; Sampson *et al.*, Nature. 2013 May 9; 497(7448):254-7; and Jinek, *et al.*, Science. 2012 Aug 17; 337(6096):816-21. The Cas9 nuclease domain can be optimized for efficient activity or enhanced stability in the host cell.

[0094] As used herein, the term “Cas9” refers to an RNA-mediated nuclease (e.g., of bacterial or archaeal origin, or derived therefrom). Exemplary RNA-mediated nucleases include the foregoing Cas9 proteins and homologs thereof, and include but are not limited to, CPF1 (See, e.g., Zetsche *et al.*, Cell, Volume 163, Issue 3, p759–771, 22 October 2015). Similarly, as used herein, the term “Cas9 ribonucleoprotein” complex and the like refers to a complex between the Cas9 protein, and a crRNA (e.g., guide RNA or small guide RNA), the Cas9 protein and a trans-activating crRNA (tracrRNA), the Cas9 protein and a small guide RNA,

or a combination thereof (*e.g.*, a complex containing the Cas9 protein, a tracrRNA, and a crRNA guide RNA).

[0095] As used herein, the terms “T lymphocyte” and “T cell” are used interchangeably and refer to cells that have completed maturation in the thymus, and identify certain foreign antigens in the body. The terms also refer to the major leukocyte types that have various roles in the immune system, including activation and deactivation of other immune cells. The T cell can be any T cell such as a cultured T cell, *e.g.*, a primary T cell, or a T cell derived from a cultured T cell line, *e.g.*, a Jurkat, SupT1, etc., or a T cell obtained from a mammal. The T cell can be a CD3 + cell. The T cell can be any type of T cell, CD4 + / CD8 + double positive T cells, CD4 + helper T cells (*e.g.* Th1 and Th2 cells), CD8 + T cells (*e.g.* cytotoxic T cells), peripheral Including but not limited to blood mononuclear cells (PBMC), peripheral blood leukocytes (PBL), tumor infiltrating lymphocytes (TIL), memory T cells, naive T cells, regulatory T cells, $\gamma\delta$ T cells, etc. It can be any T cell at any stage of development. Additional types of helper T cells include Th3 (Treg) cells, Th17 cells, Th9 cells, or Tfh cells. Additional types of memory T cells include cells such as central memory T cells (Tcm cells), effector memory T cells (Tem cells and TEMRA cells). A T cell can also refer to a genetically modified T cell, such as a T cell that has been modified to express a T cell receptor (TCR) or a chimeric antigen receptor (CAR). T cells can also be differentiated from stem cells or progenitor cells (*e.g.*, precursor cells).

[0096] “CD4 + T cells” refers to a subset of T cells that express CD4 on their surface and are associated with a cellular immune response. CD4 + T cells are characterized by a post-stimulation secretion profile that can include secretion of cytokines such as IFN- γ , TNF- α , IL-2, IL-4 and IL-10. “CD4” is a 55 kD glycoprotein originally defined as a differentiation antigen on T lymphocytes, but was also found on other cells including monocytes / macrophages. The CD4 antigen is a member of the immunoglobulin superfamily and has been implicated as an associative recognition element in MHC (major histocompatibility complex) class II restricted immune responses. On T lymphocytes, the CD4 antigen defines a helper / inducer subset.

[0097] “CD8 + T cells” refers to a subset of T cells that express CD8 on their surface, are MHC class I restricted, and function as cytotoxic T cells. The “CD8” molecule is a differentiation antigen present on thymocytes, as well as on cytotoxic and suppressor T lymphocytes. The CD8 antigen is a member of the immunoglobulin superfamily and is an

associative recognition element in major histocompatibility complex class I restriction interactions.

[0098] As used herein, the term “ex vivo” generally includes experiments or measurements made in or on living tissue, preferably in an artificial environment outside the organism, preferably with minimal differences from natural conditions.

[0099] As used herein, the term “construct” refers to a complex of molecules, including macromolecules or polynucleotides.

[0100] As used herein, the term “integration” refers to the process of stably inserting one or more nucleotides of a construct into the cell genome, i.e., covalently linking to a nucleic acid sequence in the chromosomal DNA of the cell. It may also refer to nucleotide deletions at a site of integration. Where there is a deletion at the insertion site, “integration” may further include substitution of the endogenous sequence or nucleotide deleted with one or more inserted nucleotides.

[0101] As used herein, the term “exogenous” refers to a molecule or activity that has been introduced into a host cell and is not native to that cell. The molecule can be introduced, for example, by introduction of the encoding nucleic acid into host genetic material, such as by integration into a host chromosome, or as non-chromosomal genetic material, such as a plasmid. Thus, the term, when used in connection with expression of an encoding nucleic acid, refers to the introduction of the encoding nucleic acid into a cell in an expressible form. The term “endogenous” refers to a molecule or activity that is present in a host cell under natural, unedited conditions. Similarly, the term, when used in connection with expression of the encoding nucleic acid, refers to expression of the encoding nucleic acid that is contained within the cell and not introduced exogenously.

[0102] As used herein, a “polynucleotide donor construct” refers to a nucleotide sequence (e.g. DNA sequence) that is genetically inserted into a polynucleotide and is exogenous to that polynucleotide. The polynucleotide donor construct is transcribed into RNA and optionally translated into a polypeptide. The polynucleotide donor construct can include prokaryotic sequences, cDNA from eukaryotic mRNA, genomic DNA sequences from eukaryotic (e.g., mammalian) DNA, and synthetic DNA sequences. For example, the polynucleotide donor construct can be a miRNA, shRNA, natural polypeptide (i.e., a naturally occurring polypeptide) or fragment thereof or a variant polypeptide (e.g. a natural polypeptide having less than 100% sequence identity with the natural polypeptide) or fragments thereof.

[00103] As used herein, the term “transgene” refers to a polynucleotide that has been transferred naturally, or by any of a number of genetic engineering techniques from one organism to another. It is optionally translated into a polypeptide. It is optionally translated into a recombinant protein. A “recombinant protein” is a protein encoded by a gene — recombinant DNA — that has been cloned in a system that supports expression of the gene and translation of messenger RNA (see expression system). The recombinant protein can be a therapeutic agent, e.g. a protein that treats a disease or disorder disclosed herein. As used, transgene can refer to a polynucleotide that encodes a polypeptide. A transgene can also refer to a non-encoding sequence, such as, but not limited to shRNAs, miRNAs, and miRs.

[00104] The terms “protein,” “polypeptide,” and “peptide” are used herein interchangeably.

[00105] As used herein, the term “operably linked” refers to the binding of a nucleic acid sequence to a single nucleic acid fragment such that one function is affected by the other. For example, if a promoter is capable of affecting the expression of a coding sequence or functional RNA (i.e., the coding sequence or functional RNA is under transcriptional control by the promoter), the promoter is operably linked thereto. Coding sequences can be operably linked to control sequences in both sense and antisense orientation.

[00106] As used herein, the term “developmental cell states” refers to, for example, states when the cell is inactive, actively expressing, differentiating, senescent, etc. developmental cell state may also refer to a cell in a precursor state (e.g., a T cell precursor or T cell progenitor).

[00107] As used, the term “encoding” refers to a sequence of nucleic acids which codes for a protein or polypeptide of interest. The nucleic acid sequence may be either a molecule of DNA or RNA. In preferred embodiments, the molecule is a DNA molecule. In other preferred embodiments, the molecule is a RNA molecule. When present as a RNA molecule, it will comprise sequences which direct the ribosomes of the host cell to start translation (e.g., a start codon, ATG) and direct the ribosomes to end translation (e.g., a stop codon). Between the start codon and stop codon is an open reading frame (ORF). Such terms are known to one of ordinary skill in the art.

[00108] The term “inserting” refers to a manipulation of a nucleotide sequence to introduce a non-native sequence. This is done, for example, via the use of restriction enzymes and ligases whereby the DNA sequence of interest, usually encoding the gene of interest, can be incorporated into another nucleic acid molecule by digesting both molecules with

appropriate restriction enzymes in order to create compatible overlaps and then using a ligase to join the molecules together. One skilled in the art is very familiar with such manipulations and examples may be found in Sambrook et al. (Sambrook, Fritsch, & Maniatis, "Molecular Cloning: A Laboratory Manual", 2nd ed., Cold Spring Harbor Laboratory, 1989), which is hereby incorporated by reference in its entirety including any drawings, figures and tables.

[00109] As used herein, the term "subject" refers to a mammalian subject. Exemplary subjects include humans, monkeys, dogs, cats, mice, rats, cows, horses, camels, goats, rabbits, pigs and sheep. In certain embodiments, the subject is a human. In some embodiments the subject has a disease or condition that can be treated with an engineered cell provided herein or population thereof. In some aspects, the disease or condition is a cancer.

[00110] As used herein, the term "promoter" refers to a nucleotide sequence (e.g. DNA sequence) capable of controlling the expression of a coding sequence or functional RNA. The promoter sequence consists of proximal and more distal upstream elements, the latter elements often referred to as enhancers. A promoter can be derived from natural genes in its entirety, can be composed of different elements from different promoters found in nature, and/or may comprise synthetic DNA segments. A promoter, as contemplated herein, can be endogenous to the cell of interest or exogenous to the cell of interest. It is appreciated by those skilled in the art that different promoters can induce gene expression in different tissue or cell types, or at different developmental stages, or in response to different environmental conditions. As is known in the art, a promoter can be selected according to the strength of the promoter and/or the conditions under which the promoter is active, e.g., constitutive promoter, strong promoter, weak promoter, inducible/repressible promoter, tissue specific Or developmentally regulated promoters, cell cycle-dependent promoters, and the like.

[00111] A promoter can be an inducible promoter (e.g., a heat shock promoter, tetracycline- regulated promoter, steroid-regulated promoter, metal-regulated promoter, estrogen receptor- regulated promoter, etc.). The promoter can be a constitutive promoter (e.g., CMV promoter, UBC promoter). In some embodiments, the promoter can be a spatially restricted and/or temporally restricted promoter (e.g., a tissue specific promoter, a cell type specific promoter, etc.). See for example US Application No. 15/715,068, the disclosures of which are herein incorporated by reference in their entirety.

[00112] Gene editing, as contemplated herein, may involve a gene (or nucleotide sequence) knock-in or knock-out. As used herein, the term "knock-in" refers to an addition of a DNA sequence, or fragment thereof into a genome. Such DNA sequences to be knocked-in

may include an entire gene or genes, may include regulatory sequences associated with a gene or any portion or fragment of the foregoing. For example, a polynucleotide donor construct encoding a recombinant protein may be inserted into the genome of a cell carrying a mutant gene. In some embodiments, a knock-in strategy involves substitution of an existing sequence with the provided sequence, e.g., substitution of a mutant allele with a wild-type copy. On the other hand, the term “knock-out” refers to the elimination of a gene or the expression of a gene. For example, a gene can be knocked out by either a deletion or an addition of a nucleotide sequence that leads to a disruption of the reading frame. As another example, a gene may be knocked out by replacing a part of the gene with an irrelevant (e.g., non-coding) sequence.

[00113] As used herein, the term “non-homologous end joining” or NHEJ refers to a cellular process in which cut or nicked ends of a DNA strand are directly ligated without the need for a homologous template nucleic acid. NHEJ can lead to the addition, the deletion, substitution, or a combination thereof, of one or more nucleotides at the repair site.

[00114] As used herein, the term “homology directed repair” or HDR refers to a cellular process in which cut or nicked ends of a DNA strand are repaired by polymerization from a homologous template nucleic acid. Thus, the original sequence is replaced with the sequence of the template. The homologous template nucleic acid can be provided by homologous sequences elsewhere in the genome (sister chromatids, homologous chromosomes, or repeated regions on the same or different chromosomes). Alternatively, an exogenous template nucleic acid can be introduced to obtain a specific HDR-induced change of the sequence at the target site. In this way, specific mutations can be introduced at the cut site.

[00115] The terms “vector” and “plasmid” are used interchangeably and as used herein refer to polynucleotide vehicles useful to introduce genetic material into a cell. Vectors can be linear or circular. Vectors can integrate into a target genome of a host cell or replicate independently in a host cell. Vectors can comprise, for example, an origin of replication, a multicloning site, and/or a selectable marker. An expression vector typically comprises an expression cassette. Vectors and plasmids include, but are not limited to, integrating vectors, prokaryotic plasmids, eukaryotic plasmids, plant synthetic chromosomes, episomes, viral vectors, cosmids, and artificial chromosomes.

[00116] As used herein the term “expression cassette” is a polynucleotide construct, generated recombinantly or synthetically, comprising regulatory sequences operably linked to a selected polynucleotide to facilitate expression of the selected polynucleotide in a host cell.

For example, the regulatory sequences can facilitate transcription of the selected polynucleotide in a host cell, or transcription and translation of the selected polynucleotide in a host cell. An expression cassette can, for example, be integrated in the genome of a host cell or be present in an expression vector.

[00117] As used herein, the phrase “subject in need thereof” refers to a subject that exhibits and/or is diagnosed with one or more symptoms or signs of a disease or disorder as described herein.

[00118] A “chemotherapeutic agent” refers to a chemical compound useful in the treatment of cancer. Chemotherapeutic agents include “anti-hormonal agents” or “endocrine therapeutics” which act to regulate, reduce, block, or inhibit the effects of hormones that can promote the growth of cancer.

[00119] The term “composition” refers to a mixture that contains, e.g., an engineered cell or protein contemplated herein. In some embodiments, the composition may contain additional components, such as adjuvants, stabilizers, excipients, and the like. The term “composition” or “pharmaceutical composition” refers to a preparation which is in such form as to permit the biological activity of an active ingredient contained therein to be effective in treating a subject, and which contains no additional components which are unacceptably toxic to the subject in the amounts provided in the pharmaceutical composition.

[00120] As used herein, the term “effective amount” refers to the amount of a compound (e.g., a compositions described herein, cells described herein) sufficient to effect beneficial or desired results. An effective amount can be administered in one or more administrations, applications or dosages and is not intended to be limited to a particular formulation or administration route. As used herein, the term “treating” includes any effect, e.g., lessening, reducing, modulating, ameliorating or eliminating, that results in the improvement of the condition, disease, disorder, and the like, or ameliorating a symptom thereof.

[00121] The terms “modulate” and “modulation” refer to reducing or inhibiting or, alternatively, activating or increasing, a recited variable.

[00122] The terms “increase” and “activate” refer to an increase of 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 100%, 2-fold, 3-fold, 4-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold, or greater in a recited variable.

[00123] The terms “reduce” and “inhibit” refer to a decrease of 10%, 20%, 30%, 40%, 50%, 60%, 70%, 75%, 80%, 85%, 90%, 95%, 2-fold, 3-fold, 4-fold, 5-fold, 10-fold, 20-fold, 50-fold, 100-fold, or greater in a recited variable.

Safe Harbor Loci

[00124] Gene editing therapies include, for example, viral vector integration and site specific integration. Site-specific integration is a promising alternative to random integration of viral vectors, as it mitigates the risks of insertional mutagenesis or insertional oncogenesis (Kolb *et al.* Trends Biotechnol. 2005 23:399-406; Porteus *et al.* Nat Biotechnol. 2005 23:967-973; Paques *et al.* Curr Gen Ther. 2007 7:49-66). However, site specific integration continues to face challenges such as poor knock-in efficiency, risk of insertional oncogenesis, unstable and/or anomalous expression of adjacent genes or the transgene, low accessibility (e.g. within 20 kB of adjacent genes), *etc.*. These challenges can be addressed, in part, through the identification and use of safe harbor loci or safe harbor sites (SHS), which are sites in which genes or genetic elements can be incorporated without disruption to expression or regulation of adjacent genes.

[00125] The most widely used of the putative human safe harbor sites is the AAVS1 site on chromosome 19q, which was initially identified as a site for recurrent adenoassociated virus insertion. Other potential SHS have been identified on the basis of homology, with sites first identified in other species (e.g., the human homolog of the permissive murine Rosa26 locus) or among the growing number of human genes that appear non-essential under some circumstances. One putative SHS of this type is the CCR5 chemokine receptor gene, which, when disrupted, confers resistance to human immunodeficiency virus infection. Additional potential genomic SHS have been identified in human and other cell types on the basis of viral integration site mapping or gene-trap analyses, as was the original murine Rosa26 locus. The three top SHS, AAVS1, CCR5, and Rosa26, are in close proximity to many protein coding genes and regulatory elements. (See **FIG. 2** from Sadelain, M., et al. (2012). Safe harbours for the integration of new DNA in the human genome. Nature reviews Cancer, 12(1), 51-58, the relevant disclosures of which are herein incorporated by reference in their entirety).

[00126] The AAVS1 (also known as the PPP1R12C locus) on human chromosome 19 is a known SHS for hosting transgenes (e.g. DNA transgenes) with expected function. It is at position 19q13.42. It has an open chromatin structure and is transcription-competent. The canonical SHS locus for AAVS1 is chr19: 55,625,241–55,629,351. *See* Pellenz *et al.* “New Human Chromosomal Sites with "Safe Harbor" Potential for Targeted Transgene Insertion.” Human gene therapy vol. 30,7 (2019): 814-828, the relevant disclosures of which are herein

incorporated by reference. An exemplary AAVS1 target gRNA and target sequence are provided below:

- AAVS1-gRNA sequence:
ggggccactagggacaggatGTTTTAGAGCTAGAAATAGCAAGTTAAAATAAGGCTA
GTCCGTTATCAACTTGAAAAAGTGGCACCGAGTCGGTGCTTTTTTT
- AAVS1 target sequence: ggggccactagggacaggat

[00127] CCR5, which is located on chromosome 3 at position 3p21.31, encodes the major co-receptor for HIV-1. Disruption at this site in the CCR5 gene has been beneficial in HIV/AIDS therapy and prompted the development of zinc-finger nucleases that target its third exon. The canonical SHS locus for CCR5 is chr3: 46,414,443–46,414,942. *See* Pellenz et al. “New Human Chromosomal Sites with "Safe Harbor" Potential for Targeted Transgene Insertion.” Human gene therapy vol. 30,7 (2019): 814-828, the relevant disclosures of which are herein incorporated by reference.

[00128] The mouse Rosa26 locus is particularly useful for genetic modification as it can be targeted with high efficiency and is expressed in most cell types tested. Irion et al. 2007 (“Identification and targeting of the ROSA26 locus in human embryonic stem cells.” Nature biotechnology 25.12 (2007): 1477-1482, the relevant disclosure of which are herein incorporated by reference) identified the human homolog, human ROSA26, in chromosome 3 (position 3p25.3). The canonical SHS locus for human Rosa26 (hRosa26) is chr3: 9,415,082–9,414,043. *See* Pellenz et al. “New Human Chromosomal Sites with "Safe Harbor" Potential for Targeted Transgene Insertion.” Human gene therapy vol. 30,7 (2019): 814-828, the relevant disclosures of which are herein incorporated by reference.

[00129] Additional examples of safe harbor sites are provided in Pellenz et al. “New Human Chromosomal Sites with "Safe Harbor" Potential for Targeted Transgene Insertion.” Human gene therapy vol. 30,7 (2019): 814-828, the relevant disclosures of which are herein incorporated by reference.

[00130] The present disclosure is directed to methods for identifying safe harbor loci with benefits including, but not limited to, high knock-in efficiency and high expression of transgene. An example of applications of the presently disclosed methods is the identification of safe harbor loci for insertion of transgenes (e.g., chimeric antigen receptors (CAR)) into T-cells. In some embodiments, the safe harbor loci of the present disclosure are useful for the insertion of a sequence encoding a transgene. In some embodiments, the safe harbor sites allow for high transgene expression (sufficient to allow for transgene functionality or

treatment of a disease of interest) and stable expression of the transgene over several days, weeks or months. In some embodiments, knockout of the gene at the safe harbor locus confers benefit to the function of the cell, or the gene at the safe harbor locus has no known function within the cell. In some embodiments the safe harbor locus results in stable transgene expression *in vitro* with or without CD3/CD28 stimulation, negligible off-target cleavage as detected by iGuide-Seq or CRISPR-Seq, less off-target cleavage relative to other loci as detected by iGuide-Seq or CRISPR-Seq, negligible transgene-independent cytotoxicity, negligible transgene-independent cytokine expression, negligible transgene-independent chimeric antigen receptor expression, negligible deregulation or silencing of nearby genes, and positioned outside of a cancer-related gene.

[00131] As used, a “nearby gene” can refer to a gene that is within about 100kB, about 125kB, about 150kB, about 175kB, about 200kB, about 225kB, about 250kB, about 275kB, about 300kB, about 325kB, about 350kB, about 375kB, about 400kB, about 425kB, about 450kB, about 475kB, about 500kB, about 525kB, about 550kB away from the safe harbor locus (integration site).

[00132] In some embodiments, the present disclosure contemplates inserts that comprise one or more transgenes. The transgene can encode a therapeutic protein, an antibody, a peptide, a suicide gene, an apoptosis gene or any other gene of interest. The safe harbor loci identified using the method described herein allow for transgene integration that results in , for example, enhanced therapeutic properties. These enhanced therapeutic properties, as used herein, refer to an enhanced therapeutic property of a cell when compared to a typical immune cell of the same normal cell type. For example, an NK cell having “enhanced therapeutic properties” has an enhanced, improved, and/or increased treatment outcome when compared to a typical, unmodified and/or naturally occurring NK cell. The therapeutic properties of immune cells can include, but are not limited to, cell transplantation, transport, homing, viability, self-renewal, persistence, immune response control and regulation, survival, and cytotoxicity. The therapeutic properties of immune cells are also manifested by: antigen-targeted receptor expression; HLA presentation or lack thereof; tolerance to the intratumoral microenvironment; induction of bystander immune cells and immune regulation; improved target specificity with reduction; resistance to treatments such as chemotherapy.

[00133] As used herein, the term “insert size” refers to the length of the nucleotide sequence being integrated (inserted) at the safe harbor site. In some embodiments, the insert size comprises at least about 100, 200, 300, 400 or 500 basepairs. In some embodiments, the

insert size comprises about 500 nucleotides or basepairs. In some embodiments, the insert size comprises up to 0.5, 0.6, 0.7, 0.8, 0.9, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 kbp (kilo basepairs) or the sizes in between. In some embodiments, the insert size is greater than 0.5, 0.6, 0.7, 0.8, 0.9, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20 kbp or the sizes in between. In some embodiments, the insert size is within the range of 3-15 kbp or is any number in that range. In some embodiments, the insert size is within the range of 1.5-8.3 kbp or is any number in that range. In some embodiments, the insert size is within the range of 1.5-15 kbp or is any number in that range. In some embodiments, the insert size is within the range of 0.5-20 kbp or is any number in that range. In some embodiments, the insert size is 0.5-10, 0.6-10, 0.7-10, 0.8-10, 0.9-10, 1-10, 2-10, 3-10, 4-10, 5-10, 6-10, 7-10, 8-10, 9-10 kbp. In some embodiments, the insert size is 0.5-11, 0.6-11, 0.7-11, 0.8-11, 0.9-11, 1-11, 2-11, 3-11, 4-11, 5-11, 6-11, 7-11, 8-11, 9-11, or 10-11 kbp. In some embodiments, the insert size is 0.5-12, 0.6-12, 0.7-12, 0.8-12, 0.9-12, 1-12, 2-12, 3-12, 4-12, 5-12, 6-12, 7-12, 8-12, 9-12, 10-12, or 11-12 kbp. In some embodiments, the insert size is 0.5-13, 0.6-13, 0.7-13, 0.8-13, 0.9-13, 1-13, 2-13, 3-13, 4-13, 5-13, 6-13, 7-13, 8-13, 9-13, 10-13, 11-13, or 12-13 kbp. In some embodiments, the insert size is 0.5-14, 0.6-14, 0.7-14, 0.8-14, 0.9-14, 1-14, 2-14, 3-14, 4-14, 5-14, 6-14, 7-14, 8-14, 9-14, 10-14, 11-14, 12-14 or 13-14 kbp. In some embodiments, the insert size is 0.5-15, 0.6-15, 0.7-15, 0.8-15, 0.9-15, 1-15, 2-15, 3-15, 4-15, 5-15, 6-15, 7-15, 8-15, 9-15, 10-15, 11-15, 12-15, 13-15, or 14-15 kbp. In some embodiments, the insert size is 0.5-16, 0.6-16, 0.7-16, 0.8-16, 0.9-16, 1-16, 2-16, 3-16, 4-16, 5-16, 6-16, 7-16, 8-16, 9-16, 10-16, 11-16, 12-16, 13-16, 14-16 or 15-16 kbp. In some embodiments, the insert size is 0.5-17, 0.6-17, 0.7-17, 0.8-17, 0.9-17, 1-17, 2-17, 3-17, 4-17, 5-17, 6-17, 7-17, 8-17, 9-17, 10-17, 11-17, 12-17, 13-17, or 14-17, 15-17 or 16-17 kbp. In some embodiments, the insert size is 0.5-18, 0.6-18, 0.7-18, 0.8-18, 0.9-18, 1-18, 2-18, 3-18, 4-18, 5-18, 6-18, 7-18, 8-18, 9-18, 10-18, 11-18, 12-18, 13-18, 14-18, 15-18, 16-18 or 17-18 kbp. In some embodiments, the insert size is 0.5-19, 0.6-19, 0.7-19, 0.8-19, 0.9-19, 1-19, 2-19, 3-19, 4-19, 5-19, 6-19, 7-19, 8-19, 9-19, 10-19, 11-19, 12-19, 13-19, 14-19, 15-19, 16-19, 17-19, or 18-19 kbp. In some embodiments, the insert size is 0.5-20, 0.6-20, 0.7-20, 0.8-20, 0.9-20, 1-20, 2-20, 3-20, 4-20, 5-20, 6-20, 7-20, 8-20, 9-20, 10-20, 11-20, 12-20, 13-20, 14-20, 15-20, 16-20, 17-20, 18-20, or 19-20 kbp.

[00134] The inserts of the present disclosure refer to nucleic acid molecules or polynucleotide inserted at a safe harbor site. In some embodiments, the nucleotide sequence is a DNA molecule, e.g., genomic DNA, or comprises deoxy-ribonucleotides. In some

embodiments, the insert comprises a smaller fragment of DNA, such as a plastid DNA, mitochondrial DNA, or DNA isolated in the form of a plasmid, a fosmid, a cosmid, a bacterial artificial chromosome (BAC), a yeast artificial chromosome (YAC), and/or any other sub-genome segment of DNA. In some embodiments, the insert is an RNA molecule or comprises ribonucleotides. The nucleotides in the insert are contemplated as naturally occurring nucleotides, non-naturally occurring, and modified nucleotides. Nucleotides may be modified chemically or biochemically, or may contain non-natural or derivatized nucleotide bases, as will be readily appreciated by those of skill in the art. Such modifications include, for example, labels, methylation, substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications. The polynucleotides can be in any topological conformation, including single-stranded, double-stranded, partially duplexed, triplexed, hairpinned, circular conformations, and other three-dimension conformations contemplated in the art.

[00135] The inserts can have coding and/or non-coding regions. The insert can comprises a non-coding sequence (*e.g.*, control elements, *e.g.*, a promoter sequence). In some embodiments, the insert encodes transcription factors. In some embodiments, the insert encodes an antigen binding receptors such as single receptors, T-cell receptors (TCRs), syn-notch, CARs, mAbs, etc. In some embodiments, the inserts are RNAi molecules, including, but not limited to, miRNAs, siRNA, shRNAs, *etc.* In some embodiments, the the insert is a human sequence. In some embodiments, the insert is chimeric. In some embodiments, the insert is a multi-gene/multi-module therapeutic cassette. A multi-gene/multi-module therapeutic cassette referst to an insert or cassette having one or more than one receptor (*e.g.*, synthetic receptors), other exogenous protein coding sequences, non-coding RNAs, transcriptional regulatory elements, and/or insulator sequences, *etc.*

[00136] Various cell types are contemplated as having the safe harbor sites in the present disclosure. A cell comprising a safe harbor site and/or a cell comprising an insert at a safe harbor site as described in the present disclosure can be referred to as an engineered cell. The cells can include, but are not limited to, eukaryotic cells, prokaryotic cells, animal cells, plant cells, fungal cells and the like. Optionally, the cell is a mammalian cell, for example, a human cell. In some embodiments, that engineered cell is a stem cell, a human cell, a primary cell, an hematopoietic cell, an adaptive immune cell, an innate immune cell, a T cell or a T cell progenitor. Non-limiting examples of immune cells that are contemplated in the present disclosure include T cell, B cell, natural killer (NK) cell, NKT/iNKT cell,

macrophage, myeloid cell, and dendritic cells. Non-limiting examples of stem cells that are contemplated in the present disclosure include pluripotent stem cells (PSCs), embryonic stem cells (ESCs), induced pluripotent stem cells (iPSCs), embryo-derived embryonic stem cells obtained by nuclear transfer (ntES; nuclear transfer ES), male germline stem cells (GS cells), embryonic germ cells (EG cells), hematopoietic stem/progenitor stem cells (HSPCs), somatic stem cells (adult stem cells), hemangioblasts, neural stem cells, mesenchymal stem cells and stem cells of other cells (including osteocyte, chondrocyte, myocyte, cardiac myocyte, neuron, tendon cell, adipocyte, pancreocyte, hepatocyte, nephrocyte and follicle cells and so on). In some embodiments, the engineered cells is a T cell, NK cells, iPSC, and HSPC. In some embodiments, the engineered cells used in the present disclosure are human cell lines grown *in vitro* (e.g. deliberately immortalized cell lines, cancer cell lines, *etc.*).

[00137] The methods for integrating the inserts at the safe harbor sites can be viral or non-viral delivery techniques.

[00138] In some embodiments, the nucleic acid sequence is inserted into the genome of the engineered cell by introducing a vector, for example, a viral vector, comprising the nucleic acid. Examples of viral vectors include, but are not limited to, adeno-associated viral (AAV) vectors, retroviral vectors or lentiviral vectors. In some embodiments, the lentiviral vector is an integrase-deficient lentiviral vector.

[00139] In some embodiments, the nucleic acid sequence is inserted into the genome of the T cell via non-viral delivery. In non-viral delivery methods, the nucleic acid can be naked DNA, or in a non-viral plasmid or vector. Non-viral delivery techniques can be site-specific integration techniques, as described herein or known to those of ordinary skill in the art. Examples of site-specific techniques for integration into the safe harbor loci include, without limitation, homology-dependent engineering using nucleases and homology independent targeted insertion using Cas9. In some embodiments, the non-viral delivery method comprises electroporation.

[00140] In some embodiments, the insert is integrated at a safe harbor site by introducing into the engineered cell, (a) a targeted nuclease that cleaves a target region in the safe harbor site to create the insertion site; and (b) the nucleic acid sequence (insert), wherein the insert is incorporated at the insertion site by, e.g., HDR. Examples of non-viral delivery techniques that can be used in the methods of the present disclosure are provided in US Application Nos. 16/568,116 and 16/622,843, the relevant disclosures of which are herein incorporated by reference in their entirety.

[00141] The engineered cell can retain its undifferentiated state after insertion of the transgenes. In some embodiments, the engineered cell is undifferentiated. In some embodiments, the engineered cell is undifferentiated after insert of the transgene. In some embodiments, the engineered cell is CD45RA⁺ and CCR7⁺ after insertion of the transgene. In some embodiments, the engineered cell is CD45RA⁺CCR7⁺CD27⁺ after insertion of the transgene.

CAR T cell Therapy

[00142] Chimeric antigen receptor (CAR) T cells are T cells that have been genetically engineered to produce an artificial T-cell receptor for use in immunotherapy. Chimeric antigen receptors are receptor proteins that have been engineered to confer T cells with the ability to target a specific protein. The genetic modification of lymphocytes (e.g. T cells) by incorporation of, for example, CARs, and administration of the engineered cells to a subject is an example of “adoptive cell therapy”. As used herein, the term “adoptive cell therapy” refers to cell-based immunotherapy for transfusion of autologous or allogeneic lymphocytes, referred to as T cells or B cells. In this CAR therapy approach, cells are expanded and cultured *ex vivo* and genetically modified, prior to transfusion.

[00143] The expression of CARs allows the engineered T-cells to target and bind specific proteins, for example, tumor antigens. In CAR therapy, T-cells are harvested from a subject—they can be autologous T-cells from the subject own blood or from a donor that will not be receiving the CAR therapy. Once isolated, the T-cells are genetically modified with a CAR, expanded *ex vivo*, and administered to the subject (*i.e.* patient) by, e.g. infusion.

[00144] The CARs may be introduced into the T-cells using, for example, a viral technique (e.g., retroviral integration) or site-specific technique. With site specific integration of the transgenes (e.g. CARs), the transgenes may be targeted to a safe harbor locus. Examples of site-specific techniques for integration into the safe harbor loci include, without limitation, homology-dependent engineering using nucleases and homology independent targeted insertion using Cas9.

[00145] The engineered CAR T cells have applications to immune-oncology. The CAR, for example, can be selected to target a specific tumor antigen. Examples of cancers that can be effectively targeted using CAR T cells are blood cancers. In some embodiments, CAR T cell therapy can be used to treat solid tumors.

Gene editing

[00146] The terms “gene editing” or “genome editing”, as used herein, refer to a type of genetic manipulation in which DNA is inserted, replaced, or removed from the genome using artificially manipulated nucleases or “molecular scissors”. It is a useful tool for elucidating the function and effect of sequence-specific genes or proteins or altering cell behavior (e.g. for therapeutic purposes).

[00147] Currently available genome editing tools include zinc finger nucleases (ZFN) and transcription activator-like effector nucleases (TALENs) to incorporate genes at safe harbor loci (e.g. the adeno-associated virus integration site 1 (AAVS1) safe harbor locus). The DICE (dual integrase cassette exchange) system utilizing phiC31 integrase and Bxb1 integrase is a tool for target integration. Additionally, clustered regularly interspaced short palindromic repeat/Cas9 (CRISPR/Cas9) techniques can be used for targeted gene insertion.

[00148] Site specific gene editing approaches can include homology dependent mechanisms or homology independent mechanisms.

[00149] All methods known in the art for targeted insertion of gene sequences are contemplated in the methods described herein to insert constructs at safe harbor loci.

Crispr-Cas Gene editing

[00150] One effective example of gene editing is the Crisp-Cas approach (e.g. Crisp-Cas9). This approach incorporates the use of a guide polynucleotide (e.g. guide ribonucleic acid or gRNA) and a cas endonuclease (e.g. Cas9 endonuclease).

[00151] As used herein, a polypeptide referred to as a “Cas endonuclease” or having “Cas endonuclease activity” refers to a CRISPR-related (Cas) polypeptide encoded by a Cas gene, wherein a Cas polypeptide is a target DNA sequence that can be cleaved when operably linked to one or more guide polynucleotides (see, e.g., US Pat. No. 8,697,359). Also included in this definition are variants of Cas endonuclease that retain guide polynucleotide-dependent endonuclease activity. The Cas endonuclease used in the donor DNA insertion method detailed herein is an endonuclease that introduces double-strand breaks into DNA at the target site (e.g., within the target locus or at the safe harbor site).

[00152] As used herein, the term “guide polynucleotide” relates to a polynucleotide sequence capable of complexing with a Cas endonuclease and allowing the Cas endonuclease to recognize and cleave a DNA target site. The guide polynucleotide can be a single molecule or a double molecule. The guide polynucleotide sequence can be an RNA sequence, a DNA sequence, or a combination thereof (RNA-DNA combination sequence). A guide

polynucleotide comprising only ribonucleic acid is also referred to as “guide RNA”. In some embodiments, a polynucleotide donor construct is inserted at a safe harbor locus using a guide RNA (gRNA) in combination with a Cas endonuclease (e.g. Cas9 endonuclease).

[00153] The guide polynucleotide includes a first nucleotide sequence domain (also referred to as a variable targeting domain or VT domain) that is complementary to a nucleotide sequence in the target DNA, and a second nucleotide that interacts with a Cas endonuclease polypeptide. It can be a double molecule (also referred to as a double-stranded guide polynucleotide) comprising a sequence domain (referred to as a Cas endonuclease recognition domain or CER domain). The CER domain of this double molecule guide polynucleotide comprises two separate molecules that hybridize along the complementary region. The two separate molecules can be RNA sequences, DNA sequences and/or RNA-DNA combination sequences.

[00154] Genome editing using CRISPR-Cas approaches relies on the repair of site-specific DNA double-strand breaks (DSBs) induced by the RNA-guided Cas endonuclease (e.g. Cas 9 endonuclease). Homology-directed repair (HDR) of these DSBs enables precise editing of the genome by introducing defined genomic changes, including base substitutions, sequence insertions, and deletions. Conventional HDR-based CRISPR/Cas9 genome-editing involves transfecting cells with Cas9, gRNA and donor DNA containing homologous arms matching the genomic locus of interest.

[00155] HITI (homology independent targeted insertion) uses a non-homologous end joining (NHEJ)-based homology-independent strategy and the method can be more efficient than HDR. Guide RNAs (gRNAs) target the insertion site. For HITI, donor plasmids lack homology arms and DSB repair does not occur through the HDR pathway. The donor polynucleotide construct can be engineered to include Cas9 cleavage site(s) flanking the gene or sequence to be inserted. This results in Cas9 cleavage at both the donor plasmid and the genomic target sequence. Both target and donor have blunt ends and the linearized donor DNA plasmid is used by the NHEJ pathway resulting integration into the genomic DSB site. (See, for example, Suzuki, K., et al. (2016). In vivo genome editing via CRISPR/Cas9 mediated homology-independent targeted integration. *Nature*, 540(7631), 144-149, the relevant disclosures of which are herein incorporated in their entirety).

[00156] Methods for conducting gene editing using CRISPR-Cas approaches are known to those of ordinary skill in the art. (See, for example, US Application Nos. US16/312,676, US15/303,722, and US15/628,533, the disclosures of which are herein incorporated by

reference in their entirety). Additionally, uses of endonucleases for inserting transgenes into safe harbor loci are described, for example, in US Application No. 13/036,343, the disclosures of which are herein incorporated by reference in their entirety.

[00157] The guide RNAs and/or mRNA (or DNA) encoding an endonuclease can be chemically linked to one or more moieties or conjugates that enhance the activity, cellular distribution, or cellular uptake of the oligonucleotide. Non-limiting examples of such moieties include lipid moieties such as a cholesterol moiety, cholic acid, a thioether, a thiocholesterol, an aliphatic chain (e.g., dodecandiol or undecyl residues), a phospholipid, e.g., di-hexadecyl-rac-glycerol or triethylammonium 1,2-di-O-hexadecyl- rac-glycero-3-H-phosphonate, a polyamine or a polyethylene glycol chain, adamantane acetic acid, a palmityl moiety and an octadecylamine or hexylamino-carbonyl-t oxycholesterol moiety. See for example US Application No. 15/715,068, the disclosures of which are herein incorporated by reference in their entirety.

Therapeutic Applications

[00158] For therapeutic applications, the engineered cells, populations thereof, or compositions thereof are administered to a subject, generally a mammal, generally a human, in an effective amount.

[00159] The engineered cells may be administered to a subject by infusion (e.g., continuous infusion over a period of time) or other modes of administration known to those of ordinary skill in the art.

[00160] The engineered cells provided herein can be administered as part of a pharmaceutical compositions. In some embodiments, the present disclosure provides compositions comprising a guide RNA of the present disclosure. The pharmaceutical composition may comprise one or more pharmaceutical excipients. Any suitable pharmaceutical excipient may be used, and one of ordinary skill in the art is capable of selecting suitable pharmaceutical excipients. Accordingly, the pharmaceutical excipients provided below are intended to be illustrative, and not limiting. Additional pharmaceutical excipients include, for example, those described in the *Handbook of Pharmaceutical Excipients*, Rowe *et al.* (Eds.) 6th Ed. (2009), incorporated by reference in its entirety.

[00161] The engineered cells provided herein not only find use in gene therapy but also in non-pharmaceutical uses such as, e.g., production of animal models and production of recombinant cell lines expressing a protein of interest.

[00162] The engineered cells of the present disclosure can be any cell, generally a mammalian cell, generally a human cell that has been modified by integrating a transgene at a safe harbor locus described herein. In some embodiments, the engineered cells are immune cells. In some embodiments, the engineered cells are lymphocytes. In some embodiments, the engineered cells are T cells or T cell progenitors.

[00163] The engineered cells, compositions and methods of the present disclosure are useful for therapeutic applications such as CAR T cell therapy and TCR T cell therapy. In some embodiments, the insertion of a sequence encoding a transgene within a safe harbor locus maintains the TCR expression relative to instances when there is no insertion and enables transgene expression while maintaining TCR function.

[00164] Various diseases treated using the engineered cells, populations thereof, or compositions thereof are provided herein. Non-limiting examples of such diseases include alopecia areata, autoimmune hemolytic anemia, autoimmune hepatitis, cancer, dermatomyositis, diabetes (type 1), certain juvenile idiopathic arthritis, glomerulonephritis, Graves' disease, Guillain Barre Syndrome, idiopathic thrombocytopenic purpura, myasthenia gravis, certain myocarditis, multiple sclerosis, pemphigus/pemphigoid, pernicious anemia, polyarteritis nodosa, polymyositis, primary biliary cirrhosis, psoriasis, rheumatoid arthritis, scleroderma/systemic sclerosis, Sjogren's syndrome, systemic lupus erythematosus, certain thyroiditis, certain uveitis, vitiligo, multiple vasculitis (Wegener)); autoimmune disorders including, but not limited to, granulomatosis; hematopoietic tumors including but not limited to acute and chronic leukemia, lymphoma, multiple myeloma and myelodysplastic syndrome; tumors of the prostate, breast, lung, colon, uterus, skin, liver, bone, pancreas, ovary, testis, bladder, kidney, head, neck, stomach, cervix, rectum, larynx, or esophagus solid tumors; HIV (human immunodeficiency virus) related disorders, RSV (respiratory syncytial virus) related disorders; EBV (Epstein-Barr virus) related disorders; CMV (cytomegalovirus) related disorders; and infectious diseases including, but not limited to, adenovirus-related disorders and BK polyomavirus-related disorders.

[00165] Cancers that can be treated with the engineered cells (*e.g.*, CAR T-cells) of the present disclosure, populations thereof, or compositions thereof include blood cancers. In some embodiments, the cancer treated using the engineered cells (*e.g.*, CAR T-cells) described herein, populations thereof, or compositions thereof is a hematologic malignancy or leukemia. In some embodiments, the engineered cells (*e.g.*, CAR T-cells) described herein, populations thereof, or compositions thereof are used for the treatment of acute

lymphoblastic leukemia (ALL) or diffuse large B-cell lymphoma (DLBCL). In some embodiments, the cancer is acute myeloid leukemia (AML), acute lymphoblastic leukemia (ALL), myelodysplasia, myelodysplastic syndromes, acute T-lymphoblastic leukemia, or acute promyelocytic leukemia, chronic myelomonocytic leukemia, or myeloid blast crisis of chronic myeloid leukemia. Examples of cancers treatable using the engineered cells (e.g., CAR T-cells) described herein include, without limitation, breast cancer, ovarian cancer, esophageal cancer, bladder or gastric cancer, salivary duct carcinoma, salivary duct carcinomas, adenocarcinoma of the lung or aggressive forms of uterine cancer, such as uterine serous endometrial carcinoma. In some other embodiments, the cancer is brain cancer, breast cancer, cervical cancer, colon cancer, colorectal cancer, endometrial cancer, esophageal cancer, leukemia, lung cancer, liver cancer, melanoma, ovarian cancer, pancreatic cancer, rectal cancer, renal cancer, stomach cancer, testicular cancer, or uterine cancer. In yet other embodiments, the cancer is a squamous cell carcinoma, adenocarcinoma, small cell carcinoma, melanoma, neuroblastoma, sarcoma (e.g., an angiosarcoma or chondrosarcoma), larynx cancer, parotid cancer, biliary tract cancer, thyroid cancer, acral lentiginous melanoma, actinic keratoses, acute lymphocytic leukemia, acute myeloid leukemia, adenoid cystic carcinoma, adenomas, adenosarcoma, adenosquamous carcinoma, anal canal cancer, anal cancer, anorectum cancer, astrocytic tumor, Bartholin's gland carcinoma, basal cell carcinoma, biliary cancer, bone cancer, bone marrow cancer, bronchial cancer, bronchial gland carcinoma, carcinoid, cholangiocarcinoma, chondrosarcoma, choroid plexus papilloma/carcinoma, chronic lymphocytic leukemia, chronic myeloid leukemia, clear cell carcinoma, connective tissue cancer, cystadenoma, digestive system cancer, duodenum cancer, endocrine system cancer, endodermal sinus tumor, endometrial hyperplasia, endometrial stromal sarcoma, endometrioid adenocarcinoma, endothelial cell cancer, ependymal cancer, epithelial cell cancer, Ewing's sarcoma, eye and orbit cancer, female genital cancer, focal nodular hyperplasia, gallbladder cancer, gastric antrum cancer, gastric fundus cancer, gastrinoma, glioblastoma, glucagonoma, heart cancer, hemangioblastomas, hemangioendothelioma, hemangiomas, hepatic adenoma, hepatic adenomatosis, hepatobiliary cancer, hepatocellular carcinoma, Hodgkin's disease, ileum cancer, insulinoma, intraepithelial neoplasia, interepithelial squamous cell neoplasia, intrahepatic bile duct cancer, invasive squamous cell carcinoma, jejunum cancer, joint cancer, Kaposi's sarcoma, pelvic cancer, large cell carcinoma, large intestine cancer, leiomyosarcoma, lentigo maligna melanomas, lymphoma, male genital cancer, malignant melanoma, malignant mesothelial tumors,

medulloblastoma, medulloepithelioma, meningeal cancer, mesothelial cancer, metastatic carcinoma, mouth cancer, mucoepidermoid carcinoma, multiple myeloma, muscle cancer, nasal tract cancer, nervous system cancer, neuroepithelial adenocarcinoma nodular melanoma, non-epithelial skin cancer, non-Hodgkin's lymphoma, oat cell carcinoma, oligodendroglial cancer, oral cavity cancer, osteosarcoma, papillary serous adenocarcinoma, penile cancer, pharynx cancer, pituitary tumors, plasmacytoma, pseudosarcoma, pulmonary blastoma, rectal cancer, renal cell carcinoma, respiratory system cancer, retinoblastoma, rhabdomyosarcoma, sarcoma, serous carcinoma, sinus cancer, skin cancer, small cell carcinoma, small intestine cancer, smooth muscle cancer, soft tissue cancer, somatostatin-secreting tumor, spine cancer, squamous cell carcinoma, striated muscle cancer, submesothelial cancer, superficial spreading melanoma, T cell leukemia, tongue cancer, undifferentiated carcinoma, ureter cancer, urethra cancer, urinary bladder cancer, urinary system cancer, uterine cervix cancer, uterine corpus cancer, uveal melanoma, vaginal cancer, verrucous carcinoma, VIPoma, vulva cancer, well-differentiated carcinoma, or Wilms tumor.

[00166] In some embodiments, the present disclosure provides methods of treating a subject in need of treatment by administering to the subject a composition comprising any of the engineered cells described herein. As used, the terms “treat,” “treatment,” and the like refer generally to obtaining a desired pharmacological and/or physiological effect. That effect is preventive in terms of complete or partial prevention of the disease and/or therapeutic in terms of partial or complete cure of the disease and/or adverse effects resulting from the disease. The term “treatment”, as used herein, encompasses any treatment of a disease in a subject (e.g., mammal, e.g., human). Treatment may also refer to the administration of the engineered cells provided herein to a subject that is susceptible to the disease but has not yet been diagnosed as suffering from it, including preventing the disease from occurring; inhibiting disease progression; or reducing the disease (i.e., causing a regression of the disease). Further, treatment may stabilize or reduce undesirable clinical symptoms in subjects (e.g., patients). The cells provided herein populations thereof, or compositions thereof may be administered before, during or after the occurrence of the disease or injury.

[00167] In certain embodiments, the subject has a disease, condition, and/or injury that can be treated and/or ameliorated by cell therapy. In some embodiments, the subject in need of cell therapy is a subject having an injury, disease, or condition, thereby causing cell therapy (e.g., therapy in which cellular material is administered to the subject). However, it is contemplated that it is possible to treat, ameliorate and/or reduce the severity of at least one

symptom associated with the injury, disease or condition. In certain embodiments, a subject in need of cell therapy includes, but is not limited to, a bone marrow transplant or stem cell transplant candidate, a subject who has received chemotherapy or radiation therapy, a hyperproliferative disease or cancer (e.g., a hematopoietic system), a subject having or at risk of developing a hyperproliferative disease or cancer), a subject having or at risk of developing a tumor (e.g., solid tumor), viral infection or virus. It is also intended to encompass subjects suffering from or at risk of suffering from a disease associated with an infection.

[00168] In some embodiments, the present disclosure provides a composition of the present disclosure along with instructions for use. The instructions for use can be present in the kits as a package insert, in the labeling of the container of the kit or components thereof, or can be in digital form (e.g. on a CD-ROM, via a link on the internet). A kit can include one or more of a genome-targeting nucleic acid, a polynucleotide encoding a genome-targeting nucleic acid, a site-directed polypeptide, and/or a polynucleotide encoding a site-directed polypeptide. Additional components within the kits are also contemplated, for example, buffer (such as reconstituting buffer, stabilizing buffer, diluting buffer), and/or one or more control vectors.

Combination Therapies

[00169] In some embodiments, an engineered cells of the present disclosure or composition thereof is administered with at least one additional therapeutic agent. Any suitable additional therapeutic agent may be administered with an engineered cell provided herein, populations thereof, or compositions thereof. In some aspects, the additional therapeutic agent is selected from radiation, an ophthalmologic agent, a cytotoxic agent, a chemotherapeutic agent, a cytostatic agent, an anti-hormonal agent, an immunostimulatory agent, an anti-angiogenic agent, and combinations thereof.

[00170] In some embodiments, an engineered cell of the present disclosure or composition thereof is administered with a steroid. The administration of a steroid can prevent or mitigate the risk of a subject receiving the engineered cell(s) or composition thereof having an autoimmune reaction.

[00171] The additional therapeutic agent may be administered by any suitable means. In some embodiments, the engineered cells described herein, populations thereof, or compositions thereof and the additional therapeutic agent is administered in the same pharmaceutical composition, e.g. by infusion. In some embodiments, the engineered cells

described herein and additional therapeutic agent are included in different pharmaceutical compositions.

[00172] The pharmaceutical composition may comprise one or more pharmaceutical excipients. Any suitable pharmaceutical excipient may be used, and one of ordinary skill in the art is capable of selecting suitable pharmaceutical excipients. Accordingly, the pharmaceutical excipients provided below are intended to be illustrative, and not limiting. Additional pharmaceutical excipients include, for example, those described in the *Handbook of Pharmaceutical Excipients*, Rowe *et al.* (Eds.) 6th Ed. (2009), incorporated by reference in its entirety.

[00173] Various modes of administering the additional therapeutic agents are contemplated herein. In some embodiments, the additional therapeutic agent is administered by any suitable mode of administration. Generally, modes of administration include, without limitation, intravitreal, subretinal, suprachoroidal, intraarterial, intradermal, intramuscular, intraperitoneal, intravenous, nasal, parenteral, topical, pulmonary, and subcutaneous routes.

[00174] In embodiments where the engineered cells provided herein and the additional therapeutic agent are included in different pharmaceutical compositions, administration of the engineered cells provided herein can occur prior to, simultaneously, and/or following, administration of the additional therapeutic agent.

Additional Embodiments

[00175] In some aspects, provided herein are engineered cells, comprising at least one sequence encoding a transgene, wherein the at least one sequence is inserted within a safe harbor locus; wherein the safe harbor locus is at any one or more of the sgRNA target loci selected from: chr10:33130000-33140000, chr10:72290000-72300000, chr11:128340000-128350000, chr11:65425000-65427000 (NEAT1), chr15:92830000-92840000, chr16:11220000-11230000, chr2:87460000-87470000, chr3:186510000-186520000, chr3:59450000-59460000, chr8:127980000-128000000, chr9:7970000-7980000, APRT, B2M, CAPNS1, CBLB, CD2, CD3E, CD3G, CD5, EDF1, FTL, PTEN, PTPN2, PTPN6, PTPRC, PTPRCAP, RPS23, RTRAF, SERF2, SLC38A1, SMAD2, SOCS1, SRP14, SRSF9, SUB1, TET2, TIGIT, TRAC, and TRIM28.

[00176] In some embodiments, expression of the at least one sequence encoding the transgene is operatively linked to an endogenous promoter.

[00177] In some embodiments, expression of the at least one sequence encoding the transgene is operatively linked to an exogenous promoter.

[00178] In some embodiments, the target locus is selected from: chr10:33130000-33140000, chr10:72290000-72300000, chr11:128340000-128350000, chr11:65425000-65427000 (NEAT1), chr15:92830000-92840000, chr16:11220000-11230000, chr2:87460000-87470000, chr3:186510000-186520000, chr3:59450000-59460000, chr8:127980000-128000000, and chr9:7970000-7980000.

[00179] In some embodiments, the target locus is chr11:128340000-128350000 or chr15:92830000-92840000.

[00180] In some embodiments, the target locus is a gene selected from: APRT, B2M, CAPNS1, CBLB, CD2, CD3E, CD3G, CD5, EDF1, FTL, PTEN, PTPN2, PTPN6, PTPRC, PTPRCAP, RPS23, RTRAF, SERF2, SLC38A1, SMAD2, SOCS1, SRP14, SRSF9, SUB1, TET2, TIGIT, TRAC, and TRIM28.

[00181] In some embodiments, the safe harbor locus is the GS94 or GS102 integration site in Table 4.

[00182] In some embodiments, the exogenous promoter is an EF1a promoter.

[00183] In some embodiments, the engineered cell is a natural killer (NK) cell, an induced pluripotent stem cells (iPSC), a human pluripotent stem cell (HSPC), a T cell or a T cell progenitor.

[00184] In some embodiments, the transgene encodes a recombinant protein, a therapeutic agent, or a chimeric antigen receptor (CAR).

[00185] In some aspects, provided herein are compositions comprising the engineered cell described herein and a pharmaceutical excipient.

[00186] In some aspects, provided herein are guide ribonucleic acids (gRNA) for editing a cell at a safe harbor locus, wherein the gRNA comprises any one of SEQ ID NOS:1-120.

[00187] In some aspects, provided herein are methods of editing a cell having chromosomal DNA, comprising inserting at least one sequence encoding a transgene within a safe harbor locus in the chromosomal DNA of the cell, wherein the safe harbor locus is at any one or more of the sgRNA target loci selected from: chr10:33130000-33140000, chr10:72290000-72300000, chr11:128340000-128350000, chr11:65425000-65427000 (NEAT1), chr15:92830000-92840000, chr16:11220000-11230000, chr2:87460000-87470000, chr3:186510000-186520000, chr3:59450000-59460000, chr8:127980000-128000000, chr9:7970000-7980000, APRT, B2M, CAPNS1, CBLB, CD2, CD3E, CD3G, CD5, EDF1, FTL, PTEN, PTPN2, PTPN6, PTPRC, PTPRCAP, RPS23, RTRAF, SERF2, SLC38A1, SMAD2, SOCS1, SRP14, SRSF9, SUB1, TET2, TIGIT, TRAC, and TRIM28.

[00188] In some embodiments, the target locus is selected from: chr10:33130000-33140000, chr10:72290000-72300000, chr11:128340000-128350000, chr11:65425000-65427000 (NEAT1), chr15:92830000-92840000, chr16:11220000-11230000, chr2:87460000-87470000, chr3:186510000-186520000, chr3:59450000-59460000, chr8:127980000-128000000, and chr9:7970000-7980000.

[00189] In some embodiments, the target locus is chr11:128340000-128350000 or chr15:92830000-92840000.

[00190] In some embodiments, the target locus is a gene selected from: APRT, B2M, CAPNS1, CBLB, CD2, CD3E, CD3G, CD5, EDF1, FTL, PTEN, PTPN2, PTPN6, PTPRC, PTPRCAP, RPS23, RTRAF, SERF2, SLC38A1, SMAD2, SOCS1, SRP14, SRSF9, SUB1, TET2, TIGIT, TRAC, and TRIM28.

[00191] In some embodiments, the transgene encodes a recombinant protein, a therapeutic agent, or a chimeric antigen receptor (CAR).

[00192] In some embodiments, the at least one sequence comprises an exogenous promoter and the exogenous promoter is operably linked to the transgene.

[00193] In some embodiments, the cell is a T cell or T cell progenitor.

[00194] In some embodiments, the at least one sequence is inserted using a homology-directed repair or a homology independent targeted insertion.

[00195] In some embodiments, the at least one sequence is inserted using one or more guide ribonucleic acids (gRNAs) and one or more Cas9 endonucleases, wherein the one or more gRNAs comprises any one of SEQ ID NOS: 1-120.

[00196] In some aspects, provided herein are ex vivo methods of obtaining an engineered cell or population thereof, comprising: obtaining a cell; genetically modifying the cell by inserting at least one sequence encoding a transgene within a safe harbor locus, wherein the safe harbor locus is at any one or more of the sgRNA target loci selected from: chr10:33130000-33140000, chr10:72290000-72300000, chr11:128340000-128350000, chr11:65425000-65427000 (NEAT1), chr15:92830000-92840000, chr16:11220000-11230000, chr2:87460000-87470000, chr3:186510000-186520000, chr3:59450000-59460000, chr8:127980000-128000000, chr9:7970000-7980000, APRT, B2M, CAPNS1, CBLB, CD2, CD3E, CD3G, CD5, EDF1, FTL, PTEN, PTPN2, PTPN6, PTPRC, PTPRCAP, RPS23, RTRAF, SERF2, SLC38A1, SMAD2, SOCS1, SRP14, SRSF9, SUB1, TET2, TIGIT, TRAC, and TRIM28.

[00197] In some embodiments, obtaining the cell comprises: (i) collecting a tissue sample from a subject, (ii) isolating the cells from the tissue samples, and (iii) culturing the cells in vitro.

[00198] In some embodiments, the cell is a stem cell, a natural killer (NK) cell, an induced pluripotent stem cells (iPSC), a human pluripotent stem cell (HSPC), a T cell or a T cell progenitor.

[00199] In some embodiments, the at least one sequence is inserted using a homology-directed repair or a homology independent targeted insertion.

[00200] In some embodiments, the genetically modifying in step (b) comprises contacting the cell with one or more guide ribonucleic acids (gRNAs), the at least one sequence, and one or more Cas9 endonucleases, wherein the one or more gRNAs and Cas9 endonucleases facilitate the insertion of the at least one sequence into chromosomal DNA within the safe harbor locus and wherein the one or more gRNAs comprises any one of SEQ ID NOS: 1-120.

[00201] In some embodiments, the at least one sequence comprises an exogenous promoter and the exogenous promoter is operably linked to the transgene.

[00202] In some aspects, provided herein are methods of treating a subject having or at risk of having a disease, comprising administering to the subject an effective amount of the engineered cell described herein.

[00203] In some aspects, provided herein are methods of treating a subject having or at risk of having a disease, comprising: conducting the method described herein; and administering to the subject an effective amount of a composition comprising the cell or a population thereof.

[00204] In some embodiments, the disease is cancer.

EXAMPLES

[00205] The following are examples of methods and compositions of the invention. It is understood that various other embodiments may be practiced, given the general description provided herein.

[00206] Below are examples of specific embodiments for carrying out the present invention. The examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way. Efforts have been made to ensure accuracy with respect to numbers used (*e.g.*, amounts, temperatures, etc.), but some experimental error and deviation should, of course, be allowed for.

[00207] The practice of the present invention will employ, unless otherwise indicated, conventional methods of protein chemistry, biochemistry, recombinant DNA techniques and pharmacology, within the skill of the art. Such techniques are explained fully in the literature. See, e.g., T.E. Creighton, *Proteins: Structures and Molecular Properties* (W.H. Freeman and Company, 1993); A.L. Lehninger, *Biochemistry* (Worth Publishers, Inc., current addition); Sambrook, et al., *Molecular Cloning: A Laboratory Manual* (2nd Edition, 1989); *Methods In Enzymology* (S. Colowick and N. Kaplan eds., Academic Press, Inc.); *Remington's Pharmaceutical Sciences*, 18th Edition (Easton, Pennsylvania: Mack Publishing Company, 1990).

Example 1: Identification of Knock-In Loci in Coding Regions

[00208] The objective of the experiments in this set of examples was to identify T-cell knock-in (KI) loci in coding regions outside of the T Cell Receptor Alpha Constant (TRAC) locus. To select candidate loci, the criteria and requirements shown in Table 1 were used.

Table 1: Criteria used for identification of candidate knock-in loci within coding regions

Criteria	Detailed Requirements	Datasets Considered for identification of loci
KI efficiency	<ul style="list-style-type: none"> High expression at d2 (day 2) Similar expression dynamics as TRAC (stable expression upon activation) Accessible chromatin gRNA editing efficiency 	<ul style="list-style-type: none"> Knock in efficiency data on ~90 genes derived from Roth, T. L., et al. 2019. (Rapid discovery of synthetic DNA sequences to rewrite endogenous T cell circuits. bioRxiv, 604561.) Bulk RNA-seq data at d0, d2, d3 and d4: <ul style="list-style-type: none"> (i) publicly available data; (ii) data derived from Roth, T. L., et al. 2019. (Rapid discovery of synthetic DNA sequences to rewrite endogenous T cell circuits. bioRxiv, 604561.); and (iii) internally generated data Bulk ATAC-seq data at d0, d2, d3 and d4: <ul style="list-style-type: none"> (i) data derived from Roth, T. L., et al. 2019. (Rapid discovery of synthetic DNA sequences to rewrite endogenous T cell circuits. bioRxiv, 604561.); and (ii) internally generated data
Safety	<ul style="list-style-type: none"> Does not affect proliferation, cytolytic activity or signaling of T cells Be careful with tumor suppressors and oncogenes 	<ul style="list-style-type: none"> T cell screening data Achilles' project on cancer cell lines data Annotated oncogenes and tumor suppressors from TCGA Annotated functions in immune cells

[00209] Generally, the requirements for candidate KI loci within the coding regions was that the coding gene is not essential for T cell function or the knock-out of that gene would be beneficial to chimeric antigen receptor therapy (CAR T) functions.

[00210] As shown in Table 1, some of the data utilized, for comparison purposes, to identify candidate KI loci was sourced, in part, from Roth, T. L., *et al.* 2019 (Rapid discovery of synthetic DNA sequences to rewrite endogenous T cell circuits. bioRxiv, 604561), the relevant disclosures of which are herein incorporated by reference in their entirety. A summary of data in the Roth, T.L. *et al.* paper is shown in **FIG. 3**.

[00211] **FIG 4A** and **FIG 4B** show the processed RNA-seq data, showing that samples cluster based on activation status and by cell type. Donor 4 (AKI4) was identified as an outlier, as it clustered differently than the others, and was removed from remaining analysis. The transcript expression data from RNA-seq experiments on the 90 genes cited in the Roth, T.L. *et al.* paper was correlated to transcript expression data in Roth, T.L. *et al.* paper. (See **FIG. 5A** and **FIG. 5B**).

[00212] **FIG. 6** shows the process ATAC-seq data, which focused on the 10 kb area around the transcription start site (TSS). Again, donor 4 (AKI4) was identified as an outlier, based on expression profile in both CD4 and CD8 cells, and was removed from remaining analysis. The results of the remaining ATAC-seq analysis are shown in **FIGS. 7A-8**. The data in **FIG. 7A** for TSS enrichment scores also indicated that all libraries were high quality. The data on open chromatin regions around the TRAC locus revealed the highest signal near exon 3 rather than exon 1 (**FIG. 8**).

Determination of Knock-In Efficiency:

[00213] The KI efficiency results (obtained using the model described *infra*) based on the 5 donors, 2 gRNA, and 2 replicates/gRNAs from the Roth, T.L. *et al.* paper are shown in **FIG. 9** and **FIG. 10**.

[00214] A linear model was built to estimate KI efficiency of approximately 90 genes using RNA-seq and ATAC-seq data. The linear model captured 33% of the variation in the data (i.e. $R^2=0.33$). **FIG. 11** shows KI efficiency versus day 2 (d2) RNA-seq data, day 4 (d4) RNA seq data, and d2 ATAC data. The linear model was applied to remaining candidate genes to estimate their KI efficiency.

[00215] The candidate coding loci were selected by first ranking all genes in the pooled data sets by predicted KI efficiency, using RNA-seq expression data from d2 (day 2). Candidate coding loci were required to be stably expressed during T cell activation (e.g.,

≤ 2 -fold expression change relative to day 0 (d0). The candidate loci also had to be accessible based on ATAC-seq data. Using that selection process/requirements, 16 well-characterized coding genes (with known functions) were selected as candidate genes. The knockout of these 16 would confer a benefit to the function of CAR T cells (e.g. B2M, CD5, SMAD2, PTPRC, CD3E). An additional 12 coding genes with high predicted KI efficiency and no apparent essential function (inert coding genes) were selected as candidate genes. (See Table 2).

Table 2: KI Candidate Loci selected

Genes with Known Functions		Inert Coding Genes
B2M (~70%)	CD2	SUB1
CD3E (~50%)	SMAD2	EDF1
PTPRC (~50%)	SLC38A1	CAPNS1
CD3G (~30%)	TIGIT	SRP14
↑ Tested in Roth, T.L. et al paper (reported editing efficiency from Roth, T.L. et al paper)	SOCS1	RTRAF
	PTPN2	APRT
	CBLB	PTPRCAP
	PTEN	SRSF9
	PTPN6	FTL
	CD5	TRIM28
	TET2	SERF2
	TRAC	RPS23

Example 2: Identification of Knock-In Loci in Gene Deserts

[00216] The criteria for selection of candidate loci in non-coding regions or gene deserts is summarized in Table 3.

Table 3: Criteria used for identification of candidate knock-in loci within non-coding regions

Criteria	Detailed Requirements	Datasets Considered for identification of loci
KI efficiency	<ul style="list-style-type: none"> Accessible chromatin 	<ul style="list-style-type: none"> Bulk ATAC-seq data at d0, d2, d3 and d4: <ul style="list-style-type: none"> (i) data derived from Roth, T. L., et al. 2019. (Rapid discovery of synthetic DNA sequences to rewrite endogenous T cell circuits. bioRxiv, 604561.); and (ii) internally generated data
Safety	<ul style="list-style-type: none"> >10kb from cancer-related genes or TADS 	<ul style="list-style-type: none"> Ensembl genes

	<ul style="list-style-type: none"> • >10kb from any miRNA/functional small RNAs • >10kb from any 5' gene end • >10kb from any regulatory regions (ultra-conserved elements, enhancers) 	<ul style="list-style-type: none"> • Annotated oncogenes and tumor suppressors from TCGA • Annotated enhancers from Encode and papers
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[00217] To select candidate regions within the non-coding regions, the inventors here started by looking in highly accessible regions of the genome (10 kb windows). The most accessible region overlapped with (i) annotated protein coding genes (>50% accessible regions), (ii) pseudogenes and noncoding RNAs (~20% accessible regions), and (iii) enhancer/regulatory regions (~20% accessible regions). The candidate genes were required to be < 10 kb from the coding regions. A few regions that overlapped with long intergenic noncoding RNAs (lincRNAs) but did not have apparent function in T cells were also considered.

[00218] Examples of other criteria that have been used in the art for selection of SHS are described, for example in Pellenz, S., *et al.* (2019). New human chromosomal sites with “safe harbor” potential for targeted transgene insertion. Human gene therapy, 30(7), 814-828, the relevant disclosures of which are herein incorporated by reference in their entirety.

[00219] **FIG. 12** is a plot showing the normalized ATAC SEQ data for a top candidate non-coding region.

[00220] Using the above-described selection process/requirement, 11 candidate regions in gene deserts were selected. In total, there were 39 KI candidate loci, including those in coding and non-coding regions that would be evaluated as safe harbor loci (predicted loci).

Example 3: Experimental Evaluation of Predicted Loci

[00221] *Materials*

- 120 sgRNAs were ordered from Synthego, 3 sgRNAs per region, and editing efficiency was assessed by next generation sequencings (NGS).
 - 87 targeted coding genes
 - 33 targeted gene deserts
- 189 constructs were synthesized by Genscript
 - Homology arm: 450bp each
 - eGFP was used as the reporter

- Vector backbone: pUC57-Kan backbone
- 78 with endogenous promoters
- 111 with EF1a-HTLV promoter
- Constructs were sequence verified by Genscript and majority were internally verified by sequencing. The sgRNA sequences are provided in Table 4 and the construct sequences are provided in Table 5.

[00222] *Methods*

[00223] To evaluate the effectiveness of the predicted loci, the following were used:

[00224] (87 endogenous constructs + 120 exogenous construct)*2 = 414 wells + Controls = 460

[00225] 3 donors, 2 replicates at 3 time points: wk1 (d6=day 6), wk3 (d21=day 21) and wk4 (d28=day 28)

[00226] Controls

[00227] DNA-only (no ribonucleoprotein (RNP)): episomal expression (n=8)

[00228] DNA + non-targeting guides + RNP: to check if DNA delivery is more efficient with RNP (n=8)

[00229] pMax GFP was measured to check if transfection is ok (n=3).

[00230] WT cells with no electroporation

[00231] WT cells with electroporation

[00232] Controls were spread out across plates.

[00233] Cells were electroporated without RNP/HDR to check if cell counting makes sense.

[00234] 2 more donors were added and changed to 3 replicates at 1 time point: wk1 (d6)

[00235] FACS panel: GFP, TCR, Zombie

[00236] Washed every 3 wells.

[00237] The secondary data collected included: RNA-seq data: at d0, d2, and d4 (to determine stable expression) and ATAC-seq data: at d2 (to identify activated cells). The methods used for conducting the RNA-seq and ATAC-seq experiments are in Roth, T. L., et al. 2019. (Rapid discovery of synthetic DNA sequences to rewrite endogenous T cell circuits. bioRxiv, 604561), which is herein incorporated by reference in its entirety.

[00238] Automated gating was performed on FACS data, using .fcs files. For constructs with endogenous promoters, all 5 donors and all 3 time points were used. For constructs with EF1a promoter, used 3 donors (donors 1-3) and 2 time points (wk3 and wk4).

[00239] To summarize data, wells with a %KI efficiency (% GFP high cells) $\leq 10\%$ (likely a gating error, experimental error or minimal integration) were removed. Loci were then ranked by median expression among donors and median %KI efficiency among donors.

[00240] Loci significance was calculated using robust rank aggregation, which was the methodology used for consistent ranking of loci among donors and time points. Methods for conducting robust rank aggregation are known in the art. (See, for example, Kolde, R., et al. (2012). Robust rank aggregation for gene list integration and meta-analysis. *Bioinformatics* (Oxford, England), 28(4), 573–580, the disclosure of which is herein incorporated by reference in its entirety).

[00241] **Results**

[00242] The results from the analysis of controls and experimental groups is shown in FIGS. 13A-25.

[00243] The results of the pmax_GFP control experiments revealed that donor 5 had significantly higher cell count than other donors. Generally, the GFP_high readings decreased over time, as expected. (FIGS. 13A and 13B).

[00244] Experiments to analyze non-targeting controls for changes in episomal GFP expression, revealed that episomal GFP expression decreased to less than 0.05 over time. (FIGS. 14A and 14B) Some of the outliers were attributed to gating errors, which were most severe in donor 3. WT control experiments also exhibited <0.05 GFP_high readings, as expected (FIG. 15).

[00245] As shown in FIG. 16 and FIG. 17, there was a more consistent trend among donors when using sgRNA5 to target the B2M safe harbor locus.

[00246] A comparison of GFP expression trends between sgRNA79 and sgRNA83 for TRAC insertion and expression with an endogenous reporter revealed that donor 2 trends were different between sgRNA79 and sgRNA83, while donor 4 trends were the same (FIG. 18 and FIG. 22). Some potential reasons for the observed variation between replicates and donors include:

[00247] (1) manual handling of a large number of plates (e.g., FIG. 26):

[00248] Edge effects

[00249] Electroporation errors

[00250] (2) Inherent differences among donors (e.g., FIG. 27):

[00251] There were consistent differences with certain wells throughout the assay (spanning multiple weeks)

[00252] There were variable cell numbers between donors

[00253] (3) Gating errors (e.g. FIG. 28):

[00254] 1 peak vs >2 peaks in GFP signals

Example 4: Ranking Loci by Expression and KI Efficiency

[00255] The loci were ranked based on mean florescence intensity (MFI) of reporter gene, GFP, and KI efficiency.

[00256] **FIG. 29** shows GFP MFI and KI efficiency for all significant loci having endogenous promoters. The B2M locus reported the highest GFP MFI. The TRAC locus was among the top 10 MFI. The highest GFP MFI readings were reported in week 1 and reduced slightly in weeks 3 and 4. The results also showed most top loci have more than 1 sgRNA. With regard to KI efficiency, the SOCS1 locus reported the highest KI efficiency. Overall, KI efficiency showed greater variation among donors than GFP MFI.

[00257] **FIG. 30** shows GFP MFI and KI efficiency for all significant loci having exogenous promoters (e.g. EF1a promoters). The TRAC locus reported the highest GFP MFI. There was comparable expression between weeks 3 and 4. The results also showed most top loci have more than 1 sgRNA. With regard to KI efficiency, the SOCS1 locus reported the highest KI efficiency. Overall, KI efficiency showed less variation when driven by the exogenous promoters than when driven by endogenous promoters.

[00258] **FIGS. 31A, 31B, and 31C** show GFP MFI and KI efficiency for all significant loci having endogenous and exogenous (e.g., EF1a) promoters. The results showed that expression driven by EF1a promoters is about 10 X higher than endogenous promoters (**FIG. 31A**). With regard to KI efficiency, the SOCS1 locus reported the highest KI efficiency. At weeks 3 and 4, KI efficiency was higher when driven by the exogenous promoters than when driven by endogenous promoters.

Example 5: Evaluation of TCR expression in candidate noncoding sites

[00259] This experiment was conducted to identify target loci and integration sites that enable high transgene expression without disrupting the TCR. Some gene deserts (e.g. gene deserts 2, 3, 5, and 6) were identified as having high transgene expression (**FIG. 32A**).

[00260] To evaluate and identify preferred knock-in sites, TCR expression was measured following circuit cassette knock in of PrimeR (Prime Receptor (Myc)). Myc denotes an N-terminal Myc epitope tag to facilitate detection of surface expressed primer receptor. Briefly, CD3-CD28 Dynabead-activated T cells were electroporated with sgRNA/Cas9 RNPs

targeting the indicated sites (*see* **FIG. 32B and 33A**), as well as HDRTs with homology arms directing HDR-mediated integration into the indicated sites. At day 6 post-electroporation, cells were stained with anti-TCRalpha/beta and anti-myc antibodies and analyzed on an Attune NxT flow cytometer. As shown in **FIG. 32B**, the TCR expression was maintained at GS94 and GS102 candidate integration (knock-in) sites. Only 2/3 of the cells that had circuit cassette knock in of PrimeR at GS79 (TRAC) locus maintained TCR expression. These results indicated that the GS94 and GS102 sites showed better potential for TCR stimulation.

[00261] The percentage of cells showing effective knock-in (based on measurements of PrimeR) was $36\% \pm 4\%$ when using the GS94 integration site, as compared to $32\% \pm 5\%$ when using the TRAC integration site. These results revealed integration sites, including GS94, that supported reproducibly high circuit cassette knockin rates. *See* **FIG. 33A**.

Example 6: Evaluation of GS94 circuit expression and function

[00262] GS94 is a candidate integration site located on chromosome 11's distal q arm. It is within 180-350kb of the promoters for ETS1 and FLI1 (**FIG. 33B**), however that is considered low-risk for integration vector gene therapy. The circuit expression and function potential of the GS94 gene was evaluated.

[00263] T cells underwent circuit cassette integration with PrimeR at GS79 (TRAC) integration site and GS94 integration site. The cells were cocultured with K562 C19 cells for 48 hours and then the PrimeR induced CAR MFI was compared to the PrimeR MFI.

[00264] Briefly, T cells generated as described in the Example above were cocultured with K562 CD19+/MSLN- cells at day 7 post-electroporation. MSLN (mesothelin) is a gene that is overexpressed in human pancreatic cancer. Cells were then stained with anti-FLAG antibody 48 h post initiation of coculture and analyzed on an Attune NxT flow cytometer. The results revealed that GS94 yields superior CAR induction with high prime R expression following the 48-hour coculture with the K562 C19 cells. *See* **FIG. 34A**. GS94 resulted in prime antigen-dependent CAR expression that was approximately two-fold higher than the expression in several other candidate integration sites as well as the TRAC integration site. Additionally, on average, the prime receptor surface expression level was no less than 50% of expression level when using the TRAC integration site.

Cytotoxicity and Cytokine Secretion

[00265] To evaluate the effect of the candidate integration site on cytotoxicity and cytokine secretion, T cells that had undergone circuit cassette integration with PrimeR at GS79 (TRAC) integration site and GS94 integration site were cocultured with K562

C19/MSLN cells for 48 hours. MSLN is a gene that is overexpressed in human pancreatic cancer. The cells were treated at a 1:1 effector:target cell ratio (1:1 E:T)). Briefly, T cells generated as described above were cocultured with K562 CD19+/MSLN+ cells at day 7 post-electroporation. 48h post initiation of coculture, supernatants were collected and analyzed via Luminex for cytokine levels. The cytokines measure were IL-2, INFg, and TNF. Cytotoxicity was analyzed by measuring luciferase activity of remaining target cells after 48h. Each of the data points in FIG. 34B represent two replicates and the lines represent the range of cytotoxicity for the replicates. As shown in FIG. 34B, the GS94 integration sites resulted in superior cytotoxic ability and cytokine secretion following the 48-hour coculture with K562 C19/MSLN cells.

Prime-independent cytotoxicity

[00266] To compare the effect of the candidate integration site on cytotoxicity versus prime-independent cytotoxicity, T cells that had undergone circuit cassette integration with PrimeR at GS79 (TRAC) integration site and GS94 integration site were cocultured with K562 CD19+/MSLN+ cells or K562 CD19-/MSLN+ cells ("K562_MSLN") at day 7 post-electroporation for 48 hours. 0.3, 1.0, and 3.0 E:T cell ratios were tested. See FIG. 35A and FIG. 35B. At 48h post initiation of coculture, cytotoxicity was analyzed by measuring luciferase activity of remaining target cells. As shown in FIG. 35B, the GS94 integration site resulted in equivalent cytotoxic potential to the TRAC integration site and there was no prime-independent cytotoxicity.

Prime-independent cytokine secretion

[00267] To compare the effect of the candidate integration site on cytotoxicity versus prime-independent cytotoxicity, T cells that had undergone circuit cassette integration with PrimeR at GS79 (TRAC) integration site and GS94 integration site, generated as described above, were cocultured with K562 CD19+/MSLN+ cells. A group that had target cells only (E:T = 0; Targets only) was compared to a group with an E:T cell ratio of 1. Following the 48 h coculture with the K562 CD19+/MSLN+ cells, supernatant was collected and analyzed via Luminex for cytokine levels to measure secretion of IL-2, INFg and TNF cytokines. See FIG. 36A and FIG. 36B. As shown in FIG. 36B, the GS94 integration site resulted in equivalent cytokine secretion to the TRAC integration site and there was no prime-independent secretion of IL-2, INFg or TNF.

Prime-independent CAR expression

[00268] To evaluate the effect of the candidate integration site on prime-independent CAR expression, T cells that had undergone circuit cassette integration with PrimeR at GS79 (TRAC) integration site, GS94 integration site, and GS102 integration site were cultured *in vitro* for 32 days. The cells were treated with repetitive CD3/CD28 stimulation at days 5, 12, 19 and 28 of the experiment. On Day 16, the cells were evaluated for CAR expression using a flow cytometry assay. As shown in **FIG. 37**, T cell activation through TCR did not result in prime R-independent CAR expression from circuit cassette integration at the candidate integration sites.

[00269] T cells generated as described above were cultured in 96-well plates, with T cell growth medium being exchanged every 2 days. At days 5, 12, 19 and 28, T cells were stimulated with 1:1 CD3/CD28 Dynabeads. Cells were analyzed for PrimeR expression by myc epitope tag staining, and for CAR expression by FLAG epitope tag staining at the indicated time points. Flow analysis was performed on an Attune NxT flow cytometer.

Example 7: Evaluating stability of prime receptor expression over several weeks

[00270] To evaluate the effect of the candidate integration sites on stable (sustained) expression of PrimeR, T cells that had undergone circuit cassette integration with PrimeR at the integration sites indicated in **FIG. 38** were cultured *in vitro* for 32 days. Briefly, T cells generated as described above were cultured in 96-well plates, with T cell growth medium being exchanged every 2 days. At days 5, 12, 19 and 28, T cells were stimulated with 1:1 CD3/CD28 Dynabeads repetitive stimulation. Flow cytometry assays were run on days 16 and 32 using an Attune NxT flow cytometer. The cells were analyzed for PrimeR expression by myc epitope tag staining. As shown in **FIGS. 38A and 38B**, the GS94 integration site resulted in stable PrimeR expression over at least a 4-week period.

Example 8: Evaluation of on-target editing efficiency

[00271] To evaluate the on-target editing efficiency of candidate knock-in sites, iGUIDE-Seq assay was used. The methods used for conducting the iGUIDE-Seq assay are illustrated in **FIG. 39A** and provided in Nobles *et al.*, Genome Biology (2019), which is hereby incorporated by reference in its entirety. As shown in **FIG. 39B**, the GS94 integration site had the highest on-target editing efficiency of the evaluated candidate integration sites. As shown in **FIG. 39C**, GS94 resulted in no putative off-target editing as observed with two donors.

Example 9: Evaluation of GS94 knock-in**Methods**

[00272] Elevation prediction: Computational predictions of potential off-target sites from (gs94) were performed using Elevation-search (algorithm described in Listgarten *et al.* 2018. Prediction of off-target activities for the end-to-end design of CRISPR guide RNAs. *Nat Biomed Engr* **2**, 37-48; software obtained from <https://github.com/Microsoft/Elevation>). All sites identified by Elevation-search were subjected to analysis using rhAmp-seq.

[00273] rhAmpSeq: 49 candidate off-target sites for GS94 identified by iGUIDE or the Elevation prediction algorithm and the GS94 target site were characterized by rhAmpSeq (Integrated DNA Technologies, Inc.). This targeted amplification enables NGS-based quantification of the editing occurring at numerous sites simultaneously. Genomic DNA from T cells from at least 2 donors that had been treated singly with each of the following 7 guides: GS84, GS94, GS95, GS96, GS102, GS108, and GS138 was isolated with the GenFind V3 DNA purification system (Beckman Coulter). Two separate rhAmpSeq amplification pools were used to cover the 50 loci, the procedure was performed as recommended by Integrated DNA Technologies for each of the samples. The rhAmpSeq libraries were sequenced on a MiniSeq with a Mid Output Kit (300-cycles) (Illumina). The CRISPResso2 algorithm (<https://github.com/pinellolab/CRISPResso2>) was used to determine the percentage of insertions and deletions at each of the amplified loci. Statistical significance (FDR-adjusted p-value ≤ 0.001) using a chi-squared test was only observed at the GS94 site.

[00274] RNA-seq: To evaluate changes induced by GS94 integration at the transcriptional level, a CD19/MSLN circuit was integrated at the GS79 (TRAC), GS94, and GS102 integration sites. On day 6 post-integration, 1e6 edited cells were sorted using a BD FACSAria based on transgene expression. RNA was isolated from sorted T cells with the RNeasy kit (Qiagen). Purified RNA was converted into an NGS library using the TruSeq RNA Library Prep Kit v2 (Illumina). Libraries were sequenced on either the NovaSeq 6000 or NextSeq 550 instruments (Illumina). The STAR 2.7.3a aligner (Dobin A. *et al.* Bioinformatics. 2013. 29:15-21) was used to align the RNA-seq data against the reference human GRCh38 transcriptome and to obtain gene-level read counts. edgeR (Robinson MD *et al.* Bioinformatics. 2010. 26: 139-140) was used to compute differential expression, combining data across both donors. The only genes within 300Kb of the GS94 site, ETS1 and FLI1, were not differentially expressed in cells with integration at the GS94 integration site compared to cells with integration at any of the other two loci. At an FDR-adjusted p-value

cutoff of 0.01, the number of differentially expressed genes was minimal (<100 genes genome-wide).

[00275] Cytokine-independent growth assay: To evaluate the safety of the primary T cells with GS94 locus KI, cytokine-independent growth assay was performed to evaluate the potential for oncogenic transformation. Briefly, primary human T cells that had undergone CD19/MSLN circuit cassette integration at GS94 locus were thawed and recovered overnight. 1×10^6 cells were then seeded in one well of a 24 well-GREX plate, culturing for 5 days in the medium with or without cytokines. Cell number and viability were recorded at days 0, 3 and 5. As a positive control, 1×10^6 Jurkat cells were cultured in the medium without cytokines in parallel. As shown in **FIG. 43**, while GS94 KI T cells maintained good viability and total cell count when cultured with cytokine, the viability of GS94 KI T cells drastically decreased over the course of 5 days when cultured without cytokine and there was no viable cell left on day 5. The positive control Jurkat cells maintained good viability and expansion without cytokine throughout the assay. Taken together, this data shows that GS94 edited primary human T cells still depend on exogenous cytokine for growth, survival and expansion, therefore, there is no concern for cellular transformation.

Results

[00276] The specificity of CRISPR reagents (e.g. SpCas9 complexed with sgRNA) targeting candidate loci including GS94 was evaluated by iGUIDE-seq (**FIG. 40**). GS94-targeting CRISPR RNP showed the highest percentage of iGUIDE-seq oligo cassette trapping events of all candidates evaluated, and the control sgRNA sequences from the iGUIDE-seq paper showed similar specificities to what was reported in the original publication, suggesting that the assay performed as expected.

[00277] Putative off-target sites were taken from the iGUIDE-seq output, which already suggested that the putative sites were spurious. Additional target sites were predicted by a computational approach (Elevation software package). rhAmp-seq was used to prepare high-throughput sequencing libraries for each of the putative off-target sites, and the method was applied to DNA samples from T cells electroporated with CRISPR RNPs targeting the candidate target sites. The resulting NGS data were processed with CRISPResso2 software, and the frequency of insertions and deletions (indels) was taken as indication of CRISPR cleavage activity, as is common in the field. T cells electroporated with GS94-targeting CRISPR RNP showed no greater frequency of indels at the set of putative off-target sites than T cells treated with CRISPR RNP targeting other sites, consistent with the GS94-targeting

CRISPR RNP having no consequential or detectable off-target activity, and therefore being the most specific out of the set evaluated (**FIG. 41**).

[00278] Potential effects of transgene integration at the GS94 site on the regulation of the T cell transcriptome were evaluated by knocking in a large cassette to the site, growing T cells for several days, sorting cells expressing the transgene within the cassette, and then collecting RNA from the cells. RNA-seq libraries were prepared and sequenced, and analysis of the resulting Illumina sequencing data revealed no biologically or statistically significant differences in expression of any genes within 300kb of the GS94 site in cells with integrations at GS94 compared to cells with integration at *TRAC* or the GS102 sites (**FIG. 42**). Furthermore, other gene expression differences that reached statistical significance were minimal in number and in effect size, consistent with them being noise in the comparison.

[00279] To assess whether transgene integration at GS94 could confer a transformed phenotype, cells with integrations at the GS94 site were cultured with and without cytokines *in vitro*. Cells remained alive and viable with cytokine addition, but died without cytokine supplementation and lost their viability (**FIG. 43**). The positive control Jurkat cells remained viable and proliferated. Overall, this indicates that integration of a transgene at GS94 does not confer capacity for cytokine-independent growth, which is a hallmark of T cell transformation.

Example 10: In vivo Insertion of a CAR expressing cassette

[00280] *In vivo* efficacy of T cells with a transgene cassette expressing a CAR recognizing a tumor antigen, or a CAR recognizing a tumor antigen under control of a priming receptor recognizing an antigen in the anatomical vicinity of the tumor, is assessed against human tumor cells such as K562 engineered to express the CAR antigen or to express antigens recognized by both the priming receptor and the CAR. Tumor cells (e.g. 1e6) are subcutaneously injected into the flank of NSG mice (Jackson Laboratories). Tumor growth is assessed by dimensional measurement by calipers every 2-4 days. When the tumor volume reaches ~100 cubic mm, mice are intravenously injected with 5e6 T cells with a CAR or prime-CAR circuit cassette integrated at a specific site by CRISPR-mediated insertion, or with T cells engineered with CRISPR RNP alone, or with PBS alone as a sham injection. Tumor growth is monitored and mice are euthanized when tumor volume reaches 2000 cubic mm. Peripheral blood is bled from mice through a retro-orbital procedure, and flow cytometry and/or ddPCR is used to observe engineered T cell expansion over time. At time of sacrifice, spleen, blood, tumor and/or other tissue is analyzed via flow cytometry, ddPCR,

and/or immunohistochemistry for the presence of engineered T cells. The results demonstrate that T cells engineered with cassette integration at one of the defined genomic loci lead to tumor regression and clearance in injected mice as compared to T cells without cassette integration, and that engineered T cells are detectable in the peripheral blood and tissues of injected mice.

Example 11: Evaluation of non-viral insertion of a large 8.3kb expression cassette in GS94

[00281] Next, an 8.3 kb insert was inserted into a T cell at the GS94 safe harbor loci using materials/methods as previously described. A diagram of the cassette is provided in **FIG. 44**.

[00282] Construct generation

[00283] To generate plasmid constructs for knock-in, synthetic DNA was ordered from Twist, IDT and GENEWIZ and assembled via Gibson Assembly and Golden Gate Assembly. Plasmids contained homology arms homologous to sequences flanking the CRISPR target sites in the genome of 1.2kb or 450 bp in length.

[00284] T cell engineering

[00285] T-cells were enriched from peripheral blood mononuclear cells (PBMCs) obtained from normal donor Leukopaks (STEMCELL Technologies) using Lymphoprep (STEMCELL Technologies) and the EasySep Human T-Cell Isolation Kit (STEMCELL Technologies). T-cells were subsequently activated with CD3/CD28 Dynabeads at 1:1 bead to cell ratio (ThermoFisher, 40203D) in TexMACS medium (Miltenyi 130-197-196) supplemented with 3% human AB serum (Gemini Bio) and 12.5 ng/ml human IL-7 and IL-15 (Miltenyi premium grade) and cultured at 37°C, 5% CO₂ for 48 hours before electroporation.

[00286] CRISPR RNP were prepared by combining 120 μM sgRNA (Synthego) targeting DNA sequence GAGCCATGCTTGGCTTACGA (GS94, SEQ ID NO: 94), 62.5 μM sNLS-SpCas9-sNLS (Aldevron) and P3 buffer (Lonza) at a volume ratio of 5:1:3:6, and incubated for 15 minutes at room temperature. An optimized amount of plasmid DNA, determined by dose titration experiments (ranging from 0.5-3 micrograms) was mixed with 3.5 μl of RNP. T-cells were counted, debeaded, centrifuged at 90 X G for 10 minutes and resuspended at 10⁶ cells/14.5 μl of P3 with supplement added (Lonza). 14.5 μl of T-cell suspension was added to the DNA/RNP mixture, transferred to Lonza 384-well nucleocuvette plate, and pulsed in a Lonza HT Nucleofector System with code EH-115. Cells were allowed to rest for 15 minutes at room temperature before transfer to 96-well plates (Sarstedt) in TexMACS medium supplemented with 12.5 ng/ml human IL-7 and IL-15 (Miltenyi premium grade).

[00287] Transgene expression was detected by staining with anti-Myc antibody (Cell Signaling Technology clone 9B11) and anti-Flag antibody (RnD systems, clone 1042E) and analyzed on an Attune NxT Flow Cytometer. Other antibodies used were live/dead Fixable Near-IR (Thermo Fisher), TCRalpha/beta antibody (BioLegend clone IP26), CD4 antibody (BioLegend clone RPA-T4), CD8 antibody (BioLegend clone SK1).

[00288] Priming receptor induction

[00289] To assess functional activity of the transgene (ie. synthetic circuit), edited T cells were co-cultured with target cell line expressing priming antigen at 1:1 E:T ratio, and incubated for 24hrs. T cells were harvested and stained with anti-Myc and anti-Flag antibodies to assess for Priming Receptor and CAR expression, respectively.

[00290] To assess whether the 8.3kb transgene integration at GS94 resulted in functional knock-in, cells were cultured with parental K562 cells and K562 cells expressing the cognate priming antigen at a 1:1 E:T cell ratio. Cells were assayed by flow cytometry after 48 hours as previously described. K562 cells with priming antigen induced CAR expression, while control parental K562 cells did not (**FIG. 45**). Overall, this indicates that the Priming Receptor induced CAR expression after insertion of a 8.3kb transgene circuit. Thus, insertion of the 8.3 kb transgene circuit resulted in expression of multiple functional genes.

Example 12: T cell differentiation post editing

[00291] **Methods**

[00292] Two donor T cells edited as described above with a priming receptor and CAR synthetic circuit were phenotypically profiled with cell surface T cell subset markers by flow cytometry. Resting T cells were taken from in vitro culture conditions, rinsed with PBS prior to staining with Zombie-Aqua viability dye, CD4, CD8, CD45RA, CCR7 and CD27 with FMOs used as controls for gating and analyzed with an Attune NxT. In FlowJo, single, viable lymphocytes were selected by SSC and FSC and subset profiling by a combination of CCR7, CD27, CD45RA were used to identify Naive- or stem cell memory- (Tn/Tscm: CD45RA+CCR7+CD27+), central memory- (Tcm: CD45RA-CCR7+CD27+), effector memory- (Tem: CD45RA-CCR7-CD27-), or terminal effector- (Tte: CD45RA+CCR7-CD27-) T cells on CD4+ and CD8+ subpopulations.

[00293] **Results**

[00294] The non-viral editing generated a less differentiated T cell product (**FIG. 46**). In both donors, the non-viral editing did not contribute to an expansion of terminally differentiated T cells, as the major subset of T cells in both subpopulations retained positive

expression of CD45RA and CCR7. (FIG. 46). This suggests that the edited T cells contain the capacity to expand, survive and persist *in vivo*.

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TABLE 4: SGRNA SEQUENCES USED FOR EVALUATION OF PREDICTED LOCI

sgRNA ID	sgRNA Sequence	sgRNA_start_coor GRCH38	sgRNA Target Loci	Integration Site	Median (% Modified), summarized from 2 donors, 2 primersets
sgRNA_1	GCACCTGAATACCACGCCTG (SEQ ID NO:1)	chr16:88811818	APRT	APRT	79.28
sgRNA_2	CGCCTGCGATGTAGTCGATG (SEQ ID NO:2)	chr16:88811551	APRT	APRT	78.60
sgRNA_3	CAGGACGGGCGAGATGTCCC (SEQ ID NO:3)	chr16:88811640	APRT	APRT	85.25
sgRNA_4	CTGAATCTTTGGAGTACCTG (SEQ ID NO:4)	chr15:44715425	B2M	B2M	78.51
sgRNA_5	GGCCACGGAGCGAGACATCT (SEQ ID NO:5)	chr15:44711550	B2M	B2M	94.75
sgRNA_6	AAGTCAACTTCAATGTCGGA (SEQ ID NO:6)	chr15:44715515	B2M	B2M	70.97
sgRNA_7	GCTTGGAGGCCTGATCAGCG (SEQ ID NO:7)	chr19:36141111	CAPNS1	CAPNS 1	89.34

sgRNA_ 8	CTTATCTCTTCGAGCGAGG (SEQ ID NO:8)	chr19:36142301	CAPNS1	CAPNS 1	91.09
sgRNA_ 9	CACACATTACTCCAACATTG (SEQ ID NO:9)	chr19:36142676	CAPNS1	CAPNS 1	71.98
sgRNA_ 10	TTCCGCAAAATAGAGCCCCA (SEQ ID NO:10)	chr3:105746019	CBLB	CBLB	91.55
sgRNA_ 11	TGCACAGAACTATCGTACCA (SEQ ID NO:11)	chr3:105751622	CBLB	CBLB	91.43
sgRNA_ 12	GCAATAAGACTCTTTAAAGA (SEQ ID NO:12)	chr3:105853470	CBLB	CBLB	76.18
sgRNA_ 13	CAAAGAGATTACGAATGCCT (SEQ ID NO:13)	chr1:116754658	CD2	CD2	89.80
sgRNA_ 14	CAAGGCACCCAGGTTTCCA (SEQ ID NO:14)	chr1:116754663	CD2	CD2	92.70
sgRNA_ 15	TTACGAATGCCTTGGAACC (SEQ ID NO:15)	chr1:116754666	CD2	CD2	92.82
sgRNA_ 16	CAGAGACGCATCTGACCCTC (SEQ ID NO:16)	chr11:118315540	CD3E	CD3E	90.96
sgRNA_ 17	CATGCAGTTCTCACACTG (SEQ ID NO:17)	chr11:118313715	CD3E	CD3E	87.47
sgRNA_ 18	GTGTGAGAACTGCATGGAGA (SEQ ID NO:18)	chr11:118313715	CD3E	CD3E	86.65
sgRNA_ 19	TCTATTTTCAGGAAACCACT (SEQ ID NO:19)	chr11:118349748	CD3G	CD3G	87.24
sgRNA_ 20	AGTCATACACCTTAACCAAG (SEQ ID NO:20)	chr11:118349754	CD3G	CD3G	87.99
sgRNA_ 21	TTCAAGGAAACCAGTTGAGG (SEQ ID NO:21)	chr11:118352458	CD3G	CD3G	86.55
sgRNA_ 22	GAGCCTTGCCTGGAAATCTG (SEQ ID NO:22)	chr11:61118177	CD5	CD5	84.03
sgRNA_ 23	AAGCGTCAAAAGTCTGCCAG (SEQ ID NO:23)	chr11:61118324	CD5	CD5	89.19
sgRNA_ 24	CGTTCCAACCTGAAGTGCCA (SEQ ID NO: 24)	chr11:61118121	CD5	CD5	83.11
sgRNA_ 25	GAGCGACTGGGACACGGTGA (SEQ ID NO:25)	chr9:136866246	EDF1	EDF1	88.84
sgRNA_ 26	GCTGCGCAAGAAGGGCCCTA (SEQ ID NO:26)	chr9:136866211	EDF1	EDF1	91.04
sgRNA_ 27	TTGTTCTGGCCAGCAGCCCC (SEQ ID NO: 27)	chr9:136863433	EDF1	EDF1	85.98
sgRNA_ 28	CTTCCAGAGCCACATCATCG (SEQ ID NO:28)	chr19:48965791	FTL	FTL	93.10
sgRNA_ 29	GGGACTCACCAGAGAGAGGT (SEQ ID NO:29)	chr19:48965601	FTL	FTL	88.86
sgRNA_ 30	CGGTGAAATAGAAGCCCTA (SEQ ID NO:30)	chr19:48965770	FTL	FTL	93.14
sgRNA_ 31	AAAAGGATATTGTGCAACTG (SEQ ID NO:31)	chr10:87933015	PTEN	PTEN	92.37
sgRNA_ 32	TGTGCATATTTATTACATCG (SEQ ID NO:32)	chr10:87933183	PTEN	PTEN	90.64
sgRNA_ 33	TTTGTGAAGATCTTGACCAA (SEQ ID NO:33)	chr10:87933087	PTEN	PTEN	85.36

sgRNA_ 34	TGTCATGCTGAACCGCATTG (SEQ ID NO:34)	chr18:12830972	PTPN2	PTPN2	87.94
sgRNA_ 35	CCACTCTATGAGGATAGTCA (SEQ ID NO:35)	chr18:12859219	PTPN2	PTPN2	92.45
sgRNA_ 36	TTGACATAGAAGAGGCACAA (SEQ ID NO:36)	chr18:12836828	PTPN2	PTPN2	93.96
sgRNA_ 37	GAGTACTACACTCAGCAGCA (SEQ ID NO:37)	chr12:6952098	PTPN6	PTPN6	89.61
sgRNA_ 38	TCACGCACAAGAAACGTCCA (SEQ ID NO:38)	chr12:6954872	PTPN6	PTPN6	82.74
sgRNA_ 39	AGGTCTCGGTGAAACACCT (SEQ ID NO:39)	chr12:6951610	PTPN6	PTPN6	91.27
sgRNA_ 40	AGCATTATCCAAAGAGTCCG (SEQ ID NO:40)	chr1:198696873	PTPRC	PTPRC	88.88
sgRNA_ 41	ATATTAATTCTTACCAGTGG (SEQ ID NO:41)	chr1:198692370	PTPRC	PTPRC	88.95
sgRNA_ 42	AGCTTTAAATCAAGGTTTCAT (SEQ ID NO:42)	chr1:198756176	PTPRC	PTPRC	96.89
sgRNA_ 43	ATCCCGAGCCCTAAGGTGCA (SEQ ID NO:43)	chr11:67436325	PTPRCAP	PTPRCA P	84.08
sgRNA_ 44	GGCAGCGCGGAGGACAGCGT (SEQ ID NO:44)	chr11:67436285	PTPRCAP	PTPRCA P	97.74
sgRNA_ 45	CTCAGGGGGCTACTACCACC (SEQ ID NO:45)	chr11:67436170	PTPRCAP	PTPRCA P	91.50
sgRNA_ 46	GTCACCGACGAGACCAGAAG (SEQ ID NO:46)	chr5:82277810	RPS23	RPS23	79.40
sgRNA_ 47	GTCGTGGACTTCGTA CTGCT (SEQ ID NO:47)	chr5:82277843	RPS23	RPS23	83.07
sgRNA_ 48	TAATTTTTAGGCAAGTGTGCG (SEQ ID NO:48)	chr5:82277860	RPS23	RPS23	61.94
sgRNA_ 49	TTAGCTGTTAGACTTGAATA (SEQ ID NO:49)	chr14:51993810	RTRAF	RTRAF	85.50
sgRNA_ 50	CGAGAGCCGTCAACTTGCGT (SEQ ID NO:50)	chr14:51989652	RTRAF	RTRAF	85.64
sgRNA_ 51	CGGCTTCAACTGCAAAGGTG (SEQ ID NO:51)	chr14:51989700	RTRAF	RTRAF	88.77
sgRNA_ 52	TATGAAAAAGCAGAGCGACT (SEQ ID NO:52)	chr15:43793025	SERF2	SERF2	89.61
sgRNA_ 53	TCTGGCGGGCGAGCTCACGC (SEQ ID NO:53)	chr15:43792989	SERF2	SERF2	86.73
sgRNA_ 54	CTCACGCTGGTTACCGCCTA (SEQ ID NO:54)	chr15:43792977	SERF2	SERF2	80.57
sgRNA_ 55	AAAGATTACGAACCTCCCTG (SEQ ID NO:55)	chr12:46207559	SLC38A1	SLC38A 1	92.24
sgRNA_ 56	GTAAAAACAGACATGCCTA (SEQ ID NO:56)	chr12:46229232	SLC38A1	SLC38A 1	91.51
sgRNA_ 57	ATGCCTAAGGAGGTTGTACC (SEQ ID NO:57)	chr12:46229246	SLC38A1	SLC38A 1	79.48
sgRNA_ 58	CTCCAGGTATCCCATCGAAA (SEQ ID NO:58)	chr18:47869418	SMAD2	SMAD2	79.53
sgRNA_ 59	CACCAAATACGATAGATCAG (SEQ ID NO:59)	chr18:47870532	SMAD2	SMAD2	86.61

sgRNA_60	TGGCGGCGTGAATGGCAAGA (SEQ ID NO:60)	chr18:47896729	SMAD2	SMAD2	82.91
sgRNA_61	TAGGATGGTAGCACACAACC (SEQ ID NO:61)	chr16:11255478	SOCS1	SOCS1	92.25
sgRNA_62	CAGCAGCAGAGCCCCGACGG (SEQ ID NO:62)	chr16:11255432	SOCS1	SOCS1	83.79
sgRNA_63	CGGCGTGCGAACGGAATGTG (SEQ ID NO:63)	chr16:11255296	SOCS1	SOCS1	84.24
sgRNA_64	TATAGACGCTGCCCGACGTC (SEQ ID NO:64)	chr15:40038895	SRP14	SRP14	95.12
sgRNA_65	TCCAAAGAAGGGTACTGTGG (SEQ ID NO:65)	chr15:40038368	SRP14	SRP14	92.14
sgRNA_66	ACAGTACCCTTCTTTGGAAT (SEQ ID NO:66)	chr15:40038358	SRP14	SRP14	65.82
sgRNA_67	GCGACGGGCGCATCTACGTG (SEQ ID NO:67)	chr12:120469572	SRSF9	SRSF9	83.68
sgRNA_68	CCCGACCTCCATAAGTCCTG (SEQ ID NO:68)	chr12:120465700	SRSF9	SRSF9	92.56
sgRNA_69	GGGGTCTCGAAGCGCACGA (SEQ ID NO:69)	chr12:120469426	SRSF9	SRSF9	89.94
sgRNA_70	TGCTCTGTTTAGAAGATGAC (SEQ ID NO:70)	chr5:32591641	SUB1	SUB1	79.36
sgRNA_71	ATATTCTTTCTAGTTAAAG (SEQ ID NO:71)	chr5:32591566	SUB1	SUB1	70.93
sgRNA_72	CCTGTAAAGAAACAAAAGAC (SEQ ID NO:72)	chr5:32591614	SUB1	SUB1	93.66
sgRNA_73	TGGAGAAAGACGTAACCTCG (SEQ ID NO:73)	chr4:105234315	TET2	TET2	83.53
sgRNA_74	TCTGCCCTGAGGTATGCGAT (SEQ ID NO:74)	chr4:105234747	TET2	TET2	90.97
sgRNA_75	ATTCCGCTTGGTGAAAACGA (SEQ ID NO:75)	chr4:105235656	TET2	TET2	89.62
sgRNA_76	CAGGCACAATAGAAACAACG (SEQ ID NO:76)	chr3:114295571	TIGIT	TIGIT	92.65
sgRNA_77	CCATTGTAAATGCTGACTTG (SEQ ID NO:77)	chr3:114295700	TIGIT	TIGIT	60.75
sgRNA_78	CTGGGTCACTTGTCGGTGG (SEQ ID NO:78)	chr3:114295634	TIGIT	TIGIT	87.99
sgRNA_79	GTCAGGGTTCTGGATATCTG (SEQ ID NO:79)	chr14:22547508	TRAC	TRAC	98.20
sgRNA_80	TGGATTAGAGTCTCTCAGC (SEQ ID NO:80)	chr14:22547541	TRAC	TRAC	88.15
sgRNA_81	CTGCGGCTGTGGTCCAGCTG (SEQ ID NO:81)	chr14:22550661	TRAC	TRAC	94.77
sgRNA_82	ACAAAAGTGTGCTAGACATG (SEQ ID NO:82)	chr14:22547658	TRAC	TRAC	87.86
sgRNA_83	TTCTTCCCAGCCAGGTAA (SEQ ID NO:83)	chr14:22547778	TRAC	TRAC	89.85
sgRNA_84	CGTCATGAGCAGATTAAACC (SEQ ID NO:84)	chr14:22550625	TRAC	TRAC	95.81
sgRNA_85	GAGAGCGCTGCGACCCGAG (SEQ ID NO:85)	chr19:58544980	TRIM28	TRIM28	89.44

sgRNA_ 86	CCAGCGGGTGAAGTACACCA (SEQ ID NO:86)	chr19:58544869	TRIM28	TRIM28	94.79
sgRNA_ 87	GGAGCGCTTTTCGCCGCCAG (SEQ ID NO:87)	chr19:58544839	TRIM28	TRIM28	91.81
sgRNA_ 88	TGAGGCCTGGACCTTATGCA (SEQ ID NO:88)	chr10:33134193	chr10:3313 0000- 33140000	desert_ 1 (GS88)	69.44
sgRNA_ 89	CCTGGTGGAGTGAACCATGA (SEQ ID NO:89)	chr10:33132917	chr10:3313 0000- 33140000	desert_ 1 (GS89)	95.25
sgRNA_ 90	CAAGCACTTAGGTTCCCTG (SEQ ID NO:90)	chr10:33134633	chr10:3313 0000- 33140000	desert_ 1 (GS90)	91.13
sgRNA_ 91	GGTCTCCCTACAATTCAGCG (SEQ ID NO:91)	chr10:72294568	chr10:7229 0000- 72300000	desert_ 2 (GS91)	92.02
sgRNA_ 92	CACAGCGCGTGAATGCAATG (SEQ ID NO:92)	chr10:72298268	chr10:7229 0000- 72300000	desert_ 2 (GS92)	90.22
sgRNA_ 93	TCTGGGGCACCAATTCTAGG (SEQ ID NO:93)	chr10:72292786	chr10:7229 0000- 72300000	desert_ 2 (GS93)	86.35
sgRNA_ 94	GAGCCATGCTTGGCTTACGA (SEQ ID NO:94)	chr11:128342576	chr11:1283 40000- 128350000	desert_ 3 (GS94)	91.24
sgRNA_ 95	GTACAAGTACTTATCTCATG (SEQ ID NO:95)	chr11:128343592	chr11:1283 40000- 128350000	desert_ 3 (GS95)	89.02
sgRNA_ 96	GAGATAACAACATAACAACA (SEQ ID NO:96)	chr11:128347170	chr11:1283 40000- 128350000	desert_ 3 (GS96)	96.47
sgRNA_ 97	CATATTCATAGTCTTTGGG (SEQ ID NO:97)	chr11:65425000	chr11:6542 5000- 65427000 (NEAT1)	desert_ 4 (GS97)	88.54
sgRNA_ 98	CTGCCCCTTAGCAACTTAGG (SEQ ID NO:98)	chr11:65425507	chr11:6542 5000- 65427000 (NEAT1)	desert_ 4 (GS98)	92.76
sgRNA_ 99	TGTTTAAAAATATGTTGACA (SEQ ID NO:99)	chr11:65426264	chr11:6542 5000- 65427000 (NEAT1)	desert_ 4 (GS99)	90.76
sgRNA_ 100	CCAGGAATGGAACTCACGC (SEQ ID NO:100)	chr15:92830315	chr15:9283 0000- 92840000	desert_ 5 (GS100)	87.84
sgRNA_ 101	GAGGCCGCTGAATTAACCCG (SEQ ID NO:101)	chr15:92831850	chr15:9283 0000- 92840000	desert_ 5 (GS101)	85.32

sgRNA_ 102	ATACACGCACACTTGCAGAA (SEQ ID NO:102)	chr15:92831131	chr15:9283 0000- 92840000	desert_ 5 (GS102)	99.92
sgRNA_ 103	GAGCAGACAGAAACCCAGGG (SEQ ID NO:103)	chr16:11225670	chr16:1122 0000- 11230000	desert_ 6 (GS103)	87.92
sgRNA_ 104	TGAGTCTCCAAACAGAACAG (SEQ ID NO:104)	chr16:11226284	chr16:1122 0000- 11230000	desert_ 6 (GS104)	88.53
sgRNA_ 105	TAATATCACTGACTTCACGG (SEQ ID NO:105)	chr16:11225029	chr16:1122 0000- 11230000	desert_ 6 (GS105)	87.65
sgRNA_ 106	TACACACAATGTAAGCAGCA (SEQ ID NO:106)	chr2:87467461	chr2:87460 000- 87470000	desert_ 7 (GS106)	71.79
sgRNA_ 107	GGGAGCTCAATTCGAAACCA (SEQ ID NO:107)	chr2:87468809	chr2:87460 000- 87470000	desert_ 7 (GS107)	65.89
sgRNA_ 108	TTGGACAGGTGAGACAGTCG (SEQ ID NO:108)	chr2:87467001	chr2:87460 000- 87470000	desert_ 7 (GS108)	72.64
sgRNA_ 109	AAGCTCACTCAGATAGTGTG (SEQ ID NO:109)	chr3:186511316	chr3:18651 0000- 186520000	desert_ 8 (GS109)	76.89
sgRNA_ 110	CAGGAGAACCACCTTACACG (SEQ ID NO:110)	chr3:186515260	chr3:18651 0000- 186520000	desert_ 8 (GS110)	86.31
sgRNA_ 111	GGACAGACCCTGATTCACAA (SEQ ID NO:111)	chr3:186519655	chr3:18651 0000- 186520000	desert_ 8 (GS111)	85.47
sgRNA_ 112	ACATGGCAGTCTATGAACAG (SEQ ID NO:112)	chr3:59451154	chr3:59450 000- 59460000	desert_ 9 (GS112)	87.77
sgRNA_ 113	CCTATAGAGAGTACTACTTG (SEQ ID NO:113)	chr3:59456416	chr3:59450 000- 59460000	desert_ 9 (GS113)	79.33
sgRNA_ 114	CCAACCGGGTCTTCATTACG (SEQ ID NO:114)	chr3:59457029	chr3:59450 000- 59460000	desert_ 9 (GS114)	92.21

sgRNA_115	TCAAGCGTAGAGTTCCGAGT (SEQ ID NO:115)	chr8:127993006	chr8:127980000-128000000	desert_10 (GS115)	93.07
sgRNA_116	TCATGCAATTATGGACCCAG (SEQ ID NO:116)	chr8:127994663	chr8:127980000-128000000	desert_10 (GS116)	89.40
sgRNA_117	CGGGAAAGTGACTGGCCATG (SEQ ID NO:117)	chr8:127996766	chr8:127980000-128000000	desert_10 (GS117)	87.45
sgRNA_118	TGAGATTGAAATCAAATCGG (SEQ ID NO:118)	chr9:7974159	chr9:7970000-7980000	desert_11 (GS118)	84.84
sgRNA_119	TATGCAATATTCATCAGCG (SEQ ID NO:119)	chr9:7977914	chr9:7970000-7980000	desert_11 (GS119)	85.44
sgRNA_120	AATGTGTAAATCAAATGCA (SEQ ID NO:120)	chr9:7976895	chr9:7970000-7980000	desert_11 (GS120)	83.48

TABLE 5: CONSTRUCTS USED FOR EVALUATION OF PREDICTED LOCI

Construct name	Sequence	Length
pARBI-903: APRT_1_Endogenous_1	ATCTCGGCCAATAAAGGAGAAAGGGCGCGGCCGTACGCGGCCAGGTGCGTGGGCGAG ACCAGCTACGCCCCCTCTCCAGCCGCCAAGGCCCCGCCACAGCTGCCTGGCTGCAGTC AGAAGCGTAGCCCGAGACAAGGAAGGGCGCCTTGACTCGCACTTTTGTCCGGTTCAACGT TCTGctcagtgtgctggaatgcgagcgctcttaaaatcgatggcgctaggagtcctgaaatacggTACAGG CTTCCGCGACGATGCCCCGCCCTCACCCACGCTCCGCCCTCCGGGGATGCCCCACCCCT CGTGGCGGTCCCGCCCGTCCCCGCGCAGGCGCGCTCGGGCTGCCGTGCTCTTCGCACGC GGCCATGGCCGACTCCGAGCTGCAGCTGGTTGAGCAGCGGATCCGCAGCTTCCCCGACTTC CCCACCCCAtcggatccggagagggcaggggatctctcttactgtggcgacgtggaggagaacccggccccA TGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCATCCTGGTCGAGCTGGACG GCGACGTAAACGGCCACAAGTTCAAGCTGTCCGGCGAGGGCGAGGGCGATGCCACCTACG GCAAGCTGACCCTGAAGTTCATCTGCACCAACCGGCAAGCTGCCGTGCCCTGGCCACCCCTC GTGACCAACCTGACCTACGGCGTGCACTGCTTACGCCGTACCCCGACCATGAAGCAGC ACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAG GACGACGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCTGGTGAAC CGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTG GAGTACAACACTACAAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCA AGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGACGCTCGCCGACCACTA CCAGCAGAACACCCCATCGGGCAGCGCCCGTGCTGCTGCCCCACAACCACTACCTGAGC ACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTCTGAGAG TTCGTGACCGCCCGGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagctt ataatggttacaataaagcaatagcatcacaatttcacaataaagcatttttttactgcattctagtgtgttgc caaactcatcaatgtatcttatGGCGTGGTATTAGGTGCACGCACAGGCCGCCCTCGTGGCGCCC CGACCTGCGGGCTACGATGGGAGCGGTGGCCCGCGACCTCCGGGCGGGCGGGGCGG GAACCTCGTCTTTGCCCCCGGGGCCCTGCCCTCCTTCGGCCCCGGCGTCACAGGCCTGT	1806

	CCTTGGGTCCAGGGACATCTCGCCCGTCTGAAGGACCCCGCTCCTCCGCGCCGCGCATCG GCCTCTGGCGCGACACCTGAAGGCGACCCACGGGGGCGCATCGACTACATCGCAGGCG AGTGCCCAAGTGCCCGCATCTAGGCGCTTCCGCTCTGCGCGCGCCGAGGGCAGCAGTG GGCTCTGCGCTGTGCTTGGGGGAGGGCCTTGGGGTGCTTCAGGGGGCGCCGGGACGG GCGCCGTGCTTGGGTGCGCCGGGAAGGGTTGTGAGATTGAGCCC	
pARBI- 904: APRT_2_E ndogeno us_2	TGCCCCGCCCTCACCCACGCTCCGCCCTCCGGGGATGCCCCACCCCTCGTGCGGGTCCCGC CCGTCCCGCGCAGGCGCGCTCGGGCTGCCGTGGCTCTTCGCACGCGGCCATGGCCGACT CCGAGCTGCAGCTGGTTGAGCAGCGGATCCGACGTTCCCGACTTCCCCACCCAGGCGT GGTATTAGGTGCACGCACAGGCCGCCCTCGTGCGGCCCGACCTGCGGGCTACCGGATG GGAGCGCTGGCCCCGCGACCTCCGGGCGGGCGGGGCGGGAACCCCTCGTCTTTCGCCCCCG GGGCCCTGCCCTCCTTCGGCCCCGGCGTCAACAGGCCTGTCTTGGGTCCAGGGACATCTC GCCCCGTCTGAAGGACCCCGCTCCTCCGCGCGGCCATCGGCCCTCTGGCGCGACACCTG AAGGCGACCCACGGGGGCGCATCtccggatccggagaggcaggggatctctcttacttggcgacgtg gaggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCC TGGTCGAGCTGGACGGCGAGCTAAACGGCCACAAGTTCAAGCTGTCCGGCGAGGGCGAG GGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTTCATCTGCACACCCGGCAAGCTGCCCG TGCCCTGGCCACCCCTCGTGACCACCTGACCTACGGCGTGAGTGCTTCAGCCGCTACCCC GACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGC GCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGG GCGACACCCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACA TCCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAACGTCTATATCATGGCCGACAA GCAGAAGAACGGCATCAAGGTGAAGTTCAAGATCCGCCACAACATCGAGGACGGCAGCGT GCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCC GACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGAT CACATGGTCTGCTGGAGTTCGTGACCGCCCGCGGATCACTCTCGGCATGGACGAGCTGT ACAAatgattgtttattgagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattttt cactgcattctagttgtgtgttgcctaaactcatatgtatcttatGACTACATCGCAGGCGAGTGCCAGT GGCCGATCTAGGGCGCTTCCGCTCTGCGCGCGCCGAGGGCAGCAGTGGGCTGTGCGC GTCTGCTTGGGGGAGGGCCTTGGGGTGCTTCAGGGGGCGCCGGGACGGGCGCGCTGCTT GGGTGCGCCGGGAAGGGTTGTGAGATTGAGCCCCGAGGCCGCGCGCTGTGCAGGCGTC CTTCCCGCAGGTTCCGGGTCCCCAGCCAGGACAGGCGTGACCGAGTTGCCGGTCAAGTG GTCTCCCTGGAGTGCCCAAGCTGAATCCACAGGGCCAGTGCTTGTCTTGTTCCTTCT GCGAGCTGGTATTGAGCGCTGCCACGAGCCAGGCCTCCCTGGTGAAGATCACGGAATG CCCCCAGGGAAGGGAGGCCTGGAGGCCTCCGGGAGAGCCCAAGAGGTGGCCAGGGA GA	1806
pARBI- 905: APRT_3_E ndogeno us_3	CGTTCTGctcagtggtgctggaatgcgagcgctcttaaatcgatggcgctaggagtcgatgaatacggTAC AGGCTTCCGGCGACGGATGCCCGCCCCCTACCCACGCTCCGCCCTCCGGGGATGCCCCAC CCCTCGTGGCGGTCCCGCCCGTCCCGCGCAGGCGCGCTCGGGCTGCCGTGGCTCTTCGC ACGCGGCCATGGCCGACTCCGAGCTGCAGCTGTTGAGCAGCGGATCCGCACTTCCCCG ACTTCCCCACCCAGGCGTGGTATTAGGTGCACGCACAGGCCGCCCTCGTGCGCCCCGA CCTGCGGGCTACGGATGGGAGCGCGTGGCCCGCACCTCCGGGCGGGCGGGGCGGGAA CCCTCGTCTTTCGCCCGGGGCCCTGCCCTCCTTCGGCCCCGGCGTACCAAGGCCTGTCTT GGGTCCAGGtccggatccggagaggcaggggatctctcttacttggcgacgtggaggagaaccccgcccc ATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGGTCGAGCTGGAC GGCGACGTAAACGGCCACAAGTTCAAGCTGTCCGGCGAGGGCGAGGGCGATGCCACCTAC GGCAAGCTGACCCTGAAGTTTCATCTGCACACCCGGCAAGCTGCCCGTGCCCTGGCCACCC TCGTGACCACCTGACCTACGGCGTGAGTGCTTCAGCCGCTACCCGACCATATGAAGCA GCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCA AGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTTCAGGGCGACACCTGGTGA ACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGGGCACAAGC TGGAGTACAATAACAAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCAT CAAGGTGAAGTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGAGCTCGCCGACCA CTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGTGCTGCCGACAACCACTACCTG AGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCTG GAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgc	1806

	agcttataatgggtacaaataaagcaatagcatcacaaatttcacaaataaagcatttttttactgcattctagtgtggt ttgtccaaactcatcaatgtatcttatGACATCTCGCCGCTCTGAAGGACCCCGCTCCTTCCGCGCC GCCATCGGCCCTCTGGCGCGACACCTGAAGGCGACCCACGGGGGCCGATCGACTACATC GCAGGCGAGTGCCAGTGGCCGCTCTAGGGCGCTTCCGCTCTGCGCGCGCCGAGGGCA GCACGTGGGCTCTGCGCTCTGCTTGGGGGAGGGCCTTGGGGTGCTTCAGGGGGCGCCG GGACGGGCGCCGTGCTTGGGTGCGCCGGGAAGGGTTGTGAGATTGAGCCCCGAGGCCG CCGCGCTGTGACGGCGTCTTCCCGCAGGTTCCGGGTCCCGAGCCAGGACAGGCGTGACC GATTGCCGGGTGAGTTGGTCTCCCTGGAGTGCCCAAGCTGAATCCACAGGGCCAGCTGC CTGCTTCTTGTCTTCTGCGAGCTGGTATTGAGCGCTGCCACGA	
pARBI- 906: B2M_1_E ndogeno us_4	AGTAATTTGATGGGGGCTATTATGAACTGAGAAATGAACCTTGAAGAGTATCTTGGGGCCA AATCATGTAGACTCTTGAGTGATGTGTTAAGGAATGCTATGAGTGCTGAGAGGGCATCAGA AGTCTTGAGAGCCTCCAGAGAAAGGCTCTTAAAAATGCAGCGCAATCTCCAGTGACAGAA GATACTGCTAGAAATCTGCTAGAAAAAAACAAAAAGGCATGTATAGAGGAATTATGAG GGAAAGATACCAAGTCACGTTTTATTCTTCAAATGGAGGTGGCTTGTGGGAAGGTGGA AGCTCATTTGGCCAGAGTGGAATGGAATTGGGAGAAATCGATGACCAAATGTAAACACTT GGTGCTGATATAGCTTGACACCAAGTTAGCCCCAAGTGAATACCTGGCAATATTAATGT GTCTTTTCCGATATCTCTCAGGTtccggatccggagagggcaggggatctctcttacttgtggcgacgtgga ggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTC GGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGG GCGATGCCACCTACGGCAAGCTGACCTGAAGTTTCACTCTGCACCAACGGCAAGCTGCCCGT GCCCTGGCCCAACCTCGTGACCACTGACCTACGGCGTGCACTGCTTCAGCCGTACCCCG ACCACATGAAGCAGCAGGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCG CACCATCTTCTTCAAGGACGACGGCACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGC GACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATC CTGGGGCACAAGCTGGAGTACAACACAGCCACAACGTCTATATCATGGCCGACAAGC AGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTG AGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCCGA CAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAGACCCCAACGAGAAGCGCGATCAC ATGGTCTGCTGGAGTTCTGTGACCGCCCGGGATCACTCTCGGCATGGACGAGCTGTACA Aatgattgtttattgcagcttataatgggtacaaataaagcaatagcatcacaaatttcacaaataaagcatttttttact gcattctagtgtgtgtgttccaaactcatcaatgtatcttatACTCCAAGATTCAAGTTTACTACGTCATC CAGCAGAGAATGGAAGTCAAATTTCTGAATTGCTATGTGTCTGGGTTTCATCCATCCGAC ATTGAAGTTGACTTACTGAAGAATGGAGAGAGAATTGAAAAAGTGGAGCATTCAAGCTTGT CTTTCAGCAAGGACTGGTCTTCTATCTTGTACTACACTGAATTACCCCCACTGAAAAAG ATGAGTATGCCTGCCGTGTGAACCATGTGACTTTGTACAGCCCAAGATAGTTAAGTGGGG TAAGCTTACATCTTTTGAAGCTGTGAAAGTTGTGTATGAGTAGTCATATCATAAAGCT GCTTTGATATAAAAAAGGTCTATGGCCATACTACCTGAATGAGTCCCATCCCATCTGATAT AAACAATCTGCATATTGGGATTGTGAGGAATGTTCTTAAAGATCAGA	1806
pARBI- 907: B2M_2_E ndogeno us_5	AAGATCTTAATCTTCTGGGTTTCCGTTTTCTCGAATGAAAAATGCAGGTCCGAGCAGTTAAC TGGCTGGGGCACCATTAGCAAGTCACTTAGCATCTCTGGGGCCAGTCTGCAAAGCGAGGG GGCAGCCTTAATGTGCCTCCAGCCTGAAGTCTAGAATGAGCGCCCGGTGTCCCAAGCTGG GGCGCGCACCCAGATCGGAGGGCGCCGATGTACAGACAGCAAACTCACCAGTCTAGTG CATGCTTCTTAAACATACGAGACTCTAAGAAAAGGAACTGAAAACGGGAAAGTCCCTC TCTTAACCTGGCACTGCGTCGCTGGCTTGGAGACAGGTGACGGTCCCTGCGGGCCTTGTG CTGATTGGCTGGGCACGCGTTAATATAAGTGGAGGCGTCGCGCTGGCGGGCATTCCTGAA GCTGACAGCATTGGGGCGAGATGtccggatccggagagggcaggggatctctcttacttgtggcgacgtg gaggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCC TGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAAGCTGTCCGGCGAGGGCGAG GGCGATGCCACCTACGGCAAGCTGACCTGAAGTTTCACTCTGCACCAACGGCAAGCTGCCCG TGCCCTGGCCCAACCTCGTGACCACTGACCTACGGCGTGCACTGCTTCAGCCGCTACCCC GACCACATGAAGCAGCAGGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGC GCACCATCTTCTTCAAGGACGACGGCACTACAAGACCCGCGCCGAGGTGAAGTTCGAGG GCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACA TCCTGGGGCACAAGCTGGAGTACAACACAGCCACAACGTCTATATCATGGCCGACAA GCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGT	1806

	GCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGGCAGCGCCCCGTGCTGCTGCC GACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGGAT CACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGT ACAAatgattgtttatgcagcttataatggttacaataaagcaatagcatcacaatttcacaaataaagcatttttt cactgcattctagttgtgtttgtccaaactcatcaatgtatcttatTCTCGTCCGTGGCCTTAGCTGTGCTCG CGTACTCTCTCTTTCTGGCCTGGAGGCTATCCAGCGTGAGTCTCTCTACCTCCCGCTCTG GTCCTTCTCTCCCGCTCTGCACCCTCTGTGGCCCTCGCTGTGCTCTCTCGTCCGTGACTTCC CTTCTCCAAGTTCTCTTGGTGGCCCCGCTGGGGCTAGTCCAGGGCTGGATCTCGGGGAA GCGGCGGGGTGGCCTGGGAGTGGGAAGGGGGTGCACACCGGGACGCGCGCTACTTGC CCCTTTTCGGCGGGGAGCAGGGGAGACCTTTGGCCTACGGCGACGGGAGGGTCCGGGACAA AGTTTAGGGCGTCGATAAGCGTCAGAGCGCCGAGGTTGGGGGAGGGTTTCTCTCCGCTCT TTCGCGGGGCTCTGGCTCCCCAGCGCAGCTGGAGTGGGGGACGGGTAGGCTCG	
pARBI- 908: B2M_3_E ndogeno us_6	AGGAATGCTATGAGTGCTGAGAGGGCATCAGAAGTCCTTGAGAGCCTCCAGAGAAAGGCT CTTAAAAATGCAGCGCAATCTCCAGTGACAGAAGATACTGCTAGAAATCTGCTAGAAAAA AACAAAAAAGGCATGTATAGAGGAATTATGAGGGAAAGATACCAAGTACCGTTTTATTCTT CAAAATGGAGGTGGCTTGTGGGAAGGTGGAAGCTCATTTGGCCAGAGTGGAATGGAAT TGGGAGAAATCGATGACCAAAATGTAACACTTGGTGCCTGATATAGCTTGACACCAAGTTA GCCCCAAGTGAATACCTGGCAATATTAATGTGTCTTTCCCGATATTCTCAGGTACTCCA AAGATTCAAGTTTACTCAGTCATCCAGCAGAGAATGGAAGTCAAATTTCTGAATTGCTA TGTGTCTGGGTTTCATCCATCTccggatccggagagggcaggggatctctcttacttgtggcgacgtggag agaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCATCTGG TCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGC GATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCACCGCAAGCTGCCCGTGC CCTGGCCACCTCGTGACCACCTGACCTACGGCGTGCAAGTGTTCAGCCGCTACCCCGAC CACATGAAGCAGCAGACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCA CCATCTTCTCAAGGACGACGGCACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCG ACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCC TGGGGCACAAGCTGGAGTACAACATAACAGCCACAACGTCTATATCATGGCCGACAAGCA GAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCA GCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCGAC AACCCTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACA TGGTCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAA atgattgtttatgcagcttataatggttacaataaagcaatagcatcacaatttcacaaataaagcattttttcactg cattctagttgtgtttgtccaaactcatcaatgtatcttatGACATTGAAGTTGACTTACTGAAGAATGGA GAGAGAATTGAAAAAGTGGAGCATTGAGACTTGTCTTTAGCAAGGACTGGTCTTTCTATCT CTTGACTACACTGAATTCACCCCACTGAAAAAGATGAGTATGCCTGCCGTGTGAACCATG TGACTTTGTACAGCCCAAGATAGTTAAGTGGGGTAAGTCTTACATTCTTTTGAAGTGTCT GAAAGTTGTGTATGAGTAGTCATATCATAAAGCTGCTTTGATATAAAAAAGGTCTATGGCC ATACTACCTGAATGAGTCCCATCCCATCTGATATAAACAATCTGCATATTGGGATTGTGAG GGAATGTTCTTAAAGATCAGATTAGTGGCACCTGCTGAGATACTGATGCACAGCATGGTTT CTGAACCAAGTAGTTTCCCTGCAGTTGAGCAGGGAGCAGCAGCAGCACTTG	1806
pARBI- 909: CAPNS1_ 1_Endoge nous_7	GATCTCACATTCTAGCGCCAGACATGTCCGGGAACGCCTTACGCCAATTGGGGTCCCCACC AAGAGAACCCCCACCAGATCTGCACCCTCCCCCTTACGCGTGACCCAGTCCAGGCTCCCTC AAGCCCCACGGGTGCCTTTTAGACCTGAGGAGGTTGCAAACCTGATCCCCATACCTGCCCC ACCCATCCGCGGACAACCCGCCCTCGAAACTCAGACCCCAACCCGAGGCTTACAGATTCT CCCAGGTCCAGCTGCCGAAATGCGTGTGTAAGGGAGGGTGTGGGCTCAGGGGCGAAG CACCCACTGGTCCCCTTTTTCCCCCAGCAGTGAGTCGACCCATGTTCTGGTTAACTCGT TCTTGAAGGGCGCGCGCGCGCGCGGGGAGGCGGGGGCTGGGTGGGGCCCTGGG AAATGTGCTTGAGGCTGATCccggatccggagagggcaggggatctctcttacttgtggcgacgtggag gagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCATCTG GTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGG CGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCACCGCAAGCTGCCCGTG CCCTGGCCACCTCGTGACCACCTGACCTACGGCGTGCAAGTGTTCAGCCGCTACCCCGA CCACATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGC ACCATCTTCTTCAAGGACGACGGCACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGC	1806

	GACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATC CTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCTATATCATGGCCGACAAGC AGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGC AGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTCCCGA CAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCAC ATGGTCCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGGACGAGCTGTACA Aatgattgtttattgcagcttataatggttacaataaaagcaatagcatcacaatttcacaataaaagcattttttcact gcattctagtgtgtgtgttgcacaaactcatcaatgtatcttatAGCGGGGCCGGGGCGGGCGGGCGGCG GCGGCGGGCGGGCGGGTGGTGGAGGCGGGCGGTGGCGGTGGAACGGCCATGCGCATCCTA GGCGGAGTCATCAGCGCCATCAGGTAAGGCGGAGACTATCAGAGGGGCGGGGCGCTGGGA ATGGGAGGAGCCTCAGTGAGGCGTGGTCTGGGAGGGGCGTGGTCTAAAAATAGAATAGG ATTAACCTGGAGGCTAACCTGGGTACATGAATTAGGCCGGGGAGGCCTGGTTTGAGAGTT CTGCTGAAGGGGGTGGACCCAGTGAGGCGGATATCAGTCATTGGGGGCGGTGCTTGAT ATGGGAGTAGTCTGATTGTGTGGGACCAGGACAATGTGTCCTGAGGGGACTGATGTGGA GTTTTGGCGGTGGGGCTTATGGGTCTGGGCTCAGCCTGCATTGGCTAACCTGGAGATGAA CGTT	
pARBI- 910: CAPNS1_ 2_Endoge nous_8	CGGGCATTTAGGAAGCGGGCCATGGAGTAGGGTCTTGGGCAGATGGCACCTGAGGAGGA TAAGGCCTTGGGAAGCTGGGGCAGAGCCTCTATGAAGTGAGCCCTCAAGGGGCGGGGTC TTTTGATTCTACGTGGGATTTTTAGGTTTAGGGTGCCAAAGATGACTGAAATCTGCCATC GGTAGGTGTGCTGGCAGGAGGGGAGCCTCCAGGGGACCGGTCTCTGGGTTTCTCGAG GGTGGGGTTGGCCTGAGGAAGGGAGAAGAGGGGCACGACCAGGGCAGTGTGGATTGGG ACAGATGAGGACAAGAACAATGAAAGGCACAGCAACCAAGTAAGGAAGATAACGGCTG GGGTCTGGAGCGTTGGGGCTGATGGTCTGTAGTGCTGCCCGTTGGAGGCCCGCCCTG GCACTAACCCCTCCCCCTTATCTCTCGCAGTccggatccggagagggcaggggatctctccttactgtg gcgacgtggaggagaacccggccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTG CCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAG GGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACGGCAAG CTGCCCCGTGCCCTGGCCACCCCTCGTGACCACCTGACCTACGGCGTGCAAGTTCAGCCG CTACCCCGACCACATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCC AGGAGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCGGAGGTGAAGT TCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACG GCAACATCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATGGC CGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGG CAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTG CTGCCCCACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGC GCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTCGGCATGGACGA GCTGTACAAatgattgtttattgcagcttataatggttacaataaaagcaatagcatcacaatttcacaataaaagc atTTTTtactgcattctagtgtgtgttgcacaaactcatcaatgtatcttatGAGCGGGCTGCGCAGTACAAC CCGAGGCCCCGGTAAGCCCCCTCTGCAACCAGACCCCTTCTCTGCAAGGCCTTCTCGA GGTCCCATCCCTGTTCTGTAGAGAAGCCCCACCTTCTCCCCCTTCTGTGAAATTCCTCTGC CAGTTCCTCCCATGCCGTGTCTGCAGCTTCGCCATGGGTCTTAGCCATGCCCCACATACGTG CACCCCATTCATACCACCCCTATTCTTTCTCATCAAGCTGCCAGCCCACTCTGACTTCC CCACCCAGGGTACCTGGGTTTGGGGAGCCGTCTGCGCGGGTCCCCCTCCCCCTGCTCTGA GCTCTCTCCCTTTCAGCCCCACGCACACATTACTCCAACATTGAGGCCAACGAGAGTGA GGAGGTCCGGCAGTTCGGGAGACTTTTGGCCAGCTGGCTGGAGATGTAAGTAAC	1806
pARBI- 911: CAPNS1_ 3_Endoge nous_9	GCTGATGGTCTGTAGTGCTGCCGTTGGAGGCCCCGCCCCCTGGCACTAACCCCTCCCCCTT ATCTCTTCGAGCGAGGCGGCTGCGCAGTACAACCCGAGGCCCCGGTAAGCCCCCTCTGC AACCAGACCCCTTCTCTGCCAAGGCCTTTCGAGGTCCCATCCCTGTTCTGTAGAGAAAG CCCCACCTTCTCCCCCTTCTGTGAAATTCCTCTGCCAGTTCCTCCCATGCCGTGTCTGCAGCT TCGCCATGGGTCTTAGCCATGCCCCACATACGTGCACCCCACTTCACTACCACCCCTATTCTT TTCTCATCAAGCTGCCAGCCCACTCTGACTTCCCCACCCAGGGTACCTGGGTTTGGGGAG CCGTCTGGCCGGGTTCCCCCTCCCCCTGCTCTGAGCTCTCTCCCTTTCAGCCCCACGCAC ACATTACTCCAACtccggatccggagagggcaggggatctctccttactgtggcgacgtggaggagaacccggc cccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGGTCGAGCTG GACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCAC	1806

	CTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCCGTGCCCTGGCCC ACCCTCGTGACCACCTGACCTACGGCGTGAGTGCTTCAGCCGCTACCCGACCACATGAA GCAGCAGCACTTCTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCT TCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGG TGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGGGCACA AGCTGGAGTACAACACAAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACG GCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCG ACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTA CCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTCTG CTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgttta ttgcagcttataatggttacaaataaagcaatagcatcacaatttcacaaataaagcatttttctactgcattctagt tggtttgtccaaactcatcaatgtatcttatATTGAGGCCAACGAGAGTGAGGAGGTCCGGCAGTTCGG GAGACTCTTTGCCAGCTGGCTGGAGATGTAAGTAACCTGGGGTCCCTGGCCCCGCTCTAA CCGTTCATCCCTTCCCTGTGGCTGCCCTTGACACACACCCTTGACCATGACAATCCCAGT GTTCCCATCTCCATGACATTCTCAGACCCCTTCAGTCACCCCTGACCTGCCCTAACTTCGG CCCGCAGGACATGGAGGTGAGCGCCACAGAATCATGAACATTCTCAATAAGGTTGTGACA CGACGTAAGTGACCGGGGTAAAGGAATAGGGTAGATTGAGAGGCAGAGGGGTGAGAGAG GATTTGACCTCTGGCCTCTGACTTTCAACCTGTTACCCACAGACCCTGATCTGAAGACTGAT GGTTTGGCATTGACACATGTGCGAGCATGGTGGCCGTGATG	
pARBI- 912: CBLB_1_E ndogeno us_10	ggagagttagcagatggagacaaaaagggaactgctggggatcaaaccctgtaaagtccttctaagtatatga ggactttgactttattcaagttagaaggcttgaacaaaagaattatttcattgtgtttacaatggcacaagtcg tagcgagaatagctgTGTAGAGAAGAGATTTTGTGGTTTTCTTTTGTCTCTGTATTCTCTTCC TGAAAAATCTGTTTTCTGCCTAATCATATTTCTGTAAAGAACAATAGACTTGAACGTCTGCTG TTAAGTAACAAAGGTTGACCTAAACCACATAAGGTGAGATTAACTTTTAAAAATATCCAAGAT AATGTTAAGTGATTAATATGGTTCAGTATGTAATCAAAATATTTGATATTCTCTAGATACT AATCTCtttaattttttttttttAGCCTTGgtccggatccggagagggcaggggatctctccttactgtggcgac gtggaggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCA TCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCG AGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCC CGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAAGTCTCAGCCGCTACC CCGACCACATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGA GCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAG GGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAAC ATCTGGGGGCAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATGGCCGACA AGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCG TGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCC CGACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGA TCACATGGTCTGCTGGAGTTCTGTGACCGCCCGGGATCACTCTCGGCATGGACGAGCTG TACAAatgattgtttattgagcttataatggttacaaataaagcaatagcatcacaatttcacaaataaagcattttt ttcactgcattctagtgtgtgtgtccaaactcatcaatgtatcttatGGCTCTATTTTGGGGAATTGGAATTT CTTAGCTGTGACACATCCAGGTTACATGGCATTCTCACATATGATGAAGTTAAAGCAGCAG TACAGAAATATAGACCAAACCCGGAAGGTAAGACTTTTTAGCAGTAATATTATGTGATATA TCCAAAGATGAAAAATTCTCATGGTTTGTCTTAAGTAAGTCAGCAATACCCGCTGATGGC ATGCTTGGGAGGGGGCTAGAAAAGGTAAGAACCAAAATGGTGCTTCTTAACATAATGTTT TAAATTGATACATTGTGCTTACTCTGAACTTGGTATTCATAAAGTGAAAGGGGATATGGTC TCCTTTCTGTTTTATGATATCCGTGTTTATGTGCAAAATTGAATGTATATTTGAATACTTG AATACTGTGCTAAAGAACAATAAATAGAACAGCTTATGTTCACTACTTT	1806
pARBI- 913: CBLB_2_E ndogeno us_11	CATATTACTCATTGTGCAATGAATAAAGGATTTCTATTATTATATGGACCCATCATCTTATG ACTGTTTTTAGAAAATGAGAATTAATCTTGATTCAATTATTAATAACCTTGATACACAT GAAGAGGTCATGACACATAAGACTTTGACCTAATACCTTTTTTCAGATATGTTTCTATAGCTA TCTTGATAGCCTAGGACTGTTGAGAGAAAATTAATTTAAATTTTGTGATATTCTTAGCAAA TGCAAAATAATTGAGTTAAACAGAACCCACTACATTTGTTCTGAAATATGAACAATATTCTC AAATATTTGTCTGGTAGTACAAATACAATTATTAATTTTATTATTGAATTTGTGCTTCAA AGGGAGGTATTCTTAAATGATACTTGATTCAATTATTTCCCTTTTTTCCACCTTGACAGA ACTATCGTAtccgatccggagagggcaggggatctctccttactgtggcgacgtggaggagaaccccgccccA	1806

	<p>TGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACG GCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACG GCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCCGTCCTGGCCACCCTC GTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCGACCACATGAAGCAGC ACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAG GACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAAC CGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTG GAGTACAACACTACAAGCAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAAGCGCATCA AGGTGAACTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTA CCAGCAGAACACCCCATCGGGCAGCGCCCCGTGCTGCTGCCGACAACCACTACCTGAGC ACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCAGATGGTCTGCTGGAG TTCGTGACCGCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagctt ataatggttacaaataaagcaatagcatcacaaatttcacaaataaagcattttttcactgcattctagtgtgtgtgtc caaactcatcaatgtatcttatCCATGGAAAGTATTCAGACAGTGCCTTCATGAGGTCCACCAGATT AGCTCTGGCTGGAAGCAATGGCTCTAAAATCAACAATTGATTTAACTTGCAATTGATTACAT TTCAGTTTTTGAATTTGATATTTTTACCAGGCTGTTTCAGGTAAGTTTATACTTGCTTAGTCTA TCCATTCCCTcttctctctccctgtctttctctctgttctctctctctctctctctctcacacacacacaTAAAC AAACATATGGAAAATAGTGTCACTTCTATTAGTCTGTAATTTTATTGGTATGTTTGGTCATTG TTAAAAGTTTAGAGTGAGCCATTTGGCTTAAGTTTGGAGTTATCAGATGCTGTGAGCCTGGT GGCTGCTTGTAGCTTTGAGAGGATCCATCCAAAAGAGCTTTGTTTTAACTCTCTACTTAGT TTCTTACTT</p>	
pARBI- 914: CBLB_3_E ndogeno us_12	<p>TTAAACTTTAGAGGTTCAAATAAGGATATGATATAGAAAAGATTGAATGGTAGGAGAACA GAATAGGATTTATTTATATTATGACAAACGTGACTATCAGTTAATAAATTGGAGATAGTAAG TTAAGATCATTATTTATATTATGGAATAAGGAAATAGGACATGGTTCTTAACTTTTTAA TTTTCTGTGAAATAAAATATTATGACTTATTTTATTTTATCTTTGTTTTTAAAGTAAGACTGT GCCAAAATCCCAAACCTCAGTTGAAAAATAGCCACCATATATACTTGATATTTTGCTGATA CATATCAGCATTTACGACTTATATTGAGTAAATATGATGACAACCAGAAAACCTGCCAACTC AGTGAGAATGAGTACTTTAAAATCTACATTGATAGCCTTATGAAAAAGTCAAAACGGGCAA TAAGACTCTTTAAAtccggatccggagagggcaggggatctctcttactgtggcgacgtggaggagaaccccg gccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCTGGTCGAGCT GGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCA CCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCCGTGCCCTGGCC CACCCTCGTGACCACCTGACCTACGCGTGCAGTGCTTCAGCCGCTACCCGACCACATGA AGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTT CTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCT GGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCA CAAGCTGGAGTACAACACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAAC GGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCC GACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACCACT ACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCAGATGGTCTCT GCTGGAGTTCTGTGACCGCCCGGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgttt attgcagcttataatggttacaaataaagcaatagcatcacaaatttcacaaataaagcattttttcactgcattctagt gtggtttgtccaaactcatcaatgtatcttatGAAGGCAAGGAGAGAATGTATGAAGAACAGTCACAG GACAGGTAAAGAAGATATTTAGATGTTTTGGTGTAAAGGTCAATTATGTTGCTTTTTACTT AATAGTTAACTTAAACGTACCATGTAATTGTTTTGGGGTAAATGTGAGTCGCTTTGTATAT agtcagtgtgtacttaacgatggggatactttacaagaaatgcatttttagacaatttcattgtgtgtggacatgataga gtgtacttacacagagctagatggtattacctaccgcacacctaggctgtatgtatgacctattgctcctaggctgcaaa tctatacagtatgttactgtactgaatactgtgggcagttgtaacacaatggaagtgtgtgtatctaaataaccta catagaaaaggatggtgtaaaaatactgtataaaaggccgggctgg</p>	1806
pARBI- 915: CD2_1_E ndogeno us_13_14 _15	<p>AGATGAGAAAACCTATCCTTCCCAATTTTTTTGTGTGAGAAATTAATGCAGCAAGAAAACA CACACTCATAAACACATCTGCTTTGGCAAAGGAGCACATCAGAAGGGCTGGCTTGTGCGCG CTCTTGCTCTGTGTATGTGTATTATGTTTTATGTTACTGTAAAAGATGTAAAGAGAGGCA CGTGGTTAAGCTCTCGGGGTGTGGACTCCACCAGTCTCACTTCAGTTCCTTTTGCATGAAGA GCTCAGAATCAAAAGAGGAAACCAACCCCTAAGATGAGCTTTCCATGTAAATTTGTAGCCA GCTTCCTCTGATTTTCAATGTTCTTCCAAGGTAAGCATAAGAGTCAAAGAAGTCCCAAC</p>	1806

	<p>CCAGCTTTCCCTGAAAGTGACTCTCAGTAACCTTTTGCTTTTTATAGGTGCAGTCTCCAAAG AGATTACGAATGCCTTGtccggatccggagagggcaggggatctctcttactgtggcgacgtggaggagAAC cccggccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTCCCATCTGGTCGA GCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATG CCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTG GCCCCCCTCGTGACCACCCTGACCTACGGCGTGCAAGTCTCAGCCGCTACCCCGACCA TGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCCCGAAGGCTACGTCCAGGAGCGCACCAT CTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGAGGTGAAGTTCGAGGGCGACAC CCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGG GCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAG AACGGCATCAAGGTGAAGTTCAGATCCGCCACAACATCGAGGACGGCAGCGTGACGCTC GCGGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACC ACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGT CCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGGACGAGCTGTACAAtgat tgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaaataaagcattttttcactgattc tagttgtggtttgtccaaactcatcaatgtatcttatGAAACCTGGGGTGCTTGGGTGACGACATCAACT TGGACATTCTAGTTTTCAAATGAGTGATGATATTGACGATATAAAATGGGAAAAAACTTCA GACAAGAAAAAGATTGACAATTGAGAAAAGAGAAAGAGACTTTCAAGGAAAAAGATACA TATAAGCTATTAAAAATGGAAGTCTGAAAATTAAGCATCTGAAGACCGATGATCAGGATA TCTACAAGGTATCAATATATGATACAAAAGGAAAAAATGTGTTGGAAAAAATATTTGATTT GAAGATTCAAGGTAAGTGTTTATTCCCTTAATTGCTTTATTTAGTGTGGGTGCTATTTGGC AAGTTGGAAAAATAGCATTCTAATATTTCCCGAGCGTGACCTCTGCCTCCAGGGGGGCTATA CAGGAAACCAGATGCATGTCTCTGCCCGAGTGGAGACTGTGGTCCAA</p>	
pARBI- 916: CD3E_1_ Endogeno us_16	<p>AGGATTGTTCTAGTTGATTGGTATGTGTGCACTCCTAGTTGTTAAATATTTTCACTATCACAC CTGGATATACTCAACAAATATTTGTTGAGCCAAATACTCAACACCAGCCAAACACGTAGTAT TTACTTTAGCTTAAGCGAATTATTTAGCCTGACAGAAGCCTGGAATGTGGGTCTTTAAGT TCCTATTTTTGAGATGGGAAAGCTGAGGCTCACGGAAGGAGGTGACCAGCTCAAGTCTCCT ACCGTCCATGCCAAATTAGAATTCAGCCTGCCTCCTGACTTCAAGTCCAAAGTTCTTCCAC GCACTAAAGCTAGCTCTTCAAGTGCTCTTTCTTAGGAGGTACTTCTCCCGCACCAGTACCG CCCCCTCTCTATTTACCCCCAGCCATCCGGAAGGCCAGCGGGACCTGTATTCTGGCCTG AATCAGAGACGCATCtccggatccggagagggcaggggatctctcttactgtggcgacgtggaggagAACCC cggccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTCCCATCTGGTCGAG CTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGC CACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGG CCCACCCTCGTGACCACCCTGACCTACGGCGTGCAAGTCTCAGCCGCTACCCCGACCAAT GAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATC TTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGAGGTGAAGTTCGAGGGCGACACC CTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGG CACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGA ACGGCATCAAGGTGAAGTTCAGATCCGCCACAACATCGAGGACGGCAGCGTGACGCTCG CCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCA CTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTC CTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGGACGAGCTGTACAAtgattg tttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaaataaagcattttttcactgattcta gttgtggtttgtccaaactcatcaatgtatcttatTGACCCTCTGGAGAAGCTGCCTCCGCTGGCCAG GTCTCCTCTCCAGTCCCCCTGCGACTCCTGTTTCTGGGCTAGTCTTGGACCCACGAGAG AGATCGTTCTCAGCCTCATGGTGAAGTTCGCGCCCTCCAGCCTGATCCCCGCTCCTCCTC CCTGCCCTTCTGCTGGTACCCAGTCTTAAATATTGCTGCTTCTCTTCTTGAAGCATCAT CAGTAGTCACACCCTCACAGCTGGCCTGCCCTCTGCCAGGATATTTATTTGTGCTATTCACT CCCTTCCCTTTGGATGTAAGTCTCCGTTCAAGTTCCTCTCTTTCTTGCATGTAAGTTGTCCCC CATCCCAAAGTATTCCATCTACTTTCTATCGCCGTCCCCCTTTGAGCCCTCTCTGGGGATG GACTGGGTAAATGTTGACAGAGGCCCTGCCCGTT</p>	1806
pARBI- 917: CD3E_2_	<p>AATAATAAAATAATAACAATACTTAACATTTATTGAGTGCTTATTAAGTCTCAAGCACTGTCT GTACCCAACTATTACAGGATTCTTTTTCATGTAATCCTCTCAACAATATATGGGTTAAGT ATCATTTTATCCCATGAGTAAAGGGATGAGGAAACAGAGGGTTTGTGAGTTGAAAACACA</p>	1806

Endogeno us_17_18	<p>TTTCACGCTTCTCACAGCTAGTGAGTAATAAAGCTGGGACTCAAACCCAGGGCTGTTTGACT CCAGTGCCTCTACCCACGGCCACCACTCTTTGCTTGTCATGTTGTTCTAAACATATTGAAGG GGGGGCTCTGACCGTGGCAAGCGTGTGAGTAGTAAGGGGAGAATGGCCTTCATGCACTCC CTCCTCACCTCCAGCGCCTTGTGTTTTCTTGCTTAGTGATTTCCCTCTCCCCACCCACCCC CCACAGTGTGTGAGtccggatccggagagggcaggggatctctcttacttggcgacgtggaggagaaccccg gccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGGTCGAGCT GGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCA CCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCC CACCTCGTGACCACCTGACCTACGGCGTGCACTGCTTCAGCCGCTACCCCGACCACATGA AGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTT CTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCT GGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGGGCA CAAGCTGGAGTACAACACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAAC GGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCC GACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACCACT ACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCT GCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgttt attgcagcttataatggttacaaataaagcaatagcatcacaatttcacaataaagcattttttcactgcattctagtt gtggtttgtccaaactcatcaatgtatcttatAAGTGCATGGAGATGGATGTGATGTCGGTGGCCACAA TTGTCATAGTGGACATCTGCATCACTGCGGGGCTTGCTGCTGCTGGTTTACTACTGGAGCAA GAATAGAAAGGCCAAGGCCAAGCCTGTGACACGAGGAGCGGGTGTGGCGGCAGGCAAA GGGGTAAGGCTGTGGAGTCCAGTCAGAGGAGATTCTGCCAAGGGGGACGACCAGCCTG GGCCAGGGTGGGTGGCAAGTCCACAGCTAGGTGAGAACAGCTTCTCTAGAGCTTCTATGCA CAGCTTCTATTACTGTGATGACAAGATCTCAACAGACGGTTTCAAATCTCACATCACTCCCT CCTTCCCATCTAGAAAAGTGCAAAAAGTTTATGAAAGTGATGGGCTTCTCACATACCTG TCAATGCCTGCAGTCATCCGATTCCGCCCTAAGCTGTGGGAAGAGAG</p>	
pARBI- 918: CD3G_1_ Endogeno us_19_20	<p>ACTGTGACCCATGAACCAGTAGGTATTGGCGTCACCTGGGATCCTGACGTTAGTCTCTGTCA ATCCTTCTCTTTAGTTCATCTATTCTACCCAAAGTGATCTCATCATCTGGTATGCTGTAGCAG TTTTCTTACCTGTATAGTATCTTCCAAATAACATGCCCAAAATCCCAAAGTTTTACCCCTACTA ATTACAGCAATGTCTCTTTTATTCTTACCCCTGACGCAGATATTGGCGTCACCCGAGAGC ATGTTAGTAATGCAGAATCTCCCTCCCCAGAACTACTAAATAGCACCTGAAATTTTAAACA GATCCCCATGTGATTATGTGCACATCAAAGTTTGAGAAACACTACTCTAATGATCTCCTGG TATGCAGAAGCAGGGAGAATTTAGAGGCAAGATCCTTAATAGAACCACGGCTTTTCTCAT TTCAGGAAACCACTcggatccggagagggcaggggatctctcttacttggcgacgtggaggagaaccccg ccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGGTCGAGCTG GACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCAC CTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCC ACCCTCGTGACCACCTGACCTACGGCGTGCACTGCTTCAGCCGCTACCCCGACCACATGAA GCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCT TCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGG TGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGGGCACA AGCTGGAGTACAACACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACG GCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCG ACCACTACCAGCAGAACAACCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACCACTA CCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTG CTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgttta ttgcagcttataatggttacaaataaagcaatagcatcacaatttcacaataaagcattttttcactgcattctagttg tggtttgtccaaactcatcaatgtatcttatTTGGTTAAGGTGTATGACTATCAAGAAGATGGTTCGGTA CTTCTGACTTGTGATGCAGAAGCCAAAAATATCACATGGTTTAAAGATGGGAAGATGATCG GCTTCTAACTGAAGTaaaaaaaTGGAATCTGGGAAGTAATGCCAAGGACCTCGAGGG ATGTATCAGTGTAAGGATCACAGAACAAGTCAAAACCACTCCAAGTGATTACAGAAGTA TGTAATCCCTTTGGTCTGTTGTGTGAAATTAATCAGTATTTGCTGTTCTGGTGAGCTTTT TATCTGGGGTGAAAGTGGAATAGATCCTCAACAGTAATATTATCGCCTGTTCTTAATTT CAGCTTGCCTCTTTTAAATACTGTAAGATACTCCCTCACCCTATTGAAAACTACAGCCAG TCCTGTAAAATTTGTTTACCTTTGGGTGGGCTCCATGG</p>	1806

pARBI-919: CD3G_3_ Endogeno us_21	<p>TTCGAGACAAGCCTGGCCAACATGATGAACTCTGTCTCTACTAAAAATACAAAAAAATTA ACCAGGCGTGGAGGCGCGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGGA CCACTTGAACCCAGGAGGTGCGAGTTGTCAGTGAGCTGCGATTGTGCCACTGCACTCCAGCC TGGGCAACAGAGAAAAGACTCCGTCTCAAAAAAAAAAAGAGAGAGAGAGAAAAAGAAAA AAGACAGAGCCTCCATCTCCTTGCTCTTTCCATCCTCAGGACCATGAAGTACCCACTCCAA ATTCTCACATATAAAAAACATTCAATAAACATGCATCAAATTAATTAATAGAGGATGGAAAA AATGACTTATGACTGTGCTGTCTTTCCAGCCCCCTCAAGGATCGAGAAGATGACCAGTACAG CCACCTTCAAGGAAACCAAGTTGtccggatccggagagggcaggggatctctcttacttggcgacgtggag gagaaccccgccccATGGTGAGCAAGGCGGAGGAGCTGTTACCGGGGTGGTGCCCATCTGT GTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGG CGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCGTG CCCTGGCCACCCCTCGTGACCACCCTGACCTACGGCGTGCACTGCTTACGCCGTACCCCGA CCACATGAAGCAGCACGACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGC ACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGC GACACCTGTGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATC CTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCTATATCATGGCCGACAAGC AGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGC AGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCGTGTCTGCTGCCGA CAACCATACTGAGCACCCAGTCCAAGCTGAGCAAGACCCCAACGAGAAGCGCATAC ATGGTCTGTGAGTTCGTGACCGCCGCGGGATCACTCTCGGCATGGACGAGCTGTACA Aatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattttttcact gcattctagttgtggtttgtccaaactcatcaatgtatcttatAGGAGGAATTGAACCTCAGGACTCAGAGTA GGTGGGTTCTTCAATGCCAATTCTAATAAAGGACCCTTGTCATCAACTGCCCTCGCAATTGCT TCTAAGTCTAGCTCCCTTCCCTAAGCGGCTATAAGCATCAGACTCTGGGGATCAGGGATTG GGACGTGGTTTGGGGTACTCTTTCTAAAAATCTGGGGCCATACTGATTGTCTTGGCCTAG GTAAATATGAATTTTATGTATCTGTAAATCCTGTGAGAGCAGGGCCTCAAGCCATAGAGATG CTGAATATTAATCTTAACCTACATTTGAATTTCTCATTATCTACACTATTAACATTTTGGGCTA ATTAATTATTTGTGATGAGGGGCTAGCCTGTGCATTGTAGGAGTTAGGAAGCATCCCTGG CCTCTCTCCACCAGATGCTGGTAGATTGTCCAGTGTGACAATCAAAAAAT</p>	1806
pARBI-920: CD5_1_E ndogeno us_22	<p>GACCTCAGGTGATCTGCCGCTCAGCTTCCCAAAGTCTGGGATTACAGGCATGAGCCAC CACACCTGGCCTAAAATTAATTTTTAAAGATCTCTTAAAAAGCAGACACCAGCCCAATCTC AGACCCCTTGAGACAGAATTTCCAGGACAGGGGCCATCCTGCTGGACAGTGGGTGCCGAG AACACCTTGCCATTTATCTGAGCTCCCTTCTGACTCTGAAATCTGGAGCCCCACCTCCTGG GTCTAGCTTCGGGGCTGCCTGGGTGAGGGTCTCTGGGAAGCCCCTGCAGTGCCCCAGAAG GGACGAAGCTCACAAGGGGCAAGGCAGGCAGCCACGGGGCAGGAGGGAGCTCAACTGG GCGTCTAGGGAGAGGGCAGTGAGGGGTGCCAGTGGGGAACCCCTCCCAGCCTGACCCCC ACCACACCTTTCTGACCCCAAGTtccggatccggagagggcaggggatctctcttacttggcgacgtgg aggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCC TGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAG GGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCCG TGCCCTGGCCACCCCTCGTGACCACCCTGACCTACGGCGTGCACTGCTTACGCCGTACCCC GACCACATGAAGCAGCACGACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGC GCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGG GCGACACCCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACA TCCTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCTATATCATGGCCGACAA GCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGT GCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCGTGTCTGCTGCC GACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAGACCCCAACGAGAAGCGCGAT CACATGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTCGGCATGGACGAGCTGT ACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcatttttt cactgcattctagttgtggtttgtccaaactcatcaatgtatcttatTCCAGGCAAGGCTCACCCGTTCCAAC TCGAAGTGCCAGGGCCAGCTGGAGGTCTACCTCAAGGACGGATGGCACATGGTTTGCAGC CAGAGCTGGGGCCGAGCTCCAAGCAGTGGGAGGACCCAGTCAAGCGTCAAAAGTCTGC CAGCGGTGAACCTGTGGGGTGCCCTTAAGCCTTGGCCCCCTTCTGTACCTACACACCTCA GAGCTCAATCATCTGCTACGGACAACCTGGGCTCCTTCTCCAACCTGCAGCCACAGCAGAAAT</p>	1806

	GACATGTGTCACCTCTCTGGGCTGACCTGCTTAGGTGGGTAAGTACGCCAGCCACACGGGCA CCCTGGGCTGGGCGCCAGCCCCGAGGAGACTGCCGAGGCTGTGATCTAGGGTCTGAG CAGGCTGGTGGAAGGGGTGGGGGACCCAGTTTATAACCACTCCCAAGACACATACC	
pARBI- 921: CD5_2_E ndogeno us_23	GGACAGGGGCCATCTGCTGGACAGTGGGTGCCGAGAACACCTTGCCATTATCTGAGCT CCCTTCTGACTCTGAAATCTGGAGCCCCACCCTCTGGGTCTAGCTTCGGGGTGCCTGGGT CAGGGTCTCTGGGAAGCCCTGCACTGCCCGAGAGGGACGAAAGCTCACAAGGGGCAAG GCAGGCAGCCACGGGGCAGGAGGGAGCTCAACTGGGCGTCTAGGGAGAGGGCAGTGA GGGGTGCCAGTGGGGAACCCCTCCAGCCTGACCCCCACCACACCTTTCTGACCCCCAGATT TCCAGGCAAGGCTCACCCGTTCCAATCGAAGTGCCAGGGCCAGCTGGAGGTCTACCTCAA GGACGGATGGCACATGGTTTGAGCCAGAGCTGGGGCCGAGCTCCAAGCAGTGGGAGG ACCCAGTCAAGCGTCAAAAGTCTGCTcggatccggagagggcaggggatctctccttactgtgacg tggaggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCAT CCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGA GGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACGGCAAGCTGCCC GTGCCCTGGCCACCCCTCGTGACCACCTGACCTACGCGTGCAGTGCTTCAGCCGCTACCC CGACCACATGAAGCAGCAGACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAG CGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGG CCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACA TCTGGGGCAACAAGCTGGAGTCAACTACAACGCCACAACGTCTATATCATGGCCGACAA GCAGAAAGAACGGCATCAAGGTGAAGTCAAGATCCGCCACAACATCGAGGACGGCGCT GCAGCTCGCCGACCACTACCAGCAGAACCCCCATCGGCGACGGCCCCGTGCTGCTGCC GACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGGAT CACATGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTCGGCATGGACGAGCTGT ACAAtgattgtttattgagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattttt cactgcattctagttgtgtgttgcctcaactcatcaatgtatcttatCAGCGGTGAAGTGTGGGTGCCCTTA AGCCTTGGCCCTTCTTGTACCTACACACCTCAGAGCTCAATCATCTGCTACGGACAAC GGGCTCCTTCTCAACTGCAGCCACAGCAGAAATGACATGTGTACTCTCTGGGCTGACCT GCTTAGGTGGGTAAGTACCCAGCCACAGGGCACCCCTGGGCGCCAGCCCCGAGG AGACTGCCCGAGCGCTGTGATCTAGGGTCTGAGCAGGCTGGTGGAAGGGGTGGGGGAC CCAGTTTATAACCACTCCCAAGACACATACCCAGGAGGGGGACTGGAAGGGGCCAGCA CCCATCTGTAGGATGGCAATGGAGGACCTAGTTCTGCCAATCACTGACTTCATCGTCGCTC TGAACCTCCATTCTCCCATCTGTGAAGTGGGGTGGTACTTCCCGCTCGCAGGAGGCT	1806
pARBI- 922: CD5_3_E ndogeno us_24	tgctgggattacagcatgagccaccacactggcctaaaattttaaagaTCTTTAAAAGCAGACAC CAGCCCCAATCTCAGACCCCTTGAGACAGAAATTTCCAGGACAGGGGCCATCTGCTGGACA GTGGGTGCCGAGAACACCTTGCCATTATCTGAGCTCCCTTCTGACTCTGAAATCTGGAGC CCCACCCTCTGGGTCTAGCTTCGGGGCTGCTGGGTGAGGGTCTCTGGGAAGCCCTGC AGTGCCCCAGAAAGGACGAAGCTACAAGGGGCAAGGCAGGCAGCCACGGGGCAGGAG GGAGCTCAACTGGGCGTCTAGGGAGAGGGCAGTGAGGGGTGCCAGTGGGGAACCCCTC CCAGCTGACCCCAACACCTTTCTGACCCCCAGATTTCCAGGCAAGGCTACCCGTTCC AACTCGAAGTGCTcggatccggagagggcaggggatctctccttactgtgacgacgtggaggagaacccggc cccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGGTCGAGCTG GACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCAC CTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACGGCAAGCTGCCCGTGCCTGGCCC ACCCTCGTGACCACCTGACCTACGCGTGCAGTGCTTCAGCCGCTACCCGACCATGAA GCAGCAGACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCT TCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCCTGG TGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGGGCACA AGCTGGAGTACAATAACAAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAAGC GCATCAAGGTGAAGTTCAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCG ACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAACCACTA CCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGGATCACATGGTCTCTG CTGGAGTTCGTGACCGCCGCGGGATCACTCTCGGCATGGACGAGCTGTACAAtgattgttta ttgagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcatttttctgctcattctagttg tggtttgtcctcaactcatcaatgtatcttatCAGGGCCAGCTGGAGGTCTACCTCAAGGACGGATGGCA CATGGTTTGAGCCAGAGCTGGGGCCGAGCTCCAAGCAGTGGGAGGACCCAGTCAAGC	1806

	GTCAAAAGTCTGCCAGCGGCTGAACTGTGGGGTGCCCTTAAGCCTTGCCCCCTCCTTGTCACCTACACACCTCAGAGCTCAATCATCTGCTACGGACAACCTGGGCTCCTTCTCCAATGCGAGCACAGCAGAAATGACATGTGTACTCTCTGGGCCTGACCTGCTTAGGTGGGTAACTAGCCAGCCACACGCGGCACCTGGGCCTGGGCGCCAGCCCCGAGGAGACTGCCCCAGGCCTGTGATCTAGGTCTGAGCAGGCTGGTGGAAGGGTGGGGGGACCCAGTTTATAACCACTCCCCAAGACACATAACCCAGGAGGGGACTGGAAGGGGCCAGACCCATCTGT	
pARBI-923: EDF1_1_E ndogeno us_25	GGGGGCGGCCGACGGCTAGAGCGGAGACCCGCGCCCCCTCCGCCCGCTGGCCCCGGCCGGGGTGCGGGGCCCCGGGGAGGCACGGGGGCTGCGCGTCGGGGGCGAGCCGCCGCCGCGGTGTGTCTGGAGGCCGCGGGGCCGGGCTCCGGGGTCTCCCGACCTGCAGCCCCAGCGGCTACCGCGCCTCGCCAGGCCAGGCCAGGCCCGACGTGCGCTTCCCTACGTGCGCCGCGCCCGGCCACGACGTCCCTCAGACGAGCCGAACGCCGAATGGCCCCGAGCACGGGAAGTGCCGCCCCCCGCTGCAGCCAGCCAATGGGACGCCGAAAGCGGGGAGGTGCCGAGGGGACGTAGCGTCGCGCGCCAGGTCTCTAGCAGCTGCCGCTGAGCCGCCGACGGACGCTCGTCTTCGCCCGCATGGCCGAGAGCGACTGGGACACGtccggatccggagagggcaggggatctctcttacttgtggcgacgtggagggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCGTACCCCGACCATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGACGCGACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCTATATCATGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTTCAGATCCGCCACAACATCGAGGACGGCAGCGTGACGTGCGCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGTGTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAAGCGGATCACATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattttttcactgcattctagtgtgtgtgttgcctaaactcatcaatgtatcttatGTACGGTGCTGCGCAAGAAGGGCCCTACGGCCGCCAGGCCAAATCCAAGCAGGTGCTTTGCTGACTGAGGACGCGCCGGGCCGGGCGGGCGGACGCTgggcccggggccacggaccgtggggcagggggctcggggaagggcagggcggggcctgggacagggcgagggggacggggacaaggctggGGTGCCGGGGGCGAGGACGGGGTTCGAAAGGGCGGGCGAATCGCAGGGGTAGGAGGACCGGGCCAGGACaggggtgggaaggtggggggcggaaccagggggatggacggacccagggagggcggggCGGGCGACTGGAGGAGGAGAGGAGCAGGGAACCGGACGGGGCAAGGGGCGAGCGATAGGGCCGGGACCAAGTGCAGGGTGGGCGCGGGAGGGGATAGGGGCGAGGACTGTTGGTGGGGACAGGTGTGAGGACAG	1806
pARBI-924: EDF1_2_E ndogeno us_26	ACGGCTAGAGCGGAGACCCCGCGCCCCCTCCGCCCGCTGGCCCCGCCGGGGTGGGGGCCCCGGGAGGCACGGGGGCTGCGCGTCGGGGGCGAGCCGCCGCCCGCTGTGCTCGGAGGCCGCGGGGCCCGGGTCCCGGGTCTCCCGACCTGCAGCCCCAGCGGCTACCGCGCTCCGCAGGCCAGGCCAGGCCCGGACGTGCGCTTCCCTACGTGCGCGCGCCCGGCCACGACGTCCCTCAGACGAGCCGAACGCCGAATGGCCCCGAGCACGGGAAGTGCCCGCCCCCGCGTGCAGCCAGCCAATGGGACGCCGAAAGCGGGGAGGTGCCGAGGGGACGTAGCGTCGCCGCGCCAGGTCTCTAGCAGCTGCCGCTGAGCCGCCGACGGACGCTCGTCTTCGCCCGCCATGGCCGAGAGCGACTGGGACACGGTGACGGTGCTGtccggatccggagagggcaggggatctctcttacttgtggcgacgtggagggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCATCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAAGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTTCAGATCCGCCACAACATCGAGGACGGCAGCGTGACGTGCGCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCATATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGGACGAG	1806

	CTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaaataaagca ttttttcactgcattctagttgtgtttgtccaaactcatcaatgtatcttatCGCAAGAAGGGCCCTACGGCCG CCCAGGCCAAATCCAAGCAGGTGCTTTGCTGACTGAGGAGCGGCCGGCCGGCGGGGCGGGGCG GGACGCTgggcccggggccacggaccgtggggcagggggctcggggaagggcaggcggggcctgggacagggcg aggggacgggacaaggctggGTGCGGGGGCAGGACGGGGTTCGAAGGGCGGGCGGAATCG CAGGGGTAGGAGGACCGGGCCAGGACaggggtgggaaggtggggggcggaccagggagggatggac ggaccagggaggcagggggCGGGCGACTGGAGGAGGAGAGGAGCAGGGAACCGGACGGGGCA AGGGGACAGGCATAGGGCCGGGACCAGTGCCAGGGTGGGGCGGGGAGGGGATAGGGG CAGGGAAGTGTGGTGGGGACAGGTGTGAGGACAGAGGCAGGAGGTG	
pARBI- 925: EDF1_3_E ndogeno us_27	CCCTGGAGTCGGTGTGAGGCAAAAGCAGAGGAGAGGATTTGGAATTAACCTGAAGAAAAA CCATTTCAAAGCGGTAACCAGACCCAGAGGCTGCCTGAACTCAAGGGGACATGGGAACC CAGGCTGTCCCAAGTTCACACACCTCAGGCTCGTGGACTTCCAGAGTTTTCTCTCAGTTATGA GGACAGGCAGCTGTACTCATGCCAACAGAGCTGCTCTGGGAAGATGGCTGCCTCCAGG GCTCCGGCCAGCACCGGTGCAGGCAGGCACTCAGCTGACAACGTCCCGGGGGCGCCGCA CACACCACACCCACAGCACATGACCCACAGCACAGCCTCATGTTGCAAGCGGAAACAC AAGTACCTACATTTCTTGGAGTCTCCACATCTTCTCTCTCTGTGCCGTAAGATAGCC TAGAAAATTAGAAAACATCAGTGTcgggatccggagagggcaggggatctctcttacttgtggcgacgtg gaggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCATCC TGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAG GGCGATGCCACCTACGGCAAGCTGACCCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCG TGCCCTGGCCACCCCTCGTGACCACCTGACCTACGGCGTGCACTGCTTACGCCGCTACCCC GACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGC GCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGG GCGACACCTGTGTAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACA TCCTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCTATATCATGGCCGACAA GCAGAAAGAACGGCATCAAGGTGAATTCAGATCCGCCACAACATCGAGGACGGCAGCGT GCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGGCAGCGGCCCGTGTCTGTGCCC GACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGAT CACATGGTCTGTGGAGTTCTGTGACCCCGCCGGGATCACTCTCGGCATGGACGAGCTGT ACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaaataaagcatttttt cactgcattctagttgtgtttgtccaaactcatcaatgtatcttatTTTCTAAAGAGAAGATGTGCTTTATAC ACATCAGCTCCACTAGGACTGCTGCAAAACCAGGCGCGAAGCGTCGCCTGAGAACAGCAG CTTCTAGGGCCCTGGGTACGCACCCACACGAGCTGGGTTTTGTGCGAGAGGCAGTGA GAGCCGGGCTGACCTGGCTTCCGAGGCATTCCCTGCAGGGGAACCAGGGGGGTGGAGCC CACCTCCCCGTGTATCTGAACACCGGCCATCCCCCTCCCAAACCCACAACCCAGGAGT GAGAGCCCCGGCGCAGCCTACCGTGGCCAGGTCTTCTGCGTAAGCCCCCTGTCTGTGCG ACCTTGCTGGATCACCTTGCCACCTCCAGGGTCACCTGTATGGTGCAGCTCCTGTCTC CCGGTCCAGCTTGGCCGTGTTCTTGGTAATAGAATGTTGTTTGTCTGGCCAGCAGC	1806
pARBI- 926: FTL_1_En dogenous _28_30	CTCTTGCTTCAACAGTGTTTGGACGGAACAGATCCGGGACTCTCTTCCAGCCTCCGACCGC CCTCCGATTTCTCTCCGCTTCAACCTCCGGGACCATCTTCTCGGCCATCTCTGCTTCTGG GACCTGCCAGCACCGTTTTTGTGGTTAGCTCCTTCTTGCCAACCAACCATGAGCTCCCAGATT CGTCAGAATTATTCACCGACGTGGAGGCAGCCGTCAACAGCCTGGTCAATTTGTACCTGC AGGCCTCTACACCTACCTCTCTGCTGAGTCCCAGGACGCCCCGGCCCTAATTTCTCC AGCTGCGCACCTCCGGCCCTCACTGCACGCGCCAGCCTTCTTGTGCGGTGCGGTAAACAG AGGGCGGAGTCCCCTTGGCTCGCTCCCGCTAACCATTGTTGCTCCATCTTCTCCGCTAG GGCTTCTATTTGACTcgggatccggagagggcaggggatctctcttacttgtggcgacgtggaggagaacccc ggccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGGTCCGAGC TGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCC ACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGC CCACCTCTGACCAACCTGACCTACGGCGTGCACTGCTTACGCCGCTACCCGACCACATG AAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCT TCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCC TGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGC ACAAGCTGGAGTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAA CGGCATCAAGGTGAATTCAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGC	1806

	CGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACCAC TACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCC TGCTGGAGTTCGTGACCGCCGCCGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgt ttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattttttcactgcattctag ttgtggtttgtccaaactcatcaatgtatcttatCGCGATGATGTGGCTCTGGAAGGCGTGAGCCACTTC TTCCGCGAATTGGCCGAGGAGAAGCGCGAGGGCTACGAGCGTCTCCTGAAGATGCAAAAC CAGCGTGGCGGCCGCGCTCTCTCCAGGACATCAAGGTAAGTGTGTGGGTAATGGACT ACATCTCCCAGCAGGCCGTGCGCGCGAGGAGCCTTGATTTGAGGGCGTAGGTGTGCGGTG GGCTTCTGGGAGATTGAGTTCGGTCTTGTGAGCCCTCTTAACCGCTGGAATAGAGGCGCA CCTCGTGCACTGCCCAACACGCGGCGAGTCCACACCGCTGCGTGGTCTTAGGGACGTATA GCTGTAAGAGCTAGGACAGGGTGCGGAGAGTGATAAATACAAGCTGCACATGTCTTTGT GGCCTGGGCTCTGACCCCCAACGACTCTGGGAAATGTAGGTTTAGTTCT	
pARBI- 927: FTL_2_En dogenous _29	TGGGGCGGGGGGCTGAGACTCCTATGTGCTCCGATTGGTCAGGCACGGCCTTCGGCCCC GCCTCTGCCACCGCAGATTGCGCGTAGCCCTCCCGAGCGCCTGCCTCCGAGGGCCGG CGCACCATAAAAGAAGCGCCCTAGCCACGTCCCTCGCAGTTCGGCGGTCCCGCGGGTCT GTCTCTTGCTTCAACAGTGTGGACGGAACAGATCCGGGGACTCTCTCCAGCCTCCGACC GCCCTCCGATTCTCTCCGCTTGCAACCTCCGGGACCATCTCTCGGCCATCTCTGTTCT GGGACCTGCCAGCACCCTTTTGTGGTAGCTCCTTCTTCCCAACCAACCATGAGCTCCCAG ATTGCTCAGAATTATTCACCGACGTGGAGGCAGCCGTCAACAGCCTGGTCAATTTGTACCT GCAGGCTCTACACCTACtccggatccggagagggcaggggatctctccttactgtggcgacgtggaggaga accccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCATCTGGTC GAGCTGGACGGCGACGTAACCGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGA TGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGCAAGCTGCCCCGTGCCCT GGCCACCCTCGTGACCACCTGACCTACGGCGTGCACTTCAAGCCTACCCCGACCA ATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGACCA TCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCGGAGGTGAAGTTCGAGGGCGACA CCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGG GGCACAAGCTGGAGTACAATAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAA GAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGAGCT CGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAAC CACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCATATG GTCCTGCTGGAGTTCGTGACCGCCGCCGGATCACTCTCGGCATGGACGAGCTGTACAAatg attgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattttttcactgcatt tctagttgtggtttgtccaaactcatcaatgtatcttatCTCTCTGTGTGAGTCCCCAGGACGCCCTGGC CCTAATTTCTCCAGCTGCGCACCTCCGGCCCTCACTGCACGCGCCAGCCTTCTTTGTGCGGT CGGGTAAACAGAGGGCGGAGTCCCCTTGGCCTCGCCTCCCGTAACCATTTGTCCTCCATC TCTTCCCGTAGGGCTTCTATTTGACCGCGATGATGTGGCTCTGGAAGGCGTGAGCACTTC TTCCGCGAATTGGCCGAGGAGAAGCGCGAGGGCTACGAGCGTCTCCTGAAGATGCAAAAC CAGCGTGGCGGCCGCGCTCTCTCCAGGACATCAAGGTAAGTGTGTGGGTAATGGACT ACATCTCCCAGCAGGCCGTGCGCGCGAGGAGCCTTGATTTGAGGGCGTAGGTGTGCGGTG GGCTTCTGGGAGATTGAGTTCGGTCTTGTGAGCCCTCTTAACCGCTGGA	1806
pARBI- 928: PTEN_1_ Endogeno us_31	CTTTGCATAGTTTATCCTATTAGTAATCTATTCTGTCTTTGGAATATGTTTTGTGATGATGAA ATAAATACTATAAATAGTATTATTCCTTTTGCAATTGAGAGTCTGACGAAATGTCCATGTGA CAGTTCATTTTGGGTTTAGCTCTACCTCTAATATGTGACCTATGCTACCACTCCGTATAGCGT AAATCCCAGAATATATCCTCCTGAATAAATGGGGGAAAATAATACCTGGCTTCCTTAATG ATTATATTAAGACTTATCAAGAGACTATTTTCTATTTAACAATTAGAAAGTTAAGCAATACA TTATTTTCTCTGGAATCCAGTGTTTCTTTAAATACCTGTTAAGTTGTATGCAACATTTCTA AAGTTACCTACTTGTTAATTAATAAATCAAGAGTTTTTTTTTCTTATTCTGAGGTTATCTTTT ACCACAGTTtccggatccggagagggcaggggatctctccttactgtggcgacgtggaggagaaccccgccccA TGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCATCTGGTCGAGCTGGACG GCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACG GCAAGCTGACCCTGAAGTTCATCTGCACCACCGCAAGCTGCCCCGTGCCCTGGCCACCCTC GTGACCACCTGACCTACGGCGTGCACTGCTTACGCCGTACCCCGACCATGAAGCAGC ACGACTTCTTAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAG GACGACGGCAACTACAAGACCCGCGCGGAGGTGAAGTTCGAGGGCGACACCCTGGTGAAC	1806

	CGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTG GAGTACAACACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCA AGGTGAACTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTA CCAGCAGAACACCCCATCGGCGACGGCCCGTGTCTGCTGCCGACAACCACTACCTGAGC ACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAG TTCTGTACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagctt ataatggttacaataaagcaatagcatcacaatttcacaataaagcattttttcactgcattctagttgtgtgttc caaaactcatcaatgtatcttatGCACAATATCCTTTTGAAGACCATAACCCACCACAGCTAGAACCTTA TCAAACCCCTTTTGTGAAGATCTTGACCAATGGCTAAGTGAAGATGACAATCATGTTCAGCA ATTCACTGTAAAGCTGGAAAGGGACGAACTGGTGAATGATATGTGCATATTATTACATC GGGGCAAATTTTAAAGGCACAAGAGGCCCTAGATTCTATGGGGAAGTAAGGACCAGAG ACAAAAAGGTAAGTTATTTTTGATGTTTTCTTCTCTTCTGGATCTGAGAATTTATTG GAAAACAGATTTTGGGTTCTTTTTCTTTCAGTTTTATTGAGGTGTAATTGACAAGTAAAA ATTATATATAAATACAATGTATAATATGATTTTTGATGTATGTATATACATTGTGAAATG ATTACTACAGTCAAACACTACTTAACATATTCAT	
pARBI- 929: PTEN_2_ Endogeno us_32	GCTACCACTCCGTATAGCGTAAATCCCAGAATATATCCTCCTGAATAAAATGGGGGAAAA TAATACCTGGCTTCCTTAATGATTATATTTAAGACTTATCAAGAGACTATTTTCTATTTAACA ATTAGAAAGTTAAGCAATACATTATTTTCTCTGGAATCCAGTGTTTCTTTTAAATACCTGTT AAGTTTGTATGCAACATTTCTAAAGTTACCTACTTGTAAATAAAAATTCAAGAGTTTTTTTT CTTATTCTGAGGTTATCTTTTTACCACAGTTGCACAATATCCTTTTTGAAGACCATAACCCACC ACAGCTAGAACTTATCAAACCCCTTTGTGAAGATCTTGACCAATGGCTAAGTGAAGATGACA ATCATGTTGCAGCAATTCAGTGTAAAGCTGGAAAGGGACGAACTGGTGAATGATATGTGC ATATTTATTACATccggatccggagagggcaggggatctctccttactgtggcgacgtggaggagaaccccgcc cccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCTGGTCGAGCTG GACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCAC CTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCC ACCTCTGTGACCACCTGACCTACGGCGTGCAGTGCTTACGCCGTACCCCGACCACATGAA GCAGCAGGACTTCTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATTCTT TCAAGGACGACGCAACTACAAGACCCCGCGCGAGGTGAAGTTTCGAGGGCGACACCCCTGG TGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACA AGCTGGAGTACAACACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACG GCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCG ACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACCACTA CCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTG CTGGAGTTCTGTACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgttta ttgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattttttcactgcattctagttg tggtttgtccaaactcatcaatgtatcttatCGGGGCAAATTTTAAAGGCACAAGAGGCCCTAGATTTC TATGGGGAAGTAAGGACCAGAGACAAAAAGGTAAGTTATTTTTGATGTTTTCTTCTTCTC TTCTGGATCTGAGAATTTATTGAAAAACAGATTTTGGGTTCTTTTTTCTTTCAGTTTTATT GAGGTGTAATTGACAAGTAAAAATTATATATAAATACAATGTATAATATGATGTTTTGATGT ATGTGTATATACATTGTGAAATGATTACTACAGTCAAACACTTAAACATATTCATCACCTCAC ATAATTATTATTCTCCCCCAGGGTGAAAGCATTTAAGATCTACAAGCTACAATTTTCAATTA TACAATGTTATTATTAAGTATAGTCACTATGCTGTCCAGTAGAGCTTCAGATCTTGTTTCATCT TGTGTTCTCTCCCTCCCCACCCTCAGTCCCTGGAA	1806
pARBI- 930: PTEN_3_ Endogeno us_33	ATAAATAGTATTATTCCTTTTGCATTGAGAGTCTGACGAAATGTCCATGTGACAGTTCATTT TGGGTTTAGCTCTACCTCTAATATGTGACCTATGCTACCAGTCCGTATAGCGTAAATCCCA GAATATATCCTCCTGAATAAAATGGGGGAAAAATAATACCTGGCTTCCTTAATGATTATATT AAGACTTATCAAGAGACTATTTTCTATTTAACAATTAGAAAAGTTAAGCAATACATTATTTTTCT TCTGGAATCCAGTGTTTCTTTTAAATACCTGTTAAGTTGTATGCAACATTTCTAAAGTTACC TACTTGTTAATTAATAAATCAAGAGTTTTTTTTCTTATTCTGAGGTTATCTTTTACCACAGT TGCACAATATCCTTTTGAAGACCATAACCCACCACAGCTAGAACCTTATCAAACCCCTTTTGTGA AGATCTTGACccggatccggagagggcaggggatctctccttactgtggcgacgtggaggagaaccccgcccc ATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCTGGTCGAGCTGGAC GGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTAC GGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCACCC	1806

	TCGTGACCACCTGACCTACGGCGTGAGTGCTTCAGCCGCTACCCCGACCACATGAAGCA GCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTCA AGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGA ACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGC TGGAGTACAACACTACAAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCAT CAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCA CTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACCACTACCTG AGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCTG GAGTTCTGTGACCGCCGCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgttattgc agcttataatggttacaaataaagcaatagcatcacaaattcacaaataaagcattttttcactgcattctagtgtggt ttgtccaaactcatcaatgtatcttatCAATGGCTAAGTGAAGATGACAATCATGTTGCAGCAATTCAC TGTAAGCTGGAAAGGGACGAACCTGGTGAATGATATGTGCATATTTATTACATCGGGGCA AATTTTTAAAGGCACAAGAGGCCCTAGATTTCTATGGGGAAGTAAGGACCAGAGACAAAA AGGTAAGTTATTTTTGATGTTTTCTTTCTTCTTCTGATCTGAGAATTTATTGAAAAAC AGATTTTGGGTTTCTTTTTCTTCAAGTTTATTGAGGTGTAATTGACAAGTAAAAATTATA TATAAATACAATGTATAATATGATGTTTTGATGTATGTGTATATACATTGTGAAATGATTACT ACAGTCAAACCTAATACATATTCATCACCTCACATAATTATTATTCTCCCCCAGGGTGAAA GCATTTAAGATCTACAAGCTACAATTTTCAATTAT	
pARBI- 931: PTPN2_1 _Endogen ous_34	TAGTGACGGTATCAAGAGCAGCATCCAGGTTGACTTTCTTTGGGGCAGGACCTTGCTTGT GTCTTAACCTTGGTTCCTACccaagttgtctctctagctcctcaactctgaaagccacttgatatcttacacaatt cctttttgctgagaaaataaagtcagttttagtcatttacacaaaaatcctaactaacacaGACCTGTTTTTG AAATCAGGTAGATTGGAAGTCTTGGTTTACTTCTTATAAGCCCGTCCGCTGTCTGTCTTGTA ACATCCAGGAGCAGACTTAACAAGGCCTTCTGGAGCCTTGCTCTTTCTGTCTGCTTCCCTC ATCTGctctctctctctctctTACAGGGTCCACTTCTAACACATGCTGCCATTCTGGCTTATGG TTTGGCAGCAGAAGACCAAAGCAGTTGTATGCTGAACCGCtccggatccggagagggcaggggat ctctccttactgtggcgacgtggaggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTAC CGGGGTGGTGCCCATCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGT GTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCAC CACCGCAAGCTGCCCGTGCCCTGGCCACCCTCGTGACCAACCTGACCTACGGCGTGCGAG TGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGA AGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCC GAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTC AAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACTACAACAGCCACAACGTC TATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACA TCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACG GCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCC CAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTC GGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaa tttcacaaataaagcattttttcactgcattctagtgtgtttgtccaaactcatcaatgtatcttatATTGTGAGA AAGAATCGGTGAGTAATATTTAATATTTACAACCTAGTATACTGTATGTGATCATTAGCATA TAAAGATTTTCAATTTGGGGCCAATATTCATTCTTAGTTTTGGCCTTAATTGCTAAAGGCT AGCGGTCAAAGTGTCTGTCGGAAAACTCATGTATCCTTTTCTTTTCAAGTATTTTAA TAACAATTGCAGACCTTTCATCTCCAAGATAGAAATACAATGGAATAAATATGGACTAGCA GTGACATATAGATCTTTGGAATCCCTAGGAATCCTTATTGACCTATTGTCAATAAGTCCTCTT CCAGCTTTAAGATCTTGTACTGTTCTACTTCAGATTTCTTACTTTATTCTACATTTTCAATTTG CTGGTTTTAATGATGATGAAAAATTCCTAATCCACTTCTAATTAGATGTGGCAATGACATGC C	1806
pARBI- 932: PTPN2_2 _Endogen ous_35	CAGAATTTGAATATGATGTGGCTGACCATAGATACCTCCATTGCATTAATTCTGCTTCATAA AGTGTTTATGCTTGTGAGGTGTTGAATAGAGCCTAATTAGCAGTAAGTAAACAGATCT agagcacagacttggcatctgaaggaccttggtcaatgctgggactgccactactagctatgggatcttgggtgatt tttaacctttgaaagcctttcatccctcacagatataatggggaagaaaatcgttccattagtattgtgaggattaaatg attaattgatgtaacaatgtgctttcatagtacttggcatatcataagtcttcatGTTATTTTACGCTGGCTGG GAAGATAAGTTTTGCTGTGGAGAAATTTAAGAGGGATATTAATAATATTTTTGTTATTTTAA GGAAATTCGAAATGAGTCCCATGACtccggatccggagagggcaggggatctctccttacttggcgacgt ggaggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATC	1806

	<p>CTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGA GGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACGGCAAGCTGCCC GTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGAGTGCTTCAGCCGCTACCC CGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAG CGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGG GCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACA TCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATGGCCGACAA GCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGT GCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCGTGCTGCTGCCC GACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGAT CACATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGGACGAGCTGT ACAAatgattgtttatgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcatttttt cactgcattctagttgtgtttgttccaaactcatcaatgtatcttatTATCCTCATAGAGTGGCCAAGTTTCCA GAAAACAGAAATCGAAACAGATACAGAGATGTAAGCCCATGTAAGTACTTGTGGGTTTGTG TGATGTGTATTTTTGGTTTGTAGGAGGAGGATGTAGTGAAAAGGAGGGCTTGGGG TCAGTGTGATAAATACAGTAATTTTTCTATTTACGTAAGACACGTTCTTTAAGAATTTA AAGGTGTAGAATAGTGGAAGGAAAAATAATTACCCATAATTATTTTCATCCTTCAAACATAG GCACCATTATTTGGTGTATTTCCACAACCTGTTTTCTTATGCACAGTTTCTTTCTTTAA AATAATTGTAATTATAGATGTCTATATAATATCCATATGTATTTCTTTTCATATCATTCCATC CCTTTGTAAAGTTTGTCTTAAATAGTTATTGGTGTAGTTGGTTTTT</p>	
pARBI- 933: PTPN2_3 _Endogen ous_36	<p>ACCAGTTATCGTTTTGTAGGTAGACCAATCAATTCTTAGGTACCAAGAATCTGAATGATCCT TTTACTTTTAGGAAGGTAAGTACTTTATTCATTTAACTATGTTTACTCCTGGTCGATTTTTCAA GTCACAATGGCTAATGTGCTACAAACAGAAGTGCTTCCTTTCCAGCACTATAGTAATAAACA AGATTGCATTTTATACTCCTTACAAAAAAGTAGAGAATAGTTTAGGATTTGTCTCAACTCTA TTATGATGCTAATTCATTTTTCTATTTCTCTGTCTTTTTATAAATACCTAGAAATATTAATATG AAGATAAAACAGTAATTTTGAATGACAGTTGTGGTTTATCATTCTCTATTTTCAGATGATC ACAGTCGTGTTAACTGCAAAATGCTGAGAATGATTATATTAATGCCAGTTTAGTTGACATA GAAGAGGCAtcggatccggagagggcaggggatctctccttactgtggcgagtgaggagaaacccggcccc ATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCTGGTCGAGCTGGAC GGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTAC GGCAAGCTGACCCTGAAGTTCATCTGCACCACCGCAAGCTGCCCGTGCCTGGCCACCC TCGTGACCACCCTGACCTACGGCGTGAGTGCTTCAGCCGCTACCCGACCACATGAAGCA GCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCA AGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCTGGTGA ACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGC TGGAGTACAACATAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAAGGGCAT CAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGAGCTCGCCGACCA CTACCAGCAGAACACCCCATCGGCGACGCCCCGTGCTGCTGCCGACAACCACTACCTG AGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCTG GAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttatgc agcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattttttcactgcattctagttgtgt ttgtccaaactcatcaatgtatcttatCAAAGGAGTTACATCTTAACACAGGCAAGTAATACGATACC ACGCAATGTCTGAAATGATGTGTTTGTGCTTGTCTGCTTTAAATCATAGGTAAAAGTAT ATCTTGACTTCTTTGGAAATGAAATGGTATTTTCAAGTTTTTTCTGACGATGTAATGAATTAT GGACATTATAAGGTTTTGAAGCTTTGAGTATTTAAGATAAAAGGCAAGTATTTTTGATATT ACACGTTCTGTGAAGGAAATTTAGGAAATGGCTTAGGCCAGTTCTTTGGCAGATTGTG TTCCTTACATTATATCTGACACAGAGTGCTGCTTATGCTTCTTATGCTCTTTTCTCTTCCC ATACCCTGTGGCAAAACAGAGGCCCTGGACAGCTCTTCTGTAGCTCCCTGCTCGCATA TATCTTCAGAGAGTACACCAAGCCCTGGATGGTGT</p>	1806
pARBI- 934: PTPN6_1 _Endogen ous_37	<p>CCTGCTCAAGGGCCGAGGTGTCCACGGTAGCTTCTGGCTCGGCCAGTCGCAAGAACCAG GGTGACTTCTCGCTCTCCGTCAGGTAGGTGGGCCCCCGCAACCCCGGGCATTTTGGCCACT CTCTGTGCCATCAGGCCCTGAACCACTCATTCTGGTTCCCGTGCGAGTGCTGACTCCCC GTCTGTTCCCTTGGCCCCAACCCCACTCCCCATCCTGTCTGTGCCACCCATGCCATG TGTGCCCCACCCAGGACCTCAGCCGATCCCTGCCCTCCTGCTCTACTCTGCACCGACTG GCCTACCCGCTGGTGCCTCGAGGGTGGGGGATCAGGTGACCCATATTCGGATCCAGAAC</p>	1806

	TCAGGGGATTCTATGACCTGTATGGAGGGGAGAAGTTTGGGACTCTGACAGAGCTGGTG GAGTACTACACTCAGCAGTtccggatccggagagggcaggggatctctcttacttgtggcgacgtggaggagaa ccccggccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCTGGTCG AGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGAT GCCACCTACGCAAGCTGACCCTGAAGTTCATCTGCACCACCGCAAGCTGCCCCGTGCCCT GGCCCCACCTCGTGACCACCTGACCTACGGCGTGCAGTGCTTCAAGCCGTACCCCGACCA ATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCCCAAGGCTACGTCCAGGAGCGCACCA TCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACA CCCTGGTGAAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGG GGCACAAGCTGGAGTACAACACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAA GAACGGCATCAAGGTGAAGTTCAGATCCGCCACAACATCGAGGACGGCAGCGTGACGCT CGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAAC CACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCATATG GTCCTGCTGGAGTTCGTGACCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatg attgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaaataaagcattttttcactgcat tctagtgtggtttgtccaaactcatcaatgtatcttatCAGGGTGTCTGCAAGGACCGCGACGGCACCAT CATCCACCTCAAGTACCCGCTGAAGTGTCTCCGATCCCACTAGTGAGAGGTGAGGGTCCGC ACCCCGCCATTCCCAAGCAGGGATGAGCCGGCTCCCACTGACAGCCAGGGAGGCAG GGAGACTGGCAGCCGGCGCTGCCTACCCTCCATCCCTCCCTCCCTGCAACAGCTGGGGCT CTCAATGTCCCTCCTCCTGCTGTCTGGGACCTGGTGTCTCAGAGCCTAACCTACCACTT TCCACCTAACCCGAGGAAGCCACAGAAAGCTGCCTCGCCCTACTCCGGGAGCCCTGGCCG CTGCAACCCAGGTCCCACTGGAGACAGGGAGGCCACTGCTGGTGCCAGCATGTCGTGCA GGCCAGCTCTGTTGTAGAAAGCTCTTCTCCTCTGGAATCGAGCCTGCCT	
pARBI- 935: PTPN6_2 _Endogen ous_38	CTGGGTTCGAAGCCCGGTTAGAAGTCTGGAGGCTAGGATGGCTTGAACCTGGGAGGTGCA GGCTGCAGAGAGCTGTAACCGCGCCACTGCACTCCAGCCTGGGCAACAGAGCTCTGGAAG CTTGCCCTAGAGTCAGTCAAGGGCCCTAGGCCAGTGAGTAACAGCTCAGCGTCAGTTTCCT CATCTATAAAATGGGGTAATATCATACCTAGCTCTCAGCATGTTTGTGAGAGACCTAAATG AGGTGGTGGATTGGAAGCATGTAGCGCAGTGCCTGGCACACAGTAGGTGCTTGATTTCGG CCCCCTCTCTGTGAATGTCTGTCTGCTCAGCGCCTTCCCTGTGGCTGGGTCTTACCTTCCCTG ACGCTGCCTTCTCTAGGTGGTACCATGGCCACATGTCTGGCGGGCAGGCAGAGACGCTGCT GCAGGCCAAGGGCGAGCCCTGTtccggatccggagagggcaggggatctctcttacttgtggcgacgtgga ggagaacccccggccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCT GGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGG GCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCCGT GCCCTGGCCCCACCTCGTGACCACCTGACCTACGGCGTGCAGTGCTTCAAGCCGTACCCCG ACCACATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCCCAAGGCTACGTCCAGGAGCG CACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGC GACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATC CTGGGGCACAAGCTGAGTACAACACTACAACAGCCACAACGTCTATATCATGGCCGACAAGC AGAAGAACGGCATCAAGGTGAAGTTCAGATCCGCCACAACATCGAGGACGGCAGCGTGC AGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCCGA CAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCAC ATGGTCCTGTGAGTTCGTGACCGCCCGGGGATCACTCTGGCATGGACGAGCTGTACA Aatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaaataaagcattttttcact gcattctagtgtggtttgtccaaactcatcaatgtatcttatACGTTTCTGTGCGTGAGAGCCTCAGCCAG CCTGGAGACTTCGTGCTTTCTGTGCTCAGTGACCAGCCCAAGGCTGGCCAGGCTCCCCGCT CAGGGTCACCCACATCAAGGTCAAGTGTGCGAGGTAAGGCAGCCAGGCGGGGGAGCCTC TGCTGAGGCTCCTGTCTGTGACCACAGTGTGGGTGGCAGGGAGGGTCTGCCTGGGCTTGA ATTCAAGGCTGGGGACCCAGGGAGGGAGACTCAAGTCTGTGAATGGCCTAATTTGGCTC CCCCAGGGTGGACGCTACACAGTGGGTGGTTGGAGACCTCGACAGCCTACGGACCTG GTGGAGCATTTCAAGAAGACGGGGATTGAGGAGGCCTCAGGCGCCTTTGTCTACCTGCGG CAGGTACGGGTGGGCCAGCTGCCTCCCACTTCCCTGAGCTGTCCCCAGATGT	1806
pARBI- 936: PTPN6_3	TGTCACATATGTGCAATGCCATGCTCCTGAGCCTTTGATTGCAGACGTGTGGGAAGTGGGC CCCGTCCCCACCCAGTGCCACCTGCTGCTTCTTCCCTTGCTGTGCTCTAAACGAG AAGTACAAGTGAAGTCCCCCAAGGGGTGGCGCGCCTCTCCTGTCCCCGCCCTGCCGGC	1806

_Endogenous_39	<p>TGCCCCAGGCCAGTGGAGTGGCAGCCCCAGAAGTGGGACCACCGGGGGTGGTGAGGCGG CCCCGCACTGGGAGCTGCATCTGAGGCTTAGTCCCTGAGCTCTCTGCCTGCCAGACTAGCT GCACCTCCTCATTCCCTGCGCCCCCTTCTCTCCGAAGCCCCCAGGATGGTGAGGTAAGGG CCTGCCACCCACGGTAGACAGGAGGCAAGGGTGCCTGGTGCCACGGGACCCCTCCTCACT GCCCTGCCTGGGCGCCAGGtccggatccggagagggcaggggatctctcttacttggcgacgtggagg agaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGG TCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGC GATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGC CCTGGCCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGAC CAGATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCA CCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCG ACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCC TGGGGCACAAGCTGGAGTACAACACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCA GAAGAACGGCATCAAGGTGAAGTTCAGATCCGCCACAACATCGAGGACGGCAGCGTGCA GCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC AACCCTACCTGAGCAGCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACA TGGTCTGTGGAGTTCGTGACCGCCGCGGGGATCACTCTCGGCATGGACGAGCTGTACAA atgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattttttcactg cattctagttgtgtgttgcacaaactcatcaatgtatcttatTGGTTTCACCGAGACCTCAGTGGCTGGATG CAGAGACCTGCTCAAGGGCCGAGGTGTCCACGGTAGCTTCTGGCTCGGCCAGTCGCAA GAACAGGGTGACTTCTCGCTCTCCGTGAGGTAGGTGGGCCCCCGCAACCCGGGCATTT TGGCCACTCTCTTGTGCCATCCAGGCCCTGAACCACTATTCTGGTTCCTCGTGGCAGTGC TGACTCCCCGTCTGTTCCCTTGGCCCCAACCCCACTCCCATCCCTGTCTGTGCCACCC ATGCCCATGTGTGCCCCACCCAGGACCTCAGCCGATCCCTGCCCTCTGCTCTACTCTCTGC ACCGACTGGCCTCACCGCCTGGTGCCCTGCAGGGTGGGGGATCAGGTGACCCATATTCGG ATCCAGAAGTCAAGGGGATTTCTATGACCTGTATGGAGGGGAGAAGTTTG</p>	
pARBI-937: PTPRC_1_ Endogenous_40	<p>TCCTTAGCTAATGTTCTGTAGCTTGTCTTAGCTGTGTCTACATATTATATGTATCTGTAT GCATCAATATTTGTATATATGCATGCATATATGTATGTATATTTATGAATACATATACACA CCATATACATACACTTATGTATGGTGTGTGCATATGTATGTGTAGATATATGTACATACACA CTATAGTGGACTGGGAGTTAGTATACTGGGAGGAGCATACTTTAGGGTATGATTACAT ATTTATTTTGTCTTCTCCATTTTCCATTAATTAACAGGATTGACTACAGCAAAGATGCCCA GTGTTCCACTTTCAAGTGACCCCTTACCTACTCACACCACTGCATTCTACCCGCAAGCACCT TTGAAAGAGAAAATGACTTCTCAGAGACCACAACCTTCTTAGTCCAGACAATACTTCCACC CAAGTATCCCCGtccggatccggagagggcaggggatctctcttacttggcgacgtggaggagaaccccgcc ccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGGTGCAGCTGG ACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCT ACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCGTGCCCTGGCCAC CCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTACGCCGCTACCCGACCATGAAG CAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTT CAAGGACGACGGCAACTACAAGACCCGCGCGGAGGTGAAGTTCGAGGGCGACACCCTGGT GAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGGGCACA GCTGGAGTACAACACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAAGCG CATCAAGGTGAAGTTCAGATCCGCCACAACATCGAGGACGGCAGCGTGACGCTCGCCGAC CACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACCACTACC TGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCAGTGGTCTGTCT GGAGTTCGTGACCGCCGCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattg cagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattttttcactgcattctgtg gtttgtccaaactcatcaatgtatcttatGACTCTTTGGATAATGCTAGTGCTTTTAATACCAAGGTTG GCACACAAAAGTTGTTAACTTAAATATCAGGGAATGTCATTTAGAAAATTCTACAGTTATCA GTACAACTTGTCTTTAAATTATTTGCACAGTTTCTAAGTATGTATTTTATTCAAGTGCAGAA ATTGCAGGAAATTAGTATCTGTGAAATATAGATCGACTGAAGTAATTAATGCATGTTGTTAG GGAGTGGAGAGAGAAAAGAAGGGAAGCAAGATCTCCAAGGACAATCAGGAGGGGAAATT TGTTCTAGTATCTCTGATCTATACACTCGCCATGATTCTCCCGCTTGGCTTCCCGCCACCT GGACAGATGAGAAATTCCTAGTTTCAAGAGATTATCAGTTCTACTCTCTTGGAAAGGTGCTT AAATGGGAGTCTTCCCATTTCTTTGTTTCACTCTAGA</p>	1806

pARBI-938: PTPRC_2_ Endogeno us_41	AGGGAATTTTATATGTTGGTCATATTATATCCCTAGCATGTGGCATAATGTCTAGCACAAA ATAGGTGCTCAATTAATCATCATTATCTAAATAAATAATGCATTGGGAAAAAAGTTTCA AAAGTTTTTCAAAGTCTTTTGCAGGCTTGAATTAATCCCAATAGTGATCCTTTAGTCTGTT ATGTTTCTGATTTAGCCTGGGGATTCAAAAAATAAATAACATAATTTTATATATTTGGGCTT TGTAACATGTTACTAAGAGAGGAAATATAGTTTCATTAGGGTAAAAGCTACTGAAAATTG CCACTTGGTGAATGTTCTATCATAGACTTGAGGTACATATAAAAACTAATATATGTTTACAT TAATATGAATGAAATTTGAAATTTCTAAGAGATTTTGTCTTTCTTTGCAGGGCAAAGCCC AACACCTTCCCCCtccggatccggagagggcaggggatctcttacttgtggcgacgtggaggagaacccggc cccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGGTCGAGCTG GACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCAC CTACGGCAAGCTGACCTGAAGTTCATCTGCACCACGGCAAGCTGCCCCGTGCCCTGGCCC ACCCTCGTGACCACCTGACCTACGGCGTGCACTGCTTACGCCGTACCCCGACCACATGAA GCAGCAGGACTTCTTCAAGTCCGCCATGCCCCAAGGCTACGTCCAGGAGCGCACCATCTTCT TCAAGGACGACGCAACTACAAGACCCGCGCGAGGTGAAGTTCAGGGGCGACACCCTGG TGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGGGCACA AGCTGGAGTACAATAACAAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACG GCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCG ACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACCACTA CCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCAGATGGTCTCTG CTGGAGTTCGTGACCGCCGCGGGATCACTCTCGCATGGACGAGCTGTACAAatgattgttta ttgcagcttataatggttacaataaagcaatagcatcacaatttcacaaataaagcattttttcactgcatttagtg tggtttgtccaaactcatcaatgtatcttatACTGGTAAGAATTAATATTTATATTTTACTAATTTTATTT TCTTGTGCAAAGTTATATATTTAACTACAATTTTCTATTATTAACACTGAAATTTATTTTAA GGATAAATTTTATAATCATGAGTGATTCTTGACATTCATTGTTCTTAACTTTCTGCTTATAC GTTATAGAGTTTAATAACTACCTAAACATGTTATTAATTTGTATATATATTTTGTGTATAAA TAGTAACTTTTCCAACTTGACAGTAAATCACACAACAGGTTTCTACTCTCTTTAATATTTT AAGACTATAAAAAATGCATTTAAATTAGATAACAAAAATTTATAGTCTGAAAGCAGGTAA CAGCTGTCTATGTATGTTATAGATATGTAGATAACAGATTTGCATATGTCTATATTTCTTTAA GAGTATGTTGCTTTTTCAATGGTATGCA	1806
pARBI-939: PTPRC_3_ Endogeno us_42	CCTTTAGCACCATAAAGAACTAAATTTATTTAGATGTTTTATGAGAACATATCAAAAAGTA CTTTTCTGTCATCCAATACTTCCACAATAAATCATTAGTCTTGCTAATCTTCATCTGGCATA AAAATAATGACATCAACTTTCTTCATGTAATTTCCCACTTAATTCTTTACTAGGAGCAATAT CAATTCCTATATGACGTCATTGCCAGCACCTACCCTGCTCAGAATGGACAAGTAAAGAAAAA CAACCATCAAGAAGATAAAAATTGAATTTGATAATGAAGTGGACAAAGTAAAGCAGGATGCT AATTGTGTTAATCCACTTGGTGCCCCAGAAAAGCTCCCTGAAGCAAAGGAACAGGCTGAAG GTTCTGAACCCACGAGTGGCACTGAGGGGCCAGAACATTCTGTCAATGGTCTGCAAGTCC AGCTTTAAATCAAGGTtccggatccggagagggcaggggatctcttacttgtggcgacgtggaggagaacc cggccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGCTGGTCGAG CTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGC CACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCCGTGCCCTGG CCCACCTCGTGACCACCTGACCTACGGCGTGCACTGCTTACGCCGTACCCCGACCACAT GAAGCAGCAGGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATC TTCTTCAAGGACGACGCAACTACAAGACCCGCGCGAGGTGAAGTTCGAGGGCGACACC CTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGGG CACAAGCTGGAGTACAATAACAAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGA ACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCG CCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACCA CTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCAGATGGTCT CTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattg tttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaaataaagcattttttcactgcattcta gttggtgttgccaaactcatcaatgtatcttatTCATAGGAAAAGACATAAATGAGGAACTCCAAAC CTCCTGTTAGCTGTTATTTCTATTTTGTAGAAGTAGGAAGTGAATAAGGTATACAGTGGA TTAATTAATGCAGCGAACCAATATTTGTAGAAGGGTTATATTTTACTACTGTGGAAAAATA TTTAAGATAGTTTTGCCAGAACAGTTGTACAGACGTATGCTATTTTAAATTTTATCTCTT ATTCAGTAAAAACAACCTTTTGTAAATCGTTATGTGTATATGTATGTGTATGGGTGT	1806

	GTGTTTGTGTGAGAGACAGAGAAAGAGAGAGAATTCTTTCAAGTGAATCTAAAAGCTTTTG CTTTTCCTTTGTTTTATGAAGAAAAATACATTTTATATTAGAAGTTAACTTAGCTTGAA GGATCTGTTTTAAAAATCATAACTGTGTGCAGACTCAATA	
pARBI- 940: PTPRCAP _1_Endog enous_43	aaggaaaaaggcactgagtgctgggggtgctgggggtgggctgcagtgatagacatcagggtagaggttaaggtcag gttcagcctcactgggtgaagtttgagcacggtgagcaggccatgcagcccggggaggaggatgggaggaggt ggagctttccgggcagagggaacagccagtgcgaaaggccccaggcaggtggcttaatgcagctgttggggagggtgag tggtaggaggaggctggaggatgggggtgatctcacagggccagagcctggtgaccaaataaggccttgcccttt tctGCTTGGCTGTCCCAAGAGGATCCCAAAGAGAAAAAACGAAAGTGGTCTTGGTCACCCA GCCTGCCCCACACCAGGCCCCACCCAGGTGCTGAGCCCTCTGAGCCCTGCCTGTCTCCCA CAGGCTCTGCCCTGTcggatccggagaggcaggggatctctccttactgtggcgacgtggaggagaacccc ggccccATGGTGAGCAAGGCGAGGAGCTGTTACCGGGGTGGTGCCATCCTGGTCGAGC TGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCC ACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGCAAGCTGCCCGTGCCTGGC CCACCTCTGTGACCACCTGACCTACGGCGTGCAGTGCTTACGCCGTACCCCGACCACATG AAGCAGCACGACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCCACCATCT TCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCC TGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGC ACAAGCTGGAGTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAA CGGATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGC CGACCATACAGCAGAACACCCCATCGGCGACGCCCCGTGCTGCTGCCGACAACCCAC TACCTGAGCACCCAGTCCAAGCTGAGCAAGACCCCAACGAGAAGCGCGATCACATGGTCC TGCTGGAGTTCGTGACCGCCGCCGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgt ttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattttttcactgcattctag ttgtggtttgtccaaactcatcaatgtatcttatACCTTAGGGCTCGGGATGTGCTGGCCCTGCCAGGG GCCTTGGGCTCGGGTGGCAGCGCGGAGGACAGCGTGGGCTCCAGCTCTGTACCGTTGTCTc tgctgctgctgctgctcctactgctgGCCACTGGCCTAGCACTGGCCTGGCGCCGCCTCAGCCGTGAC TCAGGGGGCTACTACCACCCGGCCCGCTAGGTGCCGCGCTGTGGGGCCGCACGCGCGC CTGCTCTGGGCCAGCCCCCAGGTGCTGCTGCTGAGGCCGAGCTGAGCTGGGGTCCACA GACAATGACCTTGAAGCAGCAGGAGGATGAGCAGGACACAGACTATGACCAGTCCGGAT GGTGGCTGACGCTGACCTGGGGAAGGCGAGCAGCAATGTGGAGAGGCGTCCAGCCC AGAGCAGGTCCCCGTGCGGGCTGAGGAAGCCAGAGACAGTGAACG	1806
pARBI- 941: PTPRCAP _2_Endog enous_44	aaggtcaggttcagcctcactgggtgaagtttgagcacggtgagcaggccatgcagcccggggaggaggatggg aggaggtggagctttccgggcagagggaacagccagtgcgaaaggccccaggcaggtggcttaatgcagctgttgggg aggtagtggttagggaggaggctggaggatgggggtgatctcacagggccagagcctggtgaccaaataaggcct tgcccttttctGCTTGGCTGTCCCAAGAGGATCCCAAAGAGAAAAAACGAAAGTGGTCTTGGT CACCAGCCTGCCCCACACCAGGCCCCACCCAGGTGCTGAGCCCTCTGAGCCCTGCCTGT TCCCCACAGGCTCTGCCCTGACCTTAGGGCTCGGGATGTGCTGCGCCCTGCCAGGGGCCT CTGGGCTCGGGTGGCAGCGCGAGGACAGCtccggatccggagaggcaggggatctctccttactgtgg cgacgtggaggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGC CCATCCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCGGCGAGG GCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGCAAGCT GCCCCGTGCCCTGGCCACCTCGTGACCACCTGACCTACGGCGTGCAGTGCTTACGCCGT ACCCCGACCACATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCA GGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTC GAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGC AACATCCTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCTATATCATGGCCG ACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCA GCGTGCACTGCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGCCCCGTGCTGCT GCCCCACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAGACCCCAACGAGAAGCG CGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGATCACTCTCGGCATGGACGAG CTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagca ttttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatGTGGGTCCAGCTCTGTACCGT TGTCTgctgctgctgctgctcctactgctgGCCACTGGCCTAGCACTGGCCTGGCGCCGCCTCAGCC GTGACTCAGGGGGTACTACCACCCGGCCCGCTAGGTGCCGCGCTGTGGGGCCGCACGC GGCGCTGCTCTGGGCCAGCCCCCAGGTGCTGCTGCTGAGGCCGAGCTGAGCTGGGGT	1806

	CCACAGACAATGACCTTGAGCGACAGGAGGATGAGCAGGACACAGACTATGACCACGTGCGGATGGTGGCTGCAGGCTGACCTGGGGAAGGCGAGCAGCAATGTGGAGAGGCGTCCAGCCCAGAGCAGTCCCCGTGCGGGCTGAGGAAGCCAGAGACAGTACACGGAGGGCGACCTGGTCTCGGCTCCCCAGGACCAGCGAGCGCAGGGGGCAGTGCTGAGGCCCTGTGAGT	
pARBI-942: PTPRCAP_3_Endogenous_45	cagtgcgaaggccccaggcaggtggcttaatgcagctgttgggggaggtgagtggttagggaggaggctggaggatggggctgatctcacagggccagagcctggttgacaaataaggccttggccttttctGCTTGGCTGTCCCAAGAGGATCCCAAAGAGAAAAAACGAAAGTGGTCTTGGTCACCCAGCCTGCCCCACACCAGGCCCCACCCCAGGTGCTGAGCCCTCTGAGCCCTGCCTGTCTCCACAGGCTCTGCCCTGCACCTTAGGGCTCGGGATGCTGCTGGCCCTGCCAGGGGCCCTTGGGCTCGGTGGCAGCGCGGAGGACAGCGTGGGCTCCAGCTCTGTACCGTTGTCTgtctgtctgtctctactgtctGCCACTGGCCTAGCACTGGCTGGCGCCGCTCAGCCGTGACTCAGGGGGCTACTACtccggatccggagaggcaggggatctctcttactgtgacgacgtggaggagaaccccgcccccATGGTGAGCAAGGGCGAGGAGCTGTTACCCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGCCACAAGTTCAGCGTGTCCGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCACCGGAAGCTGCCCGTGCCCTGGCCCCACCCTCGTGACCACCTGACCTACGGGTGTCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCATATGGTCTGTGGAGTTCGTGACCGCCGCGGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaaataaagcatttttttactgcattctagtgtgtgtgttccaaactcatatgtatcttatCACCCGCCCCGCTAGGTGCCGCGCTGTGGGGCCGACGCGGCGCCTGCTCTGGGCCAGCCCCCAGGTTCGCTGGCTGCAGGCCGAGCTGAGCTGGGGTCCACAGACAATGACCTTGAGCGACAGGAGGATGAGCAGGACACAGACTATGACCACGTGCGGATGGTGGCCTGCAGGTGACCTGGGGAAGGCGAGCAGCAATGTGGAGAGGCGTCCAGCCAGAGCAGGTCCCCGTGCGGGCTGAGGAAGCCAGAGACAGTGACACGGAGGGCGACCTGGTCTCGGCTCCCCAGGACCAGCGAGCGCAGGGGGCAGTGCTGAGGCCCTGCTGAGTGACCTGCACGCCTTTGCTGGCAGCGCAGCTGGGATGACAGCGCCAGGGCAGCTGGGGGCCAGGGCCTCCATGTACCCGCACTGTAGAGGCCGGTCTTGGTGTCCCATCCC	1806
pARBI-943: RPS23_1_Endogenous_46	ATAGAGTAGGGCGGGGGATGCCATGGAGAGGCTCCATGGGGGAGGGCCGGGGGAAGCGCCGCTCCAGGAGGCACGTGGTCCGGCGCGGAAGGGGCCCATGAGGCGTGAGAGGCCGCCGAGGTTCGGGGTACCGAGGGACGCGAGGGAGGCCAGCGCTTCTCCCGGGCATTGAGCGGGGCCTCGTCTTCGGGAGAACACATTTCTCCGGAGCCCTTTCGAACGTTTATTAGTCGGTTACGGCAACTGAAGGCCAAATGTTTGGCCACAGGCCAATAAATAGTACGAGAGCCAATCGGCTTAAGGGTTTATTCCAGGTGAGGCGAGTGCTTAGAAGATGGGAAACACGTAGATGGCGTGTTTTTACGGAAGAACTAAAATATTTAATTTTATAGGCAAGTGCTGTGGACTTCGTACTGCTAGGAAGCTCCGTAGTCACCGACGAGACCAAGtccggatccggagaggcaggggatctctcttactgtgacgacgtggaggagaaccccgcccccATGGTGAGCAAGGGCGAGGAGCTGTTACCCGGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCCGTGCCCTGGCCACCCTCGTGACCACCTGACCTACGGCGTGCAAGTCTTACGCCGATACCCCGACCATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGCAACATCCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGGATCACATGGTCTGTGGAGTTCGTGACCGCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaaataaagc	1806

	<p>atctttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatAAGTGGCATGATAAACAGTATA AGAAAGCTCATTTGGGCACAGCCCTAAAGGCCAACCCCTTTGGAGGTGCTTCTCATGCAAA AGGAATCGTGCTGGAAAAAGTGAAGTCCATTGCTCCCGTCAAGTTTTAGTTTATTATAGGA ATTCGAGACATGAACCTACGAATCTTGTTTTGAAAGTAATTGCAGGTTTTGTGTAGTAGT ATTCATTTGGGCATTGTGGGGTAAAATTGCAAAGCGTTTGTCTATTTAAAAGTTGGTAAAA TTAGTTTTTGGGAATTAGGTAGTTAAGGTTTTAATTTAACGTTGGCCTGGAAGGAATTGGA GAAGATACTAGCAATGATGAAGTAAAGGACACAAACACCTTTACTGTGGGAGTTGTTATAA GTAAATGGCACGTGTCAGCTATTGAACCTTATCGACTTGATAAACTAAGGTGAAGAGA</p>	
<p>pARBI- 944: RPS23_2_ Endogeno us_47_48</p>	<p>CAAGCGGACTTGGGGTCTTGGGGACGGGCGGGCGGATGCGAATAGAGTAGGGCGGGG GATGCCATGGAGAGGCTCCATGGGGGAGGGCCGGGGAAGCGCCGCTCCAGGAGGCACGT GGTCCGGCGCGGAAGGGGCCATGAGGCGTGAGGCGCGGAGGTGCGGGTACCGAGG GACGCAGGGAGGCCAGCGCTTCTCCCGGCATTGAGCGGGGCTCGTCTTCGGGAGA ACACATTCTCCGAGCCCTCTTGAACGTTTATTAGTCGGTTCAGGGCAACTGAAGGCCAA ATGTTTGGCCACAGGCCAATAAATAGTACGAGAGCCAATCGGCTTAAGGGTTTATCCAG GTGAGGCGAGTGTCTTAGAAGATGGGAAACACGTAGATGGCGTGTTTTACGGAAGAACT AAAATATTTAATTTTAGGCAAGTCCGCGGAtccggatccggagagggcaggggatctctcttacttgt ggcgacgtggaggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGT GCCCCCTCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCGGCGCA GGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTTCTGACACCGGCA GCTGCCCGTGCCCTGGCCACCTCTGTGACCACCTGACCTACGGCGTGCAAGTTCAGCC GCTACCCCGACCATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGTACGT CCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGAGGTGAA GTTGAGGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA CGGCAACATCCTGGGGCAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATG GCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGAC GGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGC TGCTGCCCCACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAA GCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGGAC GAGCTGTACAAAtgattgtttattgcagcttataatgggtacaaataaagcaatagcatcacaaatttcacaaataa agcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatCTTCGTACTGTAGGAAGCT CCGTAGTCACCGACGAGACCAGAAGTGGCATGATAAACAGTATAAGAAAGCTCATTTGGG CACAGCCCTAAAGGCCAACCCCTTTGGAGGTGCTTCTCATGAAAAGGAATCGTGCTGGAA AAAGTGAAGTCCATTGCTCCCGTCAAGTTTTAGTTTATTATAGGAATTCGAGACATGAAC TACGAATCTTGTTTTGAAGTAATTGCAGGTTTTGTGTAGTAGTATTCAATTTGGGCATTGT GGGGTAAAATTGCAAAGCGTTTGTCTATTTAAAAGTTGGTAAAATTAGTTTTGGGAATTA GTAGTTAAGGTTTTAATTTAACGTTGGCCTGGAAGGAATTGGAGAAGATACTAGCAATGA TGAAGTAAAGGACACAAACACCTTTACTGTGGGAGTTGTTATAAGTAAATGGCACGTGTC</p>	1806
<p>pARBI- 945: RTRAF_1_ Endogeno us_49</p>	<p>TTGTATATCCTTTTAAAGTTATTCTTTTAGTTAATTGCTCTATGTGTATTGAGACTAGGAAT CAGAAAGCTTAGATTCTAGTCCAGGTGAAGTTGTGTAAACCTTGGCAAGTGTCATCTCT AGGCCTCAGCTTCTCATCTATAAAATGAGGAAGTTGTGCTATTCTATTTTTTTCTTAAGAT GATACACTTAAATGTTCCCTTCTGTTGGGTTATATAATTGCATCAAAAGTGTAGTAATGTTAT TAAAAAATTGTTAGAGATCCAACTAAGGTCTCTTCAACTCTCCATTCTTTTTCTGTGACT TTATGGTAATAATGAACTGGTGGTTTTCTTTCTTCCCTCACAGTATCTCAGAGATGTTA ACTGTCTTTCAAGATTCAAGATCGACAAGAAGCTATTGACTGGCTTCTTGTTAGCTGTT AGACTTGAAtccggatccggagagggcaggggatctctcttacttgtggcgacgtggaggagaaccccgccccA TGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCATCCTGGTCGAGCTGGACG GCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACG GCAAGCTGACCTGAAGTTTCTGTCACCAACCGCAAGCTGCCGTGCCCTGGCCACCTC GTGACCACCTGACCTACGGCGTGAGTGCTTACGCCGTACCCGACCATGAAGCAGC ACGACTTCTTCAAGTCCGCCATGCCGAAGGTACGTCCAGGAGCGACCATCTTCTTCAAG GACGACGGCAACTACAAGACCCGCGCGAGGTGAAGTTCGAGGGCGACACCTGGTGAAC CGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGACAAGCTG GAGTACAACCTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCA AGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGACGCTCGCCGACCACTA CCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGC</p>	1806

	<p> ACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAG TTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagctt ataatggttacaaataaagcaatagcatcacaaatttcacaaataaagcattttttcactgcattctagtgtgtgttc caaactcatcaatgtatcttatTATGGAGATAATGGTACGTTTTGTGGGAATGTGTATTTTAAAGA GAGAGGAAAGATGGGAAAGGGAGTGTGAAAATGTAGGGAACTTTGCACTTTGTTTTGTCT AGTACTATTTTACCTTTGGTTTATTCTTATCACAAAGTTAAAAGCACTTTTATTGTCTTTCATTG GTGTTTATATATTTCTGTTAGAAATTTGGAATGGTGCCCTCTGGAGAAGGCTAATTGACTGT CTCTCACAGAGTAACACTACTTTGATAATATGGTCTGCACCTAGCCTTTCAAATTAATTG TTTTAGTGTCCAGAATTGATGGGACTTTGAAGTGTGTTGCAGTAGGTAATTTCTCAAAA GACTGAAACATGTCTAATGCCAATATACATTAATACTCTATAGGCCAGAATATATTACTTAT GTTTACTGTCTTAGCACAGATACTTCTATGGT </p>	
<p> pARBI- 946: RTRAF_2_ Endogeno us_50 </p>	<p> GCACCTGTTATGTAGGAGGAGTAATAAAATGAATGAATGCACTCAAAACACTAAACAGTAA TTCTGTAATCCAACGGGAGGTACAGCGAATACCAAAGCCTACATATACTATTCTCTGCATG CTATAGCAAGAAAGAAAGGAAAGTGGCTTCCCGGTGGTTTTCTGCCTATTGTACAACAGG AAGCTGACAATAAAGTTTATTTGAGCGTCGACGTGCGCCGACGTGGCCCCGCTCCCCAGC CGGAGCCGCGATTGGTGGGCATTTGCCGGCGGCCACCGCTTTAAGCCACGATTGGCGAA GGCCGCCGTCAATTCGGAGCGACTCAGCGCCTGCCCGCCTCTCGCCGCGTCGCCGGTGCC TGCGCTCCCGCTCCACCTCGCTTCTTCTCTCCGGCCGAGGCCCGGGGACCAGAGCGAG AAGCGGGGACCATGTTCCGACGCTccggatccggagagggcaggggatctctcttacttgtggcgagtg aggagaacccggccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCC TGGTCGAGCTGGACGGCGACGTAACCGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAG GGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCG TGCCCTGGCCACCTCGTGACCACCTGACCTACGGCGTGCACTGCTTACGCCGTACCCC GACCACATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGC GCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGG GCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACA TCCTGGGGCACAAGCTGGAGTAACTACAACAGCCACAACGTCTATATCATGGCCGACAA GCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGT GCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGGCAGCGCCCGTGCTGTGCCC GACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGAT CACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGATCACTCTCGGCATGGACGAGCTGT ACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaaatttcacaaataaagcatttttt cactgcattctagtgtgtgtttgtccaaactcatcaatgtatcttatAAGTTGACGGCTCTCGACTACCACAAC CCCGCCGGCTTCAACTGCAAAGGTGAGGCGCGGCCCTCAGCCCGGCCGCGTGCTCCTGACC TGGGCGGAGGTCCAGCCTCAGTGCCCGCACCCACCTCCCCGTGGGGACCTCGGGCGCC TGGTTTCCGCCGCGAGCTCCGGGCCCTCTCTCTGGGTGCGCACGTACCTCGGCTCTTCG CCGCCCCCTCCCGCCTTTAAAGCCTCTCACCTACTCTGTCTCGGCATGTTACTTTCTGCACT TGGTTAACTCCAAGCATCAGTAACTACCTTCTGTACATAAAAGGGAGAGCATTCGCTT TCTCACTCACTATTCAACTCCATGGTTCCCTGGGTAATTAGCGGATACCTTGAGCACCTGCTA ATTATGGGCCAGCGCGGTGCTGGATTCTGAGGAAGGTGCTGAGTAACTTG </p>	1806
<p> pARBI- 947: RTRAF_3_ Endogeno us_51 </p>	<p> CACTAAACAGTAATTCTGTAATCCAACGGGAGGTACAGCGAATACCAAAGCCTACATATA CTATTCTCTGCATGCTATAGCAAGAAAGAAAGGAAAGTGGCTTCCCGGTGGTTTTCTGCCTA TTGTACAACAGGAAGCTGACAATAAAGTTTATTTGAGCGTCGACGTGCGCCGACGTGGCC CCGCTCCCCAGCCGGAGCCGCGATTGGTGGGCATTTGCCGGCGGCCACCGCTTTAAGCC ACGATTGGCGAAGGCCCGCGTCAATTCGGAGCGACTCAGCGCCTGCCCGCCTCTCGCCGC GTCGCCGGTGCTGCGCTCCCGCTCCACCTCGCTTCTTCTCTCCGGCCGAGGCCCGGGG ACCAGAGCGAGAAGCGGGGACCATGTTCCGACGCAAGTTGACGGCTCTCGACTACCACAA CCCCGCCGGCTTCAACTGCAAAAtccggatccggagagggcaggggatctctcttacttgtggcgagtg gagaacccggccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTG GTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGG CGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTG CCCTGGCCACCTCGTGACCACCTGACCTACGGCGTGCACTGCTTACGCCGTACCCGA CCACATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGC ACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGC GACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATC </p>	1806

	CTGGGGCACAAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATCATGGCCGACAAGC AGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGC AGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGA CAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCAC ATGGTCCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGGACGAGCTGTACA Aatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattttttcact gcattctagtgtgtgttgcctaaactcatcaatgtatcttatGGTGAGGCGGCGGCTCAGCCCCGGCCG TGTCCTGACCTGGGCGGAGGTCCAGCCTCAGTGCCCGCACCCACCTCCCCGTGGGAC CCTCGGCGGCTGGTTTCCGCGGCGAGCCTCCGGGCCCCCTCTCTCTGGGTGCCACGTACC TCGGCTCTTCGCGCCCCCTCCCGCTTTAAAGCCCTCTCACCTACTCTGTCTCGGCATGTT ACTTCTGCACTTGCTTAACTCCAAGCATCACGTAACCTCTCTGTACATAAAAGGGAGA GCATTCTGTTCTCACTCACTATTCAACTCCATGGTCCCTGGGTAATTAGGCGATACCTTG AGCACCTGCTAATTATGGGCCAGCGCGGTGCTGGATTCTGAGGAAGGTGCTGAGTAACTTG AAGACTAGTCACTGCCTGCCAGGAGCTAAAGGGACGAGGGGTGGAAG	
pARBI- 948: SERF2_1_ Endogeno us_52	CCGGGTTAGGCATAGGCCCTCCCGGATCTTCCGCGGTGTAAGGAGAAGGCCAGCGCCCCT GTGATAGGCCAGAGCCCCCACTCCACAAGCCAGCCCATCCCCACGGAGACCCAAACCGT CCACACACACCTTGCCAGCTGTTTGGGCCCCACGCCGCCCAAAACACGCCTCCAGCTGGCC CCTTGGGACCTCCCTTCTCTAGTCCGTATTTTACCTGGCCCGTGGCAGATTGCCACTCCCC CCTACCCCAAGCAGCCTGGGCTCGATGGGCGGTTGTCTGGGGCCCCGAGATTGAAGTGGT GTTGGATCCTGCTGCTGGCCGCGTGGGGTAGAAGGGTCTCGCGGTGTGTGGCGACAGCG GCCCCGCGTCTACCTTTAATTTTCTTCTTAGGCGGTAACCAAGCGTGAGCTCGCCGCCA GAAGAATATGAAAAAGCAGAGCTcctcgatccggagagggcaggggatctctcttactgtggcgactgga ggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCT GGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTACGCGTGTCCGGCGAGGGCGAGG GCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGT GCCCTGGCCCAACCTCGTGACCACCTGACCTACGGCGTGCACTGCTTACGCCGTACCCCG ACCACATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCG CACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGAGGTGAAGTTCGAGGGC GACACCTGGTGAAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATC CTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATCATGGCCGACAAGC AGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGC AGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGA CAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCAC ATGGTCCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGGACGAGCTGTACA Aatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattttttcact gcattctagtgtgtgttgcctaaactcatcaatgtatcttatGACTCGGTTAAGGGAAAGCGCCGAGATGA CGGGCTTTCTGCTGCCGCCCAAGCAGAGGTAGCCCCAGGGAGGGGAGGGAAAGGGAC GGTGAGACCTGGGTAGACCAAGGGTTATAGAAGGAAAGAGAGCTACCTCAGGGCTTGA ATGTGGACTAGTCTGAGGAGCAGAGTGATTGCTTCTCTAGGGTTTTATTCTCCCCAC CCTCCAAATTGTTAGCTCACAGCCTTACAGGAAAGGACGGGGGCGGGCGCTGCCCTCAGT CTGATTCTGAGCGTCCCTGGGTCTGACCTTAAGGGCAAGGGCAGGGAGCTTACATTTCA AATACAGTTGTGGTTACGGCAGCCAGTACTTTTGGCCCTCCTTGCTGTTGCTTCTCTCCC TTCTCCCAACCTCTCACTGGTGTGCTGGGTGTGGTCTCAATACAGAATAGAG	1806
pARBI- 949: SERF2_2_ Endogeno us_53_54	AATCAGGCCCTTTGCCACGGCTACTTACGGGACCACCTCCCGGGTTAGGCATAGGCCCT CCCGGATCTTCCGCGGTGTAAGGAGAAGGCCAGCGCCCTGTGATAGGCCAGAGCCCC ACTCCACAAGCCAGCCCATCCCCACGGAGACCCAAACCGTCCACACACACCTTGCCAGCTG TTTGGGCCCCACGCCGCCCAAAACACGCCTCCAGCTGGCCCCCTGGGACCTCCCTTCTCTA GTCCGTATTTTACCTGGCCGCTGGCAGATTGCGCACTCCCCCTACCCCAAGCAGCCTGGG CCTCGATGGGCGTGTGCGGGGCCGAGATTGAAGTGGTGTGGATCCTGCTGCTGGCC GCGCTGGGGTAGAAGGGTCGCCGTGTGTGGGCAGAGCGGCCCGCGTCTCACCTTTAA TTTTCTTCTTAGGCGGTAACtccgatccggagagggcaggggatctctcttactgtggcgactggaagg agaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCTGG TCGAGCTGGACGGCGACGTAAACGGCCACAAGTTACGCGTGTCCGGCGAGGGCGAGGGC GATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGC CCTGGCCCAACCTCGTGACCACCTGACCTACGGCGTGCACTGCTTACGCCGTACCCCGAC	1806

	<p>CACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCA CCATCTTCTTCAAGGACGACGGCACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCG ACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCC TGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATGGCCGACAAGCA GAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCA GCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCCGAC AACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACA TGGTCTGTGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGGACGAGCTGTACAA atgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaaataaagcattttttcactg cattctagttgtggtttgtccaaactcatcaatgtatcttatCAGCGCGAGCTTGCCCGCCAGAAGAATATG AAAAAGCAGAGCGACTCGGTAAAGGGAAAGCGCCGAGATGACGGGCTTTCTGCTGCCGCC CGCAAGCAGAGGTAGCCCCAGGGAGGGGAGGGAAAGGGACGGTGGAGACCTGGGTTAG ACCAAGGGTTATAGAAGGAAAGAGAGTACCTCAGGGCTTGAATGTGGACTAGTCGTGAG GAGCAGAGTGCATTGCTTCTCTAGGGTTTTATTTCTCCCAACCTCCAAATTGTTAGCTCA CAGCCTTACAGGAAAGGACGGGGGCGGGCGCCTGCCCTCAGTCTGATTTCTGAGCGTCCCT GGGTCTGACCTTAAGGGCAAGGGCAGGGAGCTTCACATTTCAAATACAGTTGTGGTTACGG CAGCCAGTACTTTTGGCCCTCCTTGCTGTTTCGGTTCCTCCTCCTTCTCCCAACCTC</p>	
pARBI- 950: SLC38A1_1_Endogenous_55	<p>TTCAAAAGGAATCTTTTGTTCACCTATTAGGATCTTTTAAATCAAATATGTATTTAATG GTGTACACCAGACCTGAAGAAAAAGATCACAGAAGGAATTTCCCTTTGTAAAGTAGAGGT AGTTAAAAATAAGCCTTATGACCTAATAGGTTAATTGAATGTCTGGTAGCCAACTTGAAAA AAGGAGAAATGATGGTTGCATCTCACATTTTAAATGTTAAGAATTTGTTTTGAATGAGGA TACCTTAACCCCTGAAGGCCAAAATGACTATTTGTGTGAGTTTGAGAAAGGCACATAGTAA CTTGGGGAACAGTCAATAGAATGACAAAATCTTGACTATTTTAACTTTCTGAACCTGTCAT TTCTGTGTTCTCAAATTTGATTTTAAATAGGCTGCATGGTGTATGAAAAGCTGGGGGAAC AAGTCTTTGGCACCACAtccggatccggagagggcaggggatctctccttactgtggcgacgtggaggagaac cccggccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGGTCTGA GCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATG CCACTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACGGCAAGCTGCCCTGCCCTG GCCCCCCTCGTGACCACCCTGACCTACGGCGTGCAAGTCTTCAGCCGCTACCCCGACACCA TGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCAT CTTCTTCAAGGACGACGGCACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACAC CCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGG GCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATGGCCGACAAGCAGAAG AACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAAGCTC GCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACC ACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGT CCTGCTGGAGTTCTGTGACCGCCCGGGGATCACTCTCGGCATGGACGAGCTGTACAAatgat tgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaaataaagcattttttcactgcattc tagttgtggtttgtccaaactcatcaatgtatcttatGGGAAGTTCGTAATCTTTGGAGCCACCTCTCTACA GAACACTGGAGGTAAAAAGAACATGCTTTTCTTACATAACTTGAACTAATTCTGGTGGAT GAGCGGCCACATGAATTTTAACTAATTCAAGCAGTTATCATCCTATTGCTAAAATGGCAC AGGGAAAGTAAAGCAGAGACAGCAGTCACTTATTTAAAGCCACAATCTGCTAGAGTAGC TGAAGTTGCCTTTGTGCTTACTGACAGTTGGTCTAAGAACGGGCTGATAACTTTTTATGTA GCTTGCAACATAAGCCTTCGTATCTTCTTCTAAAAATGTTCTCATTTTCTTCAGCAATGCTG AGCTACCTCTTCATCGTAAAAATGAACTACCCTCTGCCATAAAGTTTCTAATGGGAAAGGA AGAGACATTTTCGTAAGTTATAGACCATTTTTTATGATATA</p>	1806
pARBI- 951: SLC38A1_2_Endogenous_57	<p>TAAAGATGTCAAGCTTCAAATCATTATCATAAGGTTAAATATATTACGCATGTCTTTACAGCA AGTTTATTTCTGATCGTGAAGTAGAAGAAGTCTACAAACAGCCATTTGGAAAAAAGAA GTGTGATGAGTATGTAAGTATCATTATAATGAAGTATGCTTATTTTTTAAATCATATAAATTG GGACAAATCTTTTAAATCAAGTAGCATAGTACCAAAAGCATAACTACCTGTATTCACCAGG ATATTCCTCATACCTTATGTATTTTCTCTTGAATCCATTCAAGGAAATAACTAGATAACTAA GAATGGATTTTCTTGAATTTTACTTCCATATTGGTTCCTGAGAGTGCATTAAAGGCTTTGGCT TGATGAACCTTCTTGGGGATTATTTGCTTAGTGCAATGTTTGTTCTTTGTTTCAGATTCCA GGTACAACCTCtccggatccggagagggcaggggatctctccttactgtggcgacgtggaggagaacccggcc ccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGGTTCGAGCTGG</p>	1806

	<p>ACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGCGAGGGCGAGGGCGATGCCACCT ACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCGTGCCCTGGCCAC CCTCGTGACCACCTGACCTACGGCGTGCACTGCTTCAGCCGCTACCCGACCACATGAAG CAGCAGCACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTT CAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGT GAACCCGATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACA GCTGGAGTACAACACAAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAAGCG CATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGAC CACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACCACTACC TGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGGATCATATGGTCTGCT GGAGTTCGTGACCGCCGCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattg cagcttataatggttacaaataaagcaatagcatcacaatttcacaaataaagcattttttcactgcattctagtgtg gttgttccaaactcatcaatgtatcttatTTAGGCATGTCAAGTTTTAACCTAAGCAACGCCATTATGGG CAGTGGGATTTTGGGACTCGCCTTTGCCCTGGCAAACACTGGAATCCTACTTTTTCTGTGAG TATTGACGTGCCGGTACTTTCCATTTTAAACTGAACTTTTTGTATGTTTCTGTATTACATAG AAGAAATGTGAAATATTTATAAATAGTTTTTTATTAACCTGGCTAAGTTACAAGTACATACT TTGATATTTATTGCTTGAGTGATTTTCCAACTGTACCTAATGCTTACAACAAAGAGGAAGG AGAAATCTTTTTATTAATCAAAAATACTGAAATAAGCATTTGTGAAAAGGATTAAACATT TGAAAATAACTTTTTTGGTATTTTGGAGTCTACCTGTGACTTTAAATCTCAGTTAAATAT TAAGAGGTGTTTAACCCAGCCAGTCAACACTT</p>	
pARBI- 952: SMAD2_1 _Endogen ous_58	<p>ATCATTCTTCACTAGTTCCTTTCTGACTCTTCAGTCACCTCCAGAATTAATATCCTTAGAA GCATCTCTAAAATGAGTTTGATTTACTAAACATAGAAGTTGACAAAGTTTTCAAGTATAAC TGCATAAACTCTCTTTTTAAAAAATCAGTTTTTCCCAAGTTGTAGCCTTTCATTGGCATTG AGTCATTTATGTGACATATTTATAAGAAACATCTGCTAGTGCTGCTGCATACTTTTATCAGAT CCATTAAATAGTACATTTTTGTTCTTGATTCTCACTAAAACTAACTAAATGGCTGTCTTTT TCTTTATGCTTTTATTTGACTAATTTAGCCCATTTGACTGCACtttttttttttttttAAAGTTCCCT CCTTTCTTTTCCCTTGCTTCCCAACAGGTCTCTTGATGGTCGTCTCCAGGTATCCCATCGAtc cggatccggagagggcaggggatctctcttacttgtggcgacgtggaggagaaccccgcccccATGGTGAGCAA GGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGCTCGAGCTGGACGGCGACGTAA CGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGAC CCTGAAGTTCACTGTGACCACCGCAAGCTGCCGTGCCCTGGCCACCCTCGTGACCACCC TGACCTACGGCGTGAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTTC AAGTCCGCGATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTCAAGGACGACGGCA ACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGC TGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAAC ACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCT CAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAA CACCCCATCGGCGACGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCC AAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACC GCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttac aaataaagcaatagcatcacaatttcacaaataaagcattttttcactgcattctagtgttggtttgtccaaactcatca atgtatcttatAAAGGATTGCCACATGTTATATATTGCCGATTATGGCGCTGGCCTGATCTTCAC AGTCATCATGAACTCAAGGCAATTGAAAACCTGCGAATATGCTTTTAATCTTAAAAAGGATGA AGTATGTGTAAACCTTACCCTATCAGAGAGTTGAGACACCAGGTAGGAATATTGCAAGT TTTTTCTTGGTTTTGAATTAATGCTGAACCTCAGTATATTTAAGTACTCTTGTGACCCAG GAAAATTTTAGTGAAATCTAATAAATTACCTAAATTTGTGCATATTATTTGGTGGTAATTA AAAtttttttatttttaaaatttttAATGAGAAAACATATCTGTTTCTTGGAAATAGCATATGTTTGG CATGAAAGTGATATCCAGGAAATCCTGTAGATTGGCAGTCTGCTCAGCGCTATGCTGATG TGCTTCTACATGTCCT</p>	1806
pARBI- 953: SMAD2_2 _Endogen ous_59	<p>TTCTATATTAATAATCAGTTGACATCTGTTTTAGATAATTTTTTAAAAAATGGATTATAAA ATGAAGCACTTAGTAAAGCTGATGGCAGAGTTTTAGATCTTTTGAATACAGGAAAGTGGT AAGGGCATTATAGGTATGATTGAGCTAGAGGGCGTTGGTGTTACATTTTAAAAACA TAATCATGACTTATCTGGAGTCACATGTTCCATTTTATTGGCTTCTCATATAGAAAAATATA GTAACCAGCACTACATGCCTGTGAAAAAGTGAAGCAATTGTATATTTCTGGGTGAAGGAA GTATTCTGTACATCTCCATGTTTTACATCATGGTATTTTGAATAACCATGCTTCCATGTTAC</p>	1806

	<p>ATCAATTTTTGTTTTCAATTTATGCACAGCACTTGCTCTGAAATTTGGGGACTGAGTACAC CAAATACGATAGATtccggatccggagagggcaggggatctctccttactgtggcgacgtggaggagaaccccg gccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGGCCATCCTGGTCGAGCT GGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCA CCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCC CACCTCTGTGACCACCTGACCTACGGCGTGCAAGTGTTCAGCCGCTACCCCGACCACATGA AGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTT CTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCT GGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCA CAAGCTGGAGTACAACACTACAAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAAC GGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCC GACCACTACCAGCAGAACACCCCATCGGCGACGGCCCGTGCTGCTGCCGACAACCACT ACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTCT GCTGGAGTTCGTGACCGCCGCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtt attgcagcttataatggttacaaataaagcaatagcatcacaatttcacaataaagcattttttcactgcattctagt gtggttgcctcaactcatcaatgtatcttatCAGTGGGATACAACAGGCCTTTACAGCTTCTCTGAACA AACCAGGTGAATATTCTGCCCTCTGTGCAATCTTAGAGATCTGTGGGAGGGGGGTATATT TTGAAAGACCTATATGGGGTTGCTTAGTATAATTTTGCCTAGGATGTTTCTTAATGTAAAA TAAGGCATAGCATTTAAATATCTGCTTGCCAGTATAAAAAATATATTAATGTTTCAGCTG ATGTTTTAATCAATGCAATTCTAGTTTGAATCTTCTTAAATTAAGTATCCCTAAAGAATA ATAATTTTGATAACTATATATTTATTTAGCTTGAGATCAGATTATAATCTGTTGTTGGCCTA ATTTTTAAGTAGATACATGATGAGTTTTGCTAAATTTCTGTTATCAGAATCTCATCTTTATAC TAATAAATACATACTTAATGAACCCCTTATATCACAA</p>	
pARBI- 954: SMAD2_3 _Endogen ous_60	<p>TCAATGTATTTTTGTATAGTCTTTGAGATTAGAGTGAAGTTCTAAAAAGTAAGAGAACCTT TTGTGAAAATATTTAATTGACACTACTAAGAGTTTAAATAGTATTGGTGGTGAAAAATCG TTAAAGTATCTGATTTTACTTGCAAAATTAAGTATTTCACCAAGAGGAGTCCTTACAAC ATTCTTGTTTTAGAAGGGTTTGTTCATCATTCAATTAATTCATAAAGATAACGTTTTCAT GGGTGGAGAAGTCTATTGGGAAAGTCATAATTCGAATTTCTATCTTGCTTGCAAGTTTGCTT TCTATGATAAGTTGAAATTATTACTTGATGTTCAAGGTAGTCTCTACATCATCCTTTCAATAT TTCTGCTAGGTTGATACAAAGAGGCTGTTTTCTAGCGTGGCTTGCTGCCTTTGGTAAGAAC ATGTCGTCCATCtccggatccggagagggcaggggatctctccttactgtggcgacgtggaggagaaccccgcc ccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGGCCATCCTGGTCGAGCTGG ACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCT ACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGCCCCAC CCTCGTGACCACCTGACCTACGGCGTGCAAGTGTTCAGCCGCTACCCCGACCACATGAAG CAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTT CAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGT GAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCAAA GCTGGAGTACAACACTACAAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGG CATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGAC CACTACCAGCAGAACACCCCATCGGCGACGGCCCGTGCTGCTGCCGACAACCACTACC TGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCT GGAGTTCTGTGACCGCCGCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgttattg cagcttataatggttacaaataaagcaatagcatcacaatttcacaataaagcattttttcactgcattctagt gttgcctcaactcatcaatgtatcttatTTGCCATTACGCGCCAGTTGTGAAGAGACTGCTGGGAT GGAAGAAGTCAGCTGGTGGGTCTGGAGGAGCAGGCGGAGGAGAGCAGAATGGGCAGGA AGAAAAGTGGTGTGAGAAAAGCAGTGAAGTCTGGTGAAGAAGCTAAAGAAAACAGGAC GATTAGATGAGCTTGAGAAAAGCCATCACCCTCAAACTGTAATACTAAATGTGTTACCATA CCAAGTAAAGTTTGTAGATCCAGGTTTGATCAAATTATGTCAAGGAATCTGAAGGAAA GTTACTGAATTTGTGTTCTTTCAAGTTGCCTGTAAAAAGTGATGATTGAAATATGACTGTTT TTAACCTTGATAAATGTTTTGCTAGCTGACTTGTTTTATAAATATTTTCTGAATAGTGA GGTTTAATCAAGCTAAATAAGATACTTAGATTTATTATCTTCA</p>	1806
pARBI- 955: SOCS1_1	<p>GGGCTCCCGCAGCACAGCCTTCTCCGGCCCTAGCCCAAATCGCCAGACCAGGCGCGGAT CCCAGCCTGGCCAGCAGGCGGCGGGCGGGGCGGCGAGCCGGGGCCGACGGCTGGA GCCAGAACCGGCTGCTCTCCACGCCCCCTCTCGGTGCTGCCCGAGGCGGACTCCGCCT</p>	1806

_ Endogenous_61	<p>CCACCGAGCCCCACCCGCCGGGAAGAGCTCCGCGGAGTACAGAGCCCATTTTCTAGCTGT GTCCACTGAGGCTGAACGGATCCGCGCGGACTTGGTGCTCCGTGCTCGCCCCCTAGGGCCG GGTCCGCCGGGAGCGCCGCCCTCCGGAGTTGTCCGGCCGGCGCACACCTGCCCGCCCCG CAGCGCCCCAGCTACCTCTTTGTCTCTCCCGCAGCGACCCCCGGACGCTATGGCCACCC CTCCGGCTGGCCCCCTTCTGTAGGATGtccggatccggagagggcaggggatctctccttactgtggcgacg tggaggagaacccggccccATGGTGAGCAAGGGCGAGGAGCTGTTACCCGGGGTGGTGCCCAT CCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCGGGCGAGGGCGA GGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCC GTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCACTGCTTCAGCCGCTACCC CGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAG CGACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGG GCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACA TCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATGGCCGACAA GCAGAAAGAACGGCATCAAGGTGAACCTTCAAGATCCGCCACAACATCGAGGACGGCAGCGT GCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCC GACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGAT CACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGT ACAAatgattgtttattgagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcatttttt cactgcattctagttgtgtttgttccaaactcatcaatgtatcttatGTAGCACACAACCAAGGTGGCAGCCGA CAATGCAGTCTCCACAGCAGCAGAGCCCCGACGGCGGCCAGAACCTTCTCTCTCTCTCTCT CCTgccccgcccccgccccgccccgccccgccccgccccgCCCCGGCGACACGCACTT CCGCACATTCCGTTGCGACGCCGATTACCGGCGCATCACGCGGCCAGCGCGCTCCTGGAC GCCTGCGGATTCTACTGGGGGCCCTGAGCGTGACGGGGCGCACGAGCGGCTGCGCGCC GAGCCCGTGGGCACCTTCTGCTGCGCGACAGCCGCCAGCGGAAGTCTTTTTCGCCCTTA GCGTGAAGATGGCCTCGGGACCCACGAGCATCCGCGTGCACTTTTACGGCCGCCGCTTTCA CCTGGATGGCAGCCGCGAGAGCTTCGACTGCCTCTTCGAGCTGCTG</p>	
pARBI-956: SOCS1_2 _ Endogenous_62	<p>GGATCCAGCTGGCCAGCAGGCGGGCGGGCGGGCGGCGAGCCGGGGCCGGACGGC TGGAGCCAGAACCGGCTGCTCTCCACGCCCCCTCTCGGTGCTGCCCGGAGGCCGACTCC GCCTCCACCGAGCCCCACCCGCCGGGAAGAGCTCCGCGGAGTACAGAGCCCATTTTCTAG CTGTGTCCACTGAGGCTGAACGGATCCGCGCGGACTTGGTGCTCCGTGCTCGCCCCCTAGG GCCGGGTCCGCCGGGAGCGCCGCCCTCCGGAGTTGTCCGGCCGGCGCACACCTGCCCGGC CCCGCAGCGCCCCAGCTACCTCTTTGTCTCTCCCGCAGCGACCCCCGGACGCTATGGCCC ACCCCTCCGGCTGGCCCTTCTGTAGGATGGTAGCACACAACAGGTGGCAGCCGACAATG CAGTCTCCACAGCAGCAGAGCCCCGAtccggatccggagagggcaggggatctctccttactgtggcgacg tggaggagaacccggccccATGGTGAGCAAGGGCGAGGAGCTGTTACCCGGGGTGGTGCCCAT CCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCGGGCGAGGGCGA GGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCC GTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCACTGCTTCAGCCGCTACCC CGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAG CGACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGG GCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACA TCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATGGCCGACAA GCAGAAAGAACGGCATCAAGGTGAACCTTCAAGATCCGCCACAACATCGAGGACGGCAGCGT GCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCC GACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGAT CACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGT ACAAatgattgtttattgagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcatttttt cactgcattctagttgtgtttgttccaaactcatcaatgtatcttatCGGCGGCCAGAACCTTCTCTCTCTCTCT CCTCCTgccccgcccccgccccgccccgccccgccccgccccgCCCCGGCGACACGCA CTTCGCGACATTCCGTTGCGACGCCGATTACCGGCGCATCACGCGGCCAGCGCGCTCCTGG ACGCTGCGGATTCTACTGGGGGCCCTGAGCGTGACGGGGCGCACGAGCGGCTGCGCG CCGAGCCCGTGGGCACCTTCTGGTGCGCGACAGCCGCCAGCGGAAGTCTTTTTCGCCCT TAGCGTGAAGATGGCCTCGGGACCCACGAGCATCCGCGTGCACTTTTACGGCCGCCGCTTT CACCTGGATGGCAGCCGCGAGAGCTTCGACTGCCTCTTCGAGCTGCTGGAGCACTACGTGG CGGCGCCGCGCCGATGCTGGGGGCCCCGCTGCGCCAGCGCCG</p>	1806

pARBI-957: SOCS1_3 _Endogenous_63	<p>CGGACTCCGCCTCCACCGAGCCCCACCCGCCGGGAAGAGCTCCGCGGAGTACAGAGCCC ATTTTCTAGCTGTGTCCACTGAGGCTGAACGGATCCGCGCGGACTTGGTGTCTCGTGCTCGC CCCCTAGGGCCGGGTCCGCCGGGAGCGCCGCCCTCCGGAGTTGTCCGGCCGGCGCACACC TGCCCGGCCCGCAGCGCCCCAGCTCACCTCTTTGTCTCTCCCGCAGCGCACCCCGGACGC TATGCCCCACCCCTCCGGCTGCCCCCTTCTGTAGGATGGTAGCACACAACCAGGTGCGAGC CGACAATGCAGTCTCCACAGCAGCAGAGCCCCGACGCGCGCCAGAACCTTCCTCCTCTCTCT CCTCCTcgccccgcccccgcgccccgccccgccccgccccgccccgCCCCCGCGACACGCA CTTCGACACatccgatccggagagggcaggggatctctcttacttggcgagtgaggagaacccccggccc ATGGTGAGCAAGGGCGAGGAGCTGTTACCCGGGGTGGTGCCCATCTGGTCGAGCTGGAG GCGGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTAC GGCAAGCTGACCTGAAGTTCATCTGCACCAACGGCAAGCTGCCCCGTGCCCTGCCCCACCC TCGTGACCACCCTGACCTACGGCGTGCACTGCTTCAGCCGCTACCCCGACCACATGAAGCA GCACGACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCA AGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGA ACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAGC TGGAGTACAATAACAAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAAGCGCAT CAAGGTGAAGTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCACTCGCCGACCA CTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACCACTACCTG AGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGTG GAGTTCGTGACCGCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgttattgc agcttataatggttacaaataaagcaatagcatcacaatttcacaataaagcatttttttactgcattctagtgtggt ttgtccaaactcatcaatgtatcttatTTCCGTTCCGACGCGGATTACCGGCGCATCACGCGCGCCAGC GCGCTCCTGGACGCGCTGCGGATTCTACTGGGGGCCCTGAGCGTGACGGGGCGCACGAG CGGCTGCGCGCCGAGCCCGTGGGCACCTTCTGCTGCGCGACAGCCGCCAGCGGAACCTGC TTTTTCGCCCTTAGCGTGAAGATGGCCTCGGGACCCACGAGCATCCCGGTGCACTTTAGGC CGGCCGCTTTCACCTGGATGGCAGCCGCGAGAGCTTCGACTGCCTCTTCGAGCTGCTGGAG CACTACGTGGCGGCGCCGCGCCGATGCTGGGGGCCCGCTGCGCCAGCGCCGCTGCGG CCGCTGCAGGAGCTGTGCCGCGAGCGCATCTGTGCCACCGTGGGCCGCGAGAACCTGGCT CGCATCCCCCTCAACCCCGTCTCCGCGACTACCTGAGCTCCTTC</p>	1806
pARBI-958: SRP14_1 _Endogenous_64	<p>GGCAGACAAACAGTTAAACAGAGGAGTGGGGTAAGTGATGACCTAACCCAGCCCCGCTG CTCTAGTTTTGTTAAACACCTCATCTGCTATCACGGTCTGGCGAAACCCTGGAGAACTATT ATTTCCACGACGGAACATGTAATATCGAAGCACGTAAATTCCTCACTCAAAGTGGCGGCGT CTGGGATCCCTGACAAAGAGCCCTGGGCTGCTTGGGGCCCATTTGTTACCAGAAGCAACCTA GGCGGCTCAGTGCTGGGGACTGAGCCAGCTACAATCCCTACTATTTCCGGGCCCGAAGCC CCGAATGTGCTCAGTACAGGGTGGGGAAAGGTAGAGGAAGGCGGCGGTCCGCGGCAGAC AGACTCCGGTGGCTCCAGACACCGGAACCCAGGGAGCATCGCCCGGCTCCCTCCCGCT GCTTACACTTCTCAAGGTGATATatccgatccggagagggcaggggatctctcttacttggcgagctg gaggagaacccccggccccATGGTGAGCAAGGGCGAGGAGCTGTTACCCGGGGTGGTGCCCATCC TGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAG GGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCAACGGCAAGCTGCCCCG TGCCCTGGCCACCCTCGTGACCACCTGACCTACGGCGTGCACTGCTTCAGCCGCTACCCC GACCACATGAAGCAGCACGACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGC GCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGG GCGACACCCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACA TCCTGGGGCACAAGCTGGAGTAACTACAACAGCCACAACGTCTATATCATGGCCGACAA GCAGAAGAAGCGCATCAAGGTGAAGTTCAGATCCGCCACAACATCGAGGACGGCAGCGT GAGACTCGCCGACCACTACAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCC GACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGAT CACATGGTCTGCTGGAGTTCGTGACCGCGCCGGGATCACTCTCGGCATGGACGAGCTGT ACAAatgattgttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaataaagcatttttt cactgcattctagtgtgtgtgtgtccaaactcatcaatgtatcttatGACGCTGCCCGACGTCCGGCACTTCTG GAAAAGTCTGGTCAGCTCCGTGAGGAAGTGGAAAACAACAGGCCAGCCCCGTTAGCCAG CCCCAAATCCTGCTGCTGCGCGTCAAGGCCCTGGTCTCCTGCGAGGAGGCACAGGTCTCG AGTAACGCCTGAGCCGCCCTTCCCTCGGCCGGCCAGGCTAGCCATACCTGCTCGCTCTC CAACAACACCATCGCGCGCAGCTGGCTCGACTCCCTCCGCTTAAGCCCTAGCAGTGAGA</p>	1806

	GCCGGAAGTTCGGCCTAGGCTGGGCGGGAATTCCGCTACTAGACTTCCATTGTCTTCCACCA ATCTCTTCTCTTCCACCAATCCCGCCTGCGCCCTCCCCCTCCCCGCCGCTAGCGCCCGC GCCCTGGGACGTCCGGGGGCTGTGACCCGGAGGCGCTGGGGCTGTCTGGGTC	
pARBI- 959: SRP14_2_ Endogeno us_65_66	GTCTGTCTGCCGCGGACCGCCGCTTCTCTACCTTTCCCAACCTGTACTGAGCACATTCCG GGCTTCGGGCCCCGAAAATAGTAGGGATTGTAGCTGGCTCAGTCCCCAGCACTGAGCCGC CTAGGTTGCTTCTGGTAACAATGGGCCCAAGCAGCCAGGGCTCTTTGTGAGGGATCCCA GACGCCGCCACTTTGAGTGGAATTTAACGTGCTTCGATATTACATGTTTCCGTCTGGAAT AATAGTTTCTCAGGGTTTCGCCAGACCGTGATAGCAGATGAGGTGTTTAAACAACTAGA GCAGCGGGGCTGGGTTAGGTCATCACTTACCCACTCCTCTGTTTTAACTGTTTGTCTGCCG CTCAGCCACGTACGCGCGCTGTTCACCAGGATGCATTTTTCTTCAGATGACGGTCGAAC CAAACCATTTCAAAGAAAGtccggatccggagagggcaggggatctcttacttctgtggcgacgtggaggag aaccgccggccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTCCCCATCTGGTC GAGCTGGACGGCGACGTAACCGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGA TGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGCAAGCTGCCCCGTGCCCT GGCCCCCCTCGTGACCACCTGACCTACGGCGTGCACTTCAGCCGCTACCCCGACCA ATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCA TCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACA CCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGG GGCACAAGCTGGAGTACAACAGCCAGCCACAACGTCTATATCATGGCCGACAGACAGAA GAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGACGT CGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAAC CACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATG GTCCTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTCGGCATGGACGAGCTGTACAAatg attgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaaataaagcattttttcactgcat tctagtgtggtttgtccaaactcatcaatgtatcttatGGTACTGTGGAGGGCTTTGAGCCCGCAGACAA CAAGTGTCTGTTAAGAGCTACCGATGGGAAGAAGAAGATCAGCACTGTGGTGAGCTTAATT TCTAAGGCTGTCTTTTGAATGTAAGACTTGAACCTAACAGAGGATGGGGCGTTTCTGAA CCAGGCTTTTATTTGTTTTCCCTTTGCCCCTGTGTGGCTATTTTTGAGACCAGGACCTTCTTA TACTTTAGTAGTGGAAACCTCAAGAATAAAATAAGAAGGTAGAGGTACAGACATCGTTAGT TCTGCTAAAGCTCTGTGGAATGAAAGTAGCATATTGGTCCTTATTCGTAGTACTGTAAGG AGCAGCTGGCATAAATATTTGATTCTTAGCCCCCTACTGTGCTGGGCCTTCAATAAGCAGT TTCTTGGTACCAGGTGATGCTATTATTTCTTATCTTTGTGGTTTAC	1806
pARBI- 960: SRSF9_1_ Endogeno us_67	CCCACGTCACTGAGTGCTCACAAGTCTGTGAGGTAGGCGGCGCCACAGAGAGAACTGAG GCGCGGGAGCCCCAAGCCACTTGTCCAGCGCCTCAGCCGAGCGCGAACCCGCTCGGGGAT GGCATCCACACGGCCCCGCCCCAGGCTCTCCCTGTGACGCGCCGAAGGCCCTTCGCACCTC CAGGGGGCGCGCGCTGCGCGACGCGCAATGGTCGACCGCGCTTCTCTTTAAGAGGAC TCCTTTTGCTCCGCGGACCCCTTCGCTTCCGCTCCGCGTTCACACAATGCAGTGCGGCTGAG CGCCTCGGAGCCCGCGGGGACGCTGCGGGGGGACCCGTGCTGAggcggcgggcgacgtgggc tgcggcgggccccgcgcgctcgggcggtgctggatgtcgggctggcgagcgagcgcgcgAGGGCGACGGG CGCATCTACTccggatccggagagggcaggggatctcttacttctgtggcgacgtggaggagaaccccgccccA TGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCATCCTGGTCGAGCTGGACG GCGACGTAAACGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACG GCAAGCTGACCCTGAAGTTCATCTGCACCACCGCAAGCTGCCCGTGCCCTGGCCACCCTC GTGACCACCCTGACCTACGGCGTGCACTGCTTACGCCGCTACCCCGACCATGAAGCAGC ACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAG GACGACGGCAACTACAAGACCCGCGCGAGGTGAAGTTCAGGGCGACACCCTGGTGAAC CGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTG GAGTACAACCTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAAGCGCATCA AGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGACGCTCGCCGACCACTA CCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGC ACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAG TTCGTGACCGCGCGGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagctt ataatggttacaaataaagcaatagcatcacaatttcacaaataaagcattttttcactgcattctagtgtgtgttc caaatcatcaatgtatcttatGTGGGAACCTTCCGACCGACGTGCGCGAGAAGGACTTGGAGGA CCTGTTCTACAAGTACGGCCGCATCCGCGAGATCGAGCTCAAGAACCGGCACGGCCTCGTG	1806

	CCCTTCGCTTCGTGCGCTTCGAGGACCCCCGGTGAGGccccgcgccccctgccctctctcctcggtgc ctgaggccccgccttccctgctgtccctccccagggtccctcccccgctccctcccccgctccgagaga cccccaCGGCGCCCCCTCACGGGTGGAGGATGAGGCAGCCTCTCCTCGCAGGCCCCGGGCGG TCCTTCGCGCCGTCGTCACTTCCTTTATTTTATTATTCCAATATTTTACTTAGAAACCCAAAA GCTGAGCCTTTGGAGGGCCCAAGCCGCTGCACCGCCTCGGGGGTCCAATGAGCCT TGTCGCC	
pARBI- 961: SRSF9_2_ Endogeno us_68	TGTGGTGTGCTTTTCGAGAAAATGCTCACGAAGATTAGAAAAACTGATGGTTTATTGGC AAAATCAATAATCTGTCAGCAGTTGATTCTtttttttCTCTGAATTAGCCCTCTTATGAGTAATCT GTTTGCTCATTATTATAATTTATACCTCTAAAAGTGCCTGTGACAGCTGTAAAGGTTAATT CCAGTATCATGAAACGCTCTCAAACCAAAGCAGAAGTGCTTCAGGATCCTGATTGTGTGT TTTTCTTCACTCTAGGTTTCCCTTTATGCTTACTACTCATGCCCTCACTTGAAAGTCACT TGGCCTCTGAACAGCACTAACTCAAACGtttttttgttgttgttgttttttAGAGATGCAGAGGA TGCTATTTATGGAAGAAATGGTTATGATTATGGCCAGTGTGGCTTCGTGTGGAGTTCCTCA GGtcggatccggagagggcaggggatctctcttacttgtggcgacgtggaggagaaccccgggcccATGGTGA GCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGGTCGAGCTGGACGGCGAC GTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAG CTGACCCTGAAGTTCATCTGCACACCGGCAAGCTGCCGTGCCCTGGCCACCCCTCGTGAC CACCTGACCTACGGCGTGAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCAGCAG TTCTTCAAGTCCGCATGCCGGAAGGCTACGTCCAGGAGCGCACCATCTTCTCAAGGACGA CGGCAACTACAAGACCCGCGCGAGGTGAAGTTCGAGGGCGACACCCCTGGTGAACCGCAT CGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTA CAACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAAGCGCATCAAGGTG AACTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGC AGAACACCCCATCGGCGACGGCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCA GTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCTGT GACCGCCGCGGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatg gttacaataaagcaatagcatcacaatttcacaataaagcatttttttactgcattctagtgtgttgcctaaact catcaatgtatcttataCTTATGGAGGTCGGGGTGGGTGGCCCCGTGGTGGGAGGAATGGGCCT CCTACAAGAAGATCTGATTTCCGAGTTCTTGTTCAGGTATGTTCTTTTCAAACAGaatgagat gatacatgtaaataacttaacacagagctgtgtctccaagaaatgatagctgttattcttCAGTGCATGGGACAG GGGGCTTTCTTTTCAATAGCCTGTGTGAAGCCTTGCCCTGGATTGCCAATGAGGAAAGTATC CTGCAATGAAATTGCGCTGGGAGTGACGCTTGGAAGAACATAACCATATTTCTTGTAAG GGAGTTTTCTAGTGGTGAGAAGGAAAGATGATGGGAAAACCTTGAGCTACAATTCTAAAGA TGCTTCTTTTGAATATACCTTGGCATCAGACATGGTAGAAAGGCATTCAAGGAGCCAGATT GAACAACTTACCCAGCC	1806
pARBI- 962: SRSF9_3_ Endogeno us_69	GATGGCATCCACACGGCCCCGGCCCCAGGCTCTCCTGTGACGCGCCGAAGGCCCTTCGCAC CTCAGGGGGGCGCGGCTGCGCGCACGCGCAATGGTCGAGCCGCGTTCTCTTTAAGAG GAGCCTTTTGCCTCCGCGACCCCTTCGCTTCCGCTCCGCGTTCCACAATGCAGTGCGGCT GAGCGCTCGGAGCCCGCGGGGACGCTGCGGGGGGACCCGTGCTGAgggcgccggcgagct gggctcgggcgggcccgcgctcgggcggtcgggatgtcgggctggcgagcgagcgggcgagAGGGCGAC GGGCGCATCTACGTGGGGAACCTTCCGACCGACGTGCGCGAGAAGGACTTGAGGACCTG TTCTACAAGTACGGCCGCATCCGCGAGATCGAGCTCAAGAACCGGCACGGCCTCGTGCCCT TCGCCTTctcggatccggagagggcaggggatctctcttacttgtggcgacgtggaggagaaccccgggcccAT GGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCATCCTGGTCGAGCTGGACG GCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACG GCAAGCTGACCCTGAAGTTCATCTGCACACCGGCAAGCTGCCGTGCCCTGGCCACCCCTC GTGACCACCCTGACCTACGGCGTGCAAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGC ACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAG GACGACGGCAACTACAAGACCCGCGCGGAGGTGAAGTTCGAGGGCGACACCCTGGTGAAC CGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTG GAGTACAACCTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAAGCGCATCA AGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTA CCAGCAGAACACCCCATCGGCGACGGCCCGTGCTGCTGCCGACAACCACTACCTGAGC ACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAG TTCGTGACCGCCGCGGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagctt	1806

	<p>ataatggttacaaataaagcaatagcatcacaaatttcacaaataaagcattttttcactgcattctagttggtttgtc caaactcatcaatgtatcttatGTGCGTCTCGAGACCCCGGTAGGcccccgcccgccctgcctctctcc tcggtgctcgaggcccccgtctctctgctgtccctccccagggtctccctcccccggtctccctccccgcctcgc cgcagaccctcaCGGCGCCCCCTCACGGGTGGAGGATGAGGCAGCCTCTCTCGCAGGCCCG GGCGTCTTCGCGCCGTGCTCACTTCTTTATTTTATTATTCCAATATTTTACTTAGAAACC CAAAAGCTGAGCCTTTGGAGGGGCCAAGCCGCCTGCACCGGCCTCGGGGGGTCCAATG AGCCTGTGCCCTCTGCTGGGGCAGCACGTAGGGGGAAGCGGCCGCGGGGACGCG GGGGTGCCTGTCGCCCTTCCCGCTCGCTCTCCCCGGCCCGTGCTCGCGTGGCTGGA GAGCAAGCT</p>	
<p>pARBI- 963: SUB1_1_ Endogeno us_70</p>	<p>GTAAGTACTAGCCTTAGTAGACTGTGGTTCCAGGTATTATCAGAAGTAGCAAGATCCCTC CatttttttTACTCAAAGAAATCGTATGTGGGATCCCAAACCACAAAATAACCGTTCTGTGG TTAATACTACTATAATGCCTGAAGTGTCTTTTGGGATCTGAGAACAGAGTTTGAAAAATT ACTAGACAGAAGGATTGGTTAGATTCATAGTTTGTGTTGAGTGAAACTTGCTTATGTATA TATTTATGATATTTGGATGTAGTCTTTTGATTGTTTAAATCTTAAAAAGTAATGGGATCTTT TGACACTGGGGTATGTTTTATTTTATGTGTGCAAAATTTAACCATATCTTTTCTAGTTAAA GAGGAAAAAGCAAGTTGCTCCAGAAAAACCTGTAAAGAAACAAAAGACAGGTGAGACTTC GAGAGCCCTGTCAccggatccggagaggggcaggggatctctcttactgtggcgacgtggaggagaaccccg cccATGGTGAGCAAGGGCGAGGAGCTGTACCAGGGGTGGTGCCATCTGGTCGAGCTG GACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGAGTGCAC CTACGGCAAGCTGACCTGAAGTTTCACTGTGACCACGGCAAGCTGCCGTGCCGTGGCC ACCTCTGTGACCACCTGACCTACGGCGTGCAGTGCTTACGCGCTACCCGACCCACATGAA GCAGCAGACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCT TCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGG TGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGCAACATCCTGGGGCACA AGCTGGAGTACAACACAACGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACG GCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGACGTGCGCG ACCACTACCAGCAGAAACACCCCCATCGGCGACGGCCCCGTGCTGTGCCGACAACCACTA CCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCAGAACGAGCGCATCATAGTTCCTG CTGGAGTTCTGTGACGCGCCGCCGGGATCACTCTCGCATGGACAGAGCTGTACAAatgattgttta ttgcagcttataatggttacaaataaagcaatagcatcacaaatttcacaaataaagcattttttcactgcattctagttg tggtttgtccaaactcatcaatgtatcttatTCTTCTAACAGAGCAGCAGCAGCAGAGATGATAACAT GTTTCAGGTAAAGTTGGCTAttttttttttttttttttttgacatggagtcagctctgtcaccaggctggagtgca gtggcgccatctcggtcactgcaacctcagcctctgagttcaagcagttctgtgctcagcctcccgagtagctaggat tacaggcatccgcaccagacctggtaattttttagtagagatggggttaccatctgtggccaggctggtctt gaactcctgacctgtgatccaactgcctcagcctccaaaagtgtcgggttacagggtgagccaccatgccttcccAA AGTTGGCTGTTTCTTAGATTACAGAGGAATTATTATCTGGCTTGATCTGAAGAATGTTAAAA GTACTATGATCTGATAATTGCTAATATG</p>	1806
<p>pARBI- 964: SUB1_2_ Endogeno us_71</p>	<p>ATAAATAAACATATCTCGAAATGGAATAAGTTGGTTATATCTTTTAAATAGTATATCTGC TTCGTAAAATAAGTAAGTACTAGCCTTAGTAGACTGTGGTTTCCAGGTATTATCAGAAGTA GCAAGATCCCTCATTTTTTTTTTCTACCAAAGAAATCGTATGTGGGATCCCAAACCACAAAAT AACCCTTCTGTGGTTAATACTACTATAATGCCTGAAGTGTCTTTGGGATCCTGAGAACAG AGTTTGAAAACATTACTAGACAGAAGGATTGGTTAGATTATAGTTTTGTTGTTGAGTGAAA CTTGCTTATGTATATATTTATGATATTTTGGATGTAGTCTTTTGATTGTTTAAATCTTAAAAAG TAATGGGATCTTTGACACTGGGGTATGTTTTATTTTATGTGTGCAAAATTTAACCATAATTC TTTTCTAGTTAtccggatccggagaggggcaggggatctctcttactgtggcgacgtggaggagaaccccgccc ATGGTGAGCAAGGGCGAGGAGCTGTTACCCGGGTGGTGCCCATCTGCTGCTGAGCTGGAC GGCGACGTAAACGGCCACAAGTTTACAGCTGTCCGCGAGGGCGAGGGCGATGCCACGTAC GGCAAGCTGACCTGAAGTTTCACTGTGACCACCGGCAAGCTGCCCGTGCCCTGGCCACCC TCGTGACCACCTGACCTACGGCGTGCAGTGCTTACGCGCTACCCGACCCACATGAAGCA GCACGACTTCTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCA AGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTGAGGGCGACACCCTGGTGA ACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGC TGGAGTACAACACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCAT CAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTGCCGACCA CTACAGCAGAAGACCCCCATCGGCGACGGCCCGTGCTGTCTGCCGACAACCACTACTCTG</p>	1806

	AGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCTG GAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgttattgc agcttataatggttacaaataaagcaatagcatcacaatttcacaataaagcatttttttactgcattctagtgtggt ttgtccaaactcatcaatgtatcttatAAGAGGAAAAAGCAAGTTGCTCCAGAAAAACCTGTAAAGAA ACAAAAGACAGGTGAGACTTCGAGAGCCCTGTCATCTTCTAAACAGAGCAGCAGCAGCAG AGATGATAACATGTTTCAGGTAAAGTTGGCTATTTTTTTTTTTTTTTTTTTGACATGGAGTCA TGCTCTGTCACCAGGCTGGAGTGCAGTGGCGCCATCTCGGCTCACTGCAACCTCAGCCTCC TGAGTTCAAGCAGTTCTGCCTCAGCCTCCCGAGTAGCTAGGATTACAGGCATCCGCCACC AGACCTGGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTACCATCTTGCCAGGCTGGT CTTGAACTCTGACCTTGTGATCCAACCTGCCTCAGCCTCAAAAAGTGTGGGTTTACAGGTG TGAGCCACCATGCCTTGCCAAAGTTGGCTGTTCTTT	
pARBI- 965: SUB1_3_ Endogeno us_72	AATTAGTATATCTGCTTCGTAAATAAGTAACTGACTAGCCTTAGTAGACTGTGGTTTCCAG GTTTATTGAGAAGTAGCAAGATCCCTCCATTTTTTTTTTCTACCAAGAAATCGTATGTTGGGAT CCCCAACACAAAATAACCGTTCCTGTGGTTAATACTACTATAATGCCTGAAGTGTCTTTTG GGATCCTGAGAACAGAGTTTGAAAACATTACTAGACAGAAGGATTGGTTAGATTCATAGTT TTGTTGTTGAGTGAACTTGCTTATGTATATATTATGATATTTTGGATGTAGTCTTTTGATT GTTTAAATCTTAAAAAGTAATGGGATCTTTTGACACTGGGGTATGTTTTATTTTATGTGTGC AAATTTTAAACCATATCTTTTCTAGTTAAAGAGGAAAAAGCAAGTTGCTCCAGAAAAACCTG TAAAGAAACAAAAGTccggatccggagagggcaggggatctctcttacttgtggcgacgtggaggagaacccc ggccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGCTGGTTCGAGC TGACGGCGCAGCTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCC ACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGCAAGCTGCCGTGCCCTGGC CCACCTCTGTGACCACCTGACCTACGGCGTGCAGTGCTTACGCCGTACCCCGACCACATG AAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCT TCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCC TGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGC ACAAGCTGGAGTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAA CGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGC CGACCATACCAGCAGAACACCCCATCGGCGACGCGCCCGTGCTGCTGCCGACAACAC TACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCC TGCTGGAGTTCTGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgt ttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaataaagcatttttttactgcattctag ttgtggtttgtccaaactcatcaatgtatcttatACAGGTGAGACTTCGAGAGCCCTGTCATCTTCTAAAC AGAGCAGCAGCAGCAGAGATGATAACATGTTTCAGGTAAAGTTGGCTATTTTTTTTTTTTTT TTTTTTGACATGGAGTCTGCTCTGTCACCAGGCTGGAGTGCAGTGGCGCCATCTCGGCTC ACTGCAACCTCAGCCTCCTGAGTTCAAGCAGTTCTCTGCCTCAGCCTCCCGAGTAGCTAGGA TTACAGGCATCCGCCACCAGACCTGGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTACC CATCTTGGCCAGGCTGGTCTTGAACCTCTGACCTTGTATCCAACCTGCCTCAGCCTCAAAA GTGCTGGGTTTACAGGTGTGAGCCACCATGCCTTGCCAAAGTTGGCTGTTTCTTTAGATTCA GAGGAATTATTATCTGGCTTGATCTGAAGAATGTTAAAAGT	1806
pARBI- 966: TET2_1_E ndogeno us_73	CACATTTTAATTTTTGTTCCATGCTCTTTAGAATTCAACTAGAGGGCAGCCTTGTTGGATGGC CCCGAAGCAAGCCTGATGGAACAGGATAGAACCAACCATGTTGAGGGCAACAGACTAAGT CCATTCTGATACCATCACCTCCATTTGCCAGACAGAACCTCTGGCTACAAAGCTCCAGAA TGGAAGCCCACTGCCTGAGAGAGCTCATCCAGAAGTAAATGGAGACACCAAGTGGCACTCT TTCAAAGTTATTATGGAATACCTGTATGAAGGGAAGCCAGAATAGTCGTGTGAGTCTCTG ACTTTACACAAGAAAGTAGAGGGTATTCCAAGTGTGCAAAATGGAGGAATAAAACGCAC AGTTAGTGAACCTTCTCTCTGGCTCCTTCAGATCAAGAAATTGAAACAAGACCAAAAAGG CTAATGGAGAAAAGACGTAACtccggatccggagagggcaggggatctctcttacttgtggcgacgtggagga gaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGGT CGAGCTGGACGGCGCAGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCG ATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGCAAGCTGCCGTGCC CTGGCCACCTCTGTGACCACCTGACCTACGGCGTGCAGTGCTTACGCCGTACCCGACC ACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCAC CATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGA CACCTGTGTAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCT	1806

	GGGGCACAAGCTGGAGTACAACATAACAGCCACAACGTCTATATCATGGCCGACAAGCA GAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCA GCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCGAC AACCCTACCTGAGCAGCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACA TGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTCGGCATGGACGAGCTGTACAA atgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaaataaagcattttttcactg cattctagttgtggtttgtccaaactcatcaatgtatcttatTTCGGGGTAAGCCAAGAAAGAAATCCAGGT GAAAGCAGTCAACCAAATGTCTCCGATTGAGTGATAAGAAAGAATCTGTGAGTTCTGTAG CCCAAGAAAATGCAGTTAAAGATTTACCCAGTTTTTCAACACATAACTGCAGTGGGCCTGAA AATCCAGAGCTTCAGATTCTGAATGAGCAGGAGGGGAAAAAGTGCTAATTACCATGACAAG AACATTGTATTACTTAAAAACAAGGCAGTGCTAATGCCTAATGGTGCTACAGTTTCTGCCTC TTCCGTGGAACACACACATGGTGAACCTCTGGAAAAAACACTGTCTCAATATTATCCAGATT GTGTTTCCATTGCGGTGCAGAAAACCATCTCACATAAATGCCATTAACAGTCAGGCTACT AATGAGTTGTCTGTGAGATCACTACCCATCGCATACCTCAGGGCAGATC	
pARBI- 967: TET2_2_E ndogeno us_74	AATGGAGAAAGACGTAACCTCGGGGTAAAGCCAAGAAAGAAATCCAGGTGAAAGCAGTCAA CCAAATGTCTCCGATTGAGTGATAAGAAAGAATCTGTGAGTTCTGTAGCCCAAGAAATG CAGTTAAAGATTTACCCAGTTTTTCAACACATAACTGCAGTGGGCCTGAAATCCAGAGCTT CAGATTCTGAATGAGCAGGAGGGGAAAAAGTGCTAATTACCATGACAAGAACATTGTATTAC TTAAAAACAAGGCAGTGCTAATGCCTAATGGTGCTACAGTTTTCTGCCTCTTCGTGGAACAC ACACATGGTGAACTCCTGGAAAAAACACTGTCTCAATATTATCCAGATTGTGTTTCCATTGC GGTGACAGAAAACCATCTCACATAAATGCCATTAACAGTCAGGCTACTAATGAGTTGTCTCT GTGAGATCACTACCCATCGTccggatccggagagggcaggggatctctccttactgtggcgacgtggagga gaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGGT CGAGCTGGACGGCGACGTAACCGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCG ATGCCACCTACGGCAAGCTGACCTGAAGTTTCTGTGACACCGGCAAGCTGCCGTGCC CTGGCCACCTCTGTGACCACCTGACCTACGGCGTGCACTGCTTACCGCGTACCCCGACC ACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCAC CATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGAGGTGAAGTTCCAGGGCGA CACCTGTGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCT GGGGCACAAGCTGGAGTACAACATAACAGCCACAACGTCTATATCATGGCCGACAAGCA GAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCA GCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCGAC AACCCTACCTGAGCAGCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACA TGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTCGGCATGGACGAGCTGTACAA atgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaaataaagcattttttcactg cattctagttgtggtttgtccaaactcatcaatgtatcttatCATACCTCAGGGCAGATCAATTCGCACAGA CCTTAACCTCTGAGCTGCCTCAAAGCCAGCTGCAGTGGTGAGTGAGGCCTGTGATGCTGA TGATGCTGATAATGCCAGTAACTAGCTGCAATGCTAAATACCTGTTCTTTTTCAGAAACAG AACTAACAACAACAAAATCAGTTTTTGAGATATGCCATCTCCTGCAGAAAATAACATC CAGGGAACCAAAAGCTAGCGTCTGGTGAAGAATTCTGTTGAGGTTCCAGCAGCAATTTGC AAGCTCCTGGTGGCAGCTCTGAACGGTATTTAAAAACAAAATGAAATGAATGGTGCTTACTT CAAGCAAAGCTCAGTGTCTACTAAGGATTCCTTTTCTGCCACTACCACACCACCACCATC ACAATTGCTTCTTTCTCCCCCTCCTCCTCTCCACAGGTTCTCAGCTT	1806
pARBI- 968: TET2_3_E ndogeno us_75	GGAAAAAGCACTCTGAATGGTGGAGTTTTAGAAGAACACCACCACTACCCCAACCAAAGTA ACACAACACTTTTTAAGGGAAGTGAAATAGAGGGTAAACCTGAGGCACCACTTCCCAGAG TCCTAATCCATCTACACATGTATGCAGCCCTTCTCCGATGCTTTCTGAAAGGCCTCAGAATAA TTGTGTGAACAGGAATGACATACAGACTGCAGGGACAATGACTGTTCCATTGTGTTCTGAG AAAACAAGACCAATGTACAGAACACTCAAGCATAACCCACCAATTTTTGGTAGCAGTGGAG AGCTACAGGACAACCTGCCAGCAGTTGATGAGAAACAAAGAGCAAGAGATTCTGAAGGGTC GAGACAAGGAGCAACACGAGATCTTGTCGCCCAACACAGCACTATCTGAAACCAGGAT GGATTGAATTGAAGGCCCTCGTtccggatccggagagggcaggggatctctccttactgtggcgacgtgga ggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCT GGTCGAGCTGGACGGCGACGTAACCGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGG GCGATGCCACCTACGGCAAGCTGACCTGAAGTTTCTGTGACACCGGGCAAGCTGCCCGT GCCCTGGCCACCTCGTGACCACCTGACCTACGGCGTGCACTGCTTACGCCGTACCCCG	1806

	<p>ACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCG CACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGAGGTGAAGTTCGAGGGC GACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATC CTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCTATATCATGGCCGACAAGC AGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGC AGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCGA CAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCAC ATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTGGCATGGACGAGCTGTACA Aatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaaataaagcattttttcact gcattctagtgtgtgttgcacaaactcatcaatgtatcttatTTTCACCAAGCGGAATCCCATCTAAAACGT AATGAGGCATCACTGCCATCAATTCTCAGTATCAACCCAATCTCTCCAATCAAATGACCTCC AAACAATACACTGGAATTTCAACATGCCTGGGGGGCTCCCAAGGCAAGCTTACACCCAGA AAACAACACAGCTGGAGCACAAGTCAAAATGTACCAAGTTGAAATGAATCAAGGGCAGT CCCAAGGTACAGTGGACCAACATCTCCAGTTCCAAAAACCTCACACCAGGTGCATTCTCC AAAACAGACATTTACCAAAAGCTCATGTGCAGTCACTGTGTGGCACTAGATTTTCAATTTTCA ACAAAGAGCAGATTCCCAAACTGAAAACTTATGTCCCAAGTGTGAAACAGCACTTGAAT CAACAGGCTTCAGAGACTGAGCCATTTTCAAACCTCACACCTTTTGCAACAT</p>	
<p>pARBI- 969: TIGIT_1_E ndogeno us_76</p>	<p>AAAGGGAGGTTGAGATGGGCTGAGGTCTTCTAGGAGGCGGGGAGGGAGTGCAGCCTTGA CAAGCCTCCTGTGGGCGAGGTGTAAAGAGGGGAGAGTACAGTACAGTCTGGAAGCATAGGGC AGTGGGTGGGGAGGAGATGGGCTGGGCTGGGCTGGAGTAGAGATGTGTGGAGAAGGGT GAGAAGACTGGAAGACAACCTGAATGGGGGACTGGGAGCCTTGAATAACAGGCATGGA GAGGAGCGTCTTGAATGGAAGAAACAGGAAATAATTACAGCCTCTATGGAGGAGCAA CAGGATGGACTGGAGAACTATCATTCCAAAATCCAGTTGGGGCCTCAAAGGCCCTTAGAA TTTTTCTAGGAAGGTTGAAGGCCAGCTGCTGACCCAGGACTCACATGTGCTTCGTCTCTTC CCTAGGAATGATGACAGGCACAATAGAAACAtccggatccggagagggcaggggatctctcttacttgt ggcgacgtggaggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGT GCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGA GGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTTCATCTGCACCACGGCAA GCTGCCCGTGCCCTGGCCACCTCGTGACCACCTGACCTACGGCGTGCACTGCTTCAGCC GCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGT CCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGAGGTGAA GTTGAGGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA CGGCAACATCCTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCTATATCATG GCGGACAAGCAGAGAAGACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGAC GGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGC TGCTGCCCCACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAA GCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGGAC GAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaaataa agcattttttcactgcattctagtgtgtgttgcacaaactcatcaatgtatcttatACGGGGAACATTTCTGCAG AGAAAGGTGGCTCTATCATCTTACAATGTCACCTCTCCTCCACCACGGCACAAGTGACCCAG GTCAACTGGGAGCAGCAGGACCAGCTTCTGGCCATTTGTAATGCTGACTTGGGGTGGCACA TCTCCCCATCCTTCAAGGATCGAGTGCCCCAGGTCCCGGCTGGGCTCACCTCCAGTCG CTGACCGTGAACGATACAGGGGAGTACTTCTGCATCTATCACACCTACCTGATGGGACGT ACACTGGGAGAATCTTCTGGAGGTCCTAGAAAGCTCAGGTATTCTGCTGGAGCAAGTTG GTGGATAAACCTCTCCCTCTAGCATAGAAAAATGCAATCCTGAAACACTGCACAGCAGGGCT TCTCAATTCGGGATCACATTTGAATCACCTGAGGAGATTTTAAATCATACTGATGCCGAGGC C</p>	1806
<p>pARBI- 970: TIGIT_2_E ndogeno us_77</p>	<p>GAGGAGATGGGCTGGGCTGGGCTGGAGTAGAGATGTGTGGAGAAGGGTGAGAAGACTG GAAAGACAACCTGAATGGGGGACTGGGAGCCTTGAATAACAGGCATGGAGAGGAGCGTC TCTTGAAATGGAAGAAACAGGAAATAATTACAGCCTCTATGGAGGAGCAACAGGATGGAC TGGAGAAACTATCATTCCAAAATCCAGTTGGGGCTCAAAGGCCCTTAGAATTTTCTAGGA AGGTTGAAGGCCAGCTGCTGACCCAGGACTCACATGTGCTTCGTCTCTTCCCTAGGAATG ATGACAGGCACAATAGAAACAACGGGGAAACATTTCTGCAGAGAAAGGTGGCTCTATCATCT TACAATGTCACCTCTCCTCCACCACGGCACAAGTGACCCAGGTCAACTGGGAGCAGCAGGA CCAGCTTCTGGCCATTTGTAATGCTGACtccggatccggagagggcaggggatctctcttacttgtggcga</p>	1806

	<p>cgtggaggagaacccccggccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCC ATCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCGGCGAGGGC GAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACGGCAAGCTGC CCGTGCCCTGGCCACCTCGTGACCACCTGACCTACGGCGTGCACTGCTTCAGCCGCTAC CCCGACCACATGAAGCAGCACGACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAGG AGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGA GGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAA CATCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAACGTCTATATCATGGCCGAC AAGCAGAAGAAGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAGGACGGCAGC GTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGTGC CCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCG ATCATATGGTCTGCTGGAGTTCGTGACCGCGCGGGATCACTCTCGGCATGGACGAGCT GTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattt ttttcactgcatttagttgtgtgttgcctcaactcatcaatgtatcttatTTGGGGTGGCACATCTCCCCATCT TCAAGGATCGAGTGCCCCAGGTCCCGGCCTGGGCCTCACCTCCAGTCGCTGACCGTGAA CGATACAGGGGAGTACTTCTGCATCTATCACACCTACCCTGATGGGACGTACACTGGGAGA ATCTTCTGGAGGTCTAGAAAGCTCAGGTATTCCTGCTGGAGCAAGTTGGTGGATAAACC TCTCCCTTAGCATAGAAAATGCAATCCTGAAACACTGCACAGCAGGGCTTCTCAATTCGGG ATCATCTTGAATCACCTGAGGAGATTTAAATCATACTGATGCCGAGGCCTCACCGAGACC AATTCATCAGAATCCCTAATAGCAGAGCTAAACAAGGGTAAGGTCTAAAAGCATTTCCAG GTGATTCTAATGGGCAGCAATACTGAGAACCACTGTTCTTATGTAAGAAGCACATC</p>	
pARBI- 971: TIGIT_3_E ndogeno us_78	<p>CCTCCCTGTGGGCGAGGTGTAAAGAGGGGCGAAGTCAGCTCTGGAAGCATAGGGCAGT GGGTGGGGAGGAGATGGGCTGGGCTGGGCTGGAGTAGAGATGTGTGGAGAAGGGTGAG AAGACTGGAAAGACAACCTGAATGGGGGACTGGGAGCCTTGAATAACAGGCATGGAGAG GAGCGTCTCTTGAAATGGAAGAAACAGGAAATAATTACAGCCTCTATGGAGGAGCAACAG GATGGACTGGAGAACTATCATTTCCAAAATCCAGTTGGGGCCTCAAAGGCCCTTAGAATTT TTCTAGGAAGGTTGAAGGCCAGCTGCTGACCCAGGACTCACATGTGCTTCGTCTCTTCCT AGGAATGATGACAGGCACAATAGAAACAACGGGGAACATTTCTGCAGAGAAAGGTGGCTC TATCATCTTACAATGTCACTCTCCTCCACtccggatccggagagggcaggggatctctccttactgtggc gacgtggaggagaacccccggccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCC CATCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGG CGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACGGCAAGCTG CCCGTGCCCTGGCCACCTCGTGACCACCTGACCTACGGCGTGCACTGCTTCAGCCGCTA CCCCGACCACATGAAGCAGCACGACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAG GAGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCG AGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCA ACATCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAACGTCTATATCATGGCCGA CAAGCAGAAGAAGCGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAGGACGGCAG CGTGCACTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGTG CCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGC GATCATATGGTCTGCTGGAGTTCGTGACCGCGCGGGATCACTCTCGGCATGGACGAGC TGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcatt ttttcactgcatttagttgtgtgttgcctcaactcatcaatgtatcttatACGGCACAAGTGACCCAGGTCAAC TGGGAGCAGCAGGACCACTTCTGGCCATTTGTAATGCTGACTTGGGGTGGCACATCTCCC CATCTTCAAGGATCGAGTGGCCCCAGGTCCCGGCCTGGGCCTCACCTCCAGTCGCTGAC CGTGAAACGATACAGGGGAGTACTTCTGCATCTATCACACCTACCCTGATGGGACGTACACT GGGAGAATCTTCTGGAGTCTAGAAAGCTCAGGTATTCTGCTGGAGCAAGTTGGTGG ATAAACCTCTCCCTTAGCATAGAAAATGCAATCCTGAAACACTGCACAGCAGGGCTTCTCA ATTCCGGATCACATTTGAATCACCTGAGGAGATTTAAATCATACTGATGCCGAGGCCTCAC CCAGACCAATTCAATCAGAATCCCTAATAGCAGAGCTAAACAAGGGTAAGGTCTAAAAG</p>	1806
pARBI- 972: TRAC_1_ Endogeno us_79	<p>TAATGCCAGCCTAAGTTGGGGAGACCACTCCAGATTCGAAGATGTACAGTTTGCTTTGCTG GGCCTTTTTCCCATGCCTGCTTTACTCTGCCAGAGTTATATTGCTGGGGTTTTGAAGAAGAT CCTATTAATAAAAGAATAAGCAGTATTATTAAGTAGCCCTGCATTTACAGTTTCTTGAGT GGCAGGCCAGGCCTGGCCGTGAACGTTCACTGAAATCATGGCCTCTTGCCCAAGATTGATA GCTTGTGCCTGTCCCTGAGTCCAGTCCATCACGAGCAGCTGGTTTCTAAGATGCTATTTC</p>	1806

	<p>CGTATAAAGCATGAGACCGTGACTTGCCAGCCCCACAGAGCCCCGCCCTTGTCATCACTG GCATCTGGACTCCAGCCTGGGTTGGGGCAAAGAGGGAAATGAGATCATGCTTAACCTG ATCCTCTTGTCACAGATtccggatccggagagggcaggggatctctcttacttggtgagcgtggaggaga accccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCATCCTGGTC GAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGA TGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGCAAGCTGCCCCGTCCT GGCCACCCCTCGTGACCACCTGACCTACGGCGTGCACTGCTTCAGCCGTACCCCGACCA ATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCCCAAGGCTACGTCCAGGAGCGCACCA CTTCTTCAAGGACGACGGCACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACA CCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGG GGCACAAGCTGGAGTACAATAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAA GAACGGCATCAAGGTGAAGTTCAGATCCGCCACAACATCGAGGACGGCAGCGTGAGCT CGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAAC CACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATG GTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatg attgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaataaagcattttttactgcat tctagtgtggtttgtccaaactcatcaatgtatcttatATCCAGAACCCTGACCTGCCGTGACCACTG AGAGACTCTAAATCCAGTGACAAGTCTGTCTGCCTATTACCGATTTTGATTCTCAAAACAAAT GTGTACAAAGTAAGGATTCTGATGTGTATATCACAGACAAAAGTGTGCTAGACATGAGGT CTATGGACTTCAAGAGCAACAGTGTGTGGCCTGGAGCAACAATCTGACTTTGCATGTGC AAACGCCTTCAACAACAGCATTATTCAGAAGACACCTTCTCCCCAGCCAGGTAAGGGCA GCTTTGGTGCCTTCGAGGCTGTTTCCTTGCTTCAGGAATGGCCAGGTTCTGCCAGAGCTC TGGTCAATGATGTCTAAACTCCTCTGATTGGTGGTCTCGGCCTTATCCATTGCCACCAAAA CCCTCTTTTACTAAGAAACAGTGAGCCTTGTCTGGCAGTCCAGA</p>	
pARBI- 973: TRAC_2_ Endogeno us_80	<p>GATTCCAAGATGTACAGTTTGCTTTGCTGGGCCCTTTTCCCATGCCTGCTTTACTCTGCCAG AGTTATATTGCTGGGGTTTTGAAGAAGATCCTATTAATAAAAAGAAATAGCAGTATTATTA GTAGCCCTGCATTTTCAGGTTTCTTGAGTGGCAGGCCAGGCCTGGCCGTGAACGTTCACTG AAATCATGGCCTCTTGCCCAAGATTGATAGCTTGCTGTCCCTGAGTCCCAGTCCATCAC GAGCAGCTGGTTTCTAAGATGCTATTTCCCGTATAAAGCATGAGACCGTGACTTGCCAGCCC CACAGAGCCCCGCCCTTGTCATCACTGGCATCTGGACTCCAGCCTGGGTTGGGGCAAGA GGGAAATGAGATCATGCTTAACCTGATCCTCTTGTCACAGATATCCAGAACCCTGACC CTGCCGTGTACCAGTGtccggatccggagagggcaggggatctctcttacttggtgagcgtggaggagaac cccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCATCCTGGTCTGA GCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATG CCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGCAAGCTGCCCCGTGCCCTG GCCCACCCCTCGTGACCACCTGACCTACGGCGTGCACTGCTTCAGCCGCTACCCCGACCA TGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCCCAAGGCTACGTCCAGGAGCGCACCAT CTTCTTCAAGGACGACGGCACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACAC CCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGG GCACAAGCTGGAGTACAATAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAG AACGGCATCAAGGTGAAGTTCAGATCCGCCACAACATCGAGGACGGCAGCGTGACGCTC GCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACC ACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGT CCTGCTGGAGTTCTGTACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgat tgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaataaagcattttttactgcatc tagttgtggtttgtccaaactcatcaatgtatcttatAGAGACTCTAAATCCAGTGACAAGTCTGTCTGCCT ATTACCGATTTTGATTCTCAACAAATGTGTACAAAGTAAGGATTCTGATGTGTATATCA CAGACAAAAGTGTGCTAGACATGAGGTCTATGGACTTCAAGAGCAACAGTGTGTGGCCTG GAGCAACAATCTGACTTTGCATGTGCAACGCCTTCAACAACAGCATTATTCAGAAGACA CCTTCTTCCCCAGCCAGGTAAGGGCAGCTTTGGTGCCTTCGAGGCTGTTTCCTTGCTTCA GGAATGGCCAGGTTCTGCCAGAGCTCTGGTCAATGATGTCTAAACTCCTCTGATTGGTG GTCTCGGCCTTATCCATTGCCACCAAAACCTCTTTTACTAAGAAACAGTGAGCCTTGTCT GGCAGTCCAGAGAATGACACGGGAAAAAAGCAGATGAAGAGAAG</p>	1806
pARBI- 974:	<p>TTCTGTGGTAGCGGAACTACTAAGGGGCCATCTGGACCCGAGGTATTGTGATGATAAA TTCTGAGCACTACCCATCCCAAGGGGCTCAGAAATAAATAAGAGCCAAGTCTAGTC</p>	1806

TRAC_3_ Endogeno us_81	<p>GGTGTTCCTGCTCTGAAACACAATACTGTTGGCCCTGGAAGAATGCACAGAATCTGTTTGT AAGGGGATATGCACAGAAGCTGCAAGGGACAGGAGGTGCAGGAGCTGCAGGCCTCCCC ACCCAGCCTGCTCTGCCTTGGGGAAAACCGTGGGTGTCTCTGCAGGCCATGCAGGCCTGG GACATGCAAGCCATAACCGCTGTGGCCTCTTGGTTTTACAGATACGAACCTAACTTTCAA AACCTGTCAGTGATTGGGTTCCGAATCTCTCTCTGAAAGTGGCCGGGTTTAATCTGCTCAT GACGCTGCGGCTGTGGTCCAGCtccggatccggagagggcaggggatctctcttactgtggcgacgtgga ggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCT GGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGG GCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGT GCCCTGGCCCAACCCTCGTGACCACCTGACCTACGGCGTGCAAGTCTCAGCCGCTACCCCG ACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCG CACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGC GACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATC CTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATGGCCGACAAGC AGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGC AGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCGA CAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCAC ATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTGGCATGGACGAGCTGTACA Aatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaaatttcacaaataaagcattttttcact gcattctagttgtggtttgtccaaactcatcaatgtatcttatTGAGGTGAGGGGCCCTTGAAGCTGGGAGTG GGGTTTAGGGACGCGGGTCTCTGGGTGCATCCTAAGCTCTGAGAGCAAACCTCCTGCAGG GTCTTGCTTTAAGTCAAAGCCTGAGCCCACTCAACTCTCTACTTCTTCTGTTACAAAT CCTCTGTGCAATAATAATGGCCTGAAACGCTGTAATAATCTCATTTCAGCCGCTCAGTT GCACTTCTCCCTATGAGGTAGGAAGAAGAGTTGTTTGAAGACGAAGAACTGAGGCCCA CAGCTAATGAGTGAGGAAGAGAGACACTTGTGTACACCACATGCCTTGTGTTGACTTCT CTCACCGTGTAACTCCTCATGTCTCTCTCCCACTACGGCTCTCTTAGCTCAGTAGAAAAG AGACATTACACTCATATTACCCCAATCCTGGCTAGAGTCTCCGCACC</p>	
pARBI- 975: TRAC_4_ Endogeno us_82	<p>ATTATTAAGTAGCCCTGCATTTAGGTTTCTTGTAGTGCCAGGCCAGGCTGGCCGTGAAC GTTCACTGAAATCATGGCCTCTTGGCCAAGATTGATAGCTTGTGCCTGTCCCTGAGTCCAG TCCATCACGAGCAGCTGGTTTCTAAGATGCTATTTCCCGTATAAAGCATGAGACCGTGACTT GCCAGCCCCACAGAGCCCCGCCCTTGTCCATCACTGGCATCTGGACTCCAGCCTGGGTTGG GGCAAAGAGGGAAATGAGATCATGTCTAACCCTGATCCTTGTCCACAGATATCCAGA ACCCTGACCCTGCCGTGTACCAGCTGAGAGACTCTAAATCCAGTGACAAGTCTGTCTGCCTA TTACCCGATTTTGATTCTCAAACAAATGTGTACAAAGTAAGGATTCTGATGTGTATAC AGACAAAAGTGTGCTAGACtccggatccggagagggcaggggatctctcttactgtggcgacgtggaggag aaccggccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCTGGTC GAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGA TGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGCAAGCTGCCCGTGCCT GGCCACCCCTCGTGACCACCTGACCTACGGCGTGCAAGTCTCAGCCGCTACCCGACCA ATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGACCA TCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACA CCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGG GGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATGGCCGACAAGCAGAA GAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGACGCT CGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAAC CACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATG GTCCTGCTGGAGTTCTGTGACCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatg attgtttattgcagcttataatggttacaaataaagcaatagcatcacaaatttcacaaataaagcattttttcactgcat tctagttgtggtttgtccaaactcatcaatgtatcttatATGAGGTCTATGGACTTCAAGAGCAACAGTGCT GTGGCCTGGAGCAACAACTGACTTTGCATGTGCAAACGCCTTCAACAACAGCATTATTCC AGAAGACACCTTCTCCCCAGCCAGGTAAGGGCAGCTTTGGTGCCTTCGAGGCTGTTTCC TTGCTTCAGGAATGGCCAGGTTCTGCCAGAGCTCTGGTCAATGATGTCTAAACCTCCTCTG ATTGGTGGTCTCGGCCTTATCCATTGCCACCAAAACCTCTTTTACTAAGAAACAGTGAGC CTTGTCTGGCAGTCCAGAGAATGACACGGGAAAAAAGCAGATGAAGAGAAGGTGGCAG</p>	1806

	GAGAGGGCACGTGGCCAGCCTCAGTCTCTCCAAGTGAAGTTCCTGCCTGCCTTTGCTC AGAGTGTGGCCCTTACTGCTCTTCTAGGCCTCATTCTAAGCCCTT	
pARBI- 976: TRAC_6_ Endogeno us_84	TTCATTTCCATTGAGTTGTTCTTATTGAGTCATCCTTCTGTGGTAGCGGAACCTACTAAGG GGCCCATCTGGACCCGAGGTATTGTGATGATAAATTCTGAGCACCTACCCCATCCCCAGAA GGGCTCAGAAATAAATAAGAGCCAAGTCTAGTCGGTGTTCCTGTCTTGAAACACAATAC TGTTGGCCCTGGAAGAATGCACAGAATCTGTTTGTAAAGGGGATATGCACAGAAGCTGCAA GGGACAGGAGGTGCAGGAGCTGCAGGCCTCCCCACCCAGCCTGCTCTGCCTTGGGGAAA ACCGTGGGTGTGTCCTGCAGGCCATGCAGGCCTGGGACATGCAAGCCCATAACCGCTGTG GCCTCTTGGTTTTACAGATACGAACCTAACTTTCAAAACCTGTCAGTGATTGGGTTCGGAA TCCTCTCTGAAAGTGGCCGGGtccggatccggagagggcaggggatctctcttactgtggcgacgtgga ggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCT GGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGG GCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCCG GCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTACGCCGTACCCCG ACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCG CACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGC GACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATC CTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATCATGGCCGACAAGC AGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGC AGCTCGCCGACCACTACCGACGAACACCCCATCGGCGACGGCCCGTGTGCTGCCCGA CAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCAC ATGGTCTGTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACA Aatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattttttact gcattctagttgtgtgttgcacaaactcatcaatgtatcttatTTAATCTGCTCATGACGTGCGGTGTGG TCCAGCTGAGGTGAGGGGCTTGAAGCTGGGAGTGGGGTTAGGGACGCGGGTCTCTGG GTGCATCCTAAGCTCTGAGAGCAAACCTCCCTGCAGGGTCTTGCTTTAAGTCCAAAGCCTG AGCCACCAAACCTCTCCTACTTCTTCTGTACAAATTCCTCTGTGCAATAATAATGGCCTG AAACGCTGTAAATATCCTCATTTAGCCGCTCAGTTGCACTTCTCCCTATGAGGTAGGA AGAACAGTTGTTTGAACAGGAAGAACTGAGGCCCCACAGCTAATGAGTGGAGGAAGAGA GACACTTGTGTACACCATGCCTTGTGTTGTACTTCTCTACCGTGTAACCTCCTCATGTCC TCTCTCCCAGTACGGCTCTTAGCTCAGTAGAAAGAAGACATTACACTC	1806
pARBI- 977: TRAC_En dogenous _83	CAGTCCATCACGAGCAGCTGGTTTCTAAGATGCTATTTCCCGTATAAAGCATGAGACCGTGA CTTGCCAGCCACAGAGCCCGCCCTGTCCATCACTGGCATCTGGACTCCAGCCTGGGTT GGGGCAAAGAGGGAAATGAGATCATGTCTAACCTGATCCTTGTCCACAGATATCCA GAACCTGACCTGCCGTGTACCAGCTGAGAGACTCTAAATCCAGTGACAAGTCTGTCTGC CTATTCACCGATTTTGATTCTCAAACAAATGTGTCAAAAGTAAGGATTCTGATGTGTATATC ACAGACAAAATGTGCTAGACATGAGGTCTATGGACTTCAAGAGCAACAGTGTGTGGCCT GGAGCAACAAATCTGACTTTGCATGTGCAACGCCTTCAACAACAGCATTATTCCAGAGA CACCTTCTTCCCAGCCCAAtccggatccggagagggcaggggatctctcttactgtggcgacgtggaggaga accccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGGTC GAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGA TGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCCGTGCCCT GGCCACCCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTACGCCGTACCCCGACCA ATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCA TCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACA CCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGG GGCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAA GAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGACGT CGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCGTGTGCTGCTGCCGACAAC CACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCATATG GTCCTGCTGGAGTTCGTGACCGCCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatg attgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattttttactgcat tctagttgtgtgttgcacaaactcatcaatgtatcttatGTAAGGGCAGCTTTGGTGCCTTCGACGGCTGT TTCTTGCTTACGAATGGCCAGGTTCTGCCAGAGCTCTGGTCAATGATGTCTAAAACCTCC TCTGATTGGTGGTCTCGGCCTTATCCATTGCCACCAAAACCTCTTTTACTAAGAAACAGTG	1806

	AGCCTGTGTTCTGGCAGTCCAGAGAATGACACGGGAAAAAGCAGATGAAGAGAAGGTGGC AGGAGAGGGCAGCTGGCCAGCCTCAGTCTCTCCAACTGAGTTCTGCCTGCCTGCTTTGC TCAGACTGTTTGGCCCTTACTGCTCTTCTAGGCCTATTCTAAGCCCTTCTCAAGTTGCCTC TCCTATTCTCCCTGTCTGCCAAAAATCTTTCCAGCTCACTAAGTCAGTCTCACGCAGTC ACTCATTAACCCACCAATCACTGATTGTGCCGGCACATGAATG	
pARBI- 978: TRIM28_ 1_Endoge nous_85	TGAGGAAGAAGCGCGGGCGGCGCTTCGGGAGGCGAGCAGGCAGAGTTGGCCGTGCCG TAGCAGCGTCCCGCGCGCGGGCAGCGGCCAGGAGGCGCGTGGCGGCGCTCGGCCT CGCGGCGGGCGGGCGGGCAGCGGCCAGCAGTTGGCGGCGAGCGCGTCTGCGCCTGCGC GGCGGGCCCCGCGCCCTCTCCCCCTGGGCGCCCCGGCGGCGTGTGAATGGCGGCCCT CCGCGGCGGCAGCCTCGGCAGCAGCGGCTCGGCCGCTCTGGCAGCCCGGGCGCGGCG AGGGCTCCGCTGGCGGCGAAAAAGCGCTCCACCGCCCCCTCGGCCGAGCCTCGGCCTCTGC CTCAGCCGCGGCGTCTGTCGCCGCGGGGGCGGCGCCGAGGCGCTGGAGCTGTGGAGC ACTCGGCGTGTGCAGAGAGCGCCTGCGACCCtccggatccggagagggcaggggatctctcttactt gtggcgacgtggaggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGG TGCCCATCCTGTGTCAGCTGGACGGCGACGTAAACGCCACAAGTTACGCGTGTCCGGCG AGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCACCGGCA AGCTGCCCCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTACG CGCTACCCCGACCACATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCGAAGGCTACG TCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGAGGTGAA GTTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA CGGCAACATCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATG GCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTTCAAGATCCGCCACAACATCGAGGAC GGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGC TGCTGCCCCACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAA GCGCGATCACATGGTCTGTGGAGTTCGTGACCGCCCGCGGGATCACTCTCGGCATGGAC GAGCTGTACAAatgattgtttattgagcttataatggttacaataaagcaatagcatcacaatttcacaataa agcatttttttactgattcttagttgtgtgtgttgcacaaactcatatgtatcttatGAGAGGGAGCCCCGCTGC TGCCCTGTTTGCATCTGGCCTGTAGTGCCTGCTTAGGGCCCCGCGCCCCCGCGCGCCGAAC AGCTCGGGGGACGCGGGGGCGGGCGGCGACGGCACCGGTAAGTACGAAGTATCGGTGC CACCCCTCCCCCTACTCTCTGCCTTTGATTCCGACTGGGTGCAGAGATGAGGATGCCACCTG GGCGAGAGGATGGGGGGCCGGACAGGGCACGGGAAATACTTTCTGGGTCTGCATACGA ACGTGGGTTTTGTGCTGGCCGCTGAGATGGGACATCTGACTAAAGTTGGAGAAAAGAAGGC TCGGGGAGGGGAGGGGCTGGTTCGCTGCGGGATAATGGTCGGGGGCCACCCAGCAGGG GAATGTGGGGGCCATAACCTGGGTGGGAACTTGTAACAGTCTCCACATCCCTGCTTCTC GAAGTGGTG	1806
pARBI- 979: TRIM28_ 2_Endoge nous_86	TCGAAGTGGTGGACTGTCCCGTGTGCAAGCAACAGTGCTTCTCAAAGACATCGTGGAGAA TTATTTTCATGCGTGATAGTGGCAGCAAGGCTGCCACCGACGCCAGGATGCGAACCAGGTG CGTCTATCTCAGCAACCACAAGGAGGTTTCTGGGGAGGGGGCATCTGCGCAGGAGGAGC TTGGCACCAAGCTCCAGGCTGTTACTCCACTTTCCAAAGGCTCTGGGTGGGCTGCCTAGGTTG GGTCAAGGGACCAATCTTAAATCTCCGTTGTATTTCTGGGATGTAAACGTGGATCTATCA AGTTGTCTTGCTTCTCTGACCCTGCCTTTGTCTGGCAGTGCTGCACTAGCTGTGAGGATAA TGCCCCAGCCACCAGCTACTGTGTGGAGTGCTCGGAGCCTCTGTGTGAGACCTGTGTAGAG GCGCACCGCGGTGAAGTACtccggatccggagagggcaggggatctctcttacttgtggcgacgtggag gagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGGCCATCCTG GTGAGCTGGACGGCGACGTAAACGGCCACAAGTTACGCGTGTCCGGCGAGGGCGAGGG CGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTG CCCTGGCCCCACCCTCGTGACCACCCTGACCTACGGCGTGCACTGCTTACGCCGTACCCCGA CCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGC ACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTTCAGAGGGC GACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATC CTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATGGCCGACAAGC AGAAGAACGGCATCAAGGTGAAGTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGC AGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCCGA CAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCAC ATGGTCTGCTGGAGTTCTGTACCGCCCGCGGGATCACTCTGGCATGGACGAGCTGTACA	1806

	Aatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaaattcacaaataaagcattttttcact gcattctagttgtggtttgtccaaactcatcaatgtatcttatACCAAGGACCATACTGTGCGCTCTACTGGT ACATGAGGCTGAGGGGGGCTGTTGAGTTGTTCTCCCATGTGTGCCCTCAGTTGCTTTTATG ATGTTGGTTGCATCTGGTGGATGGGTCCTAGAGTTCTCTAGGGGGTGCCGCCGAAGGGCC CGAGGGCAGAACTCCAGAAGCAGAAAACTGGGGTTGTGGTGTGTAGTCTCTAGGGCCTA GGTGGGAGAGGGTGGGAAGGGGAAATAAGGGAGACCTTAATGTGCTGCAGGGAGGTAC AAAGGGTTTGAGAAGGCTTATCAGGGAGTTGTGACACCTGGTGGTGAAGGGCTCAGCATA TGCAACAGGGAAAGGCATGGTGTGAAGGGCTTTCTGGGTTTGTGGTTCCCTGGCACACAT CTGGTATAAGATGCTGCTAGGGAAAGTAGACTGTGGGTCCATGGATTATAAGTGATGA	
pARBI- 980: TRIM28_ 3_Endoge nous_87	GGCGCCCAATGCGCGTGC CGCGCGGCTCGGCGCCAGTTATTTCTGTCCCGCCCCCGGCC TCGGCTCTTTCTGCGAGCGGGCGCGCGGGCGAGCGTTGTGCTTGTGCTTGTGGCGCTG GTGCGGTTTCGGCGCGGGCTGAGGAAGAAGCGCGGGCGGCGCCTTCGGGAGGCGAGCA GGCAGCAGTTGGCCGTGCCGTAGCAGCGTCCCGCGCGCGGGCGGCGAGCGGCCAGGAGG CGCGTGCGGGCGCTCGGCCTCGCGCGGGCGGCGGCGGCGAGCGGCCAGCAGTTGCGGCG GAGCGCTCTGCGCCTGCGCGCGGGCCCCGCGCCCCCTCTCCCCCCTGGGCGCCCCCGG CGGCGTGTGAATGGCGGCTCCGCGGCGGCGAGCTCGGCGAGCAGCGGCTCGGCCGCTC TGGCAGCCCCGGCCCCGGCGAGGGCTCCGCTtccggatccggagaggcgaggatctctcttactgt ggcgacgtggaggagaaccccgccccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGT GCCCCCTCTGTGTCGAGCTGAGCGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGCGCA GGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCACTCTGCACCAACCGCAA GCTGCCGTGCCCTGGCCACCTCTGTGACCACCTGACCTACGGCGTGCAGTGCTTCAGCC GCTACCCCCACCATGAAGCAGCACGACTTCTCAAGTCCGCCATGCCGAAGGCTACGT CCAGGAGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAA GTTGAGGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA CGGCAACATCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATG GCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGAC GGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGC TGCTGCCCCACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAA CGCGATCACATGGTCTGCTGGAGTTCTGTGACCGCCCGGGGATCACTCTCGGCATGGAC GAGCTGTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaaattcacaaataa agcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatGGCGGCGAAAAGCGCTCCA CCGCCCCCTCGGCCGAGCCTCGGCCTCTGCCTCAGCCGCGGCTCGTGCCTCGCGGGGGG CGGCGCCGAGGCGCTGGAGCTGCTGGAGCACTCGGCGTGTGCAGAGAGCGCCTGCGAC CCGAGAGGGAGCCCCGCTGCTGCCTGTTTGACTCGGCCTGTAGTGCCTGCTTAGGGCC CGGCCCCCGCCCGCCAACAGCTCGGGGGACGGCGGGGCGGCGGGCGACGGCACCG GTAAGTACGAAGTGATCGGTGCCACCCCTCCCCCTACTCTGCTCTTGATTCCGACTGGGT GCAGAGATGAGGATGCCACCTGGGCGAGAGGATGGGGGGCCGGACAGGGCACGGGAAA TACTTTCTGGGTCTGCATACGAACGTGGGTTTGTGCTGGCCGCTGAGATGGGACATCTGA CTAAAGTTGG	1806
pARBI- 596: APRT_1_E xogenous _1	ATCTCGGCCAATAAAGGAGAAAGGGCGCGGCCGTACGCGCGCCAGGTGCGTGGGCGAG ACCAGCTACGCCCCCTCTCCAGCCGCCAAGGCCCCGCCCCACAGCTGCCTGGCTGCAGTC AGAAGCGTAGCCCGAGACAAGGAAGGGCGCCTTGACTCGCACTTTTGTCCGGTTCAACGT TCTGctcagtggtgctggaatgcgagcgctttaaactcgatggcgctaggagtcacatgaaataggTACAGG CTTCGCGGACGGATGCCCCGCCCTCACCCACGCTCCGCCCTCCGGGGATGCCCAACCCCT CGTGGCGGTCCGCCCCGTCCCCGCGCAGGCGCGCTCGGGCTGCCGTCTTCGCACGC GGCCATGGCCGACTCCGAGCTGCAGCTGTTGAGCAGCGGATCCGACGTTCCCGACTTC CCCCCCCCAtgacgactgtgccttctagttgacgacatctgtgtttgccccctccccgtgccttcttgacccctggaa ggtgccactcccactgtcctttcctaataaaatgaggaaattgcatgcattgtctgagtaggtgtcattctattctggggg gtggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgcggtgggctctatg ggGATCTCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCG AGAAGTTGGGGGAGGGTCCGCAATTGAACGGTGCCTAGAGAAGGTGGCGGGGT AAACTGGGAAAGTGATGTGCTGTAAGTCCGCTTTTCCGAGGGTGGGGGAGAACC GTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCAGAACAC AGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCCCGGCCCTACCTGAGGCCG CCATCCACGCCGTTGAGTCGCTTCTGCCCTCCCGCTGTGGTGCCTCTGAAGTGCCT	2541

	<p>CCGCGCTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCTCCCTTG GAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGT CTTTGTTTCTGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCTAGA GCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGGCC ATCCTGGTCGAGCTGGACGGCGACGTAAACGCCACAAGTTACGCGTGTCGGCGAGGGC GAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGC CCGTGCCCTGGCCACCCCTCGTGACCACCTGACCTACGGCGTGCACTGCTTACGCCGTAC CCCACCACATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCCCAAGGCTACGTCCAGG AGCGCACCATTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGGAGGTGAAGTTCGA GGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAA CATCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATGGCCGAC AAGCAGAAGAAGCGCATCAAGGTGAAGTCAAGATCCGCCACAACATCGAGGACGGCAGC GTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGC CCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCG ATCATATGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTGGCATGGACGAGCT GTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaataaagcattt tttactgcattctagttgtggtttgtccaaactcatcaatgtatcttatGGCGTGGTATTAGGTGCACGCAC AGGCCGCCCTCGTGCGCCCCGACCTGCGGGCCTACGGATGGGAGCGCGTGGCCCCGCGAC CTCCGGGCGGGCGGGCGGGAACCCCTCGTCTTTCGCCCGCGGGCCCTGCCCTCCTTCGCG CCCGCGCTACCCAGGCTGTCTTGGGTCCAGGGACATCTCGCCCGTCTGAAGGACCCCG CCTCCTTCGCGCCGCCATCGGCCTCTGGCGCGACACCTGAAGGCGACCCACGGGGGCCG CATCGACTACATCGCAGGCGAGTGCCAGTGCGCCGATCTAGGGCGCTTCGCCCTCTGCGC GCGCCGAGGGCAGCAGTGCGCTCTGCGCGTCTGCTTGGGGGAGGGCCTTTGGGGTGCTT CAGGGGGCGCCGGGACGGGCGCCGTGCTTGGGTGCGCCGGGAAGGGTTGTGAGATTGAG CCC</p>	
<p>pARBI- 597: APRT_2_E xogenous _2</p>	<p>TGCCCCGCCCTCACCACGCTCCGCCCTCCGGGGATGCCCCACCCCTCGTGCGGTCCCGC CCGTCCCCGCGCAGGCGCGCTCGGGCTGCCGCTGGCTTTCGCACGCGGCCATGGCCGACT CCGAGCTGCAGCTGGTTGAGCAGCGGATCCGAGCTTCCCGACTTCCCCACCCACAGGCGT GGTATTCAAGTGACGCACAGGCCGCCCTCGTGCGCCCCGACCTGCGGGCCTACGGATG GGAGCGGTGGCCCGCACCTCCGGGCGGGCGGGGCGGGAACCCCTCGTCTTTCGCCCGCG GGGCCCTGCCCTCCTTCGGCCCCGGCGTCAACAGGCTGTCTTGGGTCCAGGGACATCTC GCCCCGTCTGAAGGACCCCGCTCCTTCGCGCGCCCATCGGCCTCTGGCGCGACACCTG AAGGCGACCCACGGGGCGCGCATCtgacgactgtgcttctagttgccagccatctgtgtttgcccccccc gtgcttccttgacctggaaggtgacctccactgtccttcttaataaaatgaggaaattgcatcgattgtctgagta ggtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctg gggatgcggtgggctctatggGATCTGCGATCGTCCGGTGCCCGTCAGTGGGCGAGCGCACA TCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAG AAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCTGTACTGGCTCCGCCTTTTCCCCGAG GGTGGGGGAGAACCCTATATAAGTGCAAGTGTGCGCGTGAACGTTCTTTTCGCAACGGGT TTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCCCG CCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTCTGCGCCTCCCGCTGTGGTG CCTCTGAAGTGCCTCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGT CCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCCTGACCTGCT TGCTCAACTCTACGTCTTTGTTTCTGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACC GGCGCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTT ACCGGGGTGGTGCCATCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGC GTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGC ACCACCGGCAAGCTGCCGTGCCCTGGCCACCCCTCGTGACCACCTGACCTACGGCGTGC AGTGCTTACGCGCTACCCCGACCACATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCC GAAGGTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCG CCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACT TCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACG TCTATATCATGGCCGACAAGCAGAAGAAGGCATCAAGGTGAAGTTCAGATCCGCCACAA CATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGA CGGCCCGTGTGCTGCCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGAC</p>	2541

	<p>CCCAACGAGAAGCGGATCATATGGTCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTC TCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcaca aatttcacaataaagcatttttttactgcattctagttgtgtttgtccaaactcatcaatgtatcttatGACTACATC GCAGGCGAGTGCCAGTGGCCGCATCTAGGGCGCTTCCGCTCTGCGCGCGCCGAGGGCA GCACGTGGGCTCTGCGCTCTGCTTGGGGGAGGGCCTTGGGGTGCTTCAGGGGGCGCCG GGACGGGCGCCGTGCTTGGGTGCGCCGGGAAGGGTTGTGAGATTGAGCCCCGAGGCCG CCGCGCTGTGACGGCGTCTTCCCGCAGGTTCCGGGTCCCGAGCCAGGACAGGCGTGACC GAGTTGCCGGGTGAGTTGGTCTCCCTGGAGTGCCCAAGCTGAATCCACAGGGCCAGCTGC CTTGCTTCTTGTCTTCTGCGAGCTGGTATTGAGCGCTGCCACGAGCCAGGCTTCCCTG GTGAAGATCACGGAATGCCACCCAGGGAAGGGAGGCGCTTGAGGCGCTCCGGGAGAGCCC AAGAGGTGGCCAGGGAGA</p>	
pARBI- 598: APRT_3_E xogenous _3	<p>CGTTCTGctcagtggtgctggaatgcgagcgctcttaaaatcgatggcgctaggagtccatgaataacggTAC AGGCTTCCGGCGACGGATGCCCCGCCCCTACCCACGCTCCGCCCTCCGGGGATGCCCCAC CCCTCGTGGCGGTCCCGCCCGTCCCGCGCAGGCGCGCTCGGGCTGCCGCTGGCTCTTCGC ACGCGGCCATGGCCGACTCCGAGCTGCAGCTGTTGAGCAGCGGATCCGAGCTTCCCCG ACTTCCCCACCCAGGCGTGGTATTAGGTGCACGCACAGGCCGCCCTCGTGCGCCCCGA CCTGCGGGCTACGGATGGGAGCGCGTGGCCCGCAGCTCCGGGCGGGCGGGCGGGGAA CCCTCGTCTTTCGCCCCGGGGCCCTGCCCTCCTCGGCCCGCGCTACCAAGGCTGTCTT GGGTCCAGGtgacgactgtgccttctagttgccagcatctgtgtttgccccccccgtgccttcttgacctgga agggtccactcccactgtcctttcctaataaaatgaggaaattgcatcgcatgtgctgagtaggtgtcattctattctgggg gggtgggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgctgggtctat ggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCC GAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGGGG TAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCTTTTCCGAGGGTGGGGGAGAACC GTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCAGAACAC AGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACCTGAGGCCG CCATCCACGCCGTTGAGTCGCTTCTGCCCTCCCGCTGTGGTGCCTCCTGAAGTGCCT CCGCGCTAGGTAAAGTTAAAGCTCAGGTGAGACCGGGCCTTTGTCCGGCGCTCCCTTG GAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCCTGACCTGCTTGCTCAACTCTACGT CTTGTTTCGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCTAGA GCTAGCGAATTgcgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCC ATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGC GAGGGCGATGCCACCTACGCAAGCTGACCCTGAAGTTCATCTGCACACCGGCAAGCTGC CCGTGCCCTGCCCCACCTCGTGACCACCTGACCTACGGCGTGCAAGTGTTCAGCCGCTAC CCCGACCACATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAGG AGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGA GGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAA CATCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATCATGGCCGAC AAGCAGAAGAACGGCATCAAGGTGAAGTTCAGATCCGCCACAACATCGAGGACGGCAGC GTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGTGC CCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCG ATCATATGGTCTGCTGGAGTTCGTGACCGCCCGCGGGATCACTCTCGGCATGGACGAGCT GTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattt ttttactgcattctagttgtgtttgtccaaactcatcaatgtatcttatGACATCTCGCCCGTCTGAAGGACC CCGCTCTCTCCGCGCCGCCATCGGCTCTGGCGCGACACCTGAAGGCGACCCACGGGGG CCGCATCGACTACATCGAGGCGAGTGCCAGTGCGCGCATCTAGGGCGCTTCCGCTTGG CGCGCGCCGAGGGCAGCAGTGGGCTCTGCGCTGCTTGGGGGAGGGCCTTGGGGTG CTTCAGGGGGCGCCGGACGGCGCCGTGCTTGGGTGCGCCGGGAAGGGTTGTGAGATT GAGCCCCGAGGCGCGCGCTGTGCAGGCGTCTTCCCGAGGTTCCGGGTCCCGAGCCC AGGACAGGCGTGACCGAGTTGCCGGGTGAGTTGGTCTCCCTGGAGTGCCCAAGCTGAATC CACAGGGCCAGCTGCCTTGTCTTGTCTTCTGCGAGCTGGTATTGAGCGCTGCCACG A</p>	2541
pARBI- 599: B2M_1_E	<p>AGTAATTTGATGGGGGCTATTATGAACTGAGAAATGAACTTTGAAAAGTATCTTGGGGCCA AATCATGTAGACTCTTGAGTGATGTGTTAAGGAATGCTATGAGTGCTGAGAGGGCATCAGA AGTCCTTGAGAGCCTCCAGAGAAAGGCTCTTAAAAATGCAGCGCAATCTCCAGTGACAGAA</p>	2541

xogenous _4	<p>GATACTGCTAGAAATCTGCTAGAAAAAACA AAAAGGCATGTATAGAGGAATTATGAG GGAAAGATACCAAGTCACGGTTTATTCTTCAAATGGAGGTGGCTTGTGGGAAGGTGGA AGCTCATTTGGCCAGAGTGGAATGGAATTGGGAGAAATCGATGACCAATGTAAACACTT GGTGCCTGATATAGCTTGACACCAAGTTAGCCCAAGTGAATACCCTGGCAATATTAATGT GTCTTTTCCCGATATTCTCAGGTgacgactgtgccttctagtgtccagccatctgtgtttgccccccccgt gccttccttgaccctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgattgtctgagtag gtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctgg ggatgcggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACAT CGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGA AGGTGGCGCGGGTAAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCTTTTCCCGAG GGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGT TTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCG CCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCTTCTGCCGCTCCCGCTGTGGTG CCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGT CCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCAGCTTTGCTGACCTGCT TGCTCAACTCTACGTTCTTTGTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACC GGCGCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTT ACCGGGGTGGTGCCATCCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGC GTGTCGGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCTATCTGC ACCACGGCAAGCTGCCGTGCCGTGGCCACCCTCGTGACCACTGACCTACGGCGTGC AGTGCTTCAGCCGCTACCCCGACCATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCC GAAGGCTACGTCCAGGAGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCG CCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACT TCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAACG TCTATATCATGGCCGACAAGCAGAAGACGGCATCAAGGTGAACCTCAAGATCCGCCACAA CATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGA CGGCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAAGAC CCCAACGAGAAGCGCGATCACATGCTCCTGCTGGAGTTCGTGACCGCCGCGGATCACTC TCGGCATGGACGAGCTGTACAAtgattgtttattgcagcttataatggttacaataaagcaatagcatcaca aatccacaataaagcattttttcactgcattctagtgtgtgtgttccaactcatcaatgtatcttatACTCCAAAG ATTAGGTTTACTCACGTCATCCAGCAGAGAATGGAAAGTCAAATTTCTGAATTGCTATGT GTCTGGGTTTCATCCATCCGACATTGAAGTTGACTTACTGAAGAATGGAGAGAGAATTGAA AAAGTGGAGCATTAGACTTGTCTTTCAGCAAGGACTGGTCTTTCTATCTCTGTACTACACT GAATTCACCCCACTGAAAAAGATGAGTATGCCTGCCGTGTGAACCATGTGACTTTGTGACA GCCCCAGATAGTTAAGTGGGGTAAGTCTTACATCTTTTGTAAAGCTGTGAAAGTTGTGTAT GAGTAGTCATATCATAAGCTGCTTTGATATAAAAAAGGTCTATGGCCATACTACCCTGAAT GAGTCCCATCCCATCTGATATAACAATCTGCATATTGGGATTGTCAGGGAATGTTCTTAAA GATCAGA</p>	
pARBI- 600: B2M_2_E xogenous _5	<p>AAGATCTTAATCTTCTGGGTTTCCGTTTTCTCGAATGAAAAATGCAGGTCCGAGCAGTTAAC TGGCTGGGGCACCATTAGCAAGTCATTAGCATCTCTGGGGCCAGTCTGCAAAGCGAGGG GGCAGCCTTAATGTGCCTCCAGCCTGAAGTCTAGAAATGAGCGCCCGGTGTCCCAAGCTGG GGCGCGCACCCAGATCGGAGGGCGCCGATGTACAGACAGCAAACCTACCCAGTCTAGTG CATGCCTTCTTAAACATCACGAGACTCTAAGAAAAGGAAACTGAAAACGGGAAAGTCCCTC TCTTAACCTGGCACTGCGTCGCTGGCTTGAGACAGGTGACGGTCCCTGCGGGCCTTGTC CTGATTGGCTGGGCACGCGTTTAAATATAAGTGGAGGCGTCGCGTGGCGGGCATTCTGAA GCTGACAGCATTGGGGCGAGATGtgcgactgtgccttctagtgtccagccatctgtgtttgcccccccc gtgccttccttgaccctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgattgtctgagta ggtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctg gggatgcggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACA TCGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAG AAGGTGGCGGGGTAAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCTTTTCCCGAG GGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGT TTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCG CCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCTTCTGCCGCTCCCGCTGTGGTG CCTCTGAAGTGCCTCCCGCTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGT</p>	2541

	<p>CCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCT TGCTCAACTCTACGTCTTTGTTTCTGTTTCTGCGCCGTTACAGATCCAAGCTGTGACC GGCGCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTC ACCGGGGTGGTGGCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGC GTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGC ACCACCGGCAAGCTGCCCGTGCCCTGGCCACCCTCGTGACCACCTGACCTACGGCGTG AGTGCTTCAGCCGCTACCCCGACCATGAAGCAGCACGACTTCTCAAGTCCGCCATGCCC GAAGGTACTGTCAGGAGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCG CCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACT TCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACG TCTATATCATGGCCGACAAGCAGAAGAAGCGCATCAAGGTGAAGTCAAGATCCGCCACAA CATCGAGGACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGA CGGCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGAC CCCAACGAGAAGCGCGATCACATGCTGCTGGAGTTCGTGACCGCCGCGGGGATCACTC TCGGCATGGACGAGCTGTACAAtgattgtttattgcagcttataatggttacaaataaagcaatagcatcaca aattcacaaataaagcattttttcactgcattctagtgtggtttgtccaaactcatcaatgtatcttatTCTCGTCC GTGGCCTTAGCTGTGCTCGCGTACTCTCTTTCTGGCCTGGAGGCTATCCAGCGTGAGTC TCTCTACCTCCCGCTCTGGTCTTCTCTCCGCTCTGCACCTCTGTGGCCTCGTGTGC TCTCTCGTCCGTAAGTTCCTTCTCAAGTTCCTTGGTGGCCGCGCTGGGGCTAGTCCA GGGCTGGATCTCGGGGAAGCGCGGGGTGGCCTGGGAGTGGGGAAGGGGGTGCGCACC CGGGACGCGCGTACTTGCCCTTTTCGGCGGGGAGCAGGGGAGACCTTTGGCCTACGGCG ACGGGAGGGTCGGGACAAAGTTAGGGCGTCGATAAGCGTCAGAGCGCCGAGGTTGGGG GAGGGTTTCTCTCGCTCTTCGCGGGGCTCTGGCTCCCCAGCGCAGCTGGAGTGGGG GACGGGTAGGCTCG</p>	
pARBI- 601: B2M_3_E xogenous _6	<p>AGGAATGCTATGAGTGCTGAGAGGGCATCAGAAGTCCTTGAGAGCCTCCAGAGAAAGGCT CTAAAAATGCAGCGCAATCTCCAGTGACAGAAGATACTGCTAGAAAATCTGCTAGAAAAA AACAAAAAAGGCATGTATAGAGGAATTATGAGGGAAAGATACCAAGTCACGGTTTATTCTT CAAAATGGAGGTGGCTTGTGGGAAGGTGGAAGCTCATTGGCCAGAGTGGAATGGAAT TGGGAGAAATCGATGACCAAATGTAAACACTTGGTGCCTGATATAGCTTGACACCAAGTTA GCCCCAAGTGAATACCTGGCAATATTAATGTGTCTTTCCGATATTCTCAGGTACTCCA AAGATTGAGTTTACTCACGTATCCAGCAGAGAATGGAAAGTCAAATTTCTGAATTGCTA TGTGTCTGGGTTTCATCCATCTgacgactgtgcttctagtgtccagccatctgtgttggccctccccgtgc cttcttgacctggaaggtgccactcccactgtcttcttaataaaatgaggaattgcatcgcatgtctgagtaggtg tcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctgggga tgcggtgggtcttatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGC CCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGGCAATTGAACGGGTGCCTAGAGAAGG TGGCGCGGGGTAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCTTTTCCGAGGGTG GGGAGAACCGTATATAAGTGCAAGTATCGCCGTGAACGTTCTTTTCGCAACGGGTTTGC CGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCGCCCT ACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCGCTGTGGTGCCTC CTGAACTGCGTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTGAGACCGGGCCTTTGTCCG GCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGC TCAACTCTACGTCTTTGTTTCTGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGC GCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACC GGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTG TCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC ACCGCAAGCTGCCCGTCCCTGCCACCCCTGTGACCACCCTGACCTACGGCGTGCAGT GCTTCAGCCGCTACCCCGACCATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAA GGCTACGTCCAGGAGCGACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGG AGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCA AGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCT ATATCATGGCCGACAAGCAGAAGAAGCGCATCAAGGTGAAGTCAAGATCCGCCACAACAT CGAGGACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGG CCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTCG</p>	2541

	GCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaaatt tcacaaataaagcattttttcactgcattctagtgtggtttgtccaaactcatcaatgtatcttatGACATTGAAGTT GACTTACTGAAGAATGGAGAGAGAATTGAAAAAGTGAGCATTGAGACTGTCTTTAGCA AGGACTGGTCTTTCTATCTCTGTACTACACTGAATTCACCCCACTGAAAAAGATGAGTAT GCCTGCCGTGTGAACCATGTGACTTTGTACAGCCCAAGATAGTTAAGTGGGGTAAGTCTT ACATTCTTTTGAAGCTGCTGAAAGTTGTGTATGAGTAGTCATATCATAAAGCTGCTTTGAT ATAAAAAAGGTCTATGGCCATACTACCTGAATGAGTCCCATCCCATCTGATATAAACAATC TGATATTGGGATTGTGAGGGAATGTTCTTAAAGATCAGATTAGTGGCACCTGCTGAGATA CTGATGCACAGCATGGTTTCTGAACCACTAGTTCCCTGCAGTTGAGCAGGGAGCAGCAGC AGCACTTG	
pARBI- 602: CAPNS1_ 1_Exogen ous_7	GATCTCACATTCTAGCGCCAGACATGTCGGGAACGCCTTACGCCAACTTGGGGTCCCCACC AAGAGAACCCCCACCAGATCTGCACCTCCCCTTACGCGTGCACCCAGTCCAGGCTCCCTC AAGCCCCACGGGTGCCTTTTAGACCTGAGGAGGTTGCAAACCTGATCCCCATACCTGCCCC ACCCATCCGCGGACAACCCGCCCTCGCAAACTCAGACCCCAACCCGAGGCTTCAGATTCT CCCAGGTCCAGCTGCCGGAATGCGTGTTGAAGGGAGGGTGTGGGCTCAGGGGCGAAG CACCACTGGTCCCCTTTTTCCCCCAGCAGTGAAGTCGAGCCATGTTCTGGTTAACTCGT TCTTGAAGGGCGGCGGCGGCGGCGGCGGCGGCGGAGGCGGGGGCTGGGTGGGGGCTGGG AAATGTGCTTGAGGCTGATCtagcactgtgcttctagtgtccagccatctgtgttggccctccccgtg ccttccttgaccctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatgcattgtctgagtaggt gtcattctattctgggggtggggtggggcaggacagcaaggggaggattgggaagacaatagcaggcatgtgggg atcggtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCG CCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAG GTGGCGCGGGGTAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTTCCCGAGGGT GGGGGAGAACCGTATATAAGTGCAGTAGTCGCGGTGAACGTTCTTTTCGCAACGGGTTTG CCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCC TACCTGAGGCGCCATCCACGCGGTTGAGTCGCGTCTGCCGCTCCCGCTGTGGTGCCT CCTGAAGTCGCTCCGCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCC GGCGTCCCTTGAGGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGT CTCAACTACGTCTTTGTTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCCG CGCCTACTCTAGAGTAGCGAATTgccgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCC GGGGTGGTGCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTG TCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC ACCGGCAAGCTGCCCGTCCCTGCCCCACCTCGTGACCACCTGACCTACGGCGTGCACT GCTTCAGCCGTACCCCGACCATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCCGAA GGCTACGTCCAGGAGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCGG AGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCA AGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCT ATATCATGGCCGACAAGCAGAACGACGATCAAGGTGAACCTCAAGATCCGCGCACCAACAT CGAGGACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGG CCCCGTGCTGCTGCCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGGATCACATGGTCTGCTGGAGTTCTGTGACCGCGCGGGGATCACTCTCG GCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaaatt tcacaaataaagcattttttcactgcattctagtgtggtttgtccaaactcatcaatgtatcttatAGCGGGCCGG GGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGTTGGTGGAGGCGGCGGTGGCGGTGG AACGGCCATGCGCATCTAGGCGGAGTCATCAGCGCCATCAGGTAAGGCGGAGACTATCA GAGGGCGGGGCTGGGAATGGGAGGAGCCTCAGTGAAGCGTGGTCTGGGAGGGCGGT GGTCTAAAAATAGAAATAGGATTAACCTGGAGGCTAACCTGGGTACATGAATTAGGCCGGG GAGGCTGGTTTGAGAGTTCTGCTGTAAGGGGGTGGACCCAGTGAGGCGGATATCAGTC ATTGGGGGCGGTGCTGATATGGGAGTAGTCTGATTGTGTGGGACCAGGACAATGTGGTC CTGAGGGGACTGATGTGGAGTTTGGCGGGTGGGGCTTATGGGTCTGGGCTCAGCTGCA TTGGCTAACCTGGAGATGAACGTT	2541
pARBI- 603: CAPNS1_	CGGGCATTTAGGAAGCGGGCATGGAGTAGGGTCTTGGGCAGATGGCACCTGAGGAGGA TAAGGCCTTGGGAAGCTGGGGCAGAGCCTCTATGAAGTGAGCCCTCAAAGGGGCGGGGTC TTTTGATTCTACGTGGGATTTTTAGGTTAGGGTGGCCAAGATGACTGAAATCTGCCACTG GGTAGGTGTGCTGGCAGGAGGGGAGCCTCCAGGGGACCGGTCTCTGGGTTTCTCGAG	2541

2_Exogenous_8	<p>GGTGGGGTTGGCCTGAGGAAGGGAGAAGAGGGGCACGACCAGGGCAGTGTGGATTGGG ACAGATGAGGACAAGAACAATGAAAGGCACAGCAACCAAGTAAGGAAGATAACGGCTG GGGTCTGGAGCGTTGGGGCTGATGGTTCTGTAGTCTGCCCGTTGGAGGCCCGCCCTG GCACTAACCCCTCCCCCTTATCTCTTCGACGtgcagactgtgccttctagtgtccagccatctgtgtttgcc cctccccgtgccttcttgacctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatgcattg tctgagtaggtgtcattctattctgggggtggggcaggacagcaagggggaggattgggaagacaatagcag gcatgctggggatgcgggtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAG CGCACATCGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCC TAGAGAAGGTGGCGCGGGTAAACTGGGAAAGTATGTCGTGTACTGGCTCCGCCTTTTTTC CCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAA CGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCC CGCCGCCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCCTCCCGCCTG TGGTGCTCCTGAAGTGCCTCCGCCCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGC CTTTGTCCGCGCTCCCTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGAC CCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTTTCTGTTCTGCGCGTTACAGATCCAAGCT GTGACCGCGCCTACTCTAGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAG CTGTTACCGGGGTGGTGCCATCCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAG TTCAGCGTGTCCGGCAGGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTC ATCTGCACCAACCGCAAGCTGCCGTGCCCTGGCCACCCTCGTGACCACCTGACCTACGG CGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTCAAGTCGCCA TGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGAC CCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCAT CGACTTCAAGGAGGACGGCAACATCTGGGGCACAAGCTGGAGTACAACACAACAGCCA CAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGC CACAACATCGAGGACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCG GCGACGGCCCCGTGCTGCTGCCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAA AGACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCCGGGAT CACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatg catcacaatttcacaataaagcattttttcactgcattctagtgtgtgtttgtccaaactcatcaatgtatctatGAG GCGGCTGCGCAGTACAACCCGAGCCCCGGTAAGCCCCCTCTGCAACCAGACCCCCTTCT CCTGCCAAGGCCTCTTCGAGGTCCCATCCCTGTTCTGTAGAGAAGCCCCACCTTCTCCCT TCTTGTAATTCCTCTGCCAGTTCCTCCATGCCGTGCTGACGCTTCGCCATGGGTCTTAG CCATGCCCCACATACGTGCACCCATTCACTACCACCCCTCACTTTTCTCATCAAGCTGCC CAGCCCACTCTGACTTCCCCACCCAGGGTACCTGGGTTTGGGGAGCCGTCTGGCCGGGT CCCCCTCCCTGCTCTGAGCTCTCTCCCTTTCAGCCCCACGCACACATTACTCAAACATT GAGGCCAACGAGAGTGAGGAGGTCCGGCAGTTCGGGAGACTCTTTGCCAGCTGGCTGGA GATGTAAGTAAC</p>	
pARBI-604: CAPNS1_3_Exogenous_9	<p>GCTGATGGTTCTGTAGTGCTGCCGTTGGAGGCCCGCCCTGGCACTAACCCCTCCCCCT ATCTCTTCGACGAGGCGGCTGCGCAGTACAACCCGAGCCCCGGTAAGCCCCCTCTGC AACCAGACCCCTTCTCTGCAAGGCTCTTCGAGGTCCCATCCCTGTTCTGTAGAGAAG CCCCACCTTCTCCCTTCTGTGAAATTCCTCTGCCAGTTCCTCCATGCCGTGTCTGACGCT TCGCCATGGGTCTTAGCCATGCCCCACATACGTGCACCCATTCACTACCACCCCTATTCTT TTCCTCATCAAGCTGCCAGCCCACTCTGACTTCCCCACCCAGGGTACCTGGGTTTGGGGAG CCGTCTGGCCGGGTTCCCTCCCCCTGCTCTGAGCTCTCTCCCTTTCGAGCCCCACGCAC ACATTACTCAACTgacgactgtgccttctagtgtccagccatctgtgtttgccccccccgtgccttcttgacct ggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatgcattgtctgagtaggtgtcattctattctg gggggtgggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgcgggtgggct ctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTC CCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGG GGTAAACTGGGAAAGTATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGA ACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGGCCGAGAA CACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACTGAGG CCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCCTCCCGCTGTGGTGCTCCTGAATG CGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCTCCC TTGGAGCCTACCTAGACTCAGCCGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTA</p>	2541

	<p>CGTCTTTGTTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCT AGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGT GCCCATCCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCGGCGA GGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAA GCTGCCCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAAGTGTCTCAGCC GCTACCCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGGTACGT CCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAA GTTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA CGGCAACATCCTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCTATATCATG GCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGAC GGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGC TGCTGCCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAA GCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTCGGCATGGAC GAGCTGTACAAtgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataa agcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatATTGAGGCCAACGAGAGTG AGGAGGTCCGGCAGTTCCGGGAGACTCTTGGCCAGCTGGCTGGAGATGTAAGTAACCTGG GGTCCCTGGCCCCGTCTAACCCTCCATCCCTTCCCTGTGGCTGCCCTTGACACACACCCC TTGACCATGACAATCCAGTGTCCATTCTCATGACATTCTCAGACCCCTTTCAGTCACCC CTGACTGCCCTAACTTCGCCCCGAGGACATGGAGGTGAGCGCCACAGAATCTGAAC ATTCTAATAAGGTTGTGACACGACGTAAGTGACCGGGGTTAAGGAATAGGGTAGATTCA GAGGCAGAGGGGTCAGAGAGGATTGACCTCTGGCCTCTGACTTTCAACCTGTTACCCACA GACCCTGATCTGAAGACTGATGGTTTTGGCATTGACACATGTCGCAGCATGGTGGCCGTGA TG</p>	
pARBI- 605: CBLB_1_E xogenous _10	<p>ggagagttagcatgagagacaaaaaggggaactgctggggatcaaaccttgtaaagtccttctaagtatatga ggactttgacttttattcaagttagaaggcttgaacaaaagaattatttcattgtgtttacaatgggcacaaagtcg tagcgagaataggctgTGAGAGAAGAGATTTTGTGGTTTTCTTTTTGTTCTCTGTATTCTCTTCC TGAAAAATCTGTTTTCTGCCTAATCATATTTCTGTAAAGAACATAGACTTGAACGTCTGCTG TTAAGTAACAAAGGTTGACCTAAACACATAAGGTCAGATTAACTTTTAAATATCCAAAGAT AATGTTAAGTGATTAATAATATGGTTCAAGTATGTAATCAAAATATTTGATATTTCTCTAGATACT AATCTCTtttaattttttattttttAGCCTTGgtgacgactgtgccttctagttgccagccatctgtttgtccctccc ccgtgccttcttgaccctggaaggtgccactcccactgtcctttcctaataaaatgaggaaatgcacgcattgtctgag taggtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgc tggggatgcgggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCAC ATCGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCCGCAATTGAACGGGTGCCCTAGA GAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGA GGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCGGTGAACGTTCTTTTTCGCAACGG GTTTGCCGCGCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCCG CGCCCTACCTGAGGCCGCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGG TGCCTCCTGAACTGCGTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTT GTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTG CTTGCTCAACTCTACGTCTTTGTTTCTGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGA CCGGCGCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGT TCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCA GCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCT GCACCACGGCAAGCTGCCCCGTGCCCTGGCCCCACCCTCGTGACCACCCTGACCTACGGCGT CCAGTGCTTCAGCCGCTACCCGACCATGAAGCAGCAGGACTTCTTCAAGTCCGCCATGC CGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCG CGCCGAGGTGAAGTTGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGA CTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACAGCCACA CGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCAC AACATCGAGGACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGC GACGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAG ACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCGGGGATCAC TCTCGGCATGGACGAGCTGTACAAtgattgtttattgcagcttataatggttacaataaagcaatagcatc acaatttcacaataaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatGGCTCT</p>	2541

	ATTTGCGGAATTGGAATTTCTAGCTGTGACACATCCAGGTTACATGGCATTCTCACATAT GATGAAGTTAAAGCAGCTACAGAAATATAGCACAAACCCGGAAGGTAAGACTTTTTAG CAGTAATATTATGTATATATCCAAAGATGAAAAATCTCCATGGTTTGTCTAAGTAAGT CAGCAATACCCGCTGATGGCATGCTTGGGAGGGGGCTAGAAAAGGTAAGACCAAAATG GTGCTTCTAACATAATGTTTTAAATTGATACATTGTGCTTACTCTGAACTTGGTATTCTA AAGTGAAAGGGGATATGGTCTCCTTTCTGTTTTCATGATATCCGTGTTTATGTGCAAAATTG AATGTATATATTTGAATACTTGAATACTGTGCTAAAGAACAATAAATAGAACAGTCTTATG TTCATTACTTT	
pARBI- 606: CBLB_2_E xogenous _11	CATATTACTCATTTGTGCAATGAATAAAGGATTTCTATTATTATATGGACCCATCATCTTATG ACTGTTTTTAGAAAAATGAGAATTAAATCTTGATTCAATTATTAATAAACCTTGTATACACAT GAAGAGGTCATGACACATAAGACTTTGACCTAATACCTTTTTTTCAGATATGTTTCTATAGCTA TCTTGATAGCCTAGGACTGTTTGGAGAGAAAATTAATTTAAATTTTTGTCATATTCTTAGCAAA TGCAAAATAATTGAGTTAAACAGAACCCACTACATTTGTTCTGAAATATGAACAATATTCTC AAATATTTGTCTGGTAGTACAAATACAATTATTAATTTTATTATTGAATTTTGTGCTTCAA AGGGAGGTATTTCTTAAATGATACCTTGATTCAATTATTTCCCTTTTTTCCACCTTGCACAGA ACTATCGTAtgacgactgtgcttctagtgtccagccatctgtgttggccctccccgtgcttcttgaccctggaa gggtccactccactgtccttcttaataaaatgaggaaattgcatcgattgtctgagtaggtgtcattctattctggggg gtgggtggggcaggacagcaaggaggaggattgggaagacaatagcaggcatgctgggatgagggtgggctctatg ggGATCTGCGATCGCTCCGGTGCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCG AGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCTAGAGAAGGTGGCGCGGGGT AAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGAACC GTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCAGAACAC AGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCTACCTGAGGCCG CCATCCACGCGGTTGAGTCGCTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCT CCGCGCTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCTCCCTTG GAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGTCAACTCTACGT CTTTGTTTCGTTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCTAGA GCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCC ATCCTGGTCGAGCTGGACGGGCGACGTAAACGGCCACAAGTTACGCGTGTCCGGCGAGGGC GAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGC CCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAAGTGTTCAGCCGCTAC CCCGACCACATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCCCAAGGCTACGTCCAGG AGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGAGGTGAAGTTCGA GGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAA CATCTGGGGACAAGCTGGAGTACAACACAACGCCACAACGTTCTATATCATGGCCGAC AAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGC GTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGC CCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCG ATCATATGGTCTGTGGAGTTCGTGACCGCGCGGGATCACTCTGGCATGGACGAGCT GTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattt ttttactgcattctagtgtgtttgtccaaactcatcaatgtatcttatCCATGGAAAGTATTAGACAGTGC CTTCATGAGGTCCACCAGATTAGCTCTGGCCTGGAAGCAATGGCTCTAAATCAACAATTGA TTTAACTTGCAATGATTACATTTAGTTTTTGAATTTGATTTTTTACCAGGCTGTTTCAGGTA AGTTTATACTTGCTTAGTCTATCCATTCCTtcttctctctccctgtcttttctctctgtttctctctctctgtct ctctctcacacacacacacacTAAACAAACATATGGAAAATAGTGTCAATTCCTATTAGTCTGTAATTT TATTGGTATGTTTGGTCATTGTTAAAGTTTAGAGTGAGCCATTGGCTTAAGTTTGGAGTT ATCAGATGCTGTGAGCCTGGTGGCTGCTTGTAGCTTTGAGAGGATCCATCCAAAAGAGCT TTGTTTTAACTCTCTACTTAGTTTCTTACTT	2541
pARBI- 607: CBLB_3_E xogenous _12	TTAACTTTAGAGGTTCAAAATAAGGATATGATATAGAAAAGATTGAATGGTAGGAGAACA GAATAGGATTTATTTATATTATGACAAACGTGACTATCAGTTAATAAATTGGAGATAGTAAG TTAAGATCATTATTTATATTATGGAAAAATGAAGAAATAGGACATGGTTCTTAACTTTTAA TTTTTCTGTGAAATAAAATATTATGACTTATTTTATTTTATCTTTGTTTTAGGTAAGACTGT GCCAAATCCCAAACCTCAGTTGAAAAATAGCCACCATATATACTTGATATTTTGCTGATA CATATCAGCATTTACGACTTATATTGAGTAAATATGATGACAACAGAAACTTGCCCAACTC AGTGAGAATGAGTACTTTAAATCTACATTGATAGCCTTATGAAAAAGTCAAAACGGGCAA	2541

	<p>TAAGACTCTTTAAAtgacgactgtgccttctagtgtccagccatctgtgtttgccctccccgtgccttcttgacc ctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgattgtctgagtaggtgtcattctattc tgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtggggatgcgggtggg ctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGT CCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCG GGGTAAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAG AACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGGCGCCAGA ACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCTACCTGAG GCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCTGAACT GCGTCCGCGCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCTCC CTTGAGGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGCTCAACTCT ACGTCTTTGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACTC TAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTTTCACCGGGGTGGT GCCCATCTGTCGAGCTGGACGCGCAGCTAAACGGCCACAAGTTCAGCGTGTCCGGCGA GGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTTCATCTGCACCACCGGCAA GCTGCCCGTGCCCTGGCCACCTCGTGACCACCTGACCTACGGCGTGCACTGCTTACGCC GCTACCCCGACCATGAAGCAGCAGCACTTCTTAAGTCCGCCATGCCCCAAGGCTACGT CCAGGAGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCGGAGGTGAA GTTGAGGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA CGGCAACATCTGGGGCAACAAGCTGGAGTACAACATAACAGCCACAACGTCTATATCATG GCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGAC GGCAGCGTGCACTGCGGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGC TGCTGCCCCACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAA GCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCCGCGGATCACTCTCGGCATGGAC GAGCTGTACAAatgattgtttattgacgttataatggttacaataaagcaatagcatcacaatttcacaataa agcattttttcactgcattctagtgtgtgtgtgtccaaactcatcaatgtatcttatGAAGGCAAGGAGAGAATG TATGAAGAACAGTCACAGGACAGGTAAGAAGAATATTTAGATGTTTTGGTGTAAGGTCA TTTATGTTGCTTTTACTTAATAGTTAACCTAAACGTACCATGTAATTGTTTGGGGTAAAT GTGAGTCGCTTTGTATAGtcactgtgtgtacttaacgatggggatactttacaagaaatgcatttttagacaattt cattgtgtgtggacatgatagagtgtacttacacagagctagatggattacctaccgcacacctaggctgtatgatga gcctattgtcctaggctgcaaatctatacagtatgttactgtactgaatactgtgggcagttgtaacacaatggaagta tgtgtgtatctaaatatacctaacaatagaaaaggtatggttaaaaactgtataaaaggccggcggtgg</p>	
<p>pARBI- 608: CD2_1_ Ex ogenous_ 13_14_15</p>	<p>AGATGAGAAAACCTATCCTTCCCAATTTTTTTGTGTGAGAATTAAATGCAGCAAGAAAACA CACACTCATAAACACATCTGCTTTGGCAAAGGAGCACATCAGAAGGGCTGGCTTGTGCGCG CTCTTGCTCTGTGTATGTGTATTATGTTTTATGTTACTGTAAAGATGTAAAGAGAGGCA CGTGGTTAAGCTCTCGGGGTGTGGACTCCACCAGTCTCACTTCAGTTCCTTTTGCATGAAGA GCTCAGAATCAAAAGAGGAAACCAACCCCTAAGATGAGCTTTCCATGTAAATTTGTAGCCA GCTTCCTTCTGATTTTCAATGTTTCTTCCAAAGGTAAGCATAAGAGTCAAAGAAGTCCCAAC CCAGCTTTCCCTGAAAGTGACTCTCAGTAACTCTTTTGTCTTTTATAGGTGCAGTCTCCAAAG AGATTACGAATGCCTTGtgacgactgtgccttctagtgtccagccatctgtgtttgccctccccgtgccttctt gacctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgattgtctgagtaggtgtcattc tattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtggggatgcgg tgggtctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCAC AGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAGAGAAGGTGGC GCGGGGTAACCTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTTCCCGAGGGTGGGG GAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTCCCGC GAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCTTACCT GAGGCCCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTG AACTGCGTCCGCCGTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCG CTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGCTCAA CTCTACGTCTTTGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCT ACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGG TGGTGCCATCCTGGTCGAGCTGGACGGCGACGTAACCGGCCACAAGTTCAGCGTGTCCG GCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTTCATCTGCACCACCG GCAAGCTGCCCGTGCCCTGCCCCACCTCGTGACCACCTGACCTACGGCGTGCACTGCTTC</p>	2541

	AGCCGCTACCCCGACCATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCCGAAGGCT ACGTCCAGGAGCGCACCATTCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGT GAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGA GGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATC ATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAG GACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCC GTGCTGCTGCCCGACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACG AGAAGCGCGATCAGATGGTCTGCTGGAGTTCGTGACCGCGCCGGGATCACTCTCGGCAT GGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcaca aataaagcattttttcactgcattctagttgtgtttgtccaaactcatcaatgtatcttatGAAACCTGGGGTGCC TTGGGTGAGGACATCAACTTGGACATTCTAGTTTTCAAATGAGTGATGATATTGACGATAT AAAATGGGAAAAAATTCAGACAAGAAAAAGATTGCACAATTCAGAAAAAGAGAAAGAGAC TTTCAAGGAAAAAGATACATATAAGCTATTTAAAAATGGAACCTGAAAAATTAAGCATCTGA AGACCGATGATCAGGATATCTACAAGGTATCAATATATGATACAAAAGGAAAAAATGTGTT GGAAAAAATATTTGATTTGAAGATTCAAGGTAAGTGTTATTCCCTTAATTGCTTTATTTAG TGTGGGTGCTATTTGGCAAGTTGAAAAATAGCATTTCTAATATTTCCCGAGCGCTGACCTCTG CCTCCAGGGGGGCTATACAGGAAACCAGATGCATGTCTCTGCCCGAGTGGAGACTGTGGT CCAA	
pARBI- 609: CD3E_1_ Exogenou s_16	AGGATGTTTCTAGTTGATTGGTATGTGTGCACTCCTAGTTGTTAAATATTTTCACTATCACAC CTGGATATACTCAACAAATATTTGTTGAGCCAAATACTCAACACCAGCCAAACACGTAGTAT TTACTTTAGCTTAAGCGAATTATTTAGCCTGACAGAAGCCCTGGAATGTGGGTCTTTAAGT TCCTATTTTGGAGATGGGAAAGCTGAGGCTCACGGAAGGAGGTGACCAGCTCAAGTCTCCT ACCGTCCATGCCAAATTAGAATCCAGCCTGCCTCCTGACTTCAAGTCCAAAGTTCTTCCAC GCACTAAAGCTAGCTCTTCAGTGCTCTTTCTTAGGAGGTACTTCTCCCGCACCCTGACCG CCCCCTCTCTATTTACCCCCAGCCATCCGGAAGGCCAGCGGGACCTGTATTCTGGCCTG AATCAGAGACGCATCtgacgactgtgcttctagttgccagccatctgtgtttgccccccccgctgcttcttga ccctggaaggtgccactcccactgtccttcttaataaaatgaggaaattgcattgcattgtctgagtaggtgtcattctat tctggggggtggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgcggtgg gctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAAGCGCACATCGCCCAAG TCCCGAGAAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGC GGGGTAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCGAGGGTGGGGGA GAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCA GAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCGCCCTACCTG AGGCCGCCATCCACGCCGTTGAGTCGCGTTCGCGCCTCCCGCTGTGGTGCCTCCTGAA CTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCT CCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACT CTACGTCTTTGTTTCGTTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCTAC TCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCCGGGGTG GTGCCATCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGC GAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGACCACCGGC AAGCTGCCCCGTGCCCTGGCCACCTCGTGACCACCTGACCTACGGCGTGCACTGCTTCA GCCGTACCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCGAAGGCTA CGTCCAGGAGCGCACCATTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG AAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAG GACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCA TGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGG ACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGCCCCGT GCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAG AAGCGCGATCAGATGGTCTGCTGGAGTTCGTGACCGCGCCGGGATCACTCTCGGCATGG ACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaat aaagcattttttcactgcattctagttgtgtttgtccaaactcatcaatgtatcttatTGACCTCTGGAGAACAC TGCCTCCCGCTGGCCAGGTCTCCTCTCCAGTCCCCCTGCGACTCCTGTTTCTGGGCTAGT CTTGGACCCACGAGAGAGAATCGTTCTCAGCCTCATGGTGAACCTCGCGCCTCCAGCCT GATCCCCCGCTCCCTCCTCCTGCTTCTGCTGGTACCCAGTCCCTAAATATTGCTGCTTCC TCTCTTTGAAGCATCATCAGTAGTCACACCCTCACAGCTGGCCTGCCCTCTGCCAGGATA	2541

	TTTATTTGTGCTATTTACTCCCTTCCCTTTGGATGTAACCTCTCCGTTCAAGTTCCTCCTTTCT TGATGTAAAGTTGTCCCATCCCAAAGTATTCATCTACTTTTCTATCGCCGTCCCTTTTGC AGCCCTCTCTGGGGATGGACTGGGTAAATGTTGACAGAGGCCCTGCCCGTT	
pARBI- 610: CD3E_2_ Exogenou s_17_18	AATAATAAAATAATAACAATACTTAACATTTATTGAGTGCTTATTAAGTCTCAAGCACTGTCT GTACCCAACACTTATCAAGGATTCTTTTTCATGTAATCCTCTCAACAATATATGGGTTAAGT ATCATTTTATTCCCATGAGTAAAGGGATGAGGAAACAGAGGGTTTGTGAGTTGAAAACACA TTTACGCTTCTCACAGCTAGTGAGTAATAAAGCTGGGACTCAAACCCAGGGCTGTTGACT CCAGTGCCTCTACCCACGGCCACCACTCTTTGCTTGTCATGTTGTTCTAAACATATTGAAGG GGGGGCTCTGACCGTGGCAAGCGTGTGAGTAGTAAGGGGAGAATGGCCTTCATGCACTCC CTCCTCACCTCCAGCGCTTGTGTTTTCTTGCTTAGTGATTTCCTCTCCCCACCCACCCC CCACAGTGTGTGAGtgacgactgtgcttctagtgtccagccatctgttgttggccctccccgtgcttcttgac cctggaaggtgccactcccactgtcctttcctaataaaaatgaggaaattgcatgcattgtctgagtaggtgtcattctatt ctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgcggtgg gtctctatggGATCTGCGATCGTCCGGTGCCCGTCAGTGGGAGAGCGACATCGCCACAG TCCCGGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGCGCG GGGGTAAACTGGGAAAGTGATGTCTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGA GAACCGTATATAAGTGCAAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCA GAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCGCCCTACCTG AGGCCGCCATCCACGCCGTTGAGTCGCGTTCGCGCCTCCCGCTGTGGTGCCTCGTAA CTGCGTCCGCGCTTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCTTTGTCCGCGCT CCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGCTCAACT CTACGTCTTTGTTTCTGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTAC TCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTG GTGCCCATCTGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGC GAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACACCGGC AAGTGCCCGTGCCCTGGCCACCCCTCGTGACCACCTGACCTACGGCGTGCAAGTGTCTCA GCCGCTACCCCGACCATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCGAAGGCTA CGTCCAGGAGCGACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGGAGGTG AAGTTCGAGGGCGACACCCCTGGTGAAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAG GACGGCAACATCTGGGGCACAAGCTGGAGTACAACACTACAACAGCCACAACGTCTATATCA TGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTTCAAGATCCGCCACAACATCGAGG ACGGCAGCGTGCACTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGT GCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAG AAGCGCGATCAGATGGTCTGTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGG ACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaaagcaatagcatcacaatttcacaat aaagcattttttcactgcattctagtgtgtgtgttgcacaaactcatcaatgtatcttatAAGTGCATGGAGATGGA TGATGTCGTTGGCCACAATTGTCATAGTGGACATCTGCATCACTGGGGGCTTGCTGCTG CTGGTTTACTACTGGAGCAAGAATAGAAAAGGCCAAGGCCAAGCCTGTGACACGAGGAGCG GGTGTGGCGGCAGGCAAGGGGTAAGGCTGTGGAGTCCAGTCAGAGGAGATTCTGCC AAGGGGGACGACCAAGCTGGGCCAGGGTGGGTGGCAAGTCCACAGCTAGGTGAGAACAG CTTCTCTAGAGCTTCTATGCACAGCTTCTATTACTGTGATGACAAGATCTAACAGACGGTTT CAAATCTCACATCACTCCCTCCTTCCCATCTAGAAAAAGTGAAAAAAGTTTATGAAAGTG ATGGGCTTCTCACATACCTGTCAATGCCTGCAATCCGATTCCGCCCTAAGCTGTGGG AAGAGAG	2541
pARBI- 611: CD3G_1_ Exogenou s_19_20	ACTGTGACCCATGAACCAGTAGGTATTGGCGTCACCTGGGATCCTGACGTTAGTCTCTGTCA ATCCTTCTCTTTAGTTCATCTATTCTACCAAAGTGATCTCATCATCTGGTATGCTGTAGCAG TTTCTTACCTGTATAGTATCTTCCAAATAACATGCCCCAAAATCCCAAAGTTTACCCTACTA ATTACAGCAATGTCTCTTTTATTCTTCAACCCCTGACGCAGATATTGGCGTCACCCGAGAGC ATGTTAGTAATGCAGAATCTCCCTCCCCAGAACTACTAAATAGCACCTGAAATTTTAAACA GATCCCCATGTGATTATGTGCACATCAAAGTTTGAGAAACACTACTCTAATGATCTCCTGG TATGCAGAAGCAGGGAGAATTTAGAGGGCAAGATCCTTAATAGAACACGGCTTTTCTCAT TTCAGGAAACCACTgacgactgtgcttctagtgtccagccatctgttgttggccctccccgtgcttcttgacc tggaaggtgccactcccactgtcctttcctaataaaaatgaggaaattgcatgcattgtctgagtaggtgtcattctattct gggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgcggtgggc tctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCACAGTC	2541

	<p> CCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGG GGTAAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCTTTTCCCGAGGGTGGGGGAGA ACCGTATATAAGTGCAGTAGTCGCGTGAACGTTCTTTTCGCAACGGGTTTGGCGCAGAA CACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCTGAGG CCGCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTG CGTCCGCGCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCTCCC TTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTA CGTCTTTGTTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCT AGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGT GCCCATCCTGGTCGAGCTGGACGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGA GGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAA GCTGCCCGTGGCTGGCCACCTCTGACCACCTGACCTACGGCGTGAGTGCTTCAGCC GCTACCCCGACCATGAAGCAGCAGACTTCTCAAGTCCGCCATGCCGAAGGCTACGT CCAGGAGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCGGAGGTGAA GTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA CGGCAACATCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATG GCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGAC GGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGC TGCTGCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAGACCCCAACGAGAA GCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGGAC GAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataa agcattttttcactgcattctagtgtgtgtgttgcacaaactcatcaatgtatcttatTTGGTTAAGGTGTATGACTA TCAAGAAGATGGTTCGGTACTTCTGACTTGTGATGCAGAAAGCCAAAAATATCACATGTTTA AAGATGGGAAGATGATCGGCTTCCTAACTGAAGATAaaaaaaaTGGAATCTGGGAAGTAAT GCCAAGGACCTCGAGGGATGTATCAGTGTAAAGGATCACAGAACAAGTCAAAACCACTCC AAGTGATTACAGAAGTATGTAATCCCTTTGGTCTGTTTGTGTGAAATTAATCAGTATTTG CTGTTCTGGTGAGCTTTTATCTGGGGTGAAAGTGGAATAGATCCTCAACAGTAATATTAT CGCTGTTCTCTTAATTTGAGCTTGCCTCTTTTAAATACTGTAAGATACTTCCCTCACCCAT TGA AAAACTACAGCCAGTCTGTAAATTTTGTTTACCTTTGGGTGGGCTCCATGG </p>	
<p> pARBI- 612: CD3G_3_ Exogenou s_21 </p>	<p> TTCGAGACAAGCCTGGCCAACATGATGAAACTCTGTCTCTACTAAAAATACAAAAAAATTA ACCAGGCGTGAGGCGCGCGCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAGGAGGA CCACTTGAACCCAGGAGGTGAGGTTGCAGTGAGCTGCGATTGTGCGACTGCACTCCAGCC TGGGCAACAGAGAAAGACTCCGTCTCAAAAAAAAAAAGAGAGAGAGAGAAAAAGAAAA AAGACAGAGCCTCCATCTCCTTGTCTCTTTCCATCCTCAGGACCATGAAGTACCACTCCAA ATTCTCACATATAAAAAACATTCAATAAACATGCATCAAATTAATTAATAGAGGATGGAAAA AATGACTTATGACTGTGCTGTCTTTCCAGCCCCCTCAAGGATCGAGAAGATGACCAGTACAG CCACCTTCAAGGAAACCAAGTTGtgacactgtgccttctagtgtccagccatctgttttgccttccccctgtc ctctcttgacctggaaggtgccactccactgtcctttcctaataaaatgaggaaatgcatcgcatgtgtgtagtggtg tcattctattctgggggtgggggtggggcaggacagcaaggggaggattgggaagacaatagcaggcatgctgggga tgcggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGC CCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGG TGGCGCGGGGTAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCTTTTCCCGAGGGTG GGGGAGAACCGTATATAAGTGCAGTAGTCGCGTGAACGTTCTTTTCGCAACGGGTTTGC CGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCCCT ACCTGAGGCCGCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTC CTGAAGTCCGTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCG GCGACTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTTTGTGC TCAACTCTACGTCTTTGTTTCGTTTTCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGGC GCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACC GGGGTGGTGCCATCCTGGTCGAGCTGGACGCGACGTAAACGGCCACAAGTTCAGCGTG TCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC ACCGGCAAGCTGCCCGTGCCCTGCCCCACCTCGTGACCACCTGACCTACGGCGTGCAAGT GCTTCAGCCGTACCCCGACCACATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCCGAA GGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGG AGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCA </p>	2541

	AGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAACAGCCACAACGTCT ATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACAT CGAGGACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGG CCCCGTGCTGCTGCCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCTGTGACCGCCGCCGGGATCACTCTCG GCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcaca tcacaataaagcatttttttactgcattctagttgtggtttgtccaaactcatcaatgtatcttatAGGAGGAATTG AACTCAGGACTCAGAGTAGGTGGGTCTTCAATGCCAATTCTAATAAAGGACCCCTTGCATCA ACTGCCCTCGCAATTGCTTCTAAGTCTAGCTCCCTCCCTAAGCGGCTATAAGCATCAGACTC TGGGGATCAGGGATTGGGACGTGGTTTGGGGTACTCTTTTCTAAAAATTCTGGGGCCATAC TGATTGTCTTGGCCTAGGTAAATATGAATTTTATGTATCTGTAAATCCTGTCAGAGCAGGGC CTCAAGCCATAGAGATGCTGAATATTAATCTTAACCTACATTTGAATTTCTCATTATCTACAC TATTAACATTTTGGGCTAATTAATTATTTGTGATGAGGGGCTAGCCTGTGCATTGTAGGAGT TATGGAAGCATCCCTGGCCTCTCTCCACCAGATGCTGGTAGATTGTCCAGTGTGACAATCAA AAAT	
pARBI- 613: CD5_1_ Ex ogenous_ 22	GACCTCAGGTGATCTGCCCCCTCAGCTTCCCAAAGTCTGGGATTACAGGCATGAGCCAC CACACCTGGCCTAAAATTAATTTTTAAAGATCTCTTAAAAAGCAGACACCAGCCCCAATCTC AGACCCCTTGAGACAGAATTTCCAGGACAGGGGCCATCCTGCTGGACAGTGGGTGCCGAG AACACCTTGCCATTATCTGAGCTCCCTTCTGACTCTGAAATCTGGAGCCCCACCCCTCTGG GTCTAGCTTCGGGGCTGCCTGGGTGAGGGTCTCTGGGAAGCCCTGCAGTGCCCCAGAAAG GGACGAAGCTCACAAGGGGCAAGGCAGGCAGCCACGGGGCAGGAGGGAGCTCAACTGG GCGTCTAGGGAGAGGGCAGTGAGGGGTGCCAGTGGGGAACCCCTCCAGCCTGACCCCC ACCACACCTTTCTGACCCCGAGATgacgactgtgccttctagttgccagccatctgtgtttgccccccccgt gccttccttgaccctggaaggtgcactccactgtccttcctaataaaataggaaattgcatgcattgtctgagtag gtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctgg ggatgcggtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACAT CGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGA AGGTGGCGCGGGGTAACTGGGAAAGTGATGTCGTGACTGGCTCCGCTTTTTCGCGAG GGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCGTGAACGTTCTTTTCGCAACGGGT TTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCGCCG CCCTACCTGAGGCCGCTCCACGCCGTTGAGTCGCTTCTGCCGCTCCGCTGTGGTG CCTCTGAAGTGCCTCGCCGTCTAGGTAAGTTAAAGCTCAGGTGAGACCGGGCCTTTGT CCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCCTGACCTGCT TGCTCAACTCTACGCTTTGTTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACC GGCGCTACTCTAGAGCTAGCGAATTgcccaccacATGGTGAGCAAGGGGCGAGGAGCTGTTC ACCGGGGTGGTGCCCATCCTGGTTCGAGCTGGACGCGACGTAACCGGCCACAAGTTCAGC GTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGC ACCACCGCAAGCTGCCGTGCCGTGGCCACCCCTCGTGACCACTGACCTACGCGGTGC AGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTCAAGTCCGCCATGCC GAAGGTACGTCCAGGAGCGACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCG CCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACT TCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAACAGCCACAACG TCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAA CATCGAGGACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGA CGGCCCCGTGCTGCTGCCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGAC CCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTC TCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcaca aatttcacaataaagcatttttttactgcattctagttgtggtttgtccaaactcatcaatgtatcttatTTCCAGGCA AGGCTACCCGTTCCAACCTGAAGTGCCAGGGCCAGCTGGAGGTCTACCTCAAGGACGGAT GGCACATGGTTTGAGCCAGAGCTGGGGCCGAGCTCCAAGCAGTGGGAGGACCCAGTC AAGCGTCAAAAGTCTGCCAGCGGTGAAGTGTGGGGTGCCTTAAGCCTTGGCCCCCTCCT TGTCACCTACACACCTCAGAGCTCAATCATCTGCTACGACAACTGGGCTCCTTCTCAACT GCAGCCACAGCAGAAATGACATGTGTAAGTCTCTGGGCTGACCTGCTTAGGTGGGTAACT AGCCAGCCACACGGGCACCTGGGCTGGGCGCCAGCCCCGAGGAGACTGCCCCAGGCCT	2541

	GTGATCTAGGGTCTGAGCAGGCTGGTGGAAGGGGTGGGGGGACCCAGTTTATAACCACT CCCCAAGACACATAACC	
pARBI- 614: CD5_2_ Ex ogenous_ 23	GGACAGGGGCCATCCTGCTGGACAGTGGGTGCCGAGAACACCTTGCCCATTTATCTGAGCT CCCTTCTGACTCTGAAATCTGGAGCCCCACCCTCCTGGGTCTAGCTTCGGGGTGCCTGGGT CAGGGTCTCTGGGAAGCCCTGCACTGCCCCAGAAAGGACGAAGCTCACAAGGGGCAAG GCAGGCAGCCACGGGGCAGGAGGGAGCTCAACTGGGCGTCTAGGGAGAGGGCAGTGA GGGGTGCCAGTGGGGAACCCCTCCAGCCTGACCCCCACCAACCTTTCTGACCCCCAGATT TCCAGGCAAGGCTCACCCGTTCCAACCTGAAGTGCCAGGGCCAGCTGGAGGTCTACCTCAA GGACGGATGGACATGGTTTGCAGCCAGAGCTGGGGCCGGAGCTCCAAGCAGTGGGAGG ACCCAGTCAAGCGTCAAAAGCTGTGtagcactgtgccttctagttgccagccatctgtgtttgccctccc ccgtgccttcttgacctggaaggtgccactccactgtcctttcctaataaaatgaggaaattgcatcgcatgtctgag taggtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgc tggggatcggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCAC ATCGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGA GAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCGCA GGGTGGGGGAGAACCGTATATAAGTGCACTAGTCGCCGTGAACGTTCTTTTCGCAACGG GTTTGCCGCCAGAACAAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTACGCGCCCCG CGCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGG TGCGTCTGAACTCGCTCCGCCGTAGGTAAAGTTTAAAGCTCAGGTCGAGACCGGGCTTT GTCCGGCGCTCCCTTGAGACCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTG CTTGCTCAACTCTACGTCTTTGTTTCTGTTCTGTCGCCGTACAGATCCAAGCTGTGA CCGGCGCCTACTCTAGAGCTAGCGAATTgcggccaccATGGTGAGCAAGGGCGAGGAGCTGT TCACCGGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCA GCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCACTCT GCACCACGGCAAGCTGCCCCGTGCCCTGGCCACCTCGTGACCAACCTGACCTACGGCGT GCAGTGCTTCAGCCGTACCCCGACCATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGC CCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCG CGCCGAGGTGAAGTTGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGA CTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACATAACAGGCCACA CGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCAC AACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGC GACGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAG ACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCTGTACCGCCGCCGGGATCAC TCTCGGCATGACGAGCTGTACAAtgattgtttattgcagcttataatggttacaataaagcaatagcatc acaaatttcacaaataaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatctatCAGCGG CTGAAGTGTGGGGTGCCCTTAAGCCTTGCCCCCTTCTTGTACCTACACCTCAGAGCTC AATCATCTGCTACGGACAACCTGGGCTCCTTCTCAACTGCAGCCACAGCAGAAATGACATGT GTCACTCTCTGGGCCTGACCTGCTTAGGTGGGTAAGTACCCAGCCACACGGGCACCCCTGGG CCTGGGCGCCAGCCCCGAGGAGACTGCCCGAGGCCTGTGATCTAGGGTCTGAGCAGGCTG GTGGAAGGGGTGGGGGGACCCAGTTTATAACCACTCCCCAAGACACATACCCAGGAGGG GGAAGTGAAGGGGCCAGCACCATCTGTAGGATGGCAATGGAGGACCTAGTTCTGCCAAT CACTGACTTCATCGTCGCCTCTGAACCTCCATTCTCCATCTGTGAAGTGGGGTGGTACTTCC CGCCTCGCAGGAGGCT	2541
pARBI- 615: CD5_3_ Ex ogenous_ 24	tgctgggattacaggcatgagccaccacactggcctaaaattaatttttaagaTCTCTTAAAAAGCAGACAC CAGCCCCAATCTCAGACCCCTTGAGACAGAATTTCCAGGACAGGGGCCATCCTGCTGGACA GTGGGTGCCGAGAACACCTTGCCATTATCTGAGCTCCCTTCTGACTCTGAAATCTGGAGC CCCACCCCTCTGGGTCTAGCTTCGGGGCTGCCTGGGTGAGGGTCTCTGGGAAGCCCTGC AGTCCCCAGAAAGGACGAAGCTCACAAGGGGCAAGGCAGGCAGCCACGGGCAAGGAG GGAGCTCAACTGGGCGTCTAGGGAGAGGGCAGTGAGGGGTGCCAGTGGGGAACCCCTC CCAGCTGACCCCCACCACTTTCTGACCCCCAGATTCCAGGCAAGGCTACCCGTTCC AACTCGAAGTGtagcactgtgccttctagttgccagccatctgtgtttgccctccccgtgccttcttgacct ggaaggtgccactccactgtcctttcctaataaaatgaggaaattgcatcgcatgtctgagtaggtgtcattctattctg gggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatcggtgggct ctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTC CCCAGAAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGG	2541

	<p>GGTAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGA ACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCAGAA CACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCTGAGG CCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCGCCTGTGGTGCTCTGAACTG CGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCTCCC TTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGTCTTCAACTCTA CGTCTTTGTTTCGTTTCTGTTCTGCGCCGTACAGATCCAAGCTGTGACCGGCGCCTACTCT AGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGT GCCCCATCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCGGCGA GGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCACCGGCAA GCTGCCGTGCCCTGGCCACCTCTGTGACCACCTGACCTACGGCGTGCACTGCTTACGCC GCTACCCCGACCACATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGT CCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGAGGTGAA GTTGAGGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA CGGCAACATCTCTGGGGCAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATCATG GCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGAC GGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGC TGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAA GCGCGATCACATGGTCTGTGGAGTTCGTGACCGCCGCCGAGTCACTCTCGGATGGAC GAGCTGTACAAAtgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaaatttcacaaataa agcattttttcactgcattctagtgtgtgtgttgcacaaactcatcaatgtatcttatCAGGGCCAGCTGGAGGTCT ACCTCAAGGACGGATGGCAGATGGTTTGCAGCCAGAGCTGGGGCCGAGCTCAAGCAGT GGGAGGACCCAGTCAAGCGTCAAAAGTCTGCCAGCGGTGAAGTGTGGGGTGCCCTTAA GCCTTGGCCCCCTTCTTGTACCTACACCTCAGAGCTCAATCATCTGTACGGACAACCTG GGCTCCTTCTCAACTGCAGCCACAGCAGAAATGACATGTGTCACTCTCTGGGCTGACCTG CTTAGGTGGGTAAGTACCCAGCCACACGGGCACCTGGGCTGGGCGCCAGCCCCGAGGA GACTGCCGAGGCTGTGATCTAGGGTCTGAGCAGGCTGTGGAAAGGGTGGGGGGACC CCAGTTTATAACCACTCCCAAGACATACCCAGGAGGGGGACTGGAAGGGGCCAGCAC CCATCTGT</p>	
pARBI- 616: chr2_1_E xogenous _106	<p>TGTCAAAGTGTGTGTACCTGCTCTGTGTTACCCACTGGGTTCATCAGAGGGGCACCTGA ACAAAACAGGAATGTCACTGGAGAGGGGAACAAATGCTGTCCCCAAGTCTTCCCTGCCGT TTAGAGTAACGCAGCCCTGTCCGCACATCCTACCCCATCTGCCCTCTGCTTGCCAGAATT ATCAGAATCTCTCAATTCTAATTTAGCCATTCTCTGTGAAAATGAAAAGTTAGTGGCAGGC AATGGACACCTATTGAAATAGAAATTGTTCTTCATATGTCAGAAAAGTCCCAGAGTAATCT GGGAGTAATCTGAGCAAAGTGAATCAAAGGATTATTACAATTTCTTAGTCTTCTACTGCTGC AAAAGTGGCACTCTTTGATTCTATGTTTGAGGTTCTAATTACTACCTCATGCAGGACTTACA AGAGATCAGCCATGtgcagactgtgccttctagtgtccagccatctgtgttggccctccccgtgccttcttga ccctggaagggtgccactcccactgtcctttcctaataaaatgaggaaattgcacatgcattgtctgagtaggtgtcattctat tctgggggtgggggtggggcaggacagcaaggaggaggattgggaagacaatagcaggcatgctggggatgcggtgg gctctatggGATCTGCGATCGTCCGGTGCCGTGAGTGGGCGAGCGCACATCGCCACAG TCCCCGAGAAGTTGGGGGGAGGGGTGGCAATTGAACGGGTGCCTAGAGAAGGTGGCGC GGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTCCCGAGGGTGGGGGA GAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCA GAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCTG AGGCCGCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCGCCTGTGGTGCTCCTGAA CTGCGTCCGCCGTCTAGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCT CCCTTGAGCCTACCTAGACTCAGCCGCTCTCCACGCTTTGCCTGACCCTGCTTGTCTCACT CTACGTCTTTGTTTCGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCTAC TCTAGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTG GTGCCATCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCGGC GAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCACCGGC AAGCTGCCCGTCCCTGGCCACCTCGTGACCACCTGACCTACGGCGTGCACTGCTTCA GCCGTACCCCGACCACATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCGAAGGCTA CGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGGAGGTG AAGTTCAGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAG</p>	2541

	<p>GACGGCAACATCTGGGGCACAACTGGAGTACAACACTACAACAGCCACAACGTCTATATCA TGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGG ACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGT GCTGCTGCCCCACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAG AAGCGCATCACATGGTCTGCTGGAGTTCGTGACCGCCCGGGATCACTCTCGGCATGG ACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaaat aaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatTGCTTACATTGTGTGTAG TGAATCAATGTTATTCTGAAGGGCCTCTGGAAGCAGTAGGGATTGGAGAATGTATGTCTT TTAACATGATCATTCCCATCTATGGGGGTTGGGCACTCTTAACATCATGTTGCAGATGAGTA AACTGAGGCTTTTGAGAGTTTGAGGGTGACAGCTTGAGGCAGAGGTGGAATTCCAGCTT CATCCAAGAAATCACGAATCTCCAATGGCTTGACACATCCAGGTTTGCTGGATCCTATTG TCAAGACCACATGCAGATTAGGAGCCTTCAAACAAATTATTTCAAGGGAGGGCATCTTTCT CTGTAACCCCTACCCTGGCAATTCTCATGGCTCAGGGAGTCCAGCCGGAAGCTCTGCAAT GAGTCTGGGGAACTCTCATCTGAAAAAGGCGCTCATGACAGGTGGTGCCAACCTTCCAC G</p>	
<p>pARBI- 617: chr2_2_E xogenous _107</p>	<p>CTACAAGCATGCATCACCAGGCTGGCTAATTTTTCTATTTTTGTAGGGACAGGGTTTTGCT GTGTTGCCAGGCTGGTCTCAATTTCTGGACACAAGCAATCTGCCTGCCTCAGCCTCATAA TGTTTTTTTTAATGTTAAACCCCTCTTGTTGTTGAGAGGCTGGCTTGTGTTTGAGCGCA CTGCCTACCTTTGCAGCTGTAAATGTGAGGGCTCCAGGAGGGCTGGCTGGGTCTCCCTC CTCCCTGTTGGGTGGGTGGGGCCCTGAGCTTATCCAGGCATCCCTAGGTGGATGGATGGG TGGATGGGTAGGCCCTGGCCTTCAGGGAATGCACTGTGTGTGGTCTTCCAGCCCCAGCAAA GTCTCAGGGGGCCCCGAGCGGGAAGTCGCCATCCTCAGGGGGTCCGAGTGGGGAGTCACC ATCCTCACGGTCAGCGTGGTgacgactgtgccttctagttgccagccatctgtgtttgccccctccccgtgcctt ccttgaccctggaaggtgcccactcccactgtcctttcctaataaaatgaggaaattgcatgcattgtctgtagttagtgc attctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggat gcgggtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGC CCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCCGCAATTGAACGGGTGCCTAGAGAAGG TGGCGCGGGGTAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTG GGGAGAAACCGTATATAAGTGCAAGTAGTCGCGGTGAACGTTCTTTTCGCAACGGGTTTGC CGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCGCCCT ACCTGAGGCCGCCATCCACGCCGGTTGAGTCGCGTTCTGCGCGCTCCGCTGTGGTGCCTC CTGAACTGCGTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTGAGACCGGGCCTTTGTCCG GCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGC TCAACTCTACGTCTTTGTTCTGTTTCTGTTCTGCGCGGTTACAGATCCAAGCTGTGACCGGC GCCTACTCTAGAGCTAGCGAATTgcccgcaccATGGTGAGCAAGGGCGAGGAGCTGTTACC GGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGGCCACAAGTTCAGCGTG TCCGCGCAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC ACCGGCAAGCTGCCCGTCCCTGGCCCCACCTCGTGACCACCCTGACCTACGGCGTGCAGT GCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCCGAA GGCTACGTCCAGGAGCGCACCCTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCG AGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCA AGGAGGACGGCAACATCCTGGGGCACAAAGCTGGAGTACAACACTACAACAGCCACAACGTCT ATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACAT CGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGG CCCCGTGCTGCTGCCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTCG GCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatt tcacaaataaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatTTTCGAATTGAG CTCCAGGGGGCGGAGACTCCATTCCCCCGGGGAACAATCTGATAGCCAGAAATGAGAGCA GTGAGTGACTTGGACGCTGTGTATTAGGAGGGTCCAGTCCCTCAGAGTCGCTGGACA CCAGATTGTATTTACAAAACAGATGGATGAGGAAATGGAGATTGGGTCTTCAAAAGAATTA ACCTCAGATTTTATTTATTTATTTAAAAATTTTAAATTTTCCAAGGACCTTTCCAAGTCAA GAATTGTTTTAAAAAGAAGCCTGGTGAAGGCAATGCTGTCTGTGGCCGAAGGCACCGTG AGGAGCTGAGGCTGACTTATGTTTCTCTGGGCTATGTGCGCTCTAAGGAGTTCACACA</p>	2541

	CTTTAACCCCTTAGGAACCTACATGATCATCCTCGTTTCTTAAAGAGGAAGCAGAGCCAG CAAACAAG	
pARBI- 618: chr2_3_E xogenous _108	<p>TCTTGATGGATACCCATCCTTCTCTGCTGTTCTCTCTTCTCCATCCTCAAGCACAGGGAGC TTTTGGCGAGGTTAGCTAACTTCGGGGCAGCTGTGAATTAGATACTGGCTGTAAGTTACCTC CAACATCCAGAGCATTAAACGCTCGGCTGTCAATGATTGTCAATTTTCATTGTTTACATATAG TCACATCCTCAGTTTGTGGGGTGGATGCAATTTGATTCAATTCAGATATGCCTTCAAGCTGG CCCTGCTGAGCTGGGCTGAAAGGCACATGGCTCATCTCATCTGCATGTGACAGTCTCTTTG AAGTCCCCAGAAGTGCTGCTCAGAGTCATGCTCGGGAGGGAAGAGGTAAGGCACAGAAT GAGTACAGACTGCCACCCAGCCGAGGAAAGGTGACTGCACACCAGAGGTTCTGGTAAAG GAGGTGACTCACCCGCGAtgacgactgtgccttctagttgccagccatctgtgtttgcccctccccgtgccttcc ttgacctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcacgcattgtctgagtaggttcatt ctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctgggatgcg gtgggctctatggGATCTGCGATCGCTCCGGTGCCGTCAGTGGGCAGAGCGCACATCGCCCA CAGTCCCCGAGAAGTTGGGGGGAGGGGTGGCAATTGAACGGGTGCCTAGAGAAGGTGG CGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGTCCGCCTTTTCCGAGGGTGGG GGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCG CCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCGCCCTACC TGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCCTCTG AACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGCCCTTTGTCCGCG CTCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCGTGACCTGCTTGCTCAA CTCTACGTCTTTGTTTCGTTTCTGTTCTGCGCCGTACAGATCCAAGCTGTGACCGGCGCCT ACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGG TGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCG GCGAGGGCGAGGGCGATGCCACCTACGCGCAAGCTGACCTGAAGTTCATCTGCACCACCG GCAAGCTGCCGTGCCGTGCCACCCCTCGTGACCACCTGACCTACGGCGTGCAGTGCTTC AGCCGTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGT GAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGA GGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACTACAACAGCCACAACGTCTATATC ATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAG GACGGCAGCGTGCACTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCC GTGCTGCTGCCGACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACG AGAAGCGCGATCACATGGTCTGTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCAT GGACGAGCTGTACAAtgattgtttattgcagcttataatgggtacaataaagcaatagcatcacaatttcaca aataaagcatttttctactgcattctagttgtgtttgtccaaactcatcaatgtatcttatCTGTCTACCTGTCCA AAGTGTGTGTACCTGCTCTGTGTTACCCACTGGGTTTCATCAGAGGGGCACTTGAACAAA ACAGGAATGTCACTGGAGAGGGGAACAAATGCTGTCCCAAGTCTTCCCTGCCGTTTGA GATACGACAGCCCTGTCCGCACATCCTCACCCCATCTGCCCTCTGCTTGCCAGAATTATCAG AATCTCTCAATTCTAATTCAGCCATTCTCTGTGAAAATGAAAAGTTAGTGGCAGGCAATGG ACACCTATTGAAATAGAAATTGTTCTCATATGTCAGAAAAGTCCCAGAGTAATCTGGGAG TAATCTGAGCAAACTGATTCAAAGGATTATTACAATTTCTAGTCTTCTACTGCTGCAAAAGT GGCACTCTTTGATTCTCATGTTTGAGGTTCTAATTACTACCTCATGCAGGACTTACAAGAGA</p>	2541
pARBI- 619: chr3_1_E xogenous _112	<p>TGAGCAAATAGTTCTATCCTTTTTGACACATTTCCACAGTTTGTATAATTTATTATAGAATC CTTCTAGACTACTAATAAATTCATAGGACATAGTCCTTTTATATGCGGAGGAATCCACC ACCATGAAATGTTCAAGAAATGACTTTTTAAATTTTATTTGTGGCCATGCTGATTATGAA TTTCTGAATTATGTCTGGGCTGCTTTTTCTCGGAATATGCAAAGTGGGATACTGGCATCTC TGTATCTGGAGAGTTACAGCTTCTGAGTTAAAAGATGAATGGGAAGTAGCAGGAGAGGGA GAGATCAGAAATCTCACTCCCTGAAACACAGACACTTACATACCCAGGAGGTAATTCCT GGCATGAATTGTAACAAGTATACACAGGCATTTGTACATTGTTTGCTTATGTGCTAGATGAC ATGGCAGTCTATGAAtgacgactgtgccttctagttgccagccatctgtgtttgcccctccccgtgccttctga ccctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcacgcattgtctgagtaggtgtcattctat tctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctgggatgcggtgg gtctctatggGATCTGCGATCGCTCCGGTGCCGTCAGTGGGCAGAGCGCACATCGCCACAG TCCCGGAGAAGTTGGGGGGAGGGGTGGCAATTGAACGGGTGCCTAGAGAAGGTGGCGC GGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGA</p>	2541

	<p>GAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTTCGCAACGGGTTTTGCCGCCA GAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCTACCTG AGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAA CTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCT CCCTTGGAGCTACCTAGACTCAGCCGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACT CTACGTCTTTGTTTCGTTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCTAC TCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTG GTGCCATCCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCGGC GAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGC AAGCTGCCCGTGCCCTGGCCACCCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCA GCCGCTACCCCGACCACATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCGAAGGCTA CGTCCAGGAGCGACCATCTTCTTCAAGGACGACGGCAACTACAAGACCGCGCCGAGGTG AAGTTCGAGGGGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAG GACGGCAACATCCTGGGGACAAGCTGGAGTACAACAGCCACAACGTCTATATCA TGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGG ACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGT GCTGCTGCCGACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAG AAGCGCGATCAGTGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTGGCATGG ACGAGCTGTACAAAtgattgtttattgcagcttataatggttacaaataagcaatagcatcacaatttcacaaat aaagcattttttcactgcattctagtgtgtgtgtccaaactcatcaatgtatcttatCAGGGGCCCCACATCTGC AGGCAGGACATTCAGCCCTGTATCTTGCCACTACCATGAAATCTGAGGTTCTTTCATTTTGT TTTTCTATTCTGATGAGATTGAGGTACACTGACTCACTGGTAAAGAAGACAATTTATTTGTG AACTTGTAGTCACTCCATTTGACGGCTCCCTCTACTCACTGAGGCACAGCACGTGTGGAAC AGGAAAAAGGCCTCTGGAGAGCTTGTGTTCCACTGGTTTCTTTGACTTTTGCCAACCAACTT TGCAATGTTCTCAAAAGGCATTACCTCTGCAAGGTGTGAAATAACTCTGCAGTTCAAG GGTTTGTGAAATCACGTGAAACAGCTGAAAGCTGTTCTGGCAAAGCGACCAGAGTCAGAG TtagctgtcACCAAGCCACATCCTGGCTTAAACGATGTTATTTATATCTAACTGCACTCGA</p>	
pARBI- 620: chr3_2_E xogenous _113	<p>AGATGCCCATTTGTACCACCTACCATTTGCTTGACCCCGCCCATGAGCTGTTCTTCATACCTCA TAACATAAATGCCAAATGTGTGACTTGAGTAATTAAGTACAGACCTCCAGAAGGCTTTCCTT CTTATTCTGGGTACATTGATATTTACTTTAGTATTTGTTTTGCCTTTAAAGTCATGTTCCCTTT TGATTCTTTAATATCATATCCAAAACGAAGTCCTTTTAACTATAACAATGCAAATCAAAAGT GCTGTCTTTAGCTACCTCAAGGATTTAGCAAGCGTTCCTGGAAATCTAACCAACCTTTTAA AAAGTATTTCTATGGGAATGTATTTCTGAGCCCTAAATTATGGATTTTGAAACTAAAATAGA AGAATACTGTAAAGTGCAAACTTCCAGTAGATAACAGAATTTGCAAAATCTCTAATCTCTTG TATGTGCCCAAtgacgactgtgcttctagtgtgccagcatctgtgtgttggccctccccgtgccttccttgacctg gaaggtgccactccactgtccttcttaataaaatgaggaaattgcatcgattgtctgagtaggtgtcattctattctgg ggggtggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgcggtgggctct atggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCC CGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCTAGAGAAGGTGGCGCGGG GTAACTGGGAAAGTGATGTCGTGACTGGCTCCGCTTTTTCCCGAGGGTGGGGGAGAA CCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTCCGCCAGAAC ACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCTACCTGAGGC CGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAACTGC GTCCGCCGTAGGTAAGTTTAAAGCTCAGGTGAGACCGGGCCTTTGTCCGGCGCTCCCTT GGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTAC GTCTTTGTTTCGTTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCTACTCTA GAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGC CCATCCTGGTGCAGCTGGACGGCGACGTAACGGCCACAAGTTACAGCGTGTCCGCGAGG GCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCTGCAACCACCGGCAAGCT GCCCCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCT ACCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCA GGAGCGCACCATCTTCTTCAAGGACGACGCAACTACAAGACCCGCGCCGAGGTGAAGTTC GAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGC AACATCCTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCTATATCATGGCCG ACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCA</p>	2541

	<p>GCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCGTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgagccttataatggttacaataaagcaatagcatcacaatttcacaataaagcatttttctactgattttagtgggtttgtccaaactcatcaatgtatcttatGTAGTACTCTCTATAGGCCATTGGAACAGAACATCTGGCTTAAATAATCTCAGCACCAAAACGGTCTAACTATGGTCTCCACAACATAACCCGATGGTTCTCATATTTTAGATGCTTGATGCACAAGTTGAACTGGCTAACAACTCAGACTTCAGGACTTGACTCCCCTGGGAATCTGCAGTTGTTTCCCTCCCCTTGAGTGAGACTGACTGTTGGGAGTAGAATAACCGCATGCTCTGGGTGAGAATGCCTGGCCCTTCAGAGTAACGGCAGCATGATCGCTGAGCTCCTACTGTGAGGCACATACTTCGCCACACTAACACATGGAATCCTTGCAAGCTCCTTACATAATCAGTATTTTATGCACCTTGCAAATGAGAATACTAAGGCTCAGAAGAGGCAAGCTCCTCTCCCACTGTAAACAGCTAGTGATGAACAGAGCTGGG</p>	
pARBI-621: chr3_3_E xogenous _114	<p>ACTCCCCTGGGAATCTGCAGTTGTTTCCCTCCCCTTGAGTGAGACTGACTGTTGGGAGTAGATAAACCAGCATGCTCTGGGTGAGAATGCCTGGCCCTTCAGAGTAACGGCAGCCATGATCGCTGAGCTCCTACTGTGAGGCACATACTTCGCCACACTAACACATGGAATCCTTGCAAGCTCCTTACATAATCAGTATTTTATGCACCTTGCAAATGAGAATACTAAGGCTCAGAAGAGGCAAGCTCCTCTCCCACTGTAAACAGCTAGTGATGAACAGAGCTGGGACCTAAACTTGTCTGATTTCCCACTGCTGCTCCATCAGATTGTTTGCCAGGTTAAGGATTCATGCCAGGACCTTAAATCCCTCTGAATCGACAGAGTAACCTAAAGGGCACCTTGATTTTCAGGTTTGTGCCAAACCTATGACTGTGGCCTGGCCACGTtgacgactgtgccttctagttgccagccatctgtgtttgccccctccccgtgccttcttgaccctggaaggtgccactcccactgtcctttcttaataaaatgaggaaattgcatcgattgtctgagtaggtgtcattctattctgggggtgggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtggggatggtgtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCA CAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCCTTTTCCGAGGGTGCGGAGAACCGTATATAAGTGACAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACC TGAGCCCGCCATCCACGCCGTTGAGTCGCGTTCTGCGCCTCCCGCTGTGGTGCCTCTGAAGTGCCTCCCGCTCTAGGTAAGTTTAAAGCTCAGGTGAGACCGGCCCTTTGTCCGGCGCTCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGTGCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTTCTGTTCTGCGCCGTACAGATCCAAGCTGTGACCGGCGCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCCGGGGTGGTGGCCATCCTGGTGCAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACACCGGCAAGCTGCCCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGTACCCCGACCATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGGAAGGCTACGTCCAGGAGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAACGTCTATATCATGCGCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCATCACATGGTCTGTGAGTTCTGTACCGCCCGGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgagccttataatggttacaataaagcaatagcatcacaatttcacaataaagcatttttctactgattttagtgggtttgtccaaactcatcaatgtatcttatAATGAAGACCCGGTGGTTCTAGCTTCACAATGAGCTCATTGGCATTGTCCCCACAACCACCCCTCTCCACCTGTGATCCACTATCATTTTCTATATGGCCTTTGCCAGGCTTGTCTCATATCAAAGCTTCTGCCTCTATGTTTAAATGCATAAGCTTGACAAATGTTTTCATTTGAGAAGGCAAGCTGCCTCCCGTGTGGTCTAATGTGAGCTTGGTAGAGTGACACTGCTGGATTGAGTTTGTAGTCATCAACACTTCCAGCTGATGCTGATCTGAGTAATTGCTCTATTTAGACTCTGACAGGTGAAAGTCATAGATTGAGGAAACGGAGACTCCCCCACCCTGCTATGAAGGGGAGTTTGAGAGGGTTGGGAGCTCTCCGGCAGTGGCAGGCAGTGTGGGGACACAGTATGGATAAATTGTTAATGCTCTT</p>	2541
pARBI-622:	<p>CTGCAGGTGGCAGACTTACTCATTCTCATGCTTCAGCTCCAGGGGTTCCCCTGTATGAGTCTTCTCTGCCCCCTCCACACCCAGGTAGCATTGCCCTGCTTGTGCCCTCACTGTCTC</p>	2541

chr3:1865 _Exogeno us_109	<p>CACATATATACACATCTCTTACAATAATATTAATAACCAACCAACATTTATATAGTACTTCTTA TGTACCAAGTACTGTTGTCTATCTATCTATCTATCTATCTATCTATGTACACACACTCA TATTATCTTACAATGCTATGAAATAGGTATTATTGCTGTCCATTTTACAGATGGGGAAACC AATCTATAATTGGTTTAGTGAGATTTACTGAGCATATCTACAGGTATTTGTCCTTGGTTATAG GAAACCAATCTGCTACTGGTTTCCCTTCTGTAAAATAAGTTAAATAATTTGCTTAAGCTCAC TCAGATAGTgacgactgtgccttctagttgccagccatctgtgtttgccccccccgcttccttgaccctggaa gggtccactcccactgtcctttcctaataaaaatgaggaaattgcatcgcatgtctgagtaggtgtcattctattctggggg gtggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgagggtgggctctatg gGGATCTGCGATCGCTCCGGTGCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCG AGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGGGGT AAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACC GTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCAGAACAC AGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCTACCTGAGGCCG CCATCCACGCGGTTGAGTCGCTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCT CCGCGCTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCTCCCTTG GAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGTCTGACCCTGCTTGCTCAACTCTACGT CTTTGTTTCGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCTAGA GCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGGCC ATCTGTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTACGCGTGTCCGGCGAGGGC GAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCTATGCAACACCGGCAAGCTGC CCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGAGTGCTTACGCCGTAC CCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCCAAGGCTACGTCCAGG AGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGA GGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAA CATCTGGGGCACAAGCTGGAGTACAACATAACAGCCACAACGCTCTATATCATGGCCGAC AAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGC GTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGC CCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCG ATCATATGGTCTGTGGAGTTCTGTGACCGCCGCGGGATCACTCTCGGCATGGACGACT GTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaataaagcattt ttttcactgcattctagttgtgtttgtccaaactcatcaatgtatcttatGTGTGGTTGAGTCATAATCTGAGCT ACTCTCTGGCCAACTGCTTATTGTAACCACCATCATATGGCCACTTACGACCAGTCAC ACCTCATTTTACTTGTGATGTCTAGTTTTCCCTCTATTCTGCGGGCTACTTGAGAAGACTT CTGTCTTCTCTCTAGGTATCTCTGTGCTTACTCAGTATCGAGACCATAGGTGTGTGGGT GGGGTTAATCCACACTTGCTGAACACATGTGTCCGTGCCCAATGTCCCTGTGCATAGTGGCT ACTTCCCATGGTTCACACGCATCTCATGGCTCTTGTCTTCCATTACCCATCCCATGTCCC TGCCCTGTCTCAGTGCTGAGGATGGAACCTCATTGCTGCTGCTTCCAGCCCTGGCCCTGC CCCTTGTGGGGCTCAGTGCTTCATCCCGTGAGGCTCAAGGGGTGCTG</p>	
pARBI- 623: chr3:1865 _Exogeno us_110	<p>CTTCTATCCTCACACCCATTCTTTCTAGTTTCCCATCTGACTTCTACTACCCCAAGTTC ATAAAGACCTCATGAACACAACCTGGAGAACGCCCTCAGCCTCATCTACCTCCCTGCAACA CATGGCTCACTTGTCTGCTTCTTCTTCTTAGAGTCTCTCTCTGGTTGACCTGTCAAAGATG GGATTCTCCTGTTAACGACCCTGACTCCTTGTCTCTTCTACAAAGATAATGCACTGACTTT CCAAATGTACTAAGTATGATCATCACTGTCTACTGTTGCATCGAACCCTACTAACCTCA ATAGGGAAGGCACCAAGTTCAAGAGGCCAAAGAAGAGACCCAGAGCCAGCAATGAGAC ATGGGGTTTTATGAGGGGCTCACATAGAGGGGAGAGAGTCCAGTGGCAGTGGGCTGGGC AGGAGAACCACCTTACtgcgactgtgccttctagttgccagccatctgtgtttgccccccccgcttccttcttg accctggaaggtgccactcccactgtcctttcctaataaaaatgaggaaattgcatcgcatgtctgagtaggtgtcattct attctgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgcggt gggctctatggGATCTGCGATCGCTCCGGTGCCGTCAGTGGGCAGAGCGCACATCGCCAC AGTCCCCGAGAAGTTGGGGGGAGGGGTGGCAATTGAACGGGTGCCTAGAGAAGGTGGC GCGGGGTAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGG GAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGC CAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCT GAGGCCGCCATCCACGCCGTTGAGTCGCTTCTGCCGCTCCCGCTGTGGTGCCTCCTG AACTGCGTCCGCCGTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCG</p>	2541

	<p>CTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCTGACCTGCTTGCTCAA CTCTACGTCTTTGTTTCGTTTTCTGTTCTGCGCCGTACAGATCCAAGCTGTGACCGGCGCCT ACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGG TGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCG GCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCG GCAAGCTGCCCCGTGCCCTGGCCACCTCGTGACCACCTGACCTACGGCGTGCACTGCTTC AGCCGTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGT GAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGA GGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATC ATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTCAAGATCCGCCACAACATCGAG GACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCC GTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACG AGAAGCGCGATCATATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCAT GGACGAGCTGTACAAtgattgtttattgcagcttataatgggtacaaataagcaatagcatcacaatttcaca ataaagcatttttctactgcattctagtgtgtgtgttgcacaaactcatcaatgtatcttatACGTGGTCCAGTGGT GGGAGGCTGGAAAAGAGATCTGTCTTGCCCTACAGTTCAGTGGTGGCGGGTTGGGCAGGAA AACCACAACCTGCCTGCAAACATCATGCAGTTTACATAACATTGTCACTTAGCAGCCTCCCTA ACGACCTCCACCTGGCAATCTTATTAAACCCAAAACCTAAGGCCTCAATCCCTGTATGGA CCATGTTTCATGGGACAGGCCAGGGGCTCAGAAAGTTATCATAGATAAGGAATGAATCTCC GGGTTGGCACTCCTGGATTCCCTAGCTTGAACACACATTCAAGTGTATCTGCCATTCTGA GTGTATTCTTCAATTATTGCTGTGAGGTGTGTTGACCTCTATCTACATAAGTATTCTCAA CCAGGGCCCTACGATCAGCATCAGCATACCTGGGTATATGTGAAAAATGCAGCTCCTGG ACC</p>	
<p>pARBI- 624: chr3:1865 _Exogeno us_111</p>	<p>GGGCCAAGCAAGCTCTGAGACAAGCTGTCTCACCTCCTCATCTCTGAGCACAACCTACCCA CAGCTCTGCCCTCGCTCCACCTACATCATGCCTTCTCGATGCCAACTTCCCTCTGAGGTTT CCTTACCCCACTTACAACCACAGCCTCCTTCCGGACCTCCCTACACGATGAACAGTCTGCCA GTTAATATACATCAAGCTGCCACCATGAAACAGCTCGGAAAGCCCATTTGTTCTCAATAGC ATTCCAGCTAGAAAGACCATCCACCAACCATGGCCACTGAAGAAGTCTCCCTGATGTC CAGGCAGTGGGGCTCCTAACTCTGGGCCCAATTAGCTTAGCTTGGGGGAGCAAAGGACA GGAGCACTGTTACCCAGTTGGACTAACAGCTCCACACTGTGCCTAATAGGAACCTCCTTCT CACAGTGGCACCTTTGtgacgactgtgccttctagtgtccagccatctgtgtttgccccccccgtgccttctt gaccttgaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgattgtctgagtaggtgtcattc tattctgggggtgggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgcgg tgggtctatggGGATCTGCGATCGTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCAC AGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGC GCGGGGTAACTGGGAAAGTGATGTCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGG GGAACCGTATATAAGTGCAAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGC CAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTACGCGCCCGCCGCCCTACCT GAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTG AACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTGAGACCGGGCCTTTGTCCGGCG CTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCTGACCTGCTTGCTCAA CTCTACGTCTTTGTTTCGTTTTCTGTTCTGCGCCGTACAGATCCAAGCTGTGACCGGCGCCT ACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGG TGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCG GCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCG GCAAGCTGCCGTGCCCTGGCCACCTCGTGACCACTGACCTACGGCGTGCACTGCTTC AGCCGTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGT GAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGA GGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATC ATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTCAAGATCCGCCACAACATCGAG GACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCC GTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACG AGAAGCGCGATCATATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCAT</p>	2541

	GGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcaca aataaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatTGAATCAGGGTCTGT CCTGAGCCACCCTCCCTTGGAGAGATCTGAGCACTGAGAACCACAGAGCCTGGGACACCAG CACAGGGTTTAAAACTCCACTCCAGTCAGCTGCGGTGGCTCATGCCTGTAATCCCAGC ACTTTGGGAGGCTGAGGTGGGTGGATCACAAGGTCAGGAGTTCGAGACAGCTTGACCAGC ATGGTAAAAACCCATCTCTACTAAAAGTACAAAAATTAGCCAGGCATGGTGTGGGCACCT ATAATCCCAGCTACTCGGGAGGCTGAGGCAGGGGAATTGTTTGAACCTGGGAGCTGGAGG TTGCAGTGAGCCGAGATCGCACCCTGCACTCCAGCCTGGGCGGCTGAGCGAGATTCTGTC TCAAAAAATGGGAAAAACATCATTCCCATGTGTGCTGCTGGTTGCTTCTCTTTCAAAGTA CTGCATACT	
pARBI- 625: chr8_1_E xogenous _115	CCACATCATGGACCAGAAGCCACTTGGTCTGGTTGTGAGGATGACGGAACCTTGCCCGAGG AAATGGGCAATGAACAGGAGCCTGTTGTTTCTCCTTCCAGCTCCTGACCTGTCTAGTCTCT GACCCTCTCAGTGTCACTTCTGCTACCCCTGGCCCTGCTCCCTGGATATGCAGACAGGATG GGCTTCTTCCCTTTAGACCTTCACTTTGCTCTTTTGGACTCCTTCTGGCCTTGCCTTCCCT GGTGTCTGCTGGCTCCCTGCCTGATACTGCCACACTGGTCATGCTGGCCTCTGGCCTT TGGTGACACCGCATCAGCAGGCTCCTGCTTCCCTGTCAAGGGATACAAGCCAGCACCAGGTC TTTCGCCACAAGGTATGTGTGTAAGATTGCTTCTGTACTTGGTGTCACAGGATTTTAAA GAACTCCTGGCCCACTgacgactgtgccttctagttgccagccatctgttttccccccccgtgccttcttg accctggaaggtgccactcccactgtccttcttaataaaatgaggaaattgcatgcattgtctgagtaggtgtcattct attctgggggtgggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgcggt gggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGAGAGCGCACATCGCCAC AGTCCCCGAGAAGTTGGGGGGAGGGGTGGCAATTGAACGGGTGCCTAGAGAAGGTGGC GCGGGGTAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCTTTTCCCGAGGGTGGGG GAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGC CAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTACGCGCCCGCCGCTACCT GAGGCCGCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTG AACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTGAGACCGGGCCTTTGTCCGGCG CTCCCTTGAGGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGGCTGACCTGCTTGTCTCAA CTCTACGCTCTTTGTTTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCT ACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGG TGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCG GCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCG GCAAGCTGCCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCACTGCTT AGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGT GAAGTTCGAGGGCGACACCTGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGA GGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACATAACAGCCACAACGTCTATATC ATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAG GACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCC GTGCTGCTGCCGACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACG AGAAGCGCGATCAGTGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTCGGCAT GGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcaca aataaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatCGGAACTCTACGCTTG AAACAGAAACATCTTCTCAAACACCTCTGGTATTGGCCATTTCTCTATTACTGTTTCTTGT GGTTTCATACTGAGGTTTTTGGTGCAATTGCAATTGCCCTGGAGTTTATTTTAGTAATAAAG ACAGAGTTCAATTAATGTCAAACATGAGGGTAATTGCAGAGGAAGGATTAGTAAGTCTAG GGGAAATGTGCCCAACTTTTTTTCTTCTGATAACATCTTCACTGATCATAACCCGTACAC CCACAGACACGGAGCTTCTCCGTGATGTCTGCAATGCACTAGGCCAGTCGGGGAGCAGT GGCTGCGCCACCACCTGAAAACGAAAGCATTTCTGAGTCTCTTTCAGTCCAGCTCATCTAGC AGCCAGCCACACAGGTGACCACCCACCGTAGCTGTCACTATGGGTGATGATTATCATTATG G	2541
pARBI- 626: chr8_2_E	AGGATCTTTCTCTACAGTGCCTCTTGTGGGACGGGTCTGCTGATGGGGGCTGTGTTTGG GATCTCGCCTGGAAACACGATCTCTCAACTTTCCCTGGGAGCAGAGCCTTGGGTCTCACTG AACCACCTCCCCAGCACCTTGTGTGGTGACTGGCAGGAGGTAGCCATTCCCTCTGTCTC TCTGCCCTGTCCACTTTCCTGTTATGAGTCAGTTGCTGAGATAGGCTATGAGGAGTTAACA	2541

xogenous _116	<p>GAGTGGATAAAAAAGAGCTTTGTCCTTCTTTAAAGCCTTCAAAATATACAGATGTATTAGTC AGGGCTTTCCAGAGAAACAGGACCAATAGAACATGAAGATAGATGCGTATCCATGTCTATA TCAATATCTACCTTGATATTTATATCTATATCTAGGAGATTTATTTATTATAAGGTATTGGCTC ATGCAATTATGGACCTgacgactgtgccttctagttgccagccatctgtgtttgccccccccgtgccttcctga ccctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgcatgtctgagtaggtgtcattctat tctggggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgcggtgg gtcttatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAG TCCCGGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGC GGGGTAAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCTTTTCCGAGGGTGGGGGA GAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCA GAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCTACCTG AGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAA CTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCT CCCTTGAGGCTACCTAGACTCAGCCGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACT CTACGTCTTTGTTCTGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCTAC TCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTG GTGCCATCCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCGGC GAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACACCGGC AAGCTGCCCGTGCCCTGGCCCAACCTCGTGACCACTGACCTACGGCGTGCAGTGCTTCA GCCGCTACCCGACCATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTA CGTCCAGGAGCGACCATCTTCTTCAAGGACGACGGCAACTACAAGACCGCGCCGAGGTG AAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAG GACGGCAACATCTGGGGACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATCA TGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGG ACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGT GCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAG AAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGG ACGAGCTGTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaaat aaagcatttttctactgcattctagttgtgtttgtccaaactcatcaatgtatcttatCAGAGGGGTCTGTGATT TGCCACCTGCAGGCTGGAGACCTAGGAAACAGCTGTCGTGTACAAAGGGCAGAGGGCTG GAGAACCTGTAGTGTAGATTCCAGTCCAGATTCGAAGGCTGAGGACCAGGAATGCCAAG GGCAGGAGAAGATCGATGTCCAGAACAAAGCAATCAGGCAGAGATGAAATTAACCTTCC TGTGCTTTCTGTTCTATTAGGCCTTCAGTGGGTGAATGAGGCCAACCCACATTAAGA GGACCATCTGCTTTACTCAGTCTCCTGGTTGAAGTGATAATCTCATCTGGACATACTCAGAA ATGCTGTTTAAACGCTCTCTGGAATCCTGTGGCCAGTCAAGTTGACACACAAAATTAAC CATCACACTGCAGAGACACAGTCTATCCCAATACCTGTATTACTGGGTAACGTGCATCTCA GCTC</p>	
pARBI- 627: chr8_3_E xogenous _117	<p>TAATAATGACTCTGCTGGTAATTTGTGTCCTTCTGCTTGGAAGTGTTCCTTTTATGTTGGTC ACCTCTCCAGAGCTGGTTTCAATGGGGGCATACCAATTATGGGATGCAGGGCATCCTGCAT CCTGAGGAATTTTTTCTCCAAAAATGAAACCTTGAAATGAGGACATTGTCCTGTCCACG GACTGCACAACAACACTGAGCCTCAAGGACTCATACTGGCATTCTTCTTTGAGAGTG TGGGCACCCTGGCTTCAAGCTCACGAGAAACAGGTGGGATTTAAACAATGTTGGGTTAA AGCAAAGTTTCATAAAGACAGAATCAAGAAAAAAGAAAGAGAAACCAATCTAAGTGCCA TCCTCCCTGAGTTGCATCTTACCTGAGTCTTACGCCGCCGCCCTGCTGCTGTGGGAGGAA ACGGGAAAGTGACTGGCCTgacgactgtgccttctagttgccagccatctgtgtttgccccccccgtgccttc cttgacctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgcatgtctgagtaggtgtca ttctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgc gggtgggtcttatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCC ACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTG GCGCGGGGTAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCTTTTCCGAGGGTGG GGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCC GCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCTTA CCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCC TGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGG CGCTCCCTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGCTC</p>	2541

	<p>AACTCTACGTCTTTGTTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGC CTACTCTAGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGG GGTGGTGGCCATCCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTC CGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCAC CGGCAAGCTGCCCGTGCCCTGGCCACCTCGTGACCACCTGACCTACGGCGTGCACTGC TTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAG GCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGA GGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAA GGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACATAACAGCCACAACGTCTA TATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATC GAGGACGGCAGCGTGCACTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGC CCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCA ACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTCGG CATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaattt cacaataaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatATGGGGACAGG GGTCGGGGGTGTGAGGGTGTAGTGGTAGCAGGGAGGTAGCACTTCTGTGAAGCCGGAAG GAGACCTGAACCTGGCTCTCTGCTTGTGCTTGCAGCCCTCTGGCTGGGAAGAAGGCTCT TGGCTCTTGTGAGCCTCGGTTTCTCTGCAGAGTGGCTGTTCTGAGGACAGGCTGACATTG CTGTCCATCAGTCTTCCAGGACCTGAGGATTCAGCTCTACCCATGGGCACTGAAGTGGAA CATTCACTGGTCATTGCTTCTGTTTTTTTTTTTTTTGTTTGTGTTTTTTGATACAGAGTTTAC TCTTGTGCTAGGGTGGAGTACAATGGCGTGATCTCAGCTACCACAAGCTCTGCCTCCCG GGGTCAAGCGATTCTCCCACTAGCTGAGATTACAGGCATGCGCCACCACGTCCGGCTAAT TTTGTGTA</p>	
pARBI- 628: chr9_1_E xogenous _118	<p>AAGTCAACAACAGGCTCCAGAAAAAATGGAATATAAATGGTCCCAATTTGGCATTITG GAATTTGAGGCTTATATAGTATGAGCAAAATAAATCCTCCTGCTTCTATGAATCTTTGCAC TTTTCTCTATAATTCCTTATCAAGCAATGGGTTTGTCTGTTAACCAAGACTATACATAAAAT GTATCCCGTAGTTCCTTTTATTACATTTTTTCTTTGTTGTTACTAGTGGAGAAGCTAACAAAG AGCAGAATTTCTGCCCAACCGTAGCAAATACAGAAAAACAAAAGAGAAGCTTTGATACA GCCAGTGTAGATACAGCTAGGACGTCATGAATCAGAGCTCCCAACACAGATGTAATGGAA ACATCTTATCCATATCTGATTGCTCACATATAGTTATTTAGACAACAAATTTTACATTCTCTGG ATAGGGAGCCTCCGtgacgactgtgcttctagttgccagccatctgtgttggccctccccgtgcttctctgac cctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgattgtctgagtaggtgtcattctatt ctggggggtgggggaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgctggg gctctatggGGATCTGCGATCGCTCCGCTGCCGTGAGTGGCAGAGCGCACATCGCCACAG TCCCGGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGC GGGGTAAACTGGGAAAGTGATGTCTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGA GAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCA GAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCTACCTG AGGCCGCCATCCACGCGGTTGAGTCGCGTCTGCGCGCTCCGCGCTGTGGTGCCTCCTGAA CTGCGTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCT CCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGCTCAACT CTACGTCTTTGTTTCGTTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCTAC TCTAGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTG GTGCCATCCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCGGC GAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCACCGGC AAGCTGCCCGTGCCCTGGCCACCTCGTGACCACCTGACCTACGGCGTGCACTGCTTCA GCCGTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTA CGTCCAGGAGCGACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAG GACGGCAACATCCTGGGGCACAAGCTGGAGTACAACATAACAGCCACAACGTCTATATCA TGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGG ACGGCAGCGTGAGCTCGCGACCACTACCAGCAGAACACCCCATCGGCGACGCCCCGT GCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAG AAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTCGGCATGG ACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaat</p>	2541

	aaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatATTGATTTCATCTCATA GTCCAGGTAGGTGTAATAAGTACTGCCAAGCCAGCAGACATAAATCTGTATTATCTCATTTTC ATCACAGTCTCTGCATTGGGAAAAAATGTGAGTGAAAGACATTTTCTCCACCTTGTTAA GTACACAATTACATAGTTTAAAGAAGATAAGAATTTCAAATTGTTAGAATGATATCATTATT CAAATGATTCCCTGAGAACTTCAAGTATTCCCTTCCCCAAATGTAGGCAGGGCAAAATAG AACCAGTAGGAATGAAAAATGTTAATTGTTTCAGGTTCTGTAATTTTGGGTTTAATGACTCA GGCTATGTGCTACTGAGTAAATACTCATCTGGAGAAAAAGACTGTTGCATGACATATTTCT GATTAAGGACAATTTAACTAATTCTAAGAAAACCTTACATACTGCACATGCCATAAA	
pARBI- 629: chr9_2_E xogenous _119	GATTAGGTCTGGAATAAGATTGCACCATGACTAAAATGACTTCTTTAGCCAATGACATTCTCT GAAGATTGGATCAGAGTAAAGTTAACTAACCTACTCAAGGAAGACTTTCTAAATCAGCC CCTTTGCTGTATAATTTAGTATGGAGAGCTGATTGTGGGTTTTCTGTTCATTGTTTAATA CATAGAGGTTTCACATTTCAATTTGAAACAGAAAGAGGGACTGGAAGAGATAAGTTAGTAT GAGTGAGGAAAAGATTAGAAGGTAGAGATAGGATCGCAATGCTGTTATCACCTTTGCTTTA TTGATAATCTCAGGAAGGACTAGACTGCTAAGAAAAGAGGAGCCAGATTGGAATAAAAGA GACGATGCCAGGATCAGCCTGTGAGAGGATGTCTCACTTAGTACACCTCAAGGATCATGTCT AGCTGAGCATCTATACCCCGTgagcactgtgccttctagttgccagccatctgtttgttccccctccccgtgcc ttccttgaccctggaaggtgacctcccactgtcctttcctaataaaatgaggaaatgcatgcattgtctgagtaggtgt cattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtctggggat gcgggtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGC CCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCTTAGAGAAAGG TGGCGCGGGGTAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTTCCCGAGGGTG GGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGAACGGGTTTGC CGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCGCCCT ACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCGCGCTCCCGCTGTGGTGCCTC CTGAACTGCGTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCG GCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGC TCAACTCTACGTCTTTGTTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGC GCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTCAAC GGGGTGGTGCCCATCCTGGTCGAGCTGGACGCGCAGCTAAACGGGCCACAAGTTTCAGCGTG TCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC ACCGGCAAGCTGCCCGTGCCCTGGCCACCCCTCGTGACCACCCTGACCTACGGCGTGCAGT GCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAA GGCTAGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGG AGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCA AGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACATAACAGCCACAACGTCT ATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACAT CGAGGACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGG CCCCGTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTCG GCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaat tcacaataaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatGTGATGAATATT GCATACAGACTCTGCCTTCAAGTCATCCCCATTGACAAGCATTTATTTAAGGTTCTTACAT TCCAGGACTTGTACTAGATGCTAGAAACAAACAGATAAGGAAAACGTAGGAAAATGCTTCT CTCAGGAAGCAATATTGTATATGAGTGGTGAAGAGCTTCAAATCTGGGGCCAAACTGCTGG GTTTGAAATTTGGCTTGGCCACCTACTGGCTGTGAAATCTTGGGCACTTTCTTAATCACTCT GTGCCTCAGTTTCTCATCTGAAAATGAAATAGCCATAGTACTTATTACAAATAGGTAATA ATTAGTGAGAATTAATTTGAGTCAATACATAAAAATGACTCAGAATAAAAGACCAGCTAAG AATATATACACATCACTTAGCTACTATAATCTAGTAGGAAAGATGGGTATGTTATCAGAG GACTT	2541
pARBI- 630: chr9_3_E xogenous _120	CAGATAAAAAAGCTGAAGCTCAGGGATATTGTCATTTACCCATGAGCTCACAGGCAGGAA GTGGTGAAACTATCATTAACTACGGTTGGCCTTGTCTTTGTGGTTTCATTTCTAAAGCC TCTGACACCCTGACCTCAACTTCTTCTGTAGATATGTACCTGGCCTCCTTCACTAAGAC ACTACACACTGGCCACACACTTTGTCATCTCATAGACTGACAACCTGCTCTCACATACCTG CTTCTTACTGTGAGGCTCTTTTTCTTGTCTCAGAAATGTCTTCCCCACTTCTTATGTGCCA ACTCCTAGTCATCTACAAGAACCACATTCACTTTAAGTTTCTTTGAAGCCTTTTCACTGTCC	2541

	<p>CATACCCTGATCCATTACCTCTTCTATGTATGCAGGGCTTGCTTCATGCTTGTGTAACCCAA GGGCCCTGCTgacgactgtgccttctagtgtccagccatctgtgtttgccccctccccgtgccttcttgaccctggaa ggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgattgtctgagtaggtgtcattctattctggggg gtgggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgagggtgggtctatg gGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCG AGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGGGGT AAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACC GTATATAAGTGCAGTAGTCGCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCAGAACAC AGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCTGAGGCCG CCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTCGT CCGCGCTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCTCCCTTG GAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGT CTTTGTTTCGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCTAGA GCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCC ATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGC GAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGC CCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAAGTGTTCAGCCGCTAC CCCGACCACATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAGG AGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGAGGTGAAGTTCGA GGGCGACACCCTGGTGAACGCGATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAA CATCCTGGGGCACAAGCTGGAGTACAACACTACAACGCCACAACGTCTATATCATGGCCGAC AAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGC GTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGTGC CCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCG ATCATATGGTCTGTGAGTTCGTGACCGCCCGCGGGATCACTCTGGCATGGACGAGCT GTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattt tttctactgcattctagtgtggtttgtccaaactcatcaatgtatcttatATTTGATTTAAACATTTTAAATTC TTAACAATTTATGAAAAAGGAAACCCATATGTTCAATCTGCCCTGGACCCTGCAAATATGCG AGCCAATCCTGTGTGTTTTTTCATGTTGCGTAGACTCTATTACAGTCAGTAACATATTGAG AAAGAGTGTGTCTCTCTGATAGTCTATGAGCTCCTGAAGCAAGAGGCTTGCTTAGTC ATTGCTGTATCCTCACACCAGACTCTACGGGATGCTCAGGATTCACCTGTTGATCTGTGAGG AAGCCCAAGGCTCAGTTAATGCCCCCACCCTCCTCCATAACAGTCTCCTGATTAGGAAAC AGTGCTTGACCTCTAGACAATCTGAGTATCCACTCCAGGAAGTGAACATTGCCTTCCCAAT GTTGAAACTGTAGCACTCAATCATGTTTCAGGAACATATAGAAGGTATGT</p>	
pARBI- 631: chr10_1_ Exogenou s_90	<p>TGGACCTTATGCAGGGTAATAAAACCAACACGTGGGGCCTGTGCTGTAAGGTGGCAGAG GGCGATGACTACCCCACTCATGCAGTTGAGTCATTTCAAGGCAGAGTTGTGCCAGTTCA GTACCCAGTAATAATTTCCAGTCGACGAGTATCAGTGAACAGGAGATAACCACTCATTTCTA GATTCTGCTCAGAGTCCAGCTTAGAGGCTCCACAGCTCAAAGAGACGGGATGGCAAAAC AGCCACCTTAATTTCCAGATCATCTGCCAGCTCATCTGCCAGCTGACACACAGCCATGGCT CCACTATTGCCAGTGTGTAGCTGCACCAGACCAATCTGGTTCACTTTTATGTAACAAAGT TGTGATTTGTTTTTCAGTTGCCGGGACTCCAGGTTGAAGATCATGAGCATGCCCTGATGA GCCAAGGCATGCAACCACAGtgacgactgtgccttctagtgtccagccatctgtgtttgccccctccccgtgcct tccttgaccctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgattgtctgagtaggtgtc attctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggat gagggtgggtctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGC CCACAGTCCCGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAGAGAAGG TGGCGCGGGGTAAGTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTG GGGGAGAACCCTATATAAGTGCAAGTAGTCGCGGTGAACGTTCTTTTCGCAACGGGTTTGC CGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCCCT ACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTC CTGAAGTGCCTCCCGCTTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCG GCGCTCCCTTGAGGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGC TCAACTCTACGTCTTTGTTTCTGTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGC GCCTACTCTAGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACC GGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTG</p>	2541

	<p>TCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC ACCGGCAAGCTGCCCCTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCACT GCTTCAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCCGAA GGCTACGTCCAGGAGCGCACCCTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCG AGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCA AGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCT ATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTCAAGATCCGCCACAACAT CGAGGACGGCAGCGTGACGTGCGCGACCACTACCAGCAGAACACCCCATCGGCGACGG CCCCGTGCTGCTGCCCGACAACCACTACCTGAGCAGCCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTCG GCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaatt tcacaataaagcattttttcactgcattctagtgtgtgtgttccaaactcatcaatgtatcttatGGGAACCTAAG TGCTTGAGACTGAGGAGTGGGACTGAAATAAGAAGCGGACACTGCAGGGCAGGATCAGG ATCCAATCAGATCGAGCCCTGGCATCACCTCATGGCAGGATCTAGTCAGATCGTGGCTTTTG ACATCACTTCATTGTGAAATCCAATCAGATCACACCTTATTACCTATCCTTATAAAACCGGA CCTAGCCCCAGCTCGAGGAGGCACTGCTTTGGGAGTTATCCCAGGTGTTCTTGTACTAGT TGCAAGGAATAAAATCCTCTTGCTAAATCCTCCTTGGTTGTGCAGATGTTGGCATGGATGTG GAGAGAAGGGAACACTTACGCTTTGTTGGTGAGGATGTAAATTAGCTCAACTCTGTGATAA ACAGTATGGAGAGTTTTCAAAGAACTAAAAATAGAACTTCTACTCAACCCAGCAATCCTATG AGTGCAATG</p>	
<p>pARBI- 632: chr10_2_ Exogenou s_88</p>	<p>ACATCTAATCCACACCATGACTAATAAACATGGCATGCTGCAATGGGCATTAATTTATGGG TAACAGAAGCAGATCCAAGCCTTTAGCTAATTAATAAAAAATGCACCATACAGCAACCATC CTGCCTGCTTGGGTGTAAATAGAGAGGAGAAAGATGGCATGCTGGTCATTGAGAGATAA TTACCTGCAATTTAGAGCTGGAATCTAGTGACAACATAAGAAAAATAAATACCTCTCTGGC TGTTAGGATTCTCAGTTCTAGCTGCGAGCAAGGAGCAAAGGCACCCACAGACTTGCCAAAC CTATGTCAGGAATGACGAATAGAAGGCAGAAATCCACATCCCCAGGTGGTAAATTTGTTAT CCACCTTCGTACCTCTTTCTAATGGAGGAAGTGAGGACAGGCAGCCTTGAGTCTACTT GAATGAGGCCTGGACCTTATtgacgactgtgccttctagtgtccagccatctgtgtttgccccctccccgtgcct tccttgacctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgcatgtgtgagtaggtgtc attctattctggggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtggggat gcgggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGCGGACAGCGCACATCGC CCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGG TGGCGCGGGGTAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTTCCCGAGGGTG GGGGAGAACCGTATATAAGTGCAAGTGTGCGCGTGAACGTTCTTTTCGCAACGGGTTTGC CGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCT ACCTGAGGCCGCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCCTCCCGCCTGTGGTGCCTC CTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTGAGACCGGGCCTTTGTCCG GCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGC TCAACTCTACGTCTTTGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGC GCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCC GGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTG TCCGCGAGGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC ACCGGCAAGCTGCCCCTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCACT GCTTCAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCCGAA GGCTACGTCCAGGAGCGCACCCTCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCG AGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCAAGCTCA AGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACACTGCTCT ATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTCAAGATCCGCCACAACAT CGAGGACGGCAGCGTGACGTGCGCGACCACTACCAGCAGAACACCCCATCGGCGACGG CCCCGTGCTGCTGCCCGACAACCACTACCTGAGCAGCCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTCG GCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaatt tcacaataaagcattttttcactgcattctagtgtgtgtgttccaaactcatcaatgtatcttatGCAGGGTAATA AAAACCAACAGTGGGGCCTGTGCTGTAAGGTGGCAGAGGGCGATGACTCACCCCACTCA TGCAGGTTGAGTCATTTCAAGGCAGAGTTGTGCCAGTTTCACTACCCAGTAATATTTCCAGT</p>	2541

	CGACGAGTATCAGTGAACAGGAGATAACCAAGTCATTCTAGATTCTGCTCAGAGTCCCAGC TTAGAGGCTCCACCAGCTCAAAGAGACGGGATGGCAAAACAGCCACCTTAATTTCCAGATC ATCTGCCAGCTCATCTGCCAGCTGACACACAGCCCATGGCTCCACTATTGCCAGTGCTGTAG CTGCACCAGACCAATCTGGTTCAACTTTTATGTAACAAAGTTGTGATTGTTTTTCAGTTGCC CGGGACTCCCAGGTTGAAGATCATGAGCATGCCCTGATGAGCCAAGGCATGCAACCACAG GGGAACCTAA	
pARBI- 633: chr10_3_ Exogenou s_89	TGAGGTCTTGGTATGTTGCCAGGATGGTCTCAAACCTCTGGGCTCAAGCAATCCTCCTGCC TCCACCTCCCAAAGCGCTGAGATTATAGGCATGAGACACAGAGCCCAGCCACTGTCCGCAT TTCTTTCTGGCTTCTTACTGGGTCTCTACTTTCACTTTGCTTCTTCTCTCTTCCACCAG CATAAGTTTTAGAACTGCATTCTGATCATGCTGCTCTGCTGCTTAAATCCTTCATGCAGA TCATGTAAGACCTTCTGATCCAGTGCTGCCTTGCCTCTAGAACCAGGGTGCCCTTCTCCC CTCTGCAGTTCTACTGCGCCACCTGCAGTTTCTCTCTCTGTGTTTATGTGTCTACTCCCTCTG AATGGTAGGCTCACACCCTCCACCTGGCCAACCTTACTAAATCTTGGGCTTCAACTCAAGG ATCACCTTCATgacgactgtgccttctagtgtccagccatctgtgtttgccctccccgtgccttccttgacctgga agggtgcactcccactgtcctttcctaataaaatgaggaaattgcatcgattgtctgagtaggtgtcattctattctggg gggtggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtggggatgcgggtggctctat ggGGATCTGCGATCGTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCC GAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGGGG TAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCTTTTCCGAGGGTGGGGGAGAACC GTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACAC AGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGCCG CCATCCACGCCGTTGAGTCGCTTCTGCCGCTCCCGCTGTGGTGCCTCTGAACTGCGT CCGCGCTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCTTTGTCCGGCGCTCCCTTG GAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTGCTCAACTCTACGT CTTTGTTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCTAGA GCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCC ATCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGC GAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACGGCAAGCTGC CCGTGCCCTGCCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAAGTCTTACGCCGTAC CCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCAGG AGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGA GGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAA CATCTGGGGACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATCATGGCCGAC AAGCAGAAGAACGGCATCAAGGTGAATTCAGATCCGCCACAACATCGAGGACGGCAGC GTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGTGTC CCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCG ATCACATGGTCCTGCTGGAGTTCTGTACCGCCCGCGGGATCACTCTGGCATGGACGAGCT GTACAAatgattgtttattgagccttataatggttacaaataaagcaatagcatcacaaattcacaaataaagcattt ttttactgcattctagtgtgtgttgcctcaactcatcaatgtatcttatTGGTTCACTCCACCAGGCTGGGCTG TGTGTCCTGCCAGTTCCTATAGTGCCCTAACTCACTTTTTTAAAAAATACTTTAAGTTCTG GGGTACATGTGCAGAACATGCAGGTTTGTACATAGGTATACACTTGCCATGGTGGTTTGC TGAAGCCATCAATGTCATCTACATTAGGCATTTCTCCTAATGCTGTCCCTCCCCTAGCCTCCC ACCCCCAACAGGCCCAAGTGTGTGATGTTCCCTTCTGTGTCCATGTGTTCTCGTTGTTCA GCTTCCACTTATGAGTGAGAACATGCGGTGTTTGGTTTTCTGTTCTGTGTTAGTTTGCTGA GAATGATGCTTTCAGCTTCATCCATGTCCTGCAAAGGACATGAACCTATCTTTTTTATGG CTGTCCATTATTCATGGTGTATGTGTGCCACATTTATTTATCCAGTCT	2541
pARBI- 634: chr10_1_ Exogenou s_92	CCTTCACCCCTTCTTAATAGTTTTCTCTCCGCTCCTGCACGGCTCCGCTCCGCTG ACCGTCTCGAAACCTCCAGCCGCGAGCCCGGCCCTCCAGCGGCCTGAGTGGCCTCCT CCCGCGGCGCCCCCAGCTCCGACCTCCAGCCCCCGCGAGGCGCGCCAGCGAGCGT GACCCGACCCAGGGCCACGGCTGCGCCCGTAGGATCGCGGGCGCGGGTCTCCATGAG GGACTGGGAGAGATGCGTCACCCGTAATCCCTCAACTGGGTGCAACCGGTCTGCCTTGG TTGGTCCCTTCTGATGGCGGAGCGGGACCTCGACTTGGTGCCAATGAGGAGCCTCGTG GGGGTGCTCTCGGCTGCCATGGCAACGAGGGGCGCCCGCTTCCCCGCGGGGCGAGGCC GGCTCTCCAGGACTGGCCATgacgactgtgccttctagtgtccagccatctgtgtttgccctccccgt gccttccttgacctggaaggtgcactcccactgtcctttcctaataaaatgaggaaattgcatcgattgtctgagtag	2541

	<p>gtgtcattctattctggggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctgg ggatgcggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACAT CGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGA AGGTGGCGCGGGTAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCTTTTTCCCGAG GGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGT TTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTACGCGCCCCCG CCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTG CCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGT CCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCGTCT TGCTCAACTCTACGTCTTTGTTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACC GGCGCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTT ACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGCGGACGTAAACGGCCACAAGTTCAGC GTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGC ACCACGGCAAGCTGCCCGTGCCTGGCCACCCTCGTGACCACCTGACCTACGGCGTGC AGTGCTTACGCCGTACCCCGACCACATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCC GAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCG CCGAGGTGAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACT TCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAATAACAACAGCCACAACG TCTATATCATGGCCGACAAGCAGAAGAAGCGCATCAAGGTGAACCTCAAGATCCGCCACAA CATCGAGGACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGA CGGCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGAC CCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTC TCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcaca aatttcacaataaagcattttttcactgcattctagtgtgtgttgcctcaactcatcaatgtatcttatTGCAGTCAC GCGCTGTGGCCCCAGTCTGTAGCATGAGGTGGGGGTGAGAAGTTGAGGAACAATCGG ACCTAAAGCCTTGACAATTGCCAACAGTGTAGACAAGTCCCAGCATGCCCAAAATTTATAAG AGAAGGCTGCCTGGAAGAGGGACACGATGAGGAGGGTCTGCTGAAACGGACAAAGAAAC CCAGTTCAGTGCAAGTGGAGTGGACATGGCACGGGCAGGGCAGGAGTGGGGTGGTGTCT TAGTAAGCGGATTAGGGTTTCCAAGCACAAGACCCACCCAGGGCAGGATGGGGAACCAAGG TGAGCAGGTGCGCTGAATTGTGGGTCTCAGCTGTCTTCAAGTGTCCCGCAGGAAGAGAGA GCTAAGGATCACCAGGGTCATTCCCCTGCCTCAGGCAGCCTGCACTCCACCTTAGGTACAGT CATGTCCGGTCTTCAGCA</p>	
pARBI- 635: chr10_2_ Exogenou s_91	<p>TGATCTCCACCTCAGTCTCCCAAAGAGCTGGGATTACAGGCATAAGCCACCTTGCCCCGC CAGTTTTAGCCTGTAGCTCTTTGAGGGACACTTGTTATGGTCATACCCACAGCTTTGACCC TTACCAGGTGGTCAGGTGGATGAATGAATGAGTAGAAAGAAGGAAGAGAAGGCAGGAGG GAGAAGAGGAAGAATGAAGGAAGGGTTGAGTTTGTCTGGAAGCTCCAGCTTCCATCCG CACCACACTCTCCCTCTGTCCCCAGGACACCAGGGAAGTCAAGGCTCTCCTCTTACCA GGTGCTGTGTGGGTCCAGGGAGAGAAGAGCCATTGAAATGGGGCACTGGTCTAAACTCT GGACCTGCTGCTCACTATTGACTGAACCTAGCCACTTAAATATTCTCCTCTATAAAATGGGA GTGACCATAGCAACTACCTCGTgacgactgtgccttctagtgtccagccatctgtgtttgccccccccgtgc cttcttgaccctggaaggtgccactcccactgtcctttcctaataaaataggaaattgcatcgattgtctgagtaggtg tcattctattctggggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctgggga tgcggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGC CCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGG TGGCGCGGGGTAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCTTTTTCCCGAGGGTG GGGAGAAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGC GGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTACGCGCCCCGCCCT ACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCCTC CTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCG GCGCTCCCTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGC TCAACTCTACGTCTTTGTTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGC GCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCC GGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTG TCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC ACGGCAAGCTGCCCGTGCCCTGGCCACCCTCGTGACCACCTGACCTACGGCGTGCACT</p>	2541

	<p>GCTTCAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCCGAA GGCTACGTCCAGGAGCGCACCATTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCG AGGTGAAGTTCGAGGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCA AGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCT ATATCATGGCCGACAAGCAGAAGACGGCATCAAGGTGAACCTCAAGATCCGCCACAACAT CGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGG CCCCGTGCTGCTGCCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCG GCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatt tcacaataaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatTGAATTGTAGG GAGACCCAAAAATGTATATGAATACATTTGTCAACTAAAGAGTGTAGGGATTATCTCAGT GGAGGGATAGGCAGTGCAGGCTCTGGAACCAGACTTCTGTGTTACATCCCTGCTCCACT GCTTGAGACCTTTGGCAAGGTCTTAACTCCTCTGGACCTCAGTTTTCTCATCTGTAAAACA GGGATTATACTAGTTCCTACCTCACAGAGTTGTGAAGATTAAATGAGATAATGCATGAAAG GCTTTTCAATAAGAGCAGGGCACACATTAGGCATGATGTCCATGATCAAGTGCCTAATATGT GCCTGCTCTCAGGAAGGATGCTGTGAACTACTTCACTAAAGTGTAATGAATGATAAGA TCTACTATGCTCCACTCATGCCTGTAATCCTAGCACTTTGGGAGGCCGAAGCAAGTGATCA CCTGAGG</p>	
pARBI- 636: chr10_3_ Exogenou s_93	<p>GGTGAAGTCACCCTGGGTACCTGGAGTTACTCAGAGTGACACTAGTACACGCTGGCAGG AGTGATGGATGAGCTAGGCTCCAGGAAAGCAGGTGGGGCTGGAAACCACCCAAAGACAAG GAAATTGTTGGGTTTGAATTCAGGTAAGCAGAGTATGGCCTGAGAGCAGCGGCAGAGG CTGAAAGTGGGCTTGGTCTCGGTATTTTGGAGCTGAGGTAGCTCCAACCTCTCTCCCTCTGA GTCAGCACCCCACTTAAGACAGAAATACTGAGATCTGCGACCCAGCCTCCCCACAGCAA CTCCACAGTCCCCAAACCTTTGCTCCGCTGGGTCTCCCAAGTATGGTAGCTGACACAGCCC TGAGCAGCCCACTGTCTCTGCCCTGCCAAGTCTTCTCACTCTTGTCACTTTGTCTACATCAT TTCTTTGTCTGGCACCCCTCCTtgacgactgtgccttctagttgccagccatctgtttgttccccctccccgtgcc ttccttgaccctggaaggtgccactcccactgtcctttcctaataaaatgaggaaatgcatgcattgtctgagtaggtgt cattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtctggggat gagggtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGC CCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGG TGGCGCGGGGTAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTCCCGAGGGTG GGGGAGAACCGTATATAAGTGCAGTAGTCGCGTGAACGTTCTTTTTCGCAACGGGTTTGC CGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCGCCCT ACCTGAGGCGCCATCCACGCGGTTGAGTCGCGTTCTGCGCCTCCCGCTGTGGTGCCTC CTGAACTGCGTCCGCCGTCTAGGTAAAGTTAAAGCTCAGGTGCGAGACCGGGCCTTTGTCCG GCGCTCCCTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGC TCAACTCTACGTCTTTGTTCTGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGC GCCTACTAGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACAC GGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAACGGGCCACAAGTTCAGCGTG TCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC ACCGGCAAGCTGCCCGTGCCTGGCCACCTCGTGACCACCTGACCTACGGCGTGCACT GCTTCAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCCGAA GGCTACGTCCAGGAGCGCACCATTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCG AGGTGAAGTTCGAGGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCA AGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCT ATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACAT CGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGG CCCCGTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCG GCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatt tcacaataaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatAGAATTGGTGC CCCAGAGGTGGGAAAAACCTACCTGCTCACTGCTCTATCTCTGGGCTTAGCTCAGACTCT GGCATACGTGAGTGCTTAGTAGAACTTGATGGGGTATTAAATGAGACCTGGGTGGGT CTCACATTAATTTCTAACTCCTTAGGTGGCTTGGGCCACCCCTCTGAGCCCTGTTTCCA CATCTGTAAAGTAGCAAACCATCGCCATGAAGAACAGGGAAGAACCAGGTCAGCAGGCAG</p>	2541

	GGCGGATGAAGCATCCAGCCAGTTCTAGGAAGTTTCCGATGGCTAATCCTTCAGATGCAGC TTGTAAGCAGGTCAAATACAGAATAGGAACTGAGGCGCAACGAAGTCATGCTTAGAAGT CTGTCCAGGGAGACCAGTCAAGGCCTCCCCACACCTGCAAGCCCTTCTAGGAGCTCTGG TTAAGTCACTC	
pARBI- 637: chr11_1_ Exogenou s_99	ATCTTCAAATTGTAGTCTTTGTAACAACCAAATAACCTTTTGTGGTCACTGTAAAATTAATAT TTGGTAGACAGAATCCATGTACCTTTGCTAAGTTAGAATGAATAATTTATTGTATTTTTAAT TTGAATGTTTGTGCTTTTTAAATGAGCCAAGACTAGAGGGGAAACTATCACCTAAAAATCAGT TTGGAAAACAAGACCTAAAAAGGGAAGGGGATGGGGATTGTGGGGAGAGAGTGGGCGA GGTGCCCTTACTACATGTGTGATCTGAAAACCTGCTTGGTTCTGAGCTGCGTCTATTGAAT TGGTAAAGTAATACCAATGGCTTTTTATCATTTCTTCTTCCCTTTAAGTTTCACTTGAAATTT TAAAAATCATGGTTATTTTTATCGTTGGGATCTTTCTGTCTTCTGGGTTCCATTTTTTAAATGT TTAAAAATATGTTGtgacgactgtgccttctagtgtccagccatctgttgttggccctccccgtgccttcttgacc ctggaaggtgccactcccactgtccttcttaataaaatgaggaaattgcatcgattgtctgagtaggtgtcattctattc tggggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtggggatgagggtggg ctctatggGATCTGCGATCGCTCCGGTGCCGTCAGTGGGCAGAGCGCACATCGCCACAGT CCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCG GGGTAACTGGGAAAAGTGATGTCGTGACTGGCTCCGCCCTTTTCCCGAGGGTGGGGGAG AACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCAGA ACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTACGCGCCCGCCCTACCTGAG GCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCTGA GCGTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCTCC CTTGAGGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCCTGACCTGCTTGCTCAACTCT ACGTCTTTGTTCTGTTTCTGTCGCCGTTACAGATCCAAGCTGTGACCGGCGCTACTC TAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGT GCCCATCCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCGGCGA GGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTTCATCTGCACCACCGGCAA GCTGCCCGTGCCCTGGCCACCTCGTGACCACCTGACCTACGGCGTGCACTGCTTACGCC GCTACCCCGACCATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGT CCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAA GTTGAGGGGACACCCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA CGGCAACATCCTGGGACACAAGCTGGAGTACAACACAACAGCCACAACGTCTATATCATG GCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTCAAGATCCGCCACAACATCGAGGAC GGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGC TGCTGCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAA GCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCCGCGGGATCACTCTCGGCATGGAC GAGCTGTACAAatgattgtttattgagcttataatggttacaataaagcaatagcatcacaatttcacaataa agcattttttcactgcattctagtgtgtgttgcctcaactcatcaatgtatcttatACATGGTAGTTTCAGTTCTTA ACCAATGACTTGGGGATGATGCAACAATTACTGTCTGGGATTAGAGTGATATTAGTCA CGCATGTATGGGGAAGTAGTCTCGGGTATGCTGTTGTGAAATTGAACTGTAAAAGTAGAT GGTTGAAAGTACTGGTATGTTGCTCTGTATGGTAAGAACTAATCTGTTACGTATGTACAT AATTACTAATCACTTTTCTCCCTTTACAGCACAAATAAAGTTGAGTTCTAAACTCATTAG AATTGTTGATTGCTATGTTACATTTCTGACCCCTATCACATTGCCTTCATAACGACTTTGG ATGTATCTTCATATTGTAGATTTAGGTCTAGATTTGCTAGCTCCAAGTAATTAAGGCCATGTA GGAGAGCATGGTAACCACAGATAGAACTGGTATTATCCCAAGTGGTCTGCAGACTGC	2541
pARBI- 638: chr11_2_ Exogenou s_97	TTACAGCACAAATAAAGTTTGTAGTTCTAAACTCATTAGAATTGTTGTATTGCTATGTTACATT TCTCGACCCCTATCACATTGCCTTCATAACGACTTTGGATGTATCTTCATATTGTAGATTTAG GTCTAGATTTGCTAGCTCCAAGTAATTAAGGCCATGTAGGAGAGCATGGTAACCACAGATA GAACTGGTATTATCCCAAGTGGTCTGCAGACTGCTGAGTGGGGATGGGATCTGCTCTGT TGAGAGTTGGTAATCATTGTTTGAATGTGATGAAACCACTCAAGCCAATGAAGGTGGGT GTGTAGGTGGGGAGTACTTTGCCATAATTTTTAAACATTACCTGGTTAGAGTTCTAAGTG GTACTTATTTTTGTTTGGTTAGGGGAAAGCCTGAATAAAAAACAGAAATGGACACATAATAT GCATATTCATAGTCTTTtgacgactgtgccttctagtgtccagccatctgttgttggccctccccgtgccttctt gaccttgggaaggtgccactcccactgtccttcttaataaaatgaggaaattgcatcgattgtctgagtaggtgtcattc tattctggggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtggggatgagg tgggctctatggGATCTGCGATCGCTCCGGTGCCGTCAGTGGGCAGAGCGCACATCGCCAC	2541

	AGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAGAGAAGGTGGC GCGGGGTAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCCGAGGGTGGGG GAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGC CAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCT GAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCCTCCGCCTGTGGTGCCTCCTG AACTGCGTCCGCCGTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCG CTCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGCTCAA CTCTACGCTTTTGTTCGTTTCTGTTCTGCGCCGTACAGATCCAAGCTGTGACCGGCGCCT ACTCTAGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGG TGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCG GCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCG GCAAGCTGCCCGTCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCACTGCTTC AGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGGAAGGCT ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGT GAAGTTCGAGGGCGACACCTGGTGAAACGCATCGAGCTGAAGGGCATCGACTTCAAGGA GGACGGCAACATCCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAACGTCTATATC ATGGCCGACAAGCAGAAGACGGCATCAAGGTGAAGTCAAGATCCGCCACAACATCGAG GACGGCAGCGTGCACTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCC GTGCTGTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAAG AGAAGCGCGATCATATGGTCTGCTGGAGTTCGTGACCGCCCGGGATCACTCTGGCAT GGACGAGCTGTACAAatgattgtttatgagcttataatggttacaataaagcaatagcatcacaatttcaca aataaagcattttttcactgcattctagtgtgtgttgcctaaactcatcatgtatcttatGGGAGGCTGGAATGT GCCTGGGATTTGGGTCTAAGTGTATGCGTAATTCTTACCTACTAAAGAATTTGCCTTGTTTT TTTCCTTTTGGTGAGTGACTAAAACGTCTGGGCTTCCCTGTGTGCGTGCTACAGTAAGCAAG CAGAGGCTGTGCAAAGGTGTGAGCAGGATCACGTGGAATCTGGAGGATACATCTTGCTT GCAAATGCCTCTGTCTCTGGGTGGGACTGTTCTGTCTTGCCTGCTGTTCTGTGTACCT CTTGGGGTGTAAGGTTTTGCTTACAGGAGACAACTTTGGGCGTAGAATGGAAGCCACTGC CAGCCTCTGTGCTGAGAAGGAAGGTGCTTGTTCAAAGGGAGCAGCAAGGGAGGCTTGTT CTACTCACTGGGCTGTTTGCTGAGAAGGGGAGATAAGGGGCTGAAGTGGGACTAGCCA GGGGGA	
pARBI- 639: chr11_3_ Exogenou s_98	TGGGGCTTTGGGGAATTTAGTGCGTGGGTGAGCCAAGAAAATACTAATTAATAATAGTAAG TTGTTAGTGTTGGTTAAGTTGTTGCTTGAAGTGAGAAGTTGCTTAGAACTTTCCAAAGTG CTTAGAACTTTAAGTGCAAACAGACAACTAACAAACAAAAATTGTTTGTCTTGCTACAAG GTGGGGAAGACTGAAGAAGTGTAACTGAAAACAGGTGACACAGAGTCACCAGTTTCCG AGAACCAAAGGGAGGGGTGTGTGATGCCATCTCACAGGCAGGGGAAATGTCTTTACCAGC TTCTCTGGTGGCCAAGACAGCCTGTTTCAGAGGGTTGTTTGTGTTGGGGTGTGGGTGTTA TCAAGTGAATTAGTCACTTGAAAGATGGGCGTCAGACTTGATACGCAGCAGATCAGCATC CTTCGCTGCCCTTAGCAACTTgacgactgtgcttctagtgtgagccatctgtgttgcctccctccccgtgccc ttccttgacctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgacgtgctgagtaggtg cattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggat gcggtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGC CCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAGAGAAGG TGGCGCGGGGTAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCCGAGGGTG GGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGC CGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCCCT ACCTGAGGCGCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTC CTGAAGTCCGTCCGCCGTCTAGGTAAAGTTAAAGCTCAGGTGAGACCGGGCCTTTGTCCG GCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGC TCAACTCTACGTCTTTGTTTCTGTTCTGTCGCGGTTACAGATCCAAGCTGTGACCGGC GCCTACTCTAGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACC GGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTG TCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC ACGGGCAAGCTGCCCGTCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCACT GCTTCAGCCGTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAA GGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCG	2541

	AGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCA AGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCT ATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACAT CGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGG CCCCGTGCTGCTGCCCACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCG GCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatt tcacaataaagcattttttcactgcattctagtgtgtgttgcctcaactcatcaatgtatcttatAGGTGGTTGATT TGAAACTGTGAAGGTGTGATTTTTTCAGGAGCTGGAAGTCTAGAAAAGCCTTGTAATGC CTATATTGTGGGCTTTAAACGTATTTAAGGGACCACTTAAGACGAGATTAGATGGGCTCTTC TGGATTGTCTCATTTGTACAGGTGTCTTGTGATTGAAAATCATGAGCGAAGTGAAATT GCATTGAATTTCAAGGGAATTTAGTATGTAAATCGTGCCTTAGAAACACATCTGTTGTCTTTT CTGTGTTTGGTCGATATTAATAATGGCAAAATTTTGCCTATCTAGTATCTTCAAATTGTAGT CTTTGTAAACAACCAATAACCTTTTGTGGTCACTGTAAATTAATATTTGGTAGACAGAATCC ATGTACCTTTGCTAAGGTTAGAATGAATAATTTATTTGATTTTTAATTTGAATGTTTGTGCTTT	
pARBI- 640: chr11_1_ Exogenou s_94	CGACCAACCCATCAAACCTCCCCGCCCCAGCACTTTTATTTCTCCTCTTTAGGAAGTACACTT CAGTATCTTTGGCAGAGTGCATGAGCAGCACTAAAGTAAAACATCGCAGAAAACATAGCTT TAGTCTACCTTCGTGTCTAAAGGAAAACAGTAGCTTCCCAGGCCACCGGAAGGGCAA CATATGTCCTCTGCAGTTTCTGCACAGGGAAGGTAAAGACAGAGAGGACCTACTCTC AACACAGAAAACATTTCAAATCTTTCTCGCTGCAACCCAAAGCTGAAGTCATTCTCCCCAG AAATAACAAAAGTTGGAAGAGAAGCCGGAGACAGGATAGGTGCAGGAAGCCACACTTTG AGGGCAGCACTCAGACACCCTCTCCTGTGTGCAGGACGTGCCGAATGTTAGGTGCAATGA GAATGAGCCATGCTTGGCTTAtgacgactgtgccttctagtgtgccagccatctgtgtttgccctccccgtgcc ttccttgacctggaaggtgcccactcccactgtcctttcctaataaaatgaggaaattgcatgcattgtctgagtaggtgt cattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggat gcgggtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGC CCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGG TGGCGCGGGGTAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTCCCGAGGGTG GGGAGAAACCGTATATAAGTGCAAGTAGTCGCGGTGAACGTTCTTTTCGCAACGGGTTTGC CGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCT ACCTGAGGCCGCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCCTCCGCCTGTGGTGCCTC CTGAACTGCGTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTGAGACCGGGCCTTTGTCCG GCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGC TCAACTCTACGTCTTTGTTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGC GCCTACTCTAGAGCTAGCGAATTgcccaccaccATGGTGAGCAAGGGCGAGGAGCTGTTACC GGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTG TCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC ACCGGCAAGCTGCCCGTGCCCTGGCCCAACCTCGTGACCACCTGACCTACGGCGTGCAAGT GCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAA GGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCG AGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCA AGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCT ATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACAT CGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGG CCCCGTGCTGCTGCCCACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCG GCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatt tcacaataaagcattttttcactgcattctagtgtgtgttgcctcaactcatcaatgtatcttatCGAGGGCAATC TGGCCCATCAAGTGGCCTTCGCTCTGGGAGTAACAAAAATGCACTTCAAATAGCTTCTGT AATCAAGCTGCATGGGTGGAGTACTCCCCAGCTGACTCCAGGAAGTCTCTATCCAAAGCT ATTATTAGCCAGAGCTGTGCAAATAATTAGTACCCACTTGCTCCATAACCCCTCCATGAC AGCCCAGGCATTGAGTCCAGGTGGGACCATCAAGCCATGCTCTGGTGGCTCATGCATTATC ATAGAAATGGGAGGCTTTATTTATTTACTAAAAAGAACAAAAACAACAGACTGCTGTCCTT TAGACAATAGGATCACGTCTGAGCCCTCTGTGCCCGAGTGACAAGCCAGCCCAAG	2541

	TTCTCTTTCCTCAGCCTCCCCACACATGTTCTGGAGGAGATGGGCCAGCAGGCTGCTCTGA GGCCTGGC	
pARBI- 641: chr11_2_ Exogenou s_96	TCACAGAATCTTGTGTTGAGCTAACAAACAGTTATTCTACCCAAAGTAAAGAGTAACTTAAAT TTTCCCATTTGTTCTTCCAGGCTGGAAGATGTAAGAAACACACACAGTATAGTGTAGGTTTCC TCCATAGTTAAGTACCCAGAGCTAGGCTGAAATCCAGTGTGGATTGTTTCCAACTTATAG TAGGGAACCGCCAATGACATGAAAGAGCATTACCTTACCGGACTGATTATATTCTACTTCC AGTCATAGTACAAATGATCACATGTCCACACCCACATGTGCTCTGATAAGTAGTCAATTGAG AGGAGTGAGTCAGGGAGCCGTAACCTTTCAGCCAACTGCCAAGAAGAACTGATGCTTTTA GAAATTCAGCAGCTTTTATTGGCATAGAAGTTTCAGCCTTATAGGCCAGGGTTTCTCTGAG GCAGAGGCAAAACCTGTgacgactgtgcttcttagttgccagccatctgtgttggccctccccgtgcttctt gaccttgggaaggtgccactcccactgtccttcttaataaaatgaggaaattgcatgcattgtctgagtaggtgtcattc tattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgcgg tgggctctatggGGATCTGCGATCGTCCGGTGCCCGTCAGTGGGCGAGCGCACATCGCCAC AGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGC GCGGGGTAAACTGGGAAAGTATGTCGTGTACTGGCTCCGCCTTTTCCCGAGGGTGGGG GAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGC CAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCCGCCCTACCT GAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCCTCCCGCTGTGGTGCCTCCTG AACTCGTCCGCGCTAGGTAAAGTTAAAGCTCAGGTCGAGACCGGCCCTTTGTCCGCG CTCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCTGACCTGCTTGCTCAA CTCTACGTCTTTGTTTCTGTTCTGCGCCGTACAGATCCAAGCTGTGACCGGCGCCT ACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGG TGGTGCCCATCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCG GCGAGGGCGAGGGCGATGCCACCTACGCGCAAGCTGACCTGAAGTTCATCTGCACCACCG GCAAGCTGCCGTGCCCTGGCCACCTCTGTGACCACCTGACCTACGGCGTGCACTGCTTC AGCCGTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGT GAAGTTCGAGGGCGACACCTGTTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGA GGACGGCAACATCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATC ATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAG GACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCC GTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACG AGAAGCGCGATCACATGGTCTGTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCAT GGACGAGCTGTACAAtgattgtttattgagcttataatgggttacaataaagcaatagcatcacaatttcaca aataaagcatttttttactgcattctagttgtgttgggttgcctcaactcatcaatgtatcttatTGTATGTTGTTATCT CAGGATTCTTTTTTTTTTTTTGAGACAGAGTCTCACTCTGTTGCCAGGCTGGAGTGCAGTG GCACAATCTCGGCTCACTGCAAGCTCCGCCTCCCGGGTTCAGCCATTCTCTGCCTCAGCC TCCGAGTAGCTGGGACTACAGGCGCCCGCCACACGCTTTCTAAATTTTGATTTTTAGT AGAGACGGGATTTACCATGTTAGCCAGGATGGTCTCGATCTCTGACCTCGTGATCCGCC GCCCTGGCCTCCCAAAGTGTGGGATTACAGGCGTGAGCCACTGCGCCAGCCTATCTCAG GATTCTTAATGTAAAAACAGTTCAGTATGAAAGCGTACTTATGACAGAGCTGTTGCAGAA TGTGAAATCACCCATGTGCCTAAGTGTCTCCTACTACCTGGAACACTAGACCACATGCAGC AG	2541
pARBI- 642: chr11_3_ Exogenou s_95	CAGCCCTGAACTCAGCCTTACGCGCCCTCCCTAAACACATGGGCCAGCCACAGGGAAGAAA AAAATGCCCTGTAGCAGAGGAATCTAAACATTGCTGTTGTTCTAGTTAATAAAGGACTTA GAGATTGAAAAGAAGTACCATCTGTATGGCTGGCAACAGACAGCATGATTTTGATGACTGA CTCTGGGGAGATCTGAGAAAACAGTACATAATATGTCCTTACCTCTGCTCCATCATTATGA CCCAAGCTCCTGCCCTGTCTTCTCAGGAAGATTCTTACAGTAACTCCAGTTTGGAATTTCCCT TTCATATTTGAAATAACAACAGTAATAGTGACCACTAATGCTTACCGAGTGTCCACTCTGTG CCAAGCATCGTGTTTTATCATCTTTTTGTTAGGCACTGTACATGGATTAATACAATTACAA CCCACCACAACCCCATtgacgactgtgcttcttagttgccagccatctgtgttggccctccccgtgcttcttga ccctggaaggtgccactcccactgtccttcttaataaaatgaggaaattgcatgcattgtctgagtaggtgtcattctat tctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgcgggtg gtctatggGGATCTGCGATCGTCCGGTGCCCGTCAGTGGGCGAGCGCACATCGCCACAG TCCCGGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGC	2541

	<p>GGGGTAAACTGGGAAAGTGATGTCGTGTAAGTCTCCGCTTTTCCCGAGGGTGGGGGA GAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCA GAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCTACCTG AGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAA CTGCGTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCTTTGTCCGCGCT CCCTTGAGCCTACCTAGACTCAGCCGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACT CTACGTCCTTTGTTCTGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTAC TCTAGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTG GTGCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGC GAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCAACGGC AAGTGCCCGTGGCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAAGTGTTC GCCGTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTA CGTCCAGGAGCGACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAG GACGGCAACATCTGGGGCACAAGCTGGAGTACAACAGCCACACAGTCTATATCA TGGCCGACAAGCAGAAGAAGCGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGG ACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGT GCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAG AAGCGCGATCAGATGGTCTGAGTTCGTGACCGCGCGGATCACTCTCGCATGG ACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaattcacaaat aaagcattttttcactgcattctagttgtgtttgtcctcaactcatcaatgtatcttatGAGATAAGTACTTGTACT ATCCTCATTTTTATGGGTGATGATACAAGAAACAGAAAGGTTCAAGCAACATGCCTAAAGCCA CACAGCTACTATGAGGCAAAGTCTAGGTTTGAAGTCAAGAAATTCTGACTTCAGACTCACTTA TCTTATTATACTTCACTTAGTATCTCCATTAATTAATTATTCTTCTTTTATTTGTTAAT TCACCAATATTCTGGGAAGCTACTTGTCTAGACACTGTATGAAAAATGAGAATGGATACA AAGCAACCTCAGACATGAAGTCAAGGTCCTTACAAGCTTAAACGTATATGATACATTTCAA ATAGCAATACTATGAGGACAGCTGATACTACAACATAAGTCTTGGTGGTCACAGGAGATC TATCATAGGATTTACGAAGAACCTGACACTGAAAACCAAGAACTTGAGGGAAATAAAAC</p>	
pARBI- 643: chr15_1_ Exogenou s_100	<p>GTGTCCATCTGCATGTCTCAAGTCACAATCCTCCAGATATTCAACCAAGTGCTTGATTCTG TTGGCACAAGGACCATGAAATCTTCAGTAGCTAAGGAGACTCTTTGACAAATAGATTATTG CATATGATGTAAAAGGGTCTCATTACAGAGAACTACACATTTACTACACATTTACTAGCTGT AGATGTGAGAAATTGAAGCTTTGAGAATTGTCTTTGTAAGCACGCTGTAATAATTGTGT CTCTACAAAAATGGAGAAATACTTAATCTTTGCAGGTTTTATTAGCTTCGAAAAAGGGAAT ACAAATATTTTGATACCTGACTTTATTTTAAAGATACTGGCAAGCAAGGAAAGATACTCAGT TTGTAAATTATAGCATAGATTTGAAAGACGGAAATTTTTTTTGTATTTTGATTCTTTCTGA TTCAGAACCTGCGtgacgactgtgcttctagttgccagccatctgtgttggccctccccgtgcttcttgcacc tgggaaggtgccactcccactgtccttcttaataaaaatgaggaaattgcatcgcatgtgtgtagtaggtgtcattctattct gggggtggggcaggacagcaaggggaggattgggaagacaatagcaggcatgctggggatgctgggtggc tctatggGATCTGCGATCGCTCCGCTCAGTGGGCGAGCGCACATCGCCACAGTC CCCGAGAAGTTGGGGGGAGGGTGGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGG GGTAAACTGGGAAAGTGATGTCGTGTAAGTCTCCGCTTTTCCCGAGGGTGGGGGAGA ACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCAGAA CACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCGCGCCCTACCTGAGG CCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAATG CGTCCGCCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCTCCC TTGGAGCCTACCTAGACTCAGCCGCTCTCCACGCTTTGCTGACCTGCTTGTCAACTCTA CTGCTTTTGTCTGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTACTCT AGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGT GCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGA GGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAA GCTGCCGTCGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAAGTGTCTAGCC GCTACCCGACACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGT CCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAA GTTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA CGGCAACATCTGGGGCACAAGCTGGAGTACAACAGCCACAACGCTCTATATCATG</p>	2541

	<p> GCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGAC GGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGC TGCTGCCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAA GCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGAC GAGCTGTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaataa agcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatTGAGTTTCCATTCTGGGAT AGAGAGCCCTGCCAAAGCCAACCTCAGTCTCCTGTTATTGACAGAAATTTAAAGGTTACTTGAG CTGATTGATACCAATTAATAAAAGCATCTACTGCCATTTTATTAACGCCCTATTTAATCT CCACATCCCAAGTTCATTCTCTCTCTTTTAAGGCTATACATGGGCCTCAACATTCTCTCTTC TTCAGTATCAGCTGTCCTCATCCCTATTCAAAGTCAGAATGACTTGGAATCTATTACGGGCT GCTACTTAATTGGATGAAGAAAGTACTCTGTTGCATGCTAACCTCCCAGATTGGAATTAGAA CCAAGGTCCTGAATCTACACAAGACCTTTTCCCTTCTCTTCTGCATTTATTTCTTTTTTCT ACATCTTCTTTTTGAATTTTTTTTTTTTTTTTTTCTGAGATAGAGTCTTG </p>	
<p> pARBI- 644: chr15_2_ Exogenou s_101 </p>	<p> ATCATCAAAATCTTCATTTATACAAATCACGGGTATTAGAAATAAAATCAGGTATTGTGTAC AGTCAGATCCAGGTTTACACAAACTAGAGGTTTCAATTAAGTTTCCTTCATTTTATAAAACC ATGACACAAGCTGTAAATAAAGGAGCTCTGGCTTTAGGCCTTCTTCTGTTTATAGACAGTAA ATTTAATCCTCTGTCCCTGCAGACCACTCAAAGCAGTAACCTTGGCTACCGTTGCCGCAG AAGAAACACACCCTGCAGATTTCCAGTCTATATTAGTCTTAGAAAAATTGGTCATGTTGAA AGGGAACAAAAACAATTTTACTTTGCCTCAGTTATTGACACCAAGAAGCACTCCTCAGCTGTT CAGAGGGGAAACAATGAGTCATTTCATGCTGTCAGCCAGGTGTTGTCATGAATTCAGACA GAGGCCGTGAATTAACtgacgactgtgccttctagttgccagccatctgttgttgccttccccgtgccttctt gaccttgaaggtgccactcccactgtccttcttaataaaatgaggaaattgcatgcattgtctgagtaggtgtcattc tattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtggggatgcgg tgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCAC AGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCTAGAGAAGGTGGC GCGGGGTAAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCCGAGGGGTGGGG GAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCCG CAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCTACCT GAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCCTCTG AACTGCGTCCGCCGTAGGTAAGTTTAAAGCTCAGGTGAGACCGGGCCTTGTCCGGCG CTCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGTGCTGACCCTGCTTGCTCAA CTCTACGTCTTTGTTTCTGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCT ACTTAGAGCTAGCGAATTgcccgcaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGG TGGTGCCCATCTGGTTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCG GCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCACCG GCAAGCTGCCCGTGCCCTGGCCACCCCTCGTACCACCTGACCTACGGCGTGCACTGCTTC AGCCGCTACCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCT ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGT GAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGA GGACGGCAACATCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAACGTCTATATC ATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAG GACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCC GTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACG AGAAGCGCGATCATATGGTCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTGGCAT GGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcaca ataaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatCCGTGGAGGCGTCTC TCTGAGCAGAGCCGCAATGCGCTGCTTGGGGCTCCCTGCAGCCTCTGGGGGAGGCGAGG GCGGCCAGAGCAGGCTGTGCTGGAAGGAACGCGAAGCCTGTAAACCAAGCCTGTACC TCTGAGTGCTAGTCCCAAGGGGCTCCGAGCTGTTTGTACCATGTGATTGGCTCAGGAG AGGGGTGGAGAAATGAAAACACTCTGCCAGGATATATTTAGTTGAAGTGCAGCTGGGGA AGTGCTTAACAAGGGAGCTTTTGTCTTATGTTGAAGTGTCTTCTTAACCTCTCAAGGGT GAAAAACTTGAGCCACGTACTGATCCCATTCCTCCCAACCAACCAATATATTTCTCTTCT TTAGGAAATGCTCTTATTCTGAACTTTAGAATTTCTAGGGTTTGTGCTAAGAGGAAAC TGAATAA </p>	2541

pARBI-645: chr15_3_ Exogenous s_102	<p>CTTTCCTTTCTGCATTTATTTCTTTTTTCTACATCTTTCTTTTGAATTTTTTTTTTTTTTTT CTGAGATAGAGTCTTGCTCTGTGCGCAGGCTGGAGTGCAGTGGTGTGATCTTGGCTCACTG CAGTCTCCAACCTCTGGTTCAAGCAATTCTCTGCCTCAGCCTCCGGGTAGCTGGGACTACAG GCATACACCACCATGCCCAGTAATTTTTGTATTTTAGTAGAGATGGGGTTTCACCATAGT GGCCAGGATGGTCTCCATCTCTTGACCTCGTGACCTGACCCCTCGGCCTCCCAAAGTGCTG AGATTACAGGCATGAGCCACCGCGCCCGCCTCTTTTGAATTTTTTAAAAAACACCTAA AGTTTAGGAAAGTATAAGAGGGCAAAGAAACAAGAGTTCAAAGAAACAAGAGTGTTATAC ACGCACACTTGCAtgacgactgtgccttctagttgccagccatctgtgtttgccccctccccgtgccttcttgacc tgggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgcatgtctgagtaggtgtcattctattct gggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctgggatgctgggtgggc tctatggGGATCTGCGATCGCTCCGGTGCCGTCAGTGGGCAGAGCGCACATCGCCACAGTC CCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGG GGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCGAGGGTGGGGGAGA ACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGAACGGGTTTGCCGCGAGAA CACAGCTGAAGCTTCGAGGGGTGCGCATCTCTCTTCACGCGCCCGCCGCTACCTGAGG CCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAATG CGTCCGCCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCTCCC TTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCCCTGCTTGCTCAACTCTA CGTCTTTTGTCTGTTTTCTGTTCTGCGCGCTTACAGATCCAAGCTGTGACCGCGCCCTACTCT AGAGCTAGCGAATTgcccaccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGT GCCCATCTGGTTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCGGCGA GGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAA GCTGCCGTGCCCTGGCCACCCTCGTGACCACCTGACCTACGGCGTGCAGTGCTTCAGCC GCTACCCCGACACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGT CCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAA GTTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA CGGCAACATCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATCATG GCCGACAAGCAGAAAGACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGAC GGCAGCGTGACGCTCGCGACCACTACACGAGCAAGACCCCATCGGCGACGGCCCGTGCT TGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAGACCCCAACGAGAA GCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCGCCGGGATCACTCTCGGCATGGAC GAGCTGTACAAatgattgtttattgagcttataatggttacaaataaagcaatagcatcacaatttcacaataa agcattttttcactgcattctagttgtgtgttgcacaaactcatcaatgtatcttatGAAAGGTAGTAAATATCT GTATAGTTCTGGCTGTCAAGCTTTTGGACTGAGATATGCGTAAGCAAGGCAAAAAGATCCC ATAGTCCAGGAATATCAACCACTCCAGTTTCCCAAGGAACTAAAAGTAAGTGAATGAG AAGGGTGCCATATAGGAAAATTGAAGGTGGGGCATAATTATTAATACTGCTTTGAAAT GCTGGTATGGAAGATTATATATGACTTCAAAGCATAACATGTCTTATACTTAGCTATGGGA AAATTATCATAAAAATCTTATTATACAAATCACGGGTATTAGAAATAAAATCAGGTATTG TGACAGTCAGATCCAGGTTTACACAACTAGAGGTTTCAATTAAGTTTCTTATTTTATA AAACCATGACACAAGCTGTAAATAAAGGAGCTCTGGCTTAGGCCTTCTCTGTTATAGA</p>	2541
pARBI-646: chr16_1_ Exogenous s_103	<p>TGTCTTCACGGCACGGCCCCCGCTTACCAGCTGCACTGTTTGATGAGCTTTCAGGTTCCCA GATCTTATAAGCTCATGGTGATTGATCCAAATGATGCAGAGGTGCGCCTAAAGTTAGAAGT GGGCCCCCTCTTGCCCAAGACAGCCCTTACCCCAATTCCATTCCACAGTTTGGGCATCC ACCCAGGCTGCCAAGCCAAGCGGGGGTGCCTGGGTTAGCAGGGACCTGGCCATGGGCCT CCTCAGCTAGGGGGCCGCTCTCTGAGGAGTGGGTGCCCGCCCTCCGTGGGCCGCTGGT TTCTCTTATTGGCAGCGTCTGTAGTCCCCTGGCTCTGTACCCGACGCTATTCTAGGCCTCTG GTTCTTTTACATTTCTGCTCTGCGTCTTCTGCTCGGTGGTGGTCCCAACCATCCAGCTGAGA CCTCCCCGTTGCCGCCCtgacgactgtgccttctagttgccagccatctgtgtttgccccctccccgtgccttct tgaccctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgcatgtctgagtaggtgtcatt ctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctgggatgctg gtgggctctatggGATCTGCGATCGCTCCGGTGCCGTCAGTGGGCAGAGCGCACATCGCCCA CAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGG CGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCGAGGGTGGG GGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGAACGGGTTTGCCG CCAGAACACAGCTGAAGCTTCGAGGGGTGCGCATCTCTCTTCACGCGCCCGCCGCTACC</p>	2541

	<p>TGAGGCCGCCATCCACGCCGTTGAGTCGCTTCTGCCGCTCCCGCTGTGGTGCCCTCTG AACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGCCCTTGTCCGGCG CTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGTCTGACCCTGCTTGCTCAA CTCTACGTCTTTGTTTCTGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCT ACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGG TGGTGCCCATCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCG GCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCACCG GCAAGCTGCCCGTGCCCTGCCCCACCTCGTGACCACCTGACCTACGGCGTGACGTGCTTC AGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGT GAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGA GGACGGCAACATCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAACGTCTATATC ATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTCAAGATCCGCCACAACATCGAG GACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGCCCC GTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACG AGAAGCGCGATCAGATGGTCTGCTGGAGTTCTGTACCGCCGCCGGGATCACTCTGGGCAT GGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcaca aataaagcattttttcactgcattctagttgtgtttgtccaaactcatcaatgtatcttatTGGGTTTCTGTCTGCT CCTCTCCGTGGTGGCCGGCCCTGGCTCTGCCCAAGCCATGGAGAAGGCCAAATGCAGGC TGTAAGAAAGGTCTGGGATCAGATCCCCCATCCTTCCATGGCCACGTGACCGGGCCCGCCT CTTCCCTCTGAGCCTCACATCCTCATCTGAAGAGGGAATGTGCTCATGCCACCTTGCGGG GATGTGGGGAGGGGGTGCTGCCAGTGGAGACTCCAGGGGACCCTCCAGGAGTCTCATCC TGACTCGAGACTGGGCACCTGGTGGGGGCACAGGCCCTCTCCGCCATGGGACCGCCA CATCCAGGCTCTCGTGGGTGAGATGCTGAGGAAAGGAAAGAAACAAACCTGCTGGAGGA GCAGCGAACACGGCCCTCAGCTGGGTGACCTTGGGCAAGTCACTTCCCTCTCTGGGCCTC AGTTTCCAT</p>	
pARBI- 647: chr16_2_ Exogenou s_104	<p>CTGAAGAGGGAATGCTGCTCATGCCACCTTGCGGGGATGTGGGGAGGGGGTGCTGCCAG TGGAGACTCCAGGGGACCCTCCAGGAGTCTATCCTGACTCGAGACTGGGCACCTGGTGG GGGCACAGGCCCCCTCTCCGCCATGGGACCGCCACATCCAGGCTCTCGTGGGTTGAGATG CTGAGGAAAGGAAAGAAACAAACCTGCTGGAGGAGCAGCGAACACGGCCCTCAGCTGGG TGACCTTGGGCAAGTCACTTCCCCTCTCTGGGCCTCAGTTTCCATATCTGTGAATGAGGCAG CTGGACTGAAGAATAGAGAGTCACAAAGCAGAGTGACACAACTGGGCTACAGGAAACCC TGGAGGCCCTCGACCCAGGCTGGGGCCGGGGATGTTCTGCAAAGCCTCTTGGGAGAGGG TTGCCTGAGCTGAGTCTCAAACAGAAatgacgactgtgccttctagttgccagccatctgtgtttgccctcc cccggtgccttcttgaccctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgattgtctga gtaggtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatg ctggggatgcgggtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCACTGGGCAGAGCGCA CATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGA GAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTTCCGA GGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGG GTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGC CGCCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGG TGCCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTT GTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTG CTTGCTCAACTCTACGTCTTTGTTTCTGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGA CCGGCGCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGT TCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAACCGGCCACAAGTTCA GCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCT GCACCACGGCAAGCTGCCCGTGCCTGGCCACCTCGTGACCACCTGACCTACGGCGT GCAGTGCTTCAGCCGTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGC CCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCG CGCCGAGGTGAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGA CTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAA CGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTCAAGATCCGCCAC AACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGC</p>	2541

	GACGGCCCCGTGCTGCTGCCGACAACCTACCTGAGCACCCAGTCCAAGCTGAGCAAAG ACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGGATCAC TCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatc acaaatttcacaaataaagcattttttcactgcattctagttgtgtttgtccaaactcatcaatgtatcttatCAGTGG CCTTAAGTCACGGGAGATGAGCCAGAGCAGTCCAGAGGGCACGGTCAGCACATGCTAAGG TCCTGGGGCACAGAGTACAGGGCTTGAGAAGGGTTCCTCTTGCTCCATGTGACTTTCATCAT CCAACAGCCTGTGGTGGCACTTGCTGTATCCAGCTATCTAGGAGGCTGAGGTGGGAGG ATTGCTTGAGTCTGAGAGGTCGGGCTTGTCTCCCGGTGTTGGCAGAGTCCAGAGGGAGCA AGTGGAAGCCACAGGTGTCTTGAGGCCTAGGCTGAGATCTAGCACATACCCGCTCACTTC ATCCCTTCATTTTCATCTATTGGCCAAAGCAGCCCAATTCTAGGGATGGGGATCTAGACTCA ACTTCTTGATGGGAGAAGTAGCAAAGTCACACTGCCAAGGGCAGGGACACAGGGAGGGAT GAAGAGTTAGGAATGGTT	
pARBI- 648: chr16_3_ Exogenou s_105	AAGCCACCTCCCTGCTCTGTTGCTGGCTCTCCTGAAGACAAGTGTTCATTAACCAAAG CGGTGCATGGCAATGTGATAGGGGAATGAAACACAGCAACAGAATCAATGCCCCACGCTG GGCAATAGCCGACTTTCTGTTGCTCCCATCCCTTCCTCCCTCCCGCCTCTTCCCTGCTC CTTCCATTCACAAACATTTATTGAGCACCCGCTGTGTGCCAGCCACTGTTCTAGGCCCTGA AGACACAGAAGTGAACAAAAAAGAGTCCCTGTGCACATCCTGGAGGGACTTCCCCGT GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTATACAGTGTATGGAGACAGTGGATAATAAAA GCTGTTTATGAGGCATTTCTCTGAGCTGTTCCATGTGCTTCACTTATACTCATTAGTAAAT CCTCAGGACACCCCGTgacgaactgtgacctctagttgccagccatctgtgtttgtccctccccgtgacctcttg accttgaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatgcattgtctgtagtaggtgtcattct attctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatcggt gggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCAC AGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGC GCGGGGTAAACTGGGAAAGTGTGTCGTGACTGGCTCCGCTTTTCCCGAGGGTGGGG GAGAACCGTATATAAGTGCAGTAGTCGCGGTGAACGTTCTTTTCGCAACGGGTTTGCCGC CAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTACGCGCCCCGCCCTACCT GAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTG AACTCGTCCCGCTCTAGGTAAGTTTAAAGCTCAGGTGAGACCGGCCCTTTGTCCGGCG CTCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGTGCTGACCCTGCTTGCTCAA CTCTACGTCTTTGTTTCGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCT ACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGG TGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCG GCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACACCG GCAAGCTGCCCGTGCCCTGGCCACCCCTCGTGACCACCTGACCTACGGCGTGCACTGCTTC AGCCGTACCCCGACCATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGGAAGGT ACGTTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGT GAAGTTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGA GGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATC ATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTCAAGATCCGCCACAACATCGAG GACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCC GTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACG AGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTGGCAT GGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcaca ataaagcattttttcactgcattctagttgtgtttgtccaaactcatcaatgtatcttatTGAAGTCAGTGATATT AGTCACAGAGGCCAGAGAAGTGAAGTGACTTGCCCAAGGTACACAGCCAGCAAGAGGC CAAGCCCGGATTGAACCCAGCGCTGGCTCTGGAGCCTGCAGCATAACCACAGCAGG AACTGCCACCGGAGACAGACATCGACAGCCACTAGGAGATGTTAACCAACAGGCTTGTCTT CACGGCACGGCCCCGCTTACCAGCTGCACTGTTTGATGAGCTTGCAGGTCCAGATCTT ATAAGCTCATGGTGATTGATCCAAATGATGCAGAGGTGCGCTAAAGTTAGAAGTGGGCCC CTCTGCCCCAAGACAGCCCTTACCCCAATTCCATTCCACAGTTTGGGCATCCACCCAGG CTGCCAAGCCAAGCGGGGGTGTCCGGGTAGCAGGGACCTGGCCATGGGCCTCTCAGC TAGGGGC	2541
pARBI- 649:	GGGGGCGGCCGACGGCTAGAGCGGAGACCCGCGCCCCCTCCGCCGCGTGGCCCGGCC GGGGTGCGGGGCCGGGGAGGCACGGGGGCTGCGCGTCGGGGGCGAGCCGCCGCCGC	2541

EDF1_1_E xogenous _25	<p>GTGTGCTCGGAGGCCGCGGGGCCGGGCTCCGGGCTCTCCGACCTGCAGCCCCAGCGG CTACCGCGCCTCGCCAGGCCAGGCCAGGCCCGACGTCGCTTCCCTACGTCGCCGCGGCC CGGCCACGACGTCCCTCAGACGAGCCGAACGCCGAATGGCCCCGAGCACGGGAAGTGCCC GCCCCCGCGTGCAGCCAGCCAATGGGACGCCGAAAGCGGGGAGGTGCCGAGGGGACGT AGCGTCGCCGCGCCAGGTCTCTAGCAGCTGCCGCTGAGCCGCGGACGACGCTCGTCTTC GCCCCCATGGCCGAGAGCGACTGGGACACGtgacgactgtgcctttagttgccagccatctgtgtttg ccccccccgtgccttccttgacctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgcat tgtctgagtaggtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagc aggcatgtggggatgcggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGA GCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTG CCTAGAGAAGGTGGCGGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCCTTT TTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTTCG CAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGC GCCCCCGCCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGC CTGTGGTGCTCCTGAACCTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCG GGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCT GACCCTGCTTGCTCAACTCTACGCTTTTGTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAA GCTGTGACCGGCGCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAG GAGCTGTTACCGGGGTGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAACAGGCCAC AAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAG TTCATCTGCAACCACGGCAAGCTGCCGTGCCCTGGCCACCCTCGTGACCACCTGACCTA CGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCC GCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACA AGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGG GCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACCTACAACA GCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGAT CCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCC ATCGGGCAGGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCAGTCCAAGCTGA GCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCG GGATCACTCTCGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatgggtacaataaagc aatagcatcacaatttcacaataaagcattttttcactgcattctagtgtgtgttgcacaaactcatatgtatctta tGTGACGGTGTGCGCAAGAAGGGCCCTACGGCCGCCAGGCCAAATCCAAGCAGGTGCTT TGCTGACTGAGGAGCGGCCGGGCGGGCGGGGCGGACGCTgggcccggggccacggaccgtgggg cagggggctcgggggaaggcagggcggggcctgggacagggcgaggggacggggacaaggctggGTGCCGG GGGCAGGACGGGGTTCAAGGGCGGGGCGAATCGCAGGGGTAGGAGGACCGGGCCAGG ACaggggtgggaaggtggggggcggaaccagggagggatggacggaccagggagggggCGGGCGACTG GAGGAGGAGAGGAGCAGGGAACCGGACGGGGCAAGGGGCGAGGCGATAGGGCCGGGAC CAGTGCCAGGTGGGGCGGGGAGGGGATAGGGGCGAGGACTGTTGTTGGGGACAGGTG TGAGGACAG</p>	
pARBI- 650: EDF1_2_E xogenous _26	<p>ACGGCTAGAGCGGAGACCCCGCCCCCTCCGCCCGCTGGCCCCGCCGGGGTGGCGGGC CCGGGGAGGCACGGGGGCTGCGCGTGGGGGCGAGCCGCCGCCCGCTGTGCTCGGAGG CCGCGGGGCCCGGGTCCGGGGTCTCCCGACCTGCAGCCCCAGCGGCTACCGCGCTCGC CAGGCCAGGCCAGGCCCGACGTCGCTTCCCTACGTCGCCGCGCCCGGCCACGACGTCC CTCAGACGAGCCGAACGCCGAATGGCCCCGAGCACGGGAAGTGCCCGCCCCCGCGTGCA GCCAGCCAATGGGACGCCGAAAGCGGGGAGGTGCCGAGGGGACGTAGCGTCGCCGCGCC AGGTCTTAGCAGCTGCCGCTGAGCCGCCGACGGACGCTCGTCTTCGCCGCCATGGCCG AGAGCGACTGGGACACGGTGACGGTGCTGtgacgactgtgcctttagttgccagccatctgtgtttgcc ctccccgtgccttccttgacctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgattgt ctgagtaggtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcagg catgctggggatgcggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGC GCACATCGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCT AGAGAAGGTGGCGCGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCTTTTTTC CCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTTCGAA CGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCC CGCCGCCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTCTCGCCGCTCCCGCTG</p>	2541

	<p>TGGTGCTCTGAAGTGCCTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGC CTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGAC CCTGCTTGCTCAACTCTACGTCTTTGTTTCTGTTTCTGTTCTGCGCGTTACAGATCCAAGCT GTGACCGGCGCCTACTCTAGAGTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAG CTGTTACCGGGGTGGTCCCCATCTGTCGAGCTGGACGGCGACGTAACCGGCCACAAG TTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTC ATCTGACCAACCGGCAAGCTGCCGTGCCCTGGCCACCTCGTGACCACCTGACCTACGG CGTGCAAGTGTTCAGCCGCTACCCCGACCATGAAGCAGCAGACTTCTCAAGTCCGCCA TGCCCAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCACTACAAGAC CCGCGCCGAGGTGAAGTTGAGGGCGACACCTGTGTGAACCGCATCGAGCTGAAGGGCAT CGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACTACAACGCCA CAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTTCAAGATCCGC CACAACATCGAGGACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCG GCGACGCGCCCGTGTGTGTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAA AGACCCCAACGAGAAGCGCGATCATGTCCTGTGTGAGTTCGTGACCGCCGCGGGAT CACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatag catcaaaattcacaaataaagcattttttcactgcattctagtgtgtgtgttccaaactcatatgtatcttatCGC AAGAAGGGCCCTACGGCCGCCAGGCCAAATCCAAGCAGGTGCTTTGCTGACTGAGGAGC GGCCGGCGCGGGCGGGGACGCTgggcccggggccacggaccgtggggcagggggctcggggaaggg caggcggggcctgggacagggcgaggggacggggacaaggctggGGTGCCGGGGGACAGACGGGGTT CGAAGGGCGGGGCGAATCGCAGGGGTAGGAGGACCGGGCCAGGACaggggtggggaagggtggg gggcccagccaggggggatggacggaccagggagggcagggggCGGGCGACTGGAGGAGGAGAGGAG CAGGGAACCGGACGGGGCAAGGGGAGGCGATAGGGCCGGACCAAGTCCAGGGTGGG GCGGGGAGGGGATAGGGGAGGGGACTGTTGTTGGGGACAGGTGTGAGGACAGAGGCAG GAGGTG</p>	
<p>pARBI- 651: EDF1_3_E xogenous _27</p>	<p>CCCTGGAGTCGGTGTGAGGCAAAAGCAGAGGAGAGGATTGGAATTAACCTGAAGAAAAA CCATTTCAAAGCGGTAACACAGACCCAGAGGCTGCCTGAAGTCAAGGGGACATGGGAACC CAGGCTGTCCCAAGTTCACACACCTCAGGTCGTGGACTTCCAGAGTTTTCTCAGTTATGA GGACAGGCAGCTGTACTCATGCCAACAGAGCTGCTCTGGGAAGATGGCTGCCTCCAGG GCTCCGGCCAGCACCGGTGCAGGCAGGCACTCAGCTGACAACGTCCCGGGGGCGCCGCA CACACCACACCCAGCAGCATGGACCCACAGCACAGCCTCATGTTGCAAGCGGAAACAC AAGTACCTACATTTCTTGGAAGTCTCCACATCTTCTCCTCGTCTGTGCCGTAAGATAGCC TAGAAAATTAGAAAACATCAGTGtgacgactgtgccttctagtgtccagccatgtgtgttgccttcccc gtgccttcttgaccctggaaggtgcccactgccccttcttaataaaatgaggaaattgcatcgattgtctgagta ggtgtcattctattctggggggtggggggggcagggacagcaagggggaggattgggaagacaatagcaggcatgctg gggatgagggtgggctctatggGATCTGCGATCGTCCGGTGCCCGTCAGTGGGCAGAGCGCACA TCGCCACAGTCCCGAGAAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAG AAGGTGGCGGGGTAAACTGGGAAAGTATGTGCTGTACTGGCTCCGCCTTTTCCCGAG GGTGGGGGAGAACCCTATATAAGTGCAAGTGTGCGCGTGAACGTTCTTTTCGCAACGGGT TTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTACGCGCCCCGCG CCCTACCTGAGGCCGCCATCCAGCCGTTGAGTCGCGTCTGCGCCTCCCGCTGTGGTG CCTCTGAAGTGCCTCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGT CCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCCTGACCTGCT TGCTCAACTCTACGTCTTTGTTTCTGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACC GGCGCTACTCTAGAGTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTT ACCGGGGTGGTGCCATCTGTCGAGCTGGACGGCGACGTAACGGGCCACAAGTTCAGC GTGTCCGGGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGC ACCACCGGCAAGCTGCCGTGCCCTGGCCACCTCGTGACCACCTGACCTACGGCGTGC AGTGCTTACGCGCTACCCCGACCATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCC GAAGGTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCACTACAAGACCCGCG CCGAGGTGAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACT TCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACTACAAGCCACAACG TCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTTCAAGATCCGCCACAA CATCGAGGACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGA CGGCCCGTGTGTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAAGAC</p>	2541

	CCCAACGAGAAGCGGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTC TCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcaca aatttcacaaataaagcattttttcactgcattctagtgtgtgttgcacaaactcatcaatgtatcttatTTTCTAAAG AGAAGATGTGCTTTATACACATCAGCTCCACTAGGACTGCTGCAAAACCAGGCGCGAAGCG TCGCCTGAGAACAGCAGCTTCTAGGGCCCTGGGGTACGCACCCACACGCAGCTGGGTTTT GTGCGAGAGGCAGTGAGAGCCGGGCTGACCTGGCTTCCCGAGGCATTCCCTGCAGGGGAA CCAGGGGGGTGGAGCCACCTCCCGTGCTATCTGAACACCGGCCATCCCCCTCCCCAAA CCCACAACCCAGGAGTGAGAGCCCGCGCAGCCTACCGTGCGCAGGTCTTCTGCGTA AGCCCTTGCTCTGCCGACCTTGCTGGATCACCTTGCCACCTCCAGGGTCACCTGTCTATG GTGCAGCTCCTCTGTCTCCCGTCCAGCTTGCCCGTGTCTTGGTAATAGAATGTGTTTGT CTGGCCAGCAGC	
pARBI- 652: FTL_1_Ex ogenous_ 28_30	CTCTTGCTTCAACAGTGTTTGGACGGAACAGATCCGGGGACTCTCTCCAGCCTCCGACCGC CCTCCGATTTCTCTCCGCTTGAACCTCCGGGACCATCTTCTCGGCCATCTCTGCTTCTGG GACCTGCCAGCACCGTTTTTGTGGTTAGCTCCTTCTTCCAACCAACCATGAGCTCCAGATT CGTCAGAATTATTCCACCGAGCTGGAGGCAGCCGTCAACAGCCTGGTCAATTTGTACCTGC AGGCCTCTACACCTACCTCTCTGCTGAGTCCCCAGGACGCCCCCTGGCCCTAATTTCTCC AGCTGCGCACCTCCGGCCCTCACTGCACGCGCCAGCCTTCTTTGTGCGGTGCGGTAAACAG AGGGCGGAGTCCCTTGGCCTCGCTCCCGTAACCATGTTGCTCCATCTTCTCCCGTAG GCGTCTTATTTTCGACtgacgactgtccttctagtgtccagccatctgtgtttgccccccccgtgccttcttgac cctggaaggtgccactcccactgcctttcctaataaaatgaggaaattgcatcgcatgtctgagtaggtgtcattctatt ctggggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgctgtg gctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAG TCCCGGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAGAGAAGGTGGCGC GGGGTAAACTGGGAAAGTGATGTCTGTACTGGCTCCGCCTTTTCCCGAGGGTGGGGGA GAACCGTATATAAGTGCAAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCA GAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCCGCCGCCCTACCTG AGGCCGCCATCCACGCCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCCTGAA CTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCT CCCTTGAGCCTACCTAGACTCAGCCGCTCTCCACGCTTTGCTGACCCCTGCTTGTCTCAACT CTACGTCTTTGTTTCTGTTTCTGTTCTGCGCCGTACAGATCCAAGCTGTGACCGGCGCTAC TCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTG GTGCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGC GAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGC AAGCTGCCCGTCCCTGGCCCACTCTGTGACCACTGACCTACGGCGTGCAGTGCTTCA GCCGTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTA CGTCCAGGAGCGACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG AAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAG GACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACTACAACAGCCACAACGCTCTATATCA TGGCCGACAAGCAGAAGAAGCGCATCAAGGTGAACCTTCAAGATCCGCCACAACATCGAGG ACGGCAGCGTGACGTGCGCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGT GCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAG AAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGG ACGAGCTGTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaaat aaagcattttttcactgcattctagtgtgtgttgcacaaactcatcaatgtatcttatCGCGATGATGTGGCTCTG GAAGGCGTGAGCCACTTCTTCCGCGAATTGGCCGAGGAGAAGCGCGAGGGGTACGAGCGT CTCCTGAAGATGCAAAACCAGCGTGCGGGCCGCGCTCTCTTCCAGGACATCAAGGTAATA GTGTGTGGGTAATGGAATACATCTCCAGCAGGCGGTGCGCGCAGGAGCCTTGATTGA GGGCGTAGGTGTGCGGTGGGCTTCTGGGAGATTGAGTTCGGTCTTGTGAGCCCTCTTAACC GCTGGAATAGAGGCGCACCTCGTGACGTGCCACAACACGCGGCAGTCCACACCGCTGC GTGGTCTTAGGGACGTATAGCTGTAAGAGCTAGGACAGGGTGCGGAGAGTGATAAATACA AGCTGTCACATGTCTTGTGGCCTGGGCCTTGACCCCCAACGACTCTTGGGAAATGTAGGT TTAGTTCT	2541
pARBI- 653: FTL_2_Ex	TGGGGCGGGGGGCTGAGACTCCTATGTGCTCCGATTGGTCAGGCACGGCCTTCGGCCCC GCCTCTGCCACCGCAGATTGGCCGCTAGCCCTCCCGAGCGCCTGCTCCGAGGGCCGG CGCACCATAAAGAAGCCGCCCTAGCCACGTCCCTCGCAGTTCGGCGGTCCCGCGGGTCT	2541

ogenous_ 29	<p>GTCTCTTGCTTCAACAGTGTTTGGACGGAACAGATCCGGGACTCTCTCCAGCCTCCGACC GCCCTCCGATTTCTCTCCGCTTGCAACCTCCGGGACCATCTTCTCGGCCATCTCTGCTTCT GGGACCTGCCAGACCGTTTTGTGGTTAGCTCCTTCTGCCAACCAACCATGAGCTCCAG ATTCGTGAGAATTATCCACCGACGTGGAGGCAGCCGTCAACAGCCTGGTCAATTTGTACCT GCAGGCCTCTACACCTACtgacgactgtgccttctagtgtccagccatctgtgtttgccccctccccgtgccttc cttgaccctggaaggtgccactcccactgtccttcttaataaaatgaggaaattgcatcgcatgtctgagtaggtgtca ttctattctgggggtgggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgc ggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCC ACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCTAGAGAAGGTG GCGCGGGGTAAACTGGGAAAAGTGATGTCGTGTACTGGCTCCGCCCTTTTCCCGAGGGTGG GGGAGAACCGTATATAAGTGCAGTAGTCGCGGTGAACGTTCTTTTCGCAACGGGTTTGCC GCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCCCTA CCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTCTGCCGCTCCCGCTGTGGTGCTCC TGAAGTGCCTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGG CGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTGCTGACCTGCTTGCTC AACTCTACGTCTTTGTTTCGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGC CTACTCTAGAGCTAGCGAATTgcggccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCCGG GGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTC CGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCCAC CGGCAAGCTGCCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAAGTGC TTCAGCCGCTACCCCGACCATGAAGCAGCACGACTTCTCAAGTCCGCCATGCCCGAAG GCTACGTCCAGGAGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGA GGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAA GGAGGACGCAACATCCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACGCTCTA TATCATGGCCGACAAGCAGAAGAAGCGCATCAAGGTGAACCTCAAGATCCGCCACAACATC GAGGACGGCAGCGTGCGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGC CCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCA ACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGGGATCACTCTCGG CATGGACGAGCTGTACAAatgattgtttattgagcttataatggttacaataaagcaatgcatcacaaattt cacaaataaagcattttttcactgcattctagtgtgtgtgttccaaactcatcaatgtatcttatCTCTCTGGTGA GTCCCCAGGACGCCCCTGGCCCTAATTTCTCCAGCTGCGCACCTCCGGCCCTCACTGCACG CGCCAGCCTCTTTGTGCGGTGCGGTAAACAGAGGGCGGAGTCCCTTTGGCCTCGCCTCCC GCTAACCAATTGTTGCTCCATCTCTCCCGTAGGGCTTCTATTTGACCGCGATGATGTGGCT CTGGAAGGCGTGAGCCACTTCTCCGCGAATTGGCCGAGGAGAAGCGCGAGGGCTACGAG CGTCTCCTGAAGATGCAAAACAGCGTGGCGGCGCGCTCTCTTCCAGGACATCAAGGTAA CTAGTGTGTGGTAATGGACTACATCTCCAGCAGGCCGTGCGCGGAGGAGCCTTGATTT GAGGGCGTAGGTGTCGCGTGGGCTCTGGGAGATTGAGTTCGGTCTTGAGCCCTCTTAA CCGCTGGA</p>	
pARBI- 654: PTEN_1_ Exogenou s_31	<p>CTTTCATAGTTTATCCTATTAGTAATCTATTCTGTCTTTGGAATATGTTTTGTGATGATGAA ATAAATACTATAAATAGTATTATTCCTTTTGATTGAGAGTCTGACGAAATGTCCATGTGA CAGTTCATTTTGGGTTAGCTCTACCTCTAATATGTGACCTATGCTACCACTCCGTATAGCGT AAATCCCAGAATATATCCTCCTGAATAAAATGGGGGAAAATAATACCTGGCTTCTTAAATG ATTATATTTAAGACTTATCAAGAGACTATTTTCTATTTAACAATTAGAAAGTTAAGCAATACA TTATTTTCTCTGGAATCCAGTGTTTCTTTAAATACCTGTTAAGTTTGTATGCAACATTCTA AAGTTACCTACTTGTTAATTAATAAATCAAGAGTTTTTTTTTCTATTCTGAGGTTATCTTTTT ACCACAGTTtgacgactgtgccttctagtgtccagccatctgtgtttgccccctccccgtgccttcttgaccctggaa ggtgccactcccactgtccttcttaataaaatgaggaaattgcatcgcatgtctgagtaggtgtcattctattctggggg gtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgcggtgggctctatg ggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCG AGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCTAGAGAAGGTGGCGCGGGGT AAACTGGGAAAAGTGATGTCGTGTACTGGCTCCGCCCTTTTCCCGAGGGTGGGGGAGAACC GTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCAGAACAC AGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCCCTACCTGAGGCCG CCATCCACGCCGTTGAGTCGCTTCTGCCGCTCCCGCTGTGGTGCTCTGAACTGCGT CCGCGCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGCCCTTTGTCCGGCGCTCCCTTG</p>	2541

	<p>GAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGGCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCGTGCCCTGGCCACCTCTGTGACCACCTGACCTACGGCGTGCAAGTGTTCAGCCGCTACCCCACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCCCAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAAATCCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTTCAGATCCGCCACAACATCGAGGACGGCAGCGTGCGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCATATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaataaagcattttttactgcatttagttgtggtttgtccaaactcatcaatgtatcttatGCACAATATCCTTTGAAGACCATAACCCACCACAGCTAGAACTTATCAAACCTTTTGTGAAGATCTTGACCAATGGCTAAGTGAAATGACAATCATGTTGCAGCAATTCAGTGTAAAGCTGGAAAGGGACGAACTGGTGAATGATATGTGCATATTTATTACATCGGGGCAAATTTTTAAAGGCACAAGAGGCCCTAGATTTCTATGGGGAAGTAAGGACCAGAGACAAAAAGGTAAGTTATTTTTGATGTTTTCTTTCTCTTCCTGGATCTGAGAATTTATTGGAAAACAGATTTTGGGTTTCTTTTTCTTCAGTTTTATTGAGGTGAATTGACAAGTAAAAATTATATATAAATACAATGTATAATATGATGTTTTGATGTATGTGTATATACATTGTGAAATGATTACTACAGTCAAACCTACTTAACATATTCAT</p>	
pARBI-655: PTEN_2_ Exogenous_32	<p>GCTACCACTCCGTATAGCGTAAATCCCAGAATATATCCTCCTGAATAAAATGGGGGAAAAATACCTGGCTTCCTTAATGATTATATTTAAGACTTATCAAGAGACTATTTTCTATTTAACAATTAGAAAGTTAAGCAATACATTATTTTCTCTGGAATCCAGTGTTTCTTTAAATACCTGTTAAGTTGTATGCAACATTTCTAAAGTTACCTACTTGTTAATTAATAAATCAAGAGTTTTTTTTCTTATTCTGAGGTTATCTTTTACCACAGTTGCACAATATCCTTTGAAGACCATAACCCACCACAGCTAGAACTTATCAAACCTTTTGTGAAGATCTTGACCAATGGCTAAGTGAAGATGACAATCATGTTGCAGCAATTCAGTGTAAAGCTGGAAAGGGACGAACTGGTGAATGATATGTGCATATTTATTACATtgacgactgtgccttctagttgccagccatctgtgttgccccccccgtgccttctgacctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatgcattgtctgagtaggtgtcattctattctgggggtggggtggggcaggacagcaaggggaggattgggaagacaatagcaggcatgctggggatgcggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAAGTGGGCGAGCGCACATCGCCACAGTCCCGAGAAGTTGGGGGGAGGGGTCCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGGGTAACTGGGAAAGTGATGTGCTGTAAGTCCGCTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAAGTAGTCGCGTGAACGTTCTTTTCGCAACGGGTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCGCGCCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCGCTGTGGTGCCTCCTGAATGCGTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTGAGACCGGGCCTTTGTCCGGCGTCCCTTGAGAGCTACCTAGACTCAGCCGCTCTCCACGCTTGCCTGACCTGCTTGCTCAACTCTACGTCTTTGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCTGCCCTGGCCACCCTCGTGACCACCTGACCTACGGCGTGCAAGTGTCTCAGCTACCCCGACCATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCCGAAGGTACCTCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGGAGGTGAAGTTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTTCAGATCCGCCACAACATCGAGGACGGCAGCGTGCAAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAAGCGGATCACATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaatttcacaataa</p>	2541

	agcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatCGGGGCAAATTTTTAAAGG CACAAGAGGCCCTAGATTTCTATGGGGAAGTAAGGACCAGAGACAAAAGGTAAGTTATT TTTTGATGTTTTCTTTCTCTCTCTGGATCTGAGAATTTATTGGAAAACAGATTTTGGGTTT CTTTTTTCTTCAGTTTTATTGAGGTGTAATTGACAAGTAAAAATTATATATAATACAATG TATAATATGATGTTTTGATGTATGTGTATATACATTGTGAAATGATTACTACAGTCAAACCTAC TTAACATATTCATCACCTCACATAATTATTATTCTCCCCCAGGGTGAAAGCATTTAAGATCT ACAAGCTACAATTTCAATTATACAATGTTATTATTAAGTATAGTCACTATGCTGTCCAGTAG AGCTTCAGATCTTGTTCATCTTGTGTTCTCTCCCTCCCCACCCTCAGTCCCTGGAA	
pARBI- 656: PTEN_3_ Exogenou s_33	ATAAATAGTATTATTCCTTTTGCATTGAGAGTCTGACGAAATGTCATGTGACAGTTCATT TGGGTTTAGCTCTACCTCTAATATGTGACCTATGCTACCACTCCGTATAGCGTAAATTTCCCA GAATATATCCTCCTGAATAAAATGGGGGAAAATAATACCTGGCTTCTTAATGATTATATTT AAGACTTATCAAGAGACTATTTTCTATTTAAACAATTAGAAAGTTAAGCAATACATTATTTTTC TCTGGAATCCAGTGTTTCTTTTAAATACCTGTTAAGTTGTATGCAACATTTCTAAAGTTACC TACTTGTTAATTAATAAATCAAGAGTTTTTTTTTCTTATTCTGAGGTTATCTTTTACCACAGT TGCACAATATCCTTTTGAAGACCATAACCCACCACAGCTAGAACTTATCAAACCTTTTGTGA AGATCTTGACtgacgactgtgccttctagttgccagccatctgtgtttgtccctccccgtgccttcttgaccctgga aggtgccactcccactgtccttttctaataaaatgaggaaatgcatgcattgtctgagtaggtgtcattctattctggg ggtggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtctgggagtcggtgggctctat ggGGATCTGCGATCGCTCCGTGCGCCGTGAGTGGCAGAGCGCACATCGCCACAGTCCCC GAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCTTAGAGAAGGTGGCGCGGGG TAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTCCGAGGGTGGGGGAGAACC GTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGAACGGGTTTGCCGCCAGAACAC AGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCCGCCCTACCTGAGGCCG CCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCT CCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCTCCCTTG GAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGTCAACTCTACGT CTTTGTTTCGTTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCTAGA GCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCC ATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTACGCGTGTCCGGCGAGGGC GAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCTATGCAACACCGGCAAGCTGC CCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAAGTGTTCAGCCGCTAC CCCGACCACATGAAGCAGCACGACTTCTCAAGTCCGCCATGCCCCAAGGCTACGTCCAGG AGCGCACCATCTTCTCAAGGACGACGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGA GGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAA CATCCTGGGGCACAAGCTGGAGTACAACACAACAGCCACAACGTCTATATCATGGCCGAC AAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGC GTGCAGCTCGCCGACCACTACAGCAGAACACCCCATCGCGACGGCCCCGTGTGCTGC CCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCG ATCATATGGTCTGTGGAGTTCGTGACCGCGCGGGATCACTCTGGCATGGACGAGCT GTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattt ttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatCAATGGCTAAGTGAAGATGACAAT CATGTTGCAGCAATCACTGTAAAGCTGGAAAGGGACGAAGTGGTGAATGATATGTGCAT ATTTATTACATCGGGGCAAATTTTTAAAGGCACAAGAGGCCCTAGATTTCTATGGGGAAGT AAGGACCAGAGACAAAAGGTAAGTTATTTTTGATGTTTTCTTTCTCTCTCTGGATCTG AGATTTATTGGAAAACAGATTTTGGGTTTCTTTTTCTTCAGTTTTATTGAGGTGTAATT GACAAGTAAAAATTATATATAAATACAATGTATAATATGATGTTTTGATGTATGTGTATATA CATTTGAAATGATTACTACAGTCAAACCTAATCATACCTCACATAATTATTAT TCTCCCCCAGGGTGAAAGCATTTAAGATCTACAAGCTACAATTTTCAATTAT	2541
pARBI- 657: PTPN2_1 _Exogeno us_34	TAGTGACGGTATCAAGAGCAGCATCCAGGTTGACTTTCTTTGGGGCAGGACCTTGCTGT GTCTTAACCTTGGTTCTACcCaagtttgtctctctagtcctcaactctgaaagccacttgatatcttacacaatt ccttttttgctgagaaaataaaagtcagttttgatcatttacaacaaaaatcctaactaacacaGACCTGTTTTG AAATCAGGTAGATTGGAAGTCTTGGTTTACTTCTTATAAGCCGTCCGCTGTCTGTCTGTGTA ACATCCCAGGAGCAGACTTAACAAGGCCTTCTGGAGCCTTGCTTTTCTGTCTGTCTCCCTC ATCTGctctctctctctctctTCACAGGGTCCACTTCTAACACATGCTGCCATTTCTGGCTTATGG TTTGGCAGCAGAAGACCAAAGCAGTTGTATGCTGAACCGTgacgactgtgccttctagttgccagc	2541

	catctgttgtttccctccccctgcttcttgaccctggaaggtgccactcccactgtcctttcctaataaaatgagga aattgcatcgcatgtctgagtaggtgtcattctattctgggggtgggggtggggcaggacagcaaggggaggattgg gaagacaatagcaggcatgtggggatgctgggtgggtctatggGATCTGCGATCGCTCCGGTGCCGTC AGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAAT TGAACGGGTGCCTAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTG GCTCCGCCCTTTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCCCGGTGAAC GTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTC TCCTTACGCGCGCCGCCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGGTTCCTGC CGCTCCCGCTGTGGTGCCTCTGAAGTGCCTCGCGCTAGGTAAGTTTAAAGCTCAGG TCGAGACCGGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCAC GCTTTCCTGACCTGCTTCTCACTCTACGTCTTGTTCGTTTCTGTTCTGCGCGTTAC AGATCAAGCTGTGACCGGCGCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAA GGGCGAGGAGCTGTTACCGGGGTGGTGCCATCCTGGTCGAGCTGGACGGCGACGTAAA CGGCCACAAGTTCAGCGTGTCCGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGAC CCTGAAGTTCATCTGCACCAACGGCAAGCTGCCGTGCCCTGGCCACCCTCGTGACACCC TGACCTACGGCGTGAGTGTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTC AAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCA ACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGC TGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAAC ACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCT CAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAA CACCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCC AAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACC GCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAtgattgtttattgcagcttataatggttac aaataaagcaatagcatcacaatttcacaaataaagcatttttttactgcattctagtgtgtgttgcctcaactcatca atgtatcttatATTGTGGAGAAAGAATCGGTGAGTAATATTTAATATTTACAACCTAGTATACTG TATGTGATCATTAGCATATAAAGATTTTCATTTTGGGGCCAATATTCATTCCTTAGTTTTGGC CTTTAATTGCTAAAGGCTAGCGGTCAAAGTGTTTCTGTCCGAAAAAATCATGTATCCTTTTC CTTTCTTAAGTATTTTATAACAATTGCAGACCTTTCATCTCCAAGATAGAAATACAATGGAA TAAATATGGAAGTACTGACATATAGATCTTTGGAATCCCTAGGAATCCTTATTGACCTAT TGTCATAAAGTCTCTCCAGCTTTAAGATCTTGTACTGTTCTACTTCAGATTTCTACTTTAT TCTACATTTTATAATTGCTGGTTTTAATGATGATGAAAATTCCTAATCCACTTCTAATTAGA TGTGGCAATGACATGCC	
pARBI- 658: PTPN2_2 _Exogeno us_35	CAGAATTTGAATATGATGTGGCTGACCATAGATACCTCCATTGCATTAATTCTGCTTCATAA AGTGTTTGATGCTTGCTGTGAGGTGTTGAATAGAGCCTAATTAGCAGTAAGTAAACAGATCT agagcacagacttggcatctgaaggaccttggtcaatgctgggactgccacttactagctatgggatcttgggtgatt tttaaccttgaagcctttcatccctcacagatataatggggaagaaaatcgtttccattagtattgtgaggattaaatg attaattgatgtaacaatgtgctttccatagtagtggcatatcataagtgtctcatGTTATTTACGCTGGCTGG GAAGATAAGTTTTGCTGTGGAGAATTTAAGAGGGATATTAAATATATTTTTGTTATTTTAA GGAAATTCGAAATGAGTCCCATGACTgacgactgtgcttctagtgtccagccatctgtgtttgccctcccc cgtgccttcttgaccctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgcatgtctgagt aggtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgct ggggatgctgggtgggtctatggGATCTGCGATCGCTCCGGTGCCCGTCACTGGGCAGAGCGCAC ATCGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGA GAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTCCCGA GGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCGTGAACGTTCTTTTTCGCAACGG GTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGC CGCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGG TGCTCTCTGAAGTGCCTCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACGGGGCCTTT GTCCGGCGCTCCCTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTG CTTGCTCAACTCTACGTCTTTGTTTCTGTTTCTGTCGCGGTTACAGATCCAAGCTGTGA CCGGCGCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGT TCACCGGGGTGGTGCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGGCCACAAGTTCA GCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCT GCACCACCGGCAAGCTGCCGTGCCCTGGCCACCCTCGTGACCACTGACCTACGGCGT	2541

	GCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTCAAGTCCGCCATGC CCGAAGGCTACGTCCAGGAGCGCACCATTCTTCAAGGACGACGGCAACTACAAGACCCG CGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGA CTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAACAGCCACAA CGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCAC AACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGC GACGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAG ACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGGATCAC TCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatc acaaatttcacaaataaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatTATCCTC ATAGAGTGGCCAAGTTTCCAGAAAACAGAAATCGAAACAGATACAGAGATGTAAGCCCAT GTAAGTACTTGTGGGTTTGTGTGCATGTGTATTTTTGGTTTGTGTTAGGAGGCAGGATGTA GTGAAAAGGAGGGCTTGGGGTCAGTGTGATAAATACAGTAATTTTTCTATTACGTAA GACACGTTCTTAAAGAAATTAAGGTGTAGAATAGTGAAGGAAAAATAATTACCCATAAT TATTTATCCTCTCAACATAGGCACCAATTATTTGGTGTATTTCCACAACCTGTTTTCTTAT GCACAGTTTTCTTTCTTTAAATAATTGTAATTATAGATGTCTATATAATATCCATATGTATT TCCTTTTCATATCATTCATCCATCCCTTTGTAAGTTTTGCTTAAATAGTTATTGGTGTAGTTGG TTTTT	
pARBI- 659: PTPN2_3 _Exogeno us_36	ACCAGTTATCGTTTTGTAGGTAGACCAATCAATTCTTAGGTACCAAGAATCTGAATGATCCT TTTACTTTTTAGGAAGGTAAAGTACTTTATTCATTTAACTATGTTTACTCTGGTTCGATTTTTCAA GTCACAATGGCTAATGTGCTACAAACAGAAGTGCTTCTTCCAGCACTATAGTAATAAACA AGATTGCATTTTATACTCCTTACAAAAAAGTAGAGAATAGTTTAGGATTTGTCTCAACTCTA TTATGATGCTAATTCATTTTCTTATTTCTTCTGTCTTTTATAAATACCTAGAATATTAATATG AAGATAAAAACAGTAATTTTGAATGACAGTTGTGGTTTATCATTCTCTATTTTCAGATGATC ACAGTCGTGTTAAACTGCAAAATGCTGAGAATGATTATATTAATGCCAGTTTAGTTGACATA GAAGAGGCATgacgactgtgccttctagttgccagccatctgttgttggccctccccgtgccttccttgaccctgga aggtgccactcccactgtcctttcctaataaataagaggaaatgcatgcattgtctgagtaggtgtcattctattctgggg ggtggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgcggtgggctctat ggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGCGCAGAGCGCACATCGCCACAGTCCCC GAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGGGG TAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGAACC GTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGGCCGACAGACAC AGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCTACCTGAGGCCG CCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCCTGAAGTCGT CCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCTCCCTTG GAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCCTGCTTGTCAACTCTACGT CTTTGTTTCGTTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCTAGA GCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCC ATCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGC GAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGC CCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTACGCCGTAC CCCGACCACATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAGG AGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGA GGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAA CATCTGGGGCACAAGCTGGAGTACAACACAACGCCACAACGTCTATATCATGGCCGAC AAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGC GTGCACTCGCCGACCACTACCAGCAGAACACCCCATCGCGCAGCGCCCGTGTCTGC CCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCG ATCATATGGTCTGCTGGAGTTCGTGACCGCGCCGGGATCACTCTGGCATGGACGAGCT GTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaaataaagcattt ttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatCAAAGGAGTTACATCTTAACACAG GCAAGTAATACGATACCACGCAAATGTCTGAAAATGATGTGTTTGTGCTTGTCTGCTTTAA ATCATAGGTAAAAGTATATCTTGACTTCTTTTGGAAATGAAATGGTATTTTCAAGTTTTTTCTG ACGATGTAATGAATTATGGACATTATAAGGTTTTGAAGCTTTGAGTATTTAAGATAAAAGGC AAGTTATTTTTGATATTACAGTTCGTGTAAGGAAAATCTTAGGAAATGGCTTAGGCCAGT	2541

	TCITTTGGCAGATTGTGTTCTTACATTATATCTGACACAGAGTGCTGCTTATGCTTCTTAGTG TCTTCTTTTCTCTTCCCATACCTGTGGCAAAACCAGAGGCCCTGGACAGCTCTTCTGTAGCT CCCCCTGCCTCGCATATATCTTCAGAGAGTACACCAAGCCCTGGATGGTGT	
pARBI- 660: PTPN6_1 _Exogeno us_37	CCTGCTCAAGGGCCGAGGTGTCCACGGTAGCTTCTGGCTCGGCCAGTCGCAAGAACCAG GGTGACTTCTCGCTCTCCGTCAGGTAGGTGGGGCCCCCGCAACCCCGGGCATTTTGGCCACT CTCTTGTCATCCAGGCCCTGAACCACTATTCTGTGTTCCCCGTGGCAGTGCTGACTCCCC GTCTGTTCCCTTGGCCCCAACCCCACTCCCCATCCCTGTCTGTGCCCACCCATGCCCATG TGTGCCCCACCCAGGACCTCAGCCGATCCCTGCCCTCCTGCTCTACTCTGCACCGACTG GCCTCACCGCCTGGTGCCTGCAGGGTGGGGGATCAGGTGACCCATATTCGGATCCAGAAC TCAGGGGATTTCATGACCTGTATGGAGGGGAGAAGTTTGCAGCTCTGACAGAGCTGGTG GAGTACTACACTCAGCAGTgacgactgtgccttctagttagccatctgtgtttgccctccccgtgccttc ttgacctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatgcattgtctgagtaggtgtcatt ctattctgggggtgggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtgggatgag gtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCA CAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGG CGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGG GGGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCG CCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCGCCCTACC TGAGGCGCCATCCACGCGGTTGAGTCGCGTTCTGCGCCTCCGCTGTGGTGCTCCTG AACTGCGTCCCGCTCTAGGTAAGTTTAAAGCTCAGGTGAGACCGGCCCTTTGTCCGCG CTCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGTTTGCTGACCCTGCTTGCTCAA CTCTACGTCTTGTTCGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCT ACTCTAGAGTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGG TGGTGCCCATCTGCTGAGCTGGACGGCGACGTAACCGGCCACAAGTTCAGCGTGTCCG GCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACACCG GCAAGCTGCCCGTGCCTTGCCCCACCCTCGTGACCACCTGACCTACGGCGTGCACTGCTTC AGCCGTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCT ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCACTACAAGACCGCGCCGAGGT GAAGTTGAGGGGCGACACCCTGGTGAAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGA GGACGGCAACATCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAACGTCTATATC ATGGCCGACAAGCAGAAGAAGGCATCAAGGTGAAGTCAAGATCCGCCACAACATCGAG GACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACCCCCATCGGCGACGGCCCC GTGCTGCTGCCGACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACG AGAAGCGCGATCAGATGGTCTGCTGGAGTTCGTGACCGCGCCGGGATCACTCTGGCAT GGACGAGCTGTACAAatgattgtttattgagcttataatggttacaataaagcaatagcatcacaatttcaca aataaagcatttttctactgcattctagtgtgtttgtccaaactcatcaatgtatcttatCAGGGTGTCTGCAG GACCGCGACGGCACCATCATCCACCTCAAGTACCGCTGAAGTGTCTCCGATCCCACTAGTGA GAGGTGAGGGCTCCGACCCCCGCAATCCCAAGCAGGGATGAGCCGGCTCCCAACCTGAA CAGCCAGGGAGGCGAGGAGACTGGCAGCCGGCGTGCCTACCCTCCATCCCTCCCTCCC TGCACAGCTGGGGCTCTCAATGTCCCTCCTCCTGCTGTCTGGGACCTGGTGTCTCAGAG CCTAACCTACCACCTTTCCACCTAACCCCGAGGAAGCCACAGAAAGTGCTCGCCCTACT CCGGGAGCCCTGCGCGTCAACCCAGGTCCCACTGGAGACAGGGAGGCCACTGCTGGTG GCCAGCATGTCGTGCAGGCCAGCTCTGTTGTTAGAAAGCTCTTCTCCTCTGGAATCGAGCC TGCCT	2541
pARBI- 661: PTPN6_2 _Exogeno us_38	CTGGGTTGCAAGCCCGTTAGAACTCTGGAGGCTAGGATGGCTTGAACCTGGGAGGTGCA GGCTGCAGAGAGCTGTAACCGCGCCACTGCACTCCAGCCTGGGCAACAGAGCTCTGGAAG CTTGCCCTAGAGTCAGTCAAGGGCCCTAGGCCAGTGAGTAACAGCTCAGCGTCAGTTTCT CATCTATAAATGGGGGTAATATCATACCTAGCTCTCAGCATGTTTGTGAGAGACCTAAATG AGGTGGTGGATTGGAAGCATGTAGCGCAGTGCTGGCACACAGTAGGTGCTTGATTTCG GCCCCCTCTGTGAATGTCTGTCTCAGCGCCTTCCCCTGTGGCCTGGGTCTTACCTTCCCTG ACGCTGCCTTCTTAGGTGGTACCATGGCCACATGTCTGGCGGCAGGCAGAGACGCTGCT GCAGGCCAAGGGCGAGCCCTGTgacgactgtgccttctagttagccatctgtgtttgccctccccgt gccttccttgacctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatgcattgtctgagtag gtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtgg ggatgcggtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACAT	2541

	<p>CGCCACAGTCCCGAGAAGTTGGGGGAGGGGTCGCAATTGAACGGGTGCCTAGAGA AGGTGGCGCGGGTAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCGAG GGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGT TTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCG CCCTACCTGAGGCCGCTACACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTG CCTCTGAAGTGCCTCGCCCTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGT CCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCT TGCTCAACTCTACGCTTTTGTCTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACC GGCGCTACTCTAGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTT ACCGGGGTGGTGCCCATCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTACAG GTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGC ACCACGGCAAGCTGCCGTGCCCTGGCCACCCTCGTACCACCCTGACCTACGGCGTGC AGTGCTTCAGCCGCTACCCGACCACATGAAGCAGCAGACTTCTCAAGTCCGCCATGCCC GAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCG CCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACT TCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAACG TCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTTCAGATCCGCCACAA CATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGA CGGCCCCGTGCTGCTGCCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAGAC CCCAACGAGAAGCGCATCACATGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTC TCGGCATGGACGAGCTGTACAAtgattgtttattgcagcttataatggttacaataaagcaatagcatcaca aatccacaataaagcattttttcactgcattctagtgtgtgtgttccaaactcatcaatgtatcttatACGTTTCTT GTGCGTGAGAGCCTCAGCCAGCCTGGAGACTTCGTGCTTCTGTGCTCAGTGACCAAGCCCA AGGCTGCCCCAGGCTCCCCGCTCAGGGTACCCACATCAAGGTTCATGTGCGAGGTAAGGC AGCCAGGCGGGCGGGGAGCCTCTGCTGAGGCTCCTGTCTGTGACCACAGTGTGGGTGGCA GGGAGGGTCTGCCTGGGCTTGAATTAAGGCTGGGGACCCAGGGAGGGAGACTCAAGTC CTGTGAATGGCCTAATTTGGCTCCCCCAGGGTGGACGCTACACAGTGGGTGGTTTGGAGA CCTTCGACAGCCTCAGGACCTGGTGGAGCATTTCAAGAAGACGGGGATTGAGGAGGCCT CAGGCGCCTTTGTCTACCTCGCGCAGGTCAAGGGTGGGCCAGCTGCCTCCCACTTCCCTT GAGCTGTCCCCAGATGT</p>	
pARBI- 662: PTPN6_3 _Exogeno us_39	<p>TGTACATATGTGCAATGCCATGCTCCTGAGCCTTTGATTGCAGACGTGTGGGAAGTGGGC CCCCCCCCACCCAGTGCCACCCTGCTGCTTCTCTTCCCTTGCTGTGCTCTAAAACGAG AAGTACAAGTGAGTTCCCCAAGGGGTCGGCCGCGCCTTCTCCTGTCCCCGCCCTGCCGGC TGCCCCAGGCCAGTGAGTGGCAGCCCCAGAACTGGGACCACCGGGGGTGGTGAGGCGG CCGGCACTGGGAGCTGCATCTGAGGCTTAGTCCCTGAGCTCTCTGCCTGCCAGACTAGCT GCACCTCTCATTCCCTGCGCCCCCTTCTCTCGGAAGCCCCCAGGATGGTGAGGTAAGGG CCTGCCACCCACGGTAGACAGGAGGCAAGGGTGCCTGGTGCCACGGGACCCCTCCTACT CCCTGCCTGGGCCGCCAGTgacgactgtgcttctagtgtccagccatctgtgttgcctccctccctgtg cttcttgaccctggaaggtgccactcccactgtccttctcctaataaaatgaggaaattgcatcgattgtctgagtaggtg tcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctgggga tgcggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGC CCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGAATTGAACGGGTGCCTAGAGAAGG TGGCGCGGGGTAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCCGAGGGTG GGGGAGAACCCTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGC CGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCCCT ACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTC CTGAAGTCCGTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCG GCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGC TCAACTCTACGTCTTTGTTTCTGTTCTGCTGCGCGTTACAGATCCAAGCTGTGACCGGC GCCTACTCTAGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACC GGGGTGGTGCCCATCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTG TCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC ACCGGCAAGCTGCCGTGCCCTGGCCACCCTCGTACCACCCTGACCTACGGCGTGCAGT GCTTCAGCCGTACCCCGACCACATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCCGAA GGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCG</p>	2541

	AGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCA AGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCT ATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACAT CGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGG CCCCGTGCTGTGCCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCG GCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatt tcacaataaagcattttttcactgcattctagttgtgttgcctcaactcatcaatgtatcttatTGGTTTACCGA GACCTCAGTGGGCTGGATGCAGAGACCCTGCTCAAGGGCCGAGGTGTCCACGGTAGCTTC CTGGCTCGGCCAGTCGCAAGAACCAGGGTGACTTCTCGCTCTCCGTAGGTAGGTGGGCC CCCCGCAACCCCGGGCATTGTTGGCCACTCTCTTGTGCCATCCAGGCCCTGAACCACTCATTCC TGGTCCCCGTGGCAGTGTGACTCCCCGTCTGTTCCCTTGCCCCAACCCCACTCCCCA TCCCTGTCTGTGCCACCCATGCCATGTGTGCCCCACCCAGGACCTCAGCCGATCCCTGC CCTCTGCCTCTACTCCTGCACCGACTGGCCTCACCGCCTGGTGCCCTGCAGGGTGGGGGAT CAGGTACCCATATTCGGATCCAGAACTCAGGGGATTTCTATGACCTGTATGGAGGGGAGA AGTTTG	
pARBI- 663: PTPRC_1_ Exogenou s_40	TCTTTAGCTAATGTTCTGTAGCTTGTGTTTAGATCTGTGTCTACATATTATATGTATCTGTAT GCATCAATATTTGTATATATGCATGCATATATGTGTATGTATATTTATGAATACATATACACA CCATATACATACATTATGTATGGTGTGTGCATATGTATGTGTAGATATATGTACATACACA CTATGTGGAGTGGGAGTTAGTATACTGGGAGGAGCATACTTTAGGGTATGATTCACAT ATTTATTTTGTCTTCTCCCATTTTCCATTAATTAACAGGATTGACTACAGCAAAGATGCCCA GTGTCCACTTTCAAGTGACCCCTTACCTACTCACACCACTGCATTCTACCCGCAAGCACCT TTGAAAGAGAAAATGACTTCTCAGAGACCACAACCTCTCTTAGTCCAGACAATACTTCCACC CAAGTATCCCCGtgacgactgtgccttctagttgccagccatctgttgttggccctccccgtgccttcttgacctg gaaggtgccactcccactgtccttcttaataaaatgaggaaattgcatgcattgtctgagtaggtgtcattctattctgg gggtgggtgggtgggagacagcaagggggaggattgggaagacaatagcaggcatgctgggtagtgcggtgggtctct atggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCC CGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGGG GTAAACTGGGAAAGTGATGTCTGTACTGGCTCCGCTTTTTTCCGAGGGTGGGGGAGAA CCGTATATAAGTGAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCAGAAC ACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGGC CGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGC GTCCGCGCTTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTGTCCGGCGCTCCCTT GGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTGCTCAACTCTAC GTCTTTGTTTCTGTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCTA GAGCTAGCGAATTgcccaccacATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGC CCATCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCGGCGAGG GCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTTCATCTGCACCAACGGCAAGCT GCCCCGTGCCCTGGCCACCCCTCGTGACCAACCTGACCTACGGCGTGCAAGTCTCAGCCGCT ACCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCA GGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTC GAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGC AACATCCTGGGGCACAAGCTGGAGTACAACATAACAAGCCACAACGTCTATATCATGGCCG ACAAGCAGAAGAAGCGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCA GCGTGCAAGTCCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCT GCCCCACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCG CGATCACAAGTCTGCTGGAGTTCGTGACCGCGCCGGGATCACTCTCGGCATGGACGAG CTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagca ttttttcactgcattctagttgtgttgcctcaactcatcaatgtatcttatGACTCTTGGATAATGCTAGTGC TTTTAATACCACAGGTTGGCACACAAAAGTTGTTAACTTAAATATCAGGGAATGCTATTTAG AAAATTCTACAGTTATCAGTACAACCTGTCTTTAAATTATTTGCACAGTTTCTAAGTATGTGA TTTTATTCAAGTGAGAAATTGCAGGAAATTAGTATCTGTGAAATATAGATCGACTGAAGTA ATTAATGCATGTTGTTAGGGAGTGGAGAGAGAAAAAGGAAGGAAGCAAGATCTCCAAGGAC AATCAGGAGGGGAAATTTGTTCTAGTATCCTCTGATCTATACACACTCGCCATGATTCTCCC	2541

	GCTTGGCTTCCCGCCACCTGGACAGATGAGAATTTCCCTAGTTCAGAGATTATCAGTTCTACTCTCCTTGGGAAGGTGTCTTAAATGGGAGTCTTCCCATTTCTTTGTTTCACTCTAGA	
pARBI-664: PTPRC_2_ Exogenous_41	AGGGAATTTTTATATGTTGGTCATATTATATCCCTAGCATGTGGCATAATGTCTAGCACAAA ATAGGTGCTCAATTAATCATCATTATCTAAATAAATAATGCATTGGGAAAAAAGTTTCA AAAGTTTTTCAAAAGTCTTTTGCAGGCTTGAAATTAATCCCAATAGTGATCCTTTAGTCTGTT ATGTTTCTGATTTAGCCTGGGGATTCAAAAAATAAATAACATAATTTTGATATATTTGGGCTT TGTAACATGGTACTAAGAGAGGAAATATAGTTTCATTAGGGTAAAAGCTACTGAAAATTG CCACTTGGTGAATGTTCTATCATAGACTTGAGGTACATATAAAATCTAATATATGTTTACAT TAATATGAATGAAATTTGAAATTTCTAAGAGATTTTGTCTTTTGCAGGGCAAAGCCC AACAGTTCCCCCtgacgactgtgccttctagttgccagccatctgtgttggccctccccgtgccttcttgaccct ggaaggtgccactcccactgtccttcttaataaaatgaggaaattgcatcgattgtctgagtaggtgtcattctattctg gggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgctgggtgggt ctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTC CCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGG GGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGAGA ACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGGCCGAGAA CACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTACGCGCCCCGCCCTACCTGAGG CCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGT CGTCCGCCGTCTAGGTAAAGTTAAAGCTCAGGTGAGACCGGGCCTTTGTCGGCGCTCCC TTGGAGCCTACCTAGACTCAGCCGCTCTCCACGCTTGCCTGACCTGCTTGTCTCACTCTA CGTCTTTGTTCTTTTCTGTTCTGCGCCGTACAGATCCAAGCTGTGACCGGCGCTACTCT AGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGT GCCCCATCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGA GGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTTCTGACACCGGCAA GCTGCCGTGCCCTGGCCACCTCTGTGACCACCTGACCTACGGCGTGCAGTGCTTACGCC GCTACCCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCCCGAAGGTACGT CCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGAGGTGAA GTTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA CGGCAACATCTTGGGGCAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATCATG GCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTTCAAGATCCGCCACAACATCGAGGAC GGCAGCGTGCAGCTGCGGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGC TGCTGCCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAA GCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGATCACTCTCGGCATGGAC GAGCTGTACAAAtgattgtttattgcagcttataatgggtacaaataaagcaatagcatcacaatttcacaataa agcattttttcactgcattctagttgtgttgggttgcacaaactcatcaatgtatcttatACTGTAAGAATTAATATTT ATATTTTACTAATTTTATTTTCTGTTGCAAAGTTTATATTTAACTACAATTTTCTATTATT AACACTGAAATTTATTTTAAAGATAAATTTTATAATCATGAGTGATTCTTGACATTCATTGT TCTTAAACTTTCTGCTTATACGTTATAGAGTTTAAATACTACCTAAACATGTTATTAAATTTGT ATATATATTTTGTGTATAAATAGTAACTTTTCCAACTTGACAGTAAATCACACAACAGGTT TCTACTCTTTTAAATTTTAAAGACTATAAAAAATGCATTTAAATTAGATAACAAAATTTTA TAGTCTGAAAGCAGGTTAACAGCTGTCTATGTATGTTATAGATATGTAGATAACAGATTTGC ATATGTCTATATTTCTTAAAGAGTATGTTGCTTTTTTCAATGGTATGCA	2541
pARBI-665: PTPRC_3_ Exogenous_42	CCTTTAGCACCATAAAGAACTAAATTTATTTAGATGTTTTATGAGAACATATCAAAAAGTA CTTTTCTGTCATCCAATACTTCCACAAATAAATCATTAGTTCCTTGCTAATCTTCTATCTGGCATA AAAATAATGACATCAACTTTCTTCATGTAATTTCCCACTTAATTCCTTTACTAGGAGCAATAT CAATTCCTATATGACGTCATTGCCAGCACCTACCCTGCTCAGAATGGACAAGTAAAGAAAAA CAACCATCAAGAAGATAAAATTGAATTTGATAATGAAGTGACAAAGTAAAGCAGGATGCT AATTGTGTTAATCCACTTGGTGCCCCAGAAAAGCTCCCTGAAGCAAAGGAACAGGCTGAAG GTTCTGAACCCACGAGTGGCACTGAGGGGCCAGAACATTCTGTCAATGGTCTGCAAGTCC AGCTTTAAATCAAGGTtgacgactgtgccttctagttgccagccatctgtgttggccctccccgtgccttcttg accctggaaggtgccactcccactgtccttcttaataaaatgaggaaattgcatcgattgtctgagtaggtgtcattct attctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgctgggt gggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCAC AGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGC GCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGG	2541

	<p>GAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGC CAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCTACCT GAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCTCG AACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCG CTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCTGACCTGCTTGCTCAA CTCTACGTCTTTGTTTCTGTTTCTGCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCT ACTTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCCGGGG TGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCG GCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCG GCAAGCTGCCCCGTGCCCTGGCCACCCCTCGTGACCAACCCTGACCTACGGCGTGCAAGTGCTT AGCCGTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGT GAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGA GGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATC ATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAG GACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCC GTGCTGCTGCCCGACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACG AGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCGCCGGGATCACTCTCGGCAT AGACGAGCTGTACAAtgattgttattgcagcttataatggttacaaataaagcaatagcatcacaatttcaca aataaagcatttttctactgcattctagttgtggtttgtccaaactcatcaatgtatcttatTCATAGGAAAGACA TAAATGAGGAACTCCAAACCTCCTGTTAGCTGTTATTTCTATTTTTGTAGAAGTAGGAAGT GAAAATAGGTATACAGTGGATTAATTAATGCAGCGAACCAATATTTGTAGAAGGGTTATA TTTTACTACTGTGAAAAATATTTAAGATAGTTTTGCCAGAACAGTTTGACAGACGTATGC TTATTTTAAAAATTTATCTCTTATTCAGTAAAAAACACTTCTTTGTAATCGTTATGTGTGTAT ATGTATGTGTGTATGGGTGTGTGTTGTGTGAGAGACAGAGAAAAGAGAGAGAATCTTTCA AGTGAATCTAAAGCTTTTGCTTTTCTTTGTTTTATGAAGAAAAATACATTTTATATTAG AAGTGTTAACTTAGCTGAAGGATCTGTTTTAAAAATCATAACTGTGTGCAGACTCAATA</p>	
<p>pARBI- 666: PTPRCAP _1_Exoge nous_43</p>	<p>aaggaaaaaggcactgagtgctggggggtgctgggggtgggctgcagtgatagacatcagggtagagggttaaggtag gttcagcctcactggggtgaagtttgagcacggtagcaggccatgcagccggggaggaggatgggaggaggat ggagctttccgggcagagggaacagccagtgcgaaaggccccaggcagggtggcttaatgcagctgttggggagggtgag tggtaggaggaggctggaggatgggggctgatctcacaggggcagagcctggtgaccaaataaggccttgcccttt tctGCTTGGCTGTCCCAAGAGGATCCCAAAGAGAAAAAACGAAAGTGGTCTTGGTCACCCA GCCTGCCCCACACCAGCCCCACCCAGGTGCTGAGCCCTCTGAGCCCTGCCTGTCTCCCA CAGGCTCTGCCCTGtgacgactgtgccttctagttgccagccatctgtgttggccctccccgtgccttctctgac cctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgattgtctgagtaggtgtcattctatt ctgggggggtggggtggggcaggacagcaaggggaggattgggaagacaatagcaggcatgtggggatgcggtgg gtctctatggGATCTGCGATCGTCCGCTGCCCCGTAGTGGGCGAGCGCACATCGCCACAG TCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCTAGAGAAGGTGGCGC GGGGTAACTGGGAAAGTATGTCTGTACTGGCTCCGCCTTTTTCCCGAGGGTGGGGGA GAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCA GAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCTACCTG AGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCTCTCTGAA CTGCGTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCT CCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGCTCAACT CTACGTCTTTGTTTCTGTTTCTGCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCTAC TCTAGACTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCCGGGTG GTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGC GAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGC AAGTGCCCCGTGCCCTGGCCACCCCTCGTGACCACCCTGACCTACGGCGTGCAAGTGCTTCA GCCGCTACCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTA CGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAG GACGGCAACATCCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACGTCTATATCA TGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGG ACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGT</p>	2541

	GCTGCTGCCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAG AAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGATCACTCTCGGCATGG ACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaaat aaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatACCTTAGGGCTCGGGAT GCTGCTGGCCCTGCCAGGGGCTTGGGCTCGGGTGGCAGCGCGGAGACAGCGTGGGCT CCAGCTCTGTACCGTTGTCTgctgctgctgctgctcctactgctgGCCACTGGCCTAGCACTGGCCT GGCGCCGCTCAGCCGTGACTCAGGGGGGCTACTACCAACCGGCCCGCTAGGTGCCGCGCT GTGGGGCCGCACGCGGCGCTGCTCTGGGCCAGCCCCCAGGTCGCTGGCTGCAGGCCCCG AGCTGAGCTGGGGTCCACAGACAATGACCTTGAGCGACAGGAGGATGAGCAGGACACAG ACTATGACCACGTGCGGGATGGTGGCCTGCAGGCTGACCCTGGGGAAGGCGAGCAGCAAT GTGGAGAGGCGTCCAGCCAGAGCAGGTCCCCGTGCGGGCTGAGGAAGCCAGAGACAGT GACACG	
pARBI- 667: PTPRCAP _2 Exoge nous_44	aaggtcaggttcagcctcactgggtgaagtttgagcacggtgagcaggccatgcagcccgggggaggaggatggg aggaggtggagctttccgggcagaggggaacagccagtgcgaaagcccgaggcaggtggcttaatgcagctgttggggg aggtagtggttagggaggaggctggagggtgggggctgatctcacaggccagagcctgggttgaccaaataaggcct tggccttttctGCTTGGCTGTCCCAAGAGGATCCCAAAGAGAAAAAACGAAAGTGGTCTTTGGT CACCCAGCCTGCCCCACACAGGCCCCACCCAGGTGCTGAGCCCTCTGAGCCCTGCCTGT TCCCCACAGGCTCTGCCCTGCACCTTAGGGCTCGGGATGCTGCTGGCCCTGCCAGGGGCT CTGGCTCGGGTGGCAGCGCGGAGGACAGCtgacgactgtgcttctagttgccagccatctgttgttggc cttcccccgcttcttggacccctggaaggtgccactcccactgtcctttcctaataaaatagggaattgcatcgattg tctgagtaggtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcag gcatgctggggatcggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCCGTCAGTGGGCAGAG CGCACATCGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGGCAATTGAACGGGTGCC TAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCTTTTTC CCGAGGGTGGGGGAGAACCGTATATAAGTGACAGTAGTCGCCGTGAACGTTCTTTTCGCAA CGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTACGCGGCC CGCCGCCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCCTG TGGTGCTCCTGAAGTGCCTCGCGCTAGGTAAAGTTAAAGCTCAGGTCGAGACCGGGC CTTTGTCCGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGAC CCTGCTTGCTCAACTCTACGTCTTTGTTTCTGTTTCTGTTCTGCGCGTTACAGATCCAAGCT GTGACCGCGCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAG CTGTTACCGGGGTGGTGGCCATCCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAG TTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTC ATCTGCACCAACGGCAAGCTGCCGTGCCCTGGCCACCTCTGTGACCACCTGACCTACGG CGTGACGTGCTTACCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCA TGCCCGAAGGCTACGTCCAGGAGCGACCATCTTCTTCAAGGACGACGGCAACTACAAGAC CCGCGCCGAGGTGAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCAT CGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACTACAACAGCCA CAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTTCAAGATCCGC CACAACATCGAGGACGGCAGCGTGACGCTGCCGACCACTACCAGCAGAACACCCCATCG GCGACGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAA AGACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGAT CACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatag catcacaatttcacaataaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatGTG GGCTCCAGCTCTGTACCGTTGTCTgctgctgctgctgctcctactgctgGCCACTGGCCTAGCACTG GCCTGGCGCCGCTCAGCCGTGACTCAGGGGGCTACTACCAACCGGCCCGCTAGGTGCCG GCTGTGGGGCCGCACGCGCGCCTGCTCTGGGCCAGCCCCCAGGTCGCTGGCTGACCG CCGAGCTGAGCTGGGGTCCACAGACAATGACCTTGAGCGACAGGAGGATGAGCAGGACA CAGACTATGACCAGTCGCGGATGGTGGCCTGCAGGCTGACCCTGGGGAAGGCGAGCAGC AATGTGGAGAGGCGTCCAGCCAGAGCAGGTCCCCGTGCGGGCTGAGGAAGCCAGAGAC AGTGACACGGAGGGCGACCTGGTCTCGGCTCCCCAGGACGAGCGAGCGAGGGGGCAG TGCTGAGGCCCTGCTGAGT	2541
pARBI- 668: PTPRCAP	cagtgcgaaagcccgaggcaggtggcttaatgcagctgttggggaggtagtggttagggaggaggctggaggatg ggggctgatctcacaggccagagcctggttgaccaataaaggccttggccttttctGCTTGGCTGTCCCAAGAG GATCCCAAAGAGAAAAAACGAAAGTGGTCTTTGGTCAACCCAGCCTGCCCCACACAGGCC	2541

<p>_3_Exogenou s_45</p>	<p>CACCCAGGTGCTGAGCCCTCTGAGCCCTGCTCTCCACAGGCTCTGCCCTGCACCTT AGGGCTCGGGATGCTGCTGCGCCTGCCAGGGGCTTTGGGCTCGGGTGGCAGCGCGAGG ACACGCTGGGCTCCAGCTCTGTACCGTTGTCTgtgctgtgctgctgcttactgtgctGCCACTGGCC TAGCACTGGCCTGGCGCCGCTCAGCCGTGACTCAGGGGGCTACTACTgacgactgtgcttcttag ttgccagccatctgtttgttccccctccccgtgcttcttgcacctggaagggtgccactcccactgtcttctctaataaa atgaggaaattgcatcgattgtctgtagtaggtgtcattctattctgggggggtgggggtggggcaggacagcaaggggga ggattgggaagacaatagcaggcatgctggggatgcggtgggctctatggGATCTGCGATCGCTCCGGTGC CCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGC GCAATTGAACGGGTGCCCTAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTG TACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCCTATATAAGTCAGTAGTCGCCG TGAACGTTCTTTTTCGCAACGGGTTTGCCGCGCAAGACAGTATGAAGCTTCGAGGGGTGC CATCTCTCCTTCACGCGCCCGCCCTACCTGAGGCGCCATCCACGCGGTTGAGTCGCG TTCTGCCGCTCCCGCTGTGGTGCTCTCTGAATGCGTCCGCCGTCTAGGTAAGTTAAAG CTCAGGTCGAGACCGGGCTTTGTCCGGCGCTCCCTTGAGGCTACCTAGACTCAGCCGGC TCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTACGTCTTTGTTCTGTTTTCTGTTCTGCG CCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCTAGAGCTAGCGAATTgcccgcaccATGG TGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCTGGTCGAGCTGGACGGCG ACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCA AGCTGACCTTGAAGTTCTATCTGACCACCGGCAAGCTGCCGTGCCCTGCCCACTCCGTG ACCACTCTGACCTACGGCGCTGCACTGCTTACGCGCTACCCCGACCATGAAGCAGCAGC ACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGAC GACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCTGGTGAACCGC ATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGGGCACAAGCTGGAG TACAACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGG TGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCA GCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACC CAGTCCAAGCTGAGCAAAAGACCCCAACGAGAAGCGCATCACATGGTCTGCTGGAGTTC GTGACCGCCGCGGGATCACTCTCGGCATGGACGAGCTGTACAAtgattgtttattgacgttata atggttacaataaagcaatagcatcacaataattcacaaataaagcatttttttactgacattttagttgtgttgc actcatcaatgtatcttatCACCCGGCCCGCTAGGTGCCGCGCTGTGGGGCCGACGCGGCGCCT GCTCTGGGCCAGCCCCCAGGTGCTGCTGCGTGCAGGCCGAGCTGAGCTGGGGTCCACAGA CAATGACCTTGAGCGACAGGAGGATGAGCAGGACACAGACTATGACCACGTGCGGGATGG TGGCTGCAAGCTGACCTGGGGAAGGCGAGCAGCAATGTGGAGAGGCGTCCAGCCAG AGCAGGTCCCCGTGCGGGCTGAGGAAGCCAGAGACAGTGACACGGAGGGCGACCTGGTC CTCGGCTCCCCAGGACGAGCGAGCGAGGGGGCAGTGTGAGGCCCTGCTGAGTGACCTG CAGCCCTTTGCTGGCAGCGCAGCCTGGGATGACAGCGCCAGGCGACGTGGGGGCCAGGG CCTCATGTACCGCATGTAGAGGCGGCTTGTGGTCTCCATCCC</p>	
<p>pARBI- 669: RPS23_1_ Exogenou s_46</p>	<p>ATAGAGTAGGGCGGGGATGCCATGGAGAGGCTCCATGGGGGAGGGCCGGGGAAGCGC CGCTCCAGGAGGCACGTGGTCCGGCGCGGAAGGGGCCATGAGGCGTGAGGGCCGCCGA GGTCGGGGTACCGAGGGACGCGAGGGAGGCCAGCGCTTCTCCGGGCATTGAGCGGGG CCTCGTCTTTCGGGAGAACACATTCTCCGGAGCCCTCTTGAACGTTTATTAGTCGGTTCAG GGCAACTTGAAAGCCAAATGTTTGGCCACAGGCCAATAAATAGTACGAGAGCCAATCGG CTTAAGGGTTTATTCAGGTGAGGCGAGTGTCTTAGAAGATGGGAAACACGTAGATGGCG TGTTTTACGGAAGAACTAAAAATATTTAATTTTAGGCAAGTGTCTGGACTTCGTACTGCT AGGAAGCTCCGTAGTACCGACGAGACCAAGTgacgactgtgcttcttagttgccagccatctgtgtttgcc ctccccgtgcttcttgcacctggaagggtgccactcccactgtccttctctaataaaatgaggaaattgcatgcattg tctgtaggtgttcattctattctgggggtgggggtggggcaggacagcaaggaggattgggaagcatagcag gcatgctggggatgcggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCACTGGGCAGAG CGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTGCC TAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCTTTTTTC CCGAGGGTGGGGGAGAACCCTATATAAGTGACAGTGTGCGCGTGAACGTTCTTTTCGCAA CGGGTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCC CGCCGCCCTACCTGAGGCGGCCACACGCGGTTGAGTCGCTTCCGCCCTCCCGCTG TGGTCCCTCTGAATGCGTCCGCCGTCTAGGTAAGTTTAAAGTCAAGTTCAGAGACGGGC CTTTGTCGGCGCTCCCTTGAGGCTACTAGACTCAGCGGCTCTCCAGCTTTGCTGAC</p>	<p>2541</p>

	<p>CCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCT GTGACCGGCGCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAG CTGTTACCGGGGTGGTGGCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAG TTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTC ATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGG CGTGCACTGCTTCAGCCGCTACCCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCA TGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGAC CCGCGCCGAGGTGAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCAT CGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACATAACAGGCCA CAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTTCAAGATCCGC CACAACATCGAGGACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCCATCG GCGACGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAA AGACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGGAT CACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatag catcacaatttcacaataaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatAAG TGGCATGATAAACAGTATAAGAAAGCTCATTGGGCACAGCCCTAAAGGCCAACCCTTTTG GAGGTGCTTCTCATGCAAAAGGAATCGTGCTGGAAAAAGTGTAAGTCCATTGCTCCCGTCA AGTTTTAGTTTTATTATAGGAATTCGAGACATGAACTTACGAATCTTGTGTTTGAAGTAATTG CAGGTTTTTTGTGTAGTAGTATTCTTTGGGCATTGTGGGGTAAAATTGCAAGCGTTTGTTC TATTTAAAAGTTGGTAAAATTAGTTTTTGGGAATTAGGTAGTTAAGGTTTTAATTTAACGTT GGCCTGGAAGGAATTGGAGAAGATACTAGCAATGATGAAGTAAAGGACACAAACACCTTT ACTGTGGGAGTTGTTATAAGTAAATGGCACGTGTCAGCTATTGAACCTTATCGACTTGATAA AACTAAGGTGAAGAGA</p>	
<p>pARBI- 670: RPS23_2_ Exogenou s_47_48</p>	<p>CAAGCGGGACTTGGGGTCTTGGGGACGGGCGGGCGGATGCGAATAGAGTAGGGCGGGG GATGCCATGGAGAGGCTCCATGGGGGAGGGCCGGGGAGCGCCGCTCCAGGAGGCACGT GGTCCGGCGCGGAAGGGGCCCATGAGGCGTGAGGCCGCCGAGGTCGGGGTACCGAGG GACGCAGGGAGGCCAGCGCTTCTCCCGGGCATTGAGCGGGGCCTCGTCTTCGGGAGA ACACATTCTCCGGAGCCCTCTCGAACGTTTATTAGTCGGTTCAGGGCAACTTGAAGGCCAA ATGTTTTGGCCACAGGCCAATAAATAGTACGAGAGCCAATCGGCTTAAGGTTTATTCCAG GTGAGGCGAGTGTCTTAGAAGATGGGAAACACGTAGATGGCGTGTTTTACGGAAGAACT AAAATATTTAATTTTAGGCAAGTGGCGGGAatgacgactgtgcttctagttgccagccatctgtgtttg ccccccccgtgcttcttaccctggaaggtgccactcccactgtccttcttaataaaatgaggaaattgcatcgcat tgtctgagtaggtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagc aggcatgctggggatgcggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCACTGGGCGAGA GCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGGAGGGGTGGGCAATTGAACGGGTG CCTAGAGAAGGTGGCGGGGGTAACTGGGAAAGTATGTCGTGTACTGGCTCCGCTTTT TTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGGCTGAACGTTCTTTTTCG CAACGGGTTTTGCCGCAAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTCACGC GCCCCGCCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGC CTGTGGTGCTCCTGAAGTCCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCG GGCCTTTGTCCGGCGCTCCCTGGAGCCTACCTAGACTCAGCCGGCTCCACGCTTTGCCT GACCCTGCTTGCTCAACTCTACGTCTTTGTTTCTGTTTTCTGTTCTGCGCCGTTACAGATCCAA GCTGTGACCGGCGCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAG GAGCTGTTACCGGGGTGGTGGCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCAC AAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAG TTCATCTGCACCACCGCAAGCTGCCCGTCCCTGGCCACCCTCGTGACCACCCTGACCTA CGGCGTGCAGTGCTTCAGCCGCTACCCGACCACATGAAGCAGCACGACTTCTTCAAGTCC GCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACA AGACCCGCGCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGG GCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACATAACA GCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGAT CCGCCACAACATCGAGGACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCC ATCGGCGACGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGA GCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCG GGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagc</p>	2541

	<p>aatagcatcacaatttcacaaataaagcatttttttactgcattctagttgtggtttgtccaaactcatcaatgtatctta tCTTCGTAAGCTAGGAAGCTCCGTAGTCACCGACGAGACCAGAAAGTGGCATGATAAACAG TATAAGAAAGCTCATTGGGCACAGCCCTAAAGGCCAACCTTTTGGAGGTGCTTCTCATGC AAAAGGAATCGTCTGGAAAAAGTGAAGTCCATTGCTCCCGTCAAGTTTATGTTTATTATA GGAATTCGAGACATGAACCTACGAATTCTGTTTTGAAAGTAATGCAAGTTTTTGTGTAGT AGTATTCATTGGGCATTGTGGGGTAAAATTGCAAAGCGTTTGTCTATTTAAAAGTTGGTA AAATTAGTTTTGGGAATTAGGTAGTTAAGGTTTTAATTTAACGTTGGCCTGGAAGGAATTG GAGAAGATACTAGCAATGATGAAGTAAAGGACACAAACACCTTTACTGTGGGAGTTGTTAT AAGTAAATGGCACGTGTCA</p>	
pARBI- 671: RTRAF_1_ Exogenou s_49	<p>TTGTATATCCTTTTTAAAGTTATTCTTTTTAGTTAATTGCTCTATGTGTATTGAGACTAGGAAT CAGAAAGCTTAGATTCTAGTCCCAGGTGAAGTTGTGTAACCTTGGCAAGTGCTCAATCTCT AGGCCTCAGCTTTCTCATCTATAAAATGAGGAAGTTGTCGTATTCTATTTTTTTCTTAAGAT GATACACTTAAATGTTCCCTTCTGTTGGGTTATATAATTGCATCAAAAGTGTAGTAATGTTAT TAAAAAATTGTTAGAGATCCAACTAAGGTCTCTTTCAACTCTCCCATCTTTTTCTGTGACT TTATGGTAATAATGAACTGGTGGTTTTCTTTCTTCCCTCACAGTATCTCAGAGATGTTA ACTGTCCTTTCAAGATTCAAGATCGACAAGAAGCTATTGACTGGCTTCTTGGTTAGCTGTT AGACTTGAATgacgactgtgcttctagttgccagccatctgtgttggccctcccccgcttctctgacctggaa ggtgccactcccactgtccttctataaaatgaggaaattgcatcgattgtctgagtaggtgtcattctattctggggg gtggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgagggtggctctatg gggATCTGCGATCGCTCCGGTGCCCGTCAAGTGGGCAGAGCGCACATCGCCACAGTCCCGC AGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGGGGT AACTGGGAAAGTGATGTCGTGTAAGTCCGCTTTTCCGAGGGTGGGGGAGAACC GTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGGCCGAGAACAC AGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGGCCG CCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCTGAACTGCGT CCGCCGTCTAGGTAAGTTAAAGCTCAGGTGAGACCGGGCCTTTGTCCGGCGCTCCCTTG GAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCCTGACCCTGCTTGTCAACTCTACGT CTTTGTTTCGTTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCTAGA GCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCC ATCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGC GAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACGGCAAGCTGC CCGTGCCCTGGCCACCTCGTGACCACCTGACCTACGGCGTGCAAGTTCAGCCGCTAC CCGACCATGAAGCAGCACGACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCAGG AGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCGAGGTGAAGTTCGA GGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAA CATCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAACGCTCTATATCATGGCCGAC AAGCAGAAGAAGCGCATCAAGGTGAATTCAGATCCGCCACAACATCGAGGACGGCAGC GTGACGCTCGCCGACCACTACACGAGAAACACCCCATCGCGACGGCCCGTGTGCTGC CCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCG ATCATATGGTCTGCTGGAGTTCGTGACCGCGCGGGATCACTCTGGCATGGACGAGCT GTACAAatgattgtttatgcagcttataatggttacaataaagcaatagcatcacaatttcacaaataaagcattt tttctactgcattctagttgtggtttgtccaaactcatcaatgtatcttatTATGGAGATAATGGTACGTTTTGTG GGGAATGTGTATTTTAAAGAGAGAGAAAGATGGGAAAGGGAGTGTGAAAATGTAGGGA ACTTTCAGTGTGTTTGTCTAGTACTATTTTACCTTGGTTTATTTCTATCACAAAGTAAAAAG CACTTTTATTGTCTTTCATTGGTGTATATTTCTGTGTAATTTGGAATGGTGCCTCTG GAGAAGGCTAATTGACTGTCTTCTACAGAGTAACACTACTTTGATAATATGGTCTGCACCT TAGCCTTTCAAATTAATTTGTTTTAGTGTCCAGAAATTGATGGGACTTTGAAGTGTGTTGC AGTAGGTAATTTCTCAAAGACTGAAACATGTCTAATGCCAATATACATTAATACTCTATAG GCCAGAATATATTACTTATGTTTACTGTCTTAGCACAGATACTTCTATGGT</p>	2541
pARBI- 672: RTRAF_2_ Exogenou s_50	<p>GCACCTGTTATGTAGGAGGAGTAATAAAATGAATGAATGCACTCAAAACACTAAACAGTAA TTCTGTAATCCAACGGGAGGTACAGCGAATACCAAAGCCTACATATACTATTCTCTGCATG CTATAGCAAGAAAGAAAGGAAAGTGGCTTCCGGTGGTTTTCTGCCTATTGTACAACCAGG AAGCTGACAATAAAGTTTATTGAGCGTCGACGTGCGCCGACGTGGCCCCGCTCCCGAGC CGGAGCCGCGATTGGTGGGCATTGCCGGCGGCCACCGCTTTAAGCCACGATTGGCGAA GGCCGCGTCAATTCGGAGCGACTCAGCGCTGCCCGCTCTCGCCGCTGCGCGGTGCC</p>	2541

	<p>TGCGCTCCCGCTCCACCTCGCTTCTTCTCTCCCGCCGAGGCCGGGGACCAGAGCGAG AAGCGGGGACCATGTTCCGACGCTgacgactgtgccttctagttgccagccatctgtgtttgccccccccgt gccttcttgaccctggaaggtgccactcccactgtcctttcctaataaaatgaggaaatgcatcgattgtctgagtag gtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctgg ggatgcggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACAT CGCCACAGTCCCGAGAAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGA AGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTCCCGAG GGTGGGGGAGAACCGTATATAAGTGCAAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGT TTGCCCGCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCG CCCTACCTGAGGCCGCTCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTG CCTCTGAAGTGCCTCCGCGCTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGT CCGGCGCTCCCTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCT TGCTCAACTCTACGCTTTTGTTCGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACC GGCGCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTT ACCGGGGTGGTGCCCATCTGGTCGAGCTGACGCGCAGCTAAACGGCCACAAGTTCAGC GTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGC ACCACGGCAAGCTGCCCGTGCCCTGGCCACCTCGTGACCACTGACCTACGGCGTG AGTGCTTCAGCCGCTACCCCGACCATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCC GAAGGCTACGTCCAGGAGCGACCATCTTCTCAAGGACGACGGCACTACAAGACCCGCG CCGAGGTGAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGCATCGACT TCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAACG TCTATATCATGGCCGACAAGCAGAAGACGGCATCAAGGTGAACCTCAAGATCCGCCACAA CATCGAGGACGGCAGCGTGAGCTGCGCGACCACTACCAGCAGAACACCCCATCGGCGA CGGCCCGGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGAC CCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCTGTGACCGCCGCGGGATCACTC TCGGCATGGACGAGCTGTACAAtgattgtttattgagcttataatggttacaataaagcaatagcatcaca aattcacaataaagcattttttcactgcatctagttgtgtttgtccaactcatcaatgtatcttatAAGTTGACG GCTCTCGACTACCACAACCCCGCGGCTTCAACTGCAAAGGTGAGGCGGCGGCTCAGCCG GGCCGCGTGTCCCTGACCTGGGCGGAGGTCCAGCCTCAGTGCCCGCACCCCACTCCCG TCGGGACCTCGGCGGCTGGTTCCGCGGCGAGCCTCCGGGCCCTCTCTCTGGGTGCG CACGTACCTCGGCTCTTCGCGCCCTTCCCGCTTTAAAGCCCTCTACCTACTCTGTCTC GGCATGTTACTTTCTGCACTTGCTTAAGTCCAAGCATCACGTAACCTTCTCTGTACATAA AAGGGAGAGCATTGCTCTTCTCACTCACTATTCAACTCCATGGTTCCTGGGTAATTAGGC GATACCTTGAGCACCTGCTAATTATGGGCCAGCGCGGTGCTGGATTCTGAGGAAGGTGCTG AGTAACTTG</p>	
<p>pARBI- 673: RTRAF_3_ Exogenou s_51</p>	<p>CACTAAACAGTAATTCTGTAATCCAACGGGAGGTACAGCGAATACCAAAGCCTACATATA CTATTCTCTGCATGCTATAGCAAGAAAGAAAGGAAAGTGGCTTCCCGGTGGTTTTCTGCCTA TTGTACAACAGGAAGCTGACAATAAAGTTTATTTGAGCGTCGACGTGCGCCGACGTGGCC CCGCTCCCGAGCCGGAGCCGCGATTGGTGGGCATTTGCCGGCGGCCACCGCTTTTAAGCC ACGATTGGCGAAGGCCGCGCTCATTTGGGAGCGACTCAGCGCTGCCGCGCTCTCGCCGC GTCGCCGGTGCTGCGCTCCGCTCCACCTCGCTTCTCTCTCCCGCGGAGGCCCGGGGG ACCAGAGCGAGAAGCGGGGACCATGTTCCGACGCAAGTTGACGGCTCTCGACTACCACAA CCCCGCCGGCTTCAACTGCAAAtgacgactgtgccttctagttgccagccatctgtgtttgccccccccgtgc cttcttgaccctggaaggtgccactcccactgtcctttcctaataaaatgaggaaatgcatcgattgtctgagtaggtg tcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctgggga tgcggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGC CCACAGTCCCGAGAAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGG TGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTCCCGAGGGTG GGGGAGAACCGTATATAAGTGCAAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGC CGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCT ACCTGAGGCCGCTCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTC CTGAACTGCGTCCGCGCTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCG GCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGC TCAACTCTACGTCTTTGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGC GCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACC</p>	2541

	<p>GGGGTGGTGCCCATCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTG TCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC ACCGGCAAGCTGCCCCTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCACT GCTTCAGCCGTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAA GGCTACGTCCAGGAGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCG AGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCA AGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCT ATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTTCAGATCCGCCACAACAT CGAGGACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGG CCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTCG GCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaat tcacaataaagcattttttcactgcattctagtgtgtgtgttccaaactcatcaatgtatcttatGGTGAGGCGGC GGCCTCAGCCCGCCGCGTGTCCCTGACCTGGGCGGAGGTCCAGCCTCAGTGCCCGCACC CCACCTCCCGTCCGGACCCCTCGGCGGCTGTTTCCGCCGCGAGCCTCCGGGCCCTCTCC TCTGGGTCGCCACGTACCTCGGCTCTTCGCCGCCCTTCCCGCCTTTAAAGCCCTCTACCTA CTCTGTCTCGGCATGTTACTTCTGCACTTGCTTAAGTCCAAGCATCACGTAAGTACCTTCTC TGTACATAAAAGGGAGAGCATTGCTCTTCTCACTCACTATTCAAGTCCATGGTCCCTGGG TAATTAGGCGATACCTTGAGCACCTGCTAATTATGGGCCAGCGCGGTGCTGATTCTGAGG AAGGTGCTGAGTAACTTGAAGACTAGTTCACTGCTGCCAGGAGCTAAAGGGACGAGGGG TGGAAG</p>	
pARBI- 674: SERF2_1_ Exogenou s_52	<p>CCGGGTTAGGCATAGGCCCTCCCGATCTTCGCGGTGTAAGGAGAAGGCCAGCGCCCT GTGATAGGCCCAGAGCCCCACTCCACAAGCCAGCCATCCCCACGGAGACCCAAACCGT CCACACACACCTTGCCAGCTGTTTGGGCCCCACGCCGCCCCAAACACGCCTCCAGCTGGCC CCTTGGGACCTCCCTTCTAGTCCGTATTTGACCTGGCCCGTGGCAGATTGCCACTCCCC CCTACCCCAAGCAGCTGGGCCCTCGATGGGCGGTTGTGCGGGCCCGGAGATTGAAGTGGT GTTGGATCCTGCTGCTGGCCGCGCTGGGGTAGAAGGGTCGCCGGTGTGTGGGCAGAGCG GCCCCGCGTCTACCTTTAATTTCTTTCTTAGGCGGTAACCAGCGTGAGCTCGCCGCCA GAAGAATATGAAAAAGCAGAGCTgacgactgtccttctagtgtccagccatctgtgtttgccccctccccgt gccttcttgaccctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgcatgtgtagtag gtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctgg ggatcggtgggtctatggGATCTGCGATCGCTCCGGTGCCCGTCACTGGGCGAGCGCACAT CGCCACAGTCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGA AGGTGGCGCGGGGTAACTGGGAAAGTGATGTCGTGACTGGCTCCGCTTTTCCCGAG GGTGGGGGAGAACCCTATATAAGTGCAAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGT TTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTACGCGCCCCGCG CCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTG CCTCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTGAGACCGGGCCCTTTGT CCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGCTCTCCACGCTTGCCTGACCTGCT TGCTCAACTCTACGTCTTTGTTTCGTTTCTGTTCTGCGCCGTACAGATCCAAGCTGTGACC GGCGCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTC ACCGGGGTGGTGCCCATCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGC GTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGC ACCACCGGCAAGCTGCCCGTGCCCTGGCCACCCTCGTGACCACTGACCTACGGCGTGC AGTGCTTACGCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCC GAAGGATACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCG CCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACT TCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACTACAACAGCCACAACG TCTATATCATGGCCGACAAGCAGAAGAAGCGGCATCAAGGTGAAGTTCAGATCCGCCACAA CATCGAGGACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGA CGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGAC CCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCGGGGATCACTC TCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcaca aattcacaataaagcattttttcactgcattctagtgtgtgtgttccaaactcatcaatgtatcttatGACTCGGTT AAGGGAAGCGCCGAGATGACGGGCTTCTGCTGCCGCCCGCAAGCAGAGGTAGCCCCAG</p>	2541

	GGAGGGGAGGGAAAGGGACGGTGGAGACCTGGGTAGACCAAGGGTTATAGAAGGAAA GAGAGCTACCTCAGGGCTTGAATGTGGACTAGTCGTGAGGAGCAGAGTGCATTGCTTCCTC TAGGGTTTTATTTCTCCCCACCCTCCAAATTGTTAGCTCACAGCCTTACAGGAAAGGACGG GGGCGGGCGCCTGCCCTCAGTCTGATTTCTGAGCGTCCCTGGGTCTGACCTTAAGGGCAAG GGCAGGGAGCTTACATTTCAAATACAGTTGTGGTTACGGCAGCCAGTACTTTTGGCCCTC CTTGCTGTTGCGTTCTCTCCCTTCTCCCAACCTCCTCACTGGTGTGTCTGGGTGTGGTCTC AATACAGAATAGAG	
pARBI- 675: SERF2_2_ Exogenou s_53_54	AATCGAGCCCTTTGCCACGGCTACTTCACGGGACCACCCTCCCGGGTTAGGCATAGGCCCT CCCGGATCTTCCGCGGTGTAAGGAGAAGGCCAGCGCCCTGTGATAGGCCCAGAGCCCC ACTCCACAAGCCAGCCATCCCCACGGAGACCCAAACCGTCCACACACACCTTGCCAGCTG TTTGGGCCCCACGCCGCCCAAAACACGCCTCCAGCTGGCCCTTGGGACCTCCCTTCTCTA GTCCGTATTTGACCTGGCCCGTGGCAGATTCGCCACTCCCCCTACCCCAAGCAGCTGGG CCTCGATGGGCGTGTGCGGGGCCGAGATTGAAGTGGTGTGGATCTGCTGCTGGCC GCGCTGGGTTAGAAGGGTCGCCGGTGTGTGGGCAGAGCGGCCCGCGTCTCACCTTTAA TTTTCTTTCTTAGGCGGTAACTgacgactgtgccttctagttgccagccatctgttgttggccctccccgtgcc ttccttgacctggaaggtgacctccactgtcctttcctaataaaatgaggaaattgcatcgactgtctgagtaggtg cattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggat gcggtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGC CCACAGTCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCTCTAGAGAAGG TGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCTTTTTCCCGAGGGTG GGGGAGAACCGTATATAAGTGACGTAGTCGCCGTGAACGTTCTTTTTCGAACGGGTTTGC CGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCGCCCT ACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTC CTGAACTGCGTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCG GCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGC TCAACTCTACGTCTTTGTTTCGTTTTCTGTCTGCGCCGTACAGATCCAAGCTGTGACCGGC GCCTACTCTAGAGCTAGCGAATTgcccaccacATGGTGAGCAAGGGCGAGGAGCTGTTACC GGGTGGTGCCCATCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTACGCGTG TCCGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTTCATCTGCACC ACCGGCAAGCTGCCCGTCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGT GCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAA GGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCG AGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCA AGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCT ATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACAT CGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGG CCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGCGATCACATGGTCTGTGAGTTGCTGACCGCCCGGGGATCACTCTCG GCATGGACGAGCTGTACAAatgattgtttattgcagcttataatgggttacaataaagcaatagcatcacaat tcacaataaagcattttttcactgcattctagttgtgttggttgtccaaactcatcaatgtatcttatCAGCGGAGCT TGCCCGCCAGAAGAATATGAAAAAGCAGAGCGACTCGGTTAAGGGAAAGCGCCGAGATG ACGGGCTTTCTGCTGCCGCCGCAAGCAGAGGTAGCCCCAGGGAGGGGAGGGAAAGGGA CGGTGGAGACCTGGGTTAGACCAAGGGTTATAGAAGGAAAGAGAGTACCTCAGGGCTTG AATGTGGACTAGTCGTGAGGAGCAGAGTGCATTGCTTCTCTAGGGTTTTATTTCTCCCA CCCTCCAAATTGTTAGCTCACAGCCTTACAGGAAAGGACGGGGCGGGCGCCTGCCCTCAG TCTGATTTCTGAGCGTCCCTGGGTCTGACCTTAAGGGCAAGGGCAGGGAGCTTACATTT AAATACAGTTGTGGTTACGGCAGCCAGTACTTTTGGCCCTCCTGCTTTCGTTCTCCTCC CTTCTCCCAACCTC	2541
pARBI- 676: SLC38A1_ 1_ Exogen ous_55	TTCAAAAGGAATCTTTTTGTTTCAACTATTAGGATCTTTTAAATCAAATATGTATTTAATG GTGTACACCAGACCTGAAGAAAAAGATCACAGAAGGAATTTCCCTTTGTAAGATAGAGGT AGTTAAAAATAAGCCTTATGACCTAATAGGTTAATTGTAATGCTCTGGTAGCCAACCTGAAA AAGGAGAAATGATGGTTGCATCTCACATTTTAAATGTTAAGAATTTGTTTTGTAATGAGGA TACCTTAACCCCTGAAGGCCAAAATGACTATTTGTGTGAGTTTGAGAAAGGCACATAGTAA CTTGGGGAACAGTCAATAGAATGACAAAATCTTGAATTTTAACTTTCTGAACCCTGTCAT TTCTGTGTTCTCAAATTTGATTTTAAATAGGCTGCATGGTGTATGAAAAGCTGGGGGAAC	2541

	<p>AAGTCTTTGGCACCACAtgacgactgtgccttctagtgtccagccatctgtgtttgcccctccccgtgccttctt gaccttgaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgattgtctgagtaggtgtcattc tattctgggggtgggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtggggatgcgg tgggtctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCAC AGTCCCGGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAGAGAAGGTGGC GCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTCCCGAGGGTGGGG GAGAACCGTATATAAGTGCAGTAGTCGCGTGAACGTTCTTTTCGCAACGGGTTTGCCGC CAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCCTACCT GAGGCCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCTG AACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGCTTTGTCCGCG CTCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGTTTGCCTGACCCTGCTTGCTCAA CTCTACGTCTTTGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCT ACTCTAGAGTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGG TGGTGCCCATCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCG GCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCG GCAAGCTGCCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTC AGCCGTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCGCGCCGAGGT GAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGA GGACGGCAACATCTGGGGCACAAGCTGGAGTACAATAACAACGCCACAACGTCTATATC ATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTCAAGATCCGCCACAACATCGAG GACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCC GTGCTGCTGCCGACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACG AGAAGCGCGATCACATGGTCTGTGAGTTCGTGACCGCCCGGGGATCACTCTGGCAT GGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcaca aataaagcattttttcactgcattctagtgtgtgtgttgcctaaactcatcaatgtatcttatGGGAAGTTCGTAATC TTTGAGGCCACCTCTACAGAACTGGAGGTAAAAAGAACATGCTTTTCTTTACATAACT TGAAACTAATTCTGGTGGATGAGCGGCCCATGAATTTTAAACATAATTCAAGCAGTTATCAT CCTATTGCTAAAATGGCACAGGGAAAGTAAAGCAGAGACAGCAGTCACTATTTTAAAGCC ACAAATCCTGCTAGAGTAGCTGAAGTTGCCTTTGTGTCTTACTGACAGTTGGTCTAAGAACG GGCTGATAACTTTTTATGTAGCTTGAACATAAGCCTTCGTATCTTCTTCTAAAAATGTTCT CATTTTCTTCAGCAATGCTGAGTACCTCTTCATCGTAAAAAATGAACTACCCTCTGCCATA AAGTTTCTAATGGGAAAGGAAGAGACATTTTCGTAAGTTATAGACCATTTTTTTATGATATA</p>	
pARBI- 677: SLC38A1_ 2_Exogen ous_56_5 7	<p>TAAAGATGTCAAGCTTCAAATCATTATCATAAGGTTAAATATATTACGCATGTCTTTACAGCA AGTTTATTTCTGATCGTGAAGTAGAAGAAGTCTCACAAACAGCCATTGGAAAAAAGAA GTGTGATGAGTATGTAAGTATCATTATAATGAAGTATGCTTATTTTTTAAATCATATAAATTG GGACAAATCTTTTAAATCAAGTAGCATAGTACCAAAAGCATAACTACCTGTATTACCAGG ATATTCTCATACCTTATGTATTTTCTCTTGAATCCATTCAAGGAAATAACTAGATAACTAA GAATGGATTTTCTTGAATTTTACTCCATATTGGTTCCTGAGAGTGCATTAAAGGCTTTGGCT TGATGAACCTTTCTGGGATTTATTTGCTTAGTGTCAATGTTTGTCTTTGTTTCAGATTCCA GGTACAACCTCtgacgactgtgccttctagtgtccagccatctgtgtttgcccctccccgtgccttcttgcctg gaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgattgtctgagtaggtgtcattctattctgg gggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtggggatgcgggtgggtctct atggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCC CGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGGG GTAAGTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAA CTATATAAGTGCAGTAGTCGCGTGAACGTTCTTTTCGCAACGGGTTGCCGCGAGAAC ACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCCCTACCTGAGGC CGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCTGAACTGC GTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCTTTGTCCGGCGCTCCCTT GGAGCTACCTAGACTCAGCCGGCTCTCCACGTTTGCTGACCCTGCTTGCTCAACTCTAC GTCTTTGTTTCTGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCTA GAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGC CCATCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCGGCGAGG GCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGCAAGCT</p>	2541

	<p>GCCCGTCCCTGGCCACCCCTCGTGACCACCTGACCTACGCGGTGCAGTGTCTTCACCGCT ACCCGACCATCAAGACGACGACGACTTCTTCAAGTCGCCGATGCCGGAAGGCTACGTCCA GGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTC GAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGC AACATCCTGGGGCACAAGCTGGAGTACAACACAAGCCACAACGTCTATATCATGGCCG ACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCA GCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGCT GCGCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCG CGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAG CTGTACAAtgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagca ttttttactgcattctgtgtgtgtgtccaaactcatcaatgtatcttatTTAGCGATGTGCGATTTTAACTA AGCAACGCCATTATGGGCGATGGGATTTTGGGACTCGCTTTGCCCTGGCAAACACTGGAA TCCTACTTTTTCTGTGAGTATTGACGTGCCGGTACTTTCCATTTTAAAACTGAACTTTTGTAT GTTCTGTTATTACATAGAAGAAATGTGAAATATTTATAAATAGTTTTTTTATTAACCTGGCT AAGTTACAAGTACATACTTTGATATTTATTGCTTGAGTGATTTTCCAACTGTACCTAATGCT TACAACAAAGAGGAAGGAGAAAAATCTTTTATTAATCAAAATACTGAATAAGCATTTGT GAAAAGGATTAACCATTTGAAAATAACTTTTTTGGTATTTTGGAGTCTACCTGTGACTTT AAATCTCAGTTAAAAATTAAGAGGTGTTTAAACCCAGCCAGTCACCACTT</p>	
<p>pARBI- 678: SMAD2_1 _Exogeno us_58</p>	<p>ATCATCTTCCACACTAGTCTCTTTCTGACTCTTCAGTCACTCCGACAGAAATATCCTTAGAA GCATCTCTAAAATGAGTTTGATTTTACTAAACATAGAAGTTGACAAAGTTTTTCAAGTATAAC TGCATAAATCTCTTTTTTAAAAAATCAGTTTTTCCCAAGTTGTTAGCCTTTTCATTGGCATTTG AGTCATTATGTGACATATTTATAAGAAACATCTGCTAGTGCTGCTGCATACTTTATCAGAT CCATTAATAGTACATTTTTGTTCTTGATTCTCACTAAAATACTAAATGGCTGTCATTCTTT TCTTTATGCTTTTATGTACTAATTTAGCCCATTTGACTGCACTtttttttttttttttAAAGTTCCCT CCTTCTTTTCCCTTGCTTCCCAACAGGTCTCTTGATGGTCTGCTCAGGTATCCCATCGATg acgactgtgcctctagtgtgccagccatctgtgtttgccccccccgtgccttcttgacctggaaggtgccactccac tgtcctttcctaataaataatgaggaaatgcatcgcatgtctgagtaggtgtcattctattctgggggggtggggg ggacgcaagggggaggattgggaagcaatagcaggcatgctggggatggcggtgggctctatggGGATCTGCG ATCCGTCGGTGCCGTGAGTGCGGCAGAGCGCACATCGCCAGAGTCCCCGAGAGCAAGTTGG GGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGGGGTAAACTGGGA AAGTGATGTCGTGTACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACCGTATATAAGT GCAGTAGTCGCGTGAAACGTTCTTTTTCGCAACGGGTGGCCGAGAACACAGCTGAAGC TTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCGCGCTACCTGAGGCCGCCATCCACGC CGGTTGAGTCGCTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAAGTGCCTCCGCCGTCTA GGTAAGTTTAAAGCTCAGGTGAGACCGGGCCTTTGTCGGCGCTCCCTTGGAGCCTACCT AGACTCAGCGCGCTCTCCACGCTTTGCTGACCTGCTTGCTCACTCTACGCTCTTTGTTTCG TTTTCTGTTCTGCGCCGTACAGATCCAAGCTGACCGCGCCTACTCTAGAGTAGCGAA TTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCATCCTGGTC GAGCTGGACGGCGACGTAACCGCCACAAGTTCAGCGTGTCGGCGAGGGCGAGGGCGA TGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCT GGCCACCCCTCGTGACCACCTGACCTACGGCGTGAGTGCTTACGCCGTACCCGACCCAC ATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCGGAAGGCTACGTCCAGGAGCGACCA TCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACA CCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTCTGG GGCACAAGCTGGAGTACAACATAACAGCCACAACGTCTATATCGGCCGACAAGCAGAA GAACGCATCAAGTGAACTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCT CGCCGACCACTACCAGCAGAACCCCATCGGCGACGGCCCCGTGCTGCTGCCGACAAC CACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATG GTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAatg attgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattttttactgc tctagtgtgtgtgtgtccaaactcatcaatgtatcttatAAAGGATTGCCACATGTTATATATTGCCGATTAT GGCGCTGGCCTGATCTTACAGTCATCATGAACTCAAGGCAATTGAAAACCTGCGAATATGC TTTTAATCTTAAAAAGGATGAAGTATGTGTAACCCCTTACCCTATCAGAGAGTTGAGACAC GAGTAGCTGTTGTGACCCAGGAAAAATTTTGTGTAATTTAATTAATTAACCTTAAATTTGTGC</p>	2541

	ATATTATTGGTGGTAATTAATAAtttttattttttaaaattttAATGAGAAAAACATATCTGTTTCTT GGAATAGCATATGATTGGCATGAAAGTGCATATCCAGGAAATCCTGTAGATTGGCAGTCT GCTCAGCGCTATGCTGATGTGCTTCTACATGTCCCT	
pARBI- 679: SMAD2_2 _Exogeno us_59	TTCTATATTAATAATCAGTTGACATCTGTTTTAGATAATTTTTAAAAAACTGGATTATAAA ATGAAGCACTTAGTAAAGCTGATGGCAGAGTTTTAGATCTTTGAATACAGGAAAGTGGT AAGGGCATTATAGGTATGATTGATGAGCTAGAGGGCGTTGGTGTTACATTTTAAAAACA TAATCATGACTTATCTGGAGTCACATGTTCCATTTATTGGCTTCCTCATATAGAAAAATA GTAACCAGCACTACATGCCTGTGAAAAAGTGAAGCAATTGTATTTTCTGGGTGAAGGAA GTATTCTGTACATTCTCCATGTTTTACATCATGGTATTTGAATAACCATGCTTCCATGTTAC ATCAATTTTTTGTTTTCAATTTATGCACAGCACTTGCTCTGAAATTTGGGGACTGAGTACAC CAAATACGATAGATgacgactgtgcttctagtgtccagccatctgtgtttgcccctccccgtgcttcttgacc ctggaaggtgccactcccactgtccttctctaataaaatgaggaaattgcatcgcatgtctgagtaggtgtcattctattc tgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgagggtggg ctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGT CCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCG GGGTAAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCCTTTTCCCGAGGGTGGGGGAG AACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGGCGCCAGA ACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCGCCCTACCTGAG GCCGCCATCCACGCGCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCTGAAT GCGTCCGCGCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCTTTGTCCGCGCTCC CTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCCTGACCTGCTTGCTCAACTCT ACGTCTTTGTTTCGTTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGCGCCTACTC TAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGT GCCCCATCTGGTCGAGCTGACGCGCAGCTAAACGGCCACAAGTTCAGCGTGTCCGGCGA GGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAA GCTGCCCGTGCCCTGGCCACCTCTGTGACCACCTGACCTACGGCGTGCAGTGCTTCAGCC GCTACCCCGACCATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCGAAGGCTACGT CCAGGAGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAA GTTGAGGGGCGACCCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA CGGCAACATCTGGGGCACAAGCTGGAGTACAACATAACAGCCACAACGTCTATATCATG GCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTCAAGATCCGCCACAACATCGAGGAC GGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGC TGCTGCCCCACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAA GCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCCGCGGATCACTCTCGGCATGGAC GAGCTGTACAAatgattgtttattgagcttataatggttacaataaagcaatagcatcacaatttcacaataa agcattttttcactgcattctagtgtgtgtgttgcctcaactcatcatgtatcttatCAGTGGGATACAACAGGCC TTTACAGCTTCTCTGAACAAACAGGTGAATATTCTGCCCTCTGTGCAATCTTAGAGATCTTG TGGGAGGGGGGTATATTTTGAAGACCTATATGGGGTTGCTTAGTATAATTTTGCCTAGGA TGTTTCTTAATGTAAATAAGGCATAGCATTTAAATATCTGCTTGCCAGTATAAAAAATAT ATTAAATGTTTCAGCTGATGTTTTAATCAATGCAATTCTAGTTTGAATCTTCTTAAATTACTG TATCCCCTAAAGAATAATAATTTGATACTATATTTATTTAGCTTGAGATCAGATTATA ATCTGTTGTTGGCCTAATTTTAAAGTAGATACATGATGAGTTTGTCTAAATTTCTGTTATCA GAATCTCATCTTTATACTAATAAATACATACTTAATGAACCCCTTATATCACAA	2541
pARBI- 680: SMAD2_3 _Exogeno us_60	TCAATGTATTTTGTATAGTCTTTGAGATTAGAGTGAAGTTCTAAAAAGTAAGAGAACCTT TTGTGAAAATATTTAATTGACACTACTAAGAGTTTAAATAGTATTGGTGGTGAAAAATCG TTAAAGTATCTGATTTTACTTGCAAAATTAAGTATTTCCACAAGAGGAGTCTTACAAC ATTCTGTTTTTGAAGGGTTTGTTCATCATTCTAAATTCATAAAGATAACGTTTTTCAT GGGTGGAGAAGTCTATTGGGAAAGTCATAATTCGAATTTCTATCTTGCTTTGCACTTTGCTT TCTATGATAAGTTGAAATTATTACTTGATGTTCAAGGTAGTCTCTACATCATCTTTCAATAT TTCTGCTAGGTTGATACAAGAGGCTGTTTTCTAGCGTGGCTTGCTGCCTTTGGTAAGAAC ATGTCGTCCATCtgacgactgtgcttctagtgtccagccatctgtgtttgcccctccccgtgcttcttgaccctg gaaggtgccactcccactgtccttctctaataaaatgaggaaattgcatcgcatgtctgagtaggtgtcattctattctgg gggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgagggtgggctct atggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCC CGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGGG	2541

	<p>GTAAACTGGGAAAGTGATGTCGTGTAAGTCCGCTTTTCCCGAGGGTGGGGGAGAA CCGTATATAAGTGCAGTAGTCGCGTGAACGTTCTTTTCGCAACGGGTTGCCGCCAGAAC ACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCCTACCTGAGGC CGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCTGAACTGC GTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCTTTGTCCGGCGCTCCCTT GGAGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGCTCAACTCTAC GTCTTTGTTTCTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGGCGCTACTCTA GAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGC CCATCTGGTCGAGCTGGACGGCGACGTAACGGGCCACAAGTTCAGCGTGTCCGGCGAGG GCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAAGTTCATCTGCACCACCGGCAAGCT GCCCCTGCCCTGGCCACCCTCGTGACCACCTGACCTACGGCGTGACGTGCTTACGCCGT ACCCCGACCACATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCGAAGGCTACGTCCA GGAGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCGAGGTGAAGTTC GAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGC AACATCCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAACGTCTATATCATGGCCG ACAAGCAGAAGAACGGCATCAAGGTGAAGTCAAGATCCGCCACAACATCGAGGACGGCA GCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGTGCT GCCCCACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCG CGATCACATGTCTCTGCTGGAGTTCGTGACCGCCGCGGGGATCACTCTCGCATGGACGAG CTGTACAAatgattgtttattgagcttataatggttacaataaagcaatagcatcacaatttcacaaataagca tttttttactgcattctagttgtgtttgtccaaactcatcaatgtatcttaTTGCCATTACGCGCCAGTTGT GAAGAGACTGCTGGGATGGAAGAAGTCAGCTGGTGGTCTGGAGGAGCAGGGCGGAGGA GAGCAGAATGGGCAGGAAGAAAAGTGGTGTGAGAAAGCAGTAAAAGTCTGGTGAAGAA GCTAAAGAAAACAGGACGATTAGATGAGCTTGAGAAAGCCATCACTCAAACTGTAAT ACTAAATGTGTACCATACCAAGGTAAGTTTGTGATAGTCCAGGTTTGATCAAAATTATGTC AAGGAATCTGAAGGAAAGTACTGAATTTGTGTTCTTCAAGTTGCCTGTAAAAAGTGAT GATTGAAATATGACTGTTTTAACCTTGATAAATTGTTTTGCTAGCTGACTGTTTTATAA ATTATTTCTTGAATAGTGAGGTTTAATCAAGCTAAATAAGATACTTAGATTATTATCTTCA</p>	
pARBI- 681: SOCS1_1 _Exogeno us_61	<p>GGGCTCCCGCAGCACAGCCTTTCTCCGCGCTAGCCCAAATCGCCAGACGAGCGCGAT CCCAGCCTGGCCAGCAGGCGCGGGCGGGGCGGCGAGCCGGGGCCGACGGCTGGA GCCAGAACCGGCTGCTCTCCACGCCCCCTCTCGGTGCTGCCGGAGGCCGACTCCGCCT CCACCGAGCCCCACCCGCGGGAAGAGCTCCGCGGAGTACAGAGCCATTTCTAGCTGT GTCCACTGAGGCTGAACGATCCGCGCGGACTTGGTGTCTCGTGTGCTGCCCCCTAGGGCCG GGTCCGCCGGGAGCGCCGCCCTCCGGAGTTGTCCGGCCGCGCACACCTGCCCGGCCCCG CAGCGCCCCAGCTCACCTCTTTGTCTCTCCCGCAGCGCACCCCCGGACGCTATGGCCACCC CTCCGGCTGGCCCCCTTCTGATGATGtgacgactgtgacctctagttgccagccatctgtgtttgccccctccc cgtgacctctgacctggaaggtgccactcccactgtccttttctaataaaataggaaattgcatgcattgtctgagt aggtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgt ggggatgcgggtggtctatggGATCTGCGATCGCTCCGGTGCCCGTCAAGTGGGCGAGCGCAC ATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTAGA GAAGGTGGCGGGGTAACTGGGAAAGTGATGTCGTGTAAGTCCGCTTTTCCCGA GGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCGTGAACGTTCTTTTCGCAACGG GTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGC CGCCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGG TGCTCTGAACTGCGTCCGCCGTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTT GTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTG CTTGCTCAACTCTACGTCTTTGTTTCTGTTTCTGTTCTGCGCGTTACAGATCCAAGTGTGA CCGGCGCTACTCTAGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGT TCACCGGGGTGGTGGCCATCTGGTCGAGCTGGACGGCGACGTAACGGGCCACAAGTTCA GCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCT GCACCACGGCAAGCTGCCGTGCCCTGGCCACCCTCGTGACCACCTGACCTACGGCGT GCAGTGCTTACGCCGTACCCCGACCATGAAGCAGCAGCACTTCTCAAGTCCGCCATGC CCGAAGGCTACGTCCAGGAGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCG CGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGA CTTCAAGGAGGACGGCAACATCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAA</p>	2541

	<p>CGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCAC AACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGC GACGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAG ACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCTGTGACCGCCGCCGGGATCAC TCTCGGCATGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatc acaaatttcacaaataaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatGTAGCA CACAACCAGGTGGCAGCCGACAATGCACTCTCCACAGCAGCAGAGCCCCGACGGCGGCCA GAACCTTCTCCTCTTCTCCTCTCTcgcccgcgcccccgcgcccccgcgcccccggtccccgcccc ggCCCCCGGCGACACGCACTTCCGCACATTCCGTTCCGACGCGCGATTACCGGCGCATCACGC GCGCCAGCGCGCTCTGACGCGCTGCGGATTCTACTGGGGGCCCTGAGCGTGCACGGGG CGCACGAGCGGCTGCGCGCCGAGCCCGTGGGACCTTCTGTTGCGCGACAGCCGCCAGC GGAAGTGTCTTTTCGCCCTTAGCGTGAAGATGGCCTCGGGACCCACGAGCATCCGCGTGCA CTTTCAGGCCGCGCGCTTTCACCTGGATGGCAGCCGCGAGAGCTTCGACTGCCTCTTCGAG CTGCTG</p>	
<p>pARBI- 682: SOCS1_2 _Exogeno us_62</p>	<p>GGATCCACGCTGGCCAGCAGGCGGGCGGGCGGGCGGCGAGCCGGGGCCGGACGGC TGGAGCCAGAACCGGCTGCTCTCCACGCCCCCTCTCGGTGCTGCCCGGAGGCCGGACTCC GCCTCCACCGAGCCCCACCCGCGGGAAGAGTCCGCGGAGTACAGAGCCCATTTTCTAG CTGTGTCCACTGAGGCTGAACGGATCCGCGCGGACTTGGTGTCTCGTGCTCGCCCCCTAGG CCTGGGTCCGCGGAGCGCGCCCTCCGGAGTTGTCCGGCCGGCGCACACTGCCCGGC CCCCGACGCGCCAGCTCACCTCTTTGTCTCTCCGCGAGCGACCCCCGGACGCTATGGCCC ACCCCTCCGGCTGGCCCCCTTCTGTAGGATGGTAGCACACAACAGGTGGCAGCCGACAATG CAGTCTCCACAGCAGCAGAGCCCCGAtgacgactgtgcttctagttgccagccatctgtgtttgccctccc ccgtgcttcttgaccctggaaggtgccactcccactgtccttcttaataaaatgaggaaattgcatcgattgtctgag taggtgtcattctattctggggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggatgc tggggatgcggtgggtcttatggGATCTGCGATCGCTCCGGTGCCCGTCAAGTGGGCGAGAGCGCAC ATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTCCGCAATTGAACGGGTGCCTAGA GAAGGTGGCGGGGTAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCCGA GGGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCGTGAACGTTCTTTTTCGCAACGG GTTTGCCCGCAGAACAACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGC CGCCCTACCTGAGGCCGCCATCCACGCCGTTGAGTGCCTTCTGCCGCTCCCGCTGTGG TGCCTCTGAAGTGCCTCGCCGTCTAGGTAAGTTAAAGCTCAGGTCGAGACCGGGCCTTT GTCCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGTCTGACCTG CTTGCTCAACTCTACGTCTTTGTTTCTGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGA CCGGCGCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGT TCACCGGGGTGGTGCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCA GCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCACT GCACCACGGCAAGCTGCCGTGCCCTGGCCACCCTCGTGACCACCTGACCTACGGCGT GCAAGTCTTCAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGC CCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCG CGCCGAGGTGAAGTTGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGA CTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAACAGCCACAA CGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCAC AACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGC GACGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAG ACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCTGTGACCGCCGCCGGGATCAC TCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatc acaaatttcacaaataaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatcttatCGCGG CCAGAACCTTCTCTCTTCTCCTCTCTcgcccgcgcccccgcgcccccgcgcccccggtccccg ccccggCCCCCGGCGACACGCACTTCCGCACATTCCGTTTCGACGCGCGATTACCGGCGCATCA CGCGCGCCAGCGCTCTGGACGCTCGGATTCTACTGGGGGCCCTGAGCGTGACG GGGCGCACGAGCGGCTGCGCGCGAGCCCGTGGGCACCTTCTGGTGGCGACAGCCGCC AGCGGAAGTGTCTTTTCGCCCTTAGCGTGAAGATGGCCTCGGGACCCACGAGCATCCGCGT GCACTTTCAGGCCGGCCGCTTTCACCTGGATGGCAGCCGCGAGAGCTTCGACTGCCTCTTC GAGCTGCTGGAGCACTACGTGGCGCGCCGCGCCGATGCTGGGGGCCCGCTGCGCCAG CGCCG</p>	2541

pARBI-683: SOCS1_3 _Exogeno us_63	<p>CGGACTCCGCCTCCACCGAGCCCCACCCGCCGGGAAGAGCTCCGCGGAGTACAGAGCCC ATTTTCTAGCTGTGTCCACTGAGGCTGAACGGATCCGCGCGGACTTGGTGCTCCGTGCTCGC CCCCTAGGGCCGGGTCCGCCGGGAGCGCCGCCCTCCGGAGTTGTCCGGCCGGCGCACACC TGCCCGGCCCGCAGCGCCCCAGCTCACCTCTTTGTCTCTCCCGCAGCGACCCCCGGACGC TATGCCCCACCCCTCCGGCTGCCCCCTTCTGTAGGATGGTAGCACACAACCAGGTGGCAGC CGACAATGCAGTCTCCACAGCAGCAGAGCCCCGACGCGGCCAGAACCTTCTCTCTTCTCT CCTCTCgccccgccccccgccccgccccgccccgccccgccccgccccgCCCCGGCGACACGCA CTTCGACATgacgactgtgccttctagtgtccagccatctgtgtttgccccccccctgtccttcttgacctgga aggtgccactcccactgtcctttcctaataaaataggaaattgcatcgattgtctgagtaggtgtcattctattctggg ggtggggtggggcaggacagcaaggggaggattgggaagacaatagcaggcatgctgggagtgcggtgggctctat ggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCC GAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGGGGG TAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAACC GTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCAGAACAC AGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCCCTACCTGAGGCCG CCATCCACGCCGTTGAGTCGCTTCTGCCGCTCCCGCTGTGGTGCTCTGAACTGCGT CCGCGCTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCTCCCTTG GAGCTTACCTAGACTCAGCCGGCTCTCCACGCTTGCCTGACCCTGCTTGTCAACTCTACGT CTTTGTTCGTTTTCTGTCTGCGCCGTACAGATCCAAGCTGTGACCGCGCCTACTAGA GCTAGCGAATTgccccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCC ATCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGC GAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGC CCGTGCCCTGCCCCACCTCGTGACCACCTGACCTACGGCGTGCACTGCTTACGCCGTAC CCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCAGG AGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGA GGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAA CATCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAACGTCTATATCATGGCCGAC AAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGC GTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGTGC CCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCG ATCAGATGGTCTGCTGGAGTTCGTGACCGCGCCGGGATCACTCTCGGCATGGACGAGCT GTACAAatgattgtttattgcagcttataatggttacaataaaagcaatagcatcacaatttcacaataaagcattt ttttctactgcttctagtgtgtgttgccttctatgtatcttatTTCCGTTTCGACGCCGATTACCGGC GCATACGCGCGCCAGCGCGCTCTGGACGCTGCGGATTCTACTGGGGGCCCTGAGCGT GCACGGGGCGCACGAGCGGCTGCGCGCCGAGCCCGTGGGCACCTTCTGGTGCGCGACAG CCGCCAGCGGAACTGCTTTTCGCCCTTAGCGTGAAGATGGCCTCGGGACCCACGAGCATC CGCGTGCACTTTCAGGCCGGCCGCTTTCACCTGGATGGCAGCCGCGAGAGCTTCGACTGCC TCTTCGAGCTGCTGGAGCACTACGTGGCGCGCGCGCCGATGCTGGGGGCCCGCTGC GCCAGCGCCGCTGCGGCCGCTGCAGGAGCTGTGCCGCCAGCGCATCGTGCCACCGTGG GCCGCGAGAACCTGGCTCGCATCCCCCTCAACCCGCTCTCCGCGACTACCTGAGCTCCTTC</p>	2541
pARBI-684: SRP14_1 Exogenou s_64	<p>GGCAGACAAACAGTTAAACAGAGGAGTGGGGTAAAGTGATGACCTAACCCAGCCCCGCTG CTCTAGTTTTGTTAAACACCTCATCTGCTATCACGGTCTGGCGAAACCCTGGAGAACTATT ATTTCCACGACGGAACATGTAATATCGAAGCAGTTAAATTCCACTCAAAGTGCGGCGT CTGGGATCCCTGACAAAGAGCCCTGGGCTGCTTGGGGCCCATTTGTTACCAGAAGCAACCTA GGCGGCTCAGTGCTGGGGACTGAGCCAGCTACAATCCCTACTATTTCCGGGCCCGAAGCC CCGAATGTGCTCAGTACAGGGTGGGAAAGGTAGAGGAAGGCGGCGGTCCGCGGCAGAC AGACTCCGGTGGCTCCAGACACCGGGAACCCAGGAGCATCGCCCGGCTCCCTCCCGCT GCTTACACTTCTTCAAGGTGATATAtgacgactgtgccttctagtgtccagccatctgtgtttgcccccccc gtgccttcttgacctggaaggtgccactcccactgtcctttcctaataaaataggaaattgcatcgattgtctgagta ggtgtcattctattctgggggtggggtggggcaggacagcaaggggaggattgggaagacaatagcaggcatgctg gggatgcggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACA TCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCTTAGAG AAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTCCCGAG GGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGT TTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCG</p>	2541

	<p>CCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTG CCTCCTGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGT CCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCT TGCTCAACTCTACGCTTTTGTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACC GGCGCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTT ACCGGGGTGGTGCCCATCTGGTCGAGCTGGACGGCGACGTAACCGGCCACAAGTTCAGC GTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGC ACCACGGCAAGCTGCCCGTGCCCTGGCCACCTCTGTGACCACCTGACCTACGGCGTGC AGTGCTTACGCCGTACCCCGACCACATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCC GAAGGTACGTCAGGAGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCG CCGAGGTGAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACT TCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAACG TCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAA CATCGAGGACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGA CGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGAC CCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCTGTGACCGCCGCCGGGATCACTC TCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcaca aatctcacaataaagcattttttcactgcattctagttgtgtttgtccaaactcatcaatgtatcttatGACGCTGCC CGACGTCGGCACTTCTGGAAAAGTCTGTGTCAGCTCCGTCAAGAACTGGAAAACAACAGGC CCAGCCCCGTAGCCAGCCCCAAATCCTCGTCTGCGCGTCAAGGCCCTGGTCTCTCTGCA GGAGGCACAGGTCTCGAGTAACGCCTGAGCCGCCCTTCCCTCGGCCGCCAGGCCTAGC CATACTGCTCGTCTCAACAACACCATCGCGCGACGCTGGCTCGACTCCCTCCGCTTAA GCCCCTAGCAGTGAGAGCCGGAAGTTCGGCCTAGGCTGGGCGGGACTTCCGCTACTAGAC TTCCATTGTCTCCACCAATCTCTTCTTCCACCAATCCCGCCTGCGCCCTCCCCCTCCCC GCCCCCTAGCGCCCGCGCCTGGGACGTCGGGGGGCTGTGACCCGGAGGCGCTGGGGC TGTCCTGGGTC</p>	
<p>pARBI- 685: SRP14_2_ Exogenou s_65_66</p>	<p>GTCTGTCTGCCGCGGACCGCCGCTTCTCTACCTTTCCCCACCCTGTACTGAGCACATTGCG GGCTTCGGGCCCGGAAAATAGTAGGGATTGTAGCTGGCTCAGTCCCCAGCACTGAGCCGC CTAGGTTGCTTCTGGTAACAATGGGCCCAAGCAGCCAGGGCTCTTGTGAGGGATCCCA GACGCCGCCACTTTGAGTGGAATTAACGTGCTTCGATATTACATGTTTCCGTCTGGAAAT AATAGTTTCTCAGGGTTTCGCCAGACCGTGATAGCAGATGAGGTGTTTAACAAAAGTAGA GCAGCGGGGCTGGGTTAGGTCATCACTTACCCACTCCTCTGTTTAACTGTTTGTCTGCCG CTCAGCCAGTACGCGGCCGTGTTACCAAGATGCATTTTTCTTCAGATGACGGTCAAC CAAACCCATTCCAAAGAAgtgacgactgtgccttctagttgccagccatctgtgttggccctccccgtgcctt cttgacctggaaggtgccactccactgtcctttcctaataaaatgaggaaattgcatcgattgtctgagtaggtgca ttctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtggggatgc ggtgggtcttatggGATCTGCGATCGCTCCGGTGCCGTCAGTGGGCAGAGCGCACATCGCCC ACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCTAGAGAAGGTG GCGCGGGGTAAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTTCCGAGGGTGG GGGAGAACCGTATATAAGTGCAGTAGTCGCGTGAACGTTCTTTTTCGCAACGGGTTTGCC GCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCTA CCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTCTGCGCCTCCCGCTGTGGTGCTCC TGAAGTGCCTCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGG CGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCTGACCTGCTTGCTC AACTCTACGCTTTGTTTCTGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGC TACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCCGG GTAGTGGCCCATCCTGTGTCGAGCTGGACGGCGACGTAACCGGCCACAAGTTCAGCGTGTG CGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGACCCAC CGGCAAGCTGCCCGTGCCCTGGCCACCTCTGTGACCACCTGACCTACGGCGTGCAAGTGC TTCAGCCGCTACCCCGACCACATGAAGCAGCAGCACTTCTCAAGTCCGCCATGCCGAAG GCTACGTCCAGGAGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGA GGTGAAGTTCGAGGGCGACACCCTGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAA GGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAACGCTTA TATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATC GAGGACGGCAGCGTGCACTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGC</p>	2541

	<p>CCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCA ACGAGAAGCGGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCGGATCACTCTCGG CATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaattt cacaataaagcatttttttactgcatttagttgtgtttgtccaaactcatcaatgtatcttatGGTACTGTGGAG GGCTTTGAGCCCGCAGACAACAAGTGTCTGTTAAGAGCTACCGATGGGAAGAAGAAGATC AGCACTGTGGTGAGCTTAATTTCTAAGGCTGTCTTTTGAATGTAAAGACTTGAACCTAACA GAGGATGGGGCGTTTCTGAACAGGCTTTTATTTGTTTTTCCCTTTTGCCTGTGTGGCTATT TTTGAGACCAGGACCTTCTATACCTTAGTAGTGAAACCTCAAGAATAAAATAAGAAGGT AGAGCTCAGACAGTCGTTAGTTCTGCTAAAGCTCTTGGAATGAAAGTAGCATATTGGT CCTTATTCTAGTACTGTAAGGAGCAGCTGGCATAAATATTTGATTCTTAGCCCTTACTGT GCTGGGCCCTCAATAAGCAGTTCTTGGTACCAGGTGATGCTATTATTTCTTATCTTTGTGG TTCAC</p>	
pARBI- 686: SRSF9_1_ Exogenous s_67	<p>CCCACGTCACTGAGTGCTCACAAGTCTGTGAGGTAGGCGGCGCCACAGAGAGAACTGAG GCGCGGGAGCCCAAGCCACTTGTCCAGCGCCTCAGCCGAGCGCGAACCAGCGCTCGGGGAT GGCATCCACACGCGCCCGGCCAGGCTCTCCCTGTAGCGCCCGAAGGCCCTTCGCACCTC CAGGGGGCGCCGGCTGCGCGCACGCGCAATGGTTCGAGCCGCGTCTCTTTAAGAGGAC TCCTTTTGCCTCCGCGGACCCCTTCGCTTCCGCTCCGCGTCCCAATGCAGTGCGGCTGAG CGCCTCGGAGCCCGGGGACGCTGCGGGGGACCGTGCTGAggcccggcgccgacgtgggc tgcggcgggcccgcgcgctcgggcggtgctggatgtcgggctggcgagcgcgcgcgAGGGCGACGGG CGCATCTAGcagcactgtgccttctagttgcccagcctctgtgttggccctccccgtgccttctgacctggaa gggtccactccactgtccttcttaataaaatgaggaaattgcatcgcattgtctgagtaggtgtcattctatttggggg gtgggtggggcaggacagcaaggggaggattgggaagacaatagcaggcatgctggggatgctgggtgggtctatg gGGATCTGCGATCGTCCGGTGCCCGTCAGTGGGCGAGCGCACATCGCCACAGTCCCGG AGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGGGGT AAACTGGGAAAGTGATGTCTGTACTGGCTCCGCCTTTTCCCGAGGGTGGGGGAGAAC GTATATAAGTGCAGTAGTCGCGTGAACGTTCTTTTTCGAACGGGTTTGCCGCCAGAACAC AGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCGCTACCTGAGGCCG CCATCCACGCGGTTGAGTCGCTTCTGCCGCTCCGCGCTGTGGTGCCTCTGAATCGCT CCGCGCTCTAGGTAAGTTTAAAGCTCAGGTGAGACCGGGCCTTTGTCCGGCGCTCCTTG GAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCCTGACCCTGCTTGTCAACTCTACGT CTTTGTTTCTGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCTAGA GCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGGCC ATCCTGGTTCGAGCTGGACGGCGACGTAAACGCCACAAGTTCAGCGTGTCCGGCGAGGGC GAGGGCGATGCCACCTACGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGC CCGTGCCCTGGCCACCCCTCGTGACCACCTGACCTACGGCGTGACGTGCTTACGCCGTAC CCGACCATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCCCAAGGCTACGTCCAGG AGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGA GGCGGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCA CATCCTGGGGCACAAGCTGGAGTACAACACTACAACAGCCACAACGTCTATATCATGGCCGAC AAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGGACGGCAGC GTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCGTGTGCTGCTGC CCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCG ATCATATGGTCTGTGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGGACGAGCT GTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattt ttttactgcatttagttgtgtttgtccaaactcatcaatgtatcttatGTGGGAACCTTCCGACCGACGTG CGCGAGAAGGACTTGGAGGACCTGTTCTACAAGTACGGCCGATCCGCGAGATCGAGCTC AAGAACCAGGACGGCCTCGTGCCTTCCGCTTCTGCGCTTTCGAGGACCCCGGTGAGGccc ccgccccctcccctctcctcctcggtgctgaggcccccgcttccctgctgtccccctccccagggtccccctcccccg gctccccctcccccgctccgagcagaccccccaCGGCGCCCCCTCACGGGTGGAGGATGAGGCAGCC TCTCTCGCAGGCCCGGGCGCTCCTCGCGCGCTCGTCACTTCTTTATTTTATTATTTCAAT ATTTTACTTAGAAACCCAAAAGCTGAGCCTTTGGAGGGCCCAAGCCCGCTGCACCGGCCT CGGGGGGTCCAAATGAGCCTTGTCCGCC</p>	2541
pARBI- 687: SRSF9_2_	<p>TGTGGTGTGCTTTTCGAGAAATGCTCACGAAGATTAGAAAAACTGATGGTTTATTGGC AAAATCAATAATCTGTGAGCAGTTGATTCTtttttttCTCTGAATTAGCCCTCTTATGAGTAATCT GTTTGCTCATTCAATATAATTTACATCTCTAAAAGTGGTGTGACAGCTGTAAAGGTTAAT</p>	2541

<p>Exogenous s_68</p>	<p>CCAGTATCATGAAACGCTCTCCAAACCAAGCAGAAGTCTTCAAGATCTGATTGTGTGTT TTTTTCTTCACTCTAGGTTTCCCTTTTATGCTTACTACTCATGCCCTCACTTGAAAAGTCACT TGGCCTCCTGAACAGCACTAACTCCAAACGTTTTtttggttgttggTTTTttttAGAGATGCAGAGGA TGCTATTTATGGAAGAAATGTTTATGATTATGGCCAGTGTCCGCTTCGTGTGGAGTCCCCCA GGTgacgactgtgcttctagttgccagccatctgttgtttgccctcccccgctcttctgacccctggaaggtgccact cccactgtcctttcctaataaaatgaggaaattgcatcgattgtctgagtaggtgtcattctattctgggggggtggggtgg ggcaggacagcaagggggaggattgggaagacaatagcaggcatgtcgggatgcgggtgggctctatggGGATCT GCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTT GGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGGGGTAAACTGG GAAAGTGATGTCTGTGTACTGGCTCCGCTTTTTCCCGAGGGTGGGGGAGAACCCTATATAA GTGCAGTAGTCGCGGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAA GCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCCGCCCTACCTGAGGCCGCCATCCAC GCCGGTTGAGTCGCGTTCTGCCGCTCCGCTGTGGTGCTCTGAACTGCGTCCGCGCTC TAGGTAAGTTTAAAGCTCAGGTGCAGACCGGGCCTTTGTCCGGCGCTCCCTTGGAGCCTAC CTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGCTTGCTCAACTCTACGTTCTTTGTTT CGTTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCTACTCTAGAGCTAGCG AATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCATCTGG TCGAGCTGACGGCGAGCTAAACGCGCCACAAGTTCAGCGTTCGGCGGAGGGCGAGGGC TAGGCCACCTACGGCAAGCTGACCTGAAGTTTCATCTGCACCCACGGCAAGCTGCCCTGC CCTGGCCCAACCCTCGTGACCACCTGACCTACGGCGTGCACTGCTTCAAGCGTACCCCGAC CACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGAGCGCA CCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGAGGTGAAGTTCGAGGGCG ACACCCTGTGTAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCC TGGGGCACAAGCTGGAGTACAATAACAAGCCACAACGTCTATATCATGGCCGACAAGCA GAAGAACGGCATCAAGGTGAAGTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCA GCTCGCCGACCACTACCAGCAGAACACCCCCATCGCGCAGCGCCCCGTGCTGCTGCCCGAC AACCATACTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAGCAGCGCATACACA TGGTCTGTGGAGTTCGTGACCGCGCGGGGATCACTCTCGGATGGACGAGCTGTACAA atgattgtttattgcagcttataatggtttacaataaagcaatagcatcacaatttcacaaataaagcattttttcactg cattctagttgtggtttgtccaaactcatcaatgtatcttatACTTATGGAGGTGCGGGTGGGTGCCCCGT GGTGGGAGGAATGGCCCTCTACAAGAAGATCTGATTCCGAGTCTTGTTCAGGTATGT TCCTTTCAAACAGaatgagatgatacatgtaaaatacttaacacagagctgtcttccaagaatgatagctgttat tcttCAGTGCATGGGACACGGGGGCTTTCTTTTCAATAGCCTGTGTGAAGCCTTGCCCTGGAT TGCCAATGAGGAAAGTATCCTGCAAATGAAATTGCGCTGGGAGTGCAGCCTTGAAGAAC ATAACCATATTTCTTTAAAGGAGTTTTCTAGTGGTGAGAAGGAAAGATGATGGGAAAAT TGAGCTACAATTCTAAGAGTCTTCTTTTGAATATACATTGGCATCAGACATGGTAGAAAGG CATTCAAGGAGCCAGATTGTAACAACCTTACCCAGCC</p>	
<p>pARBI- 688: SRSF9_3_ Exogenous s_69</p>	<p>GATGGCATCCACACGGCCCGGCCAGGCTCTCCCTGTGACGCGCCGAAGGCCCTTCGCAC CTCCAGGGGGCGCGCGCTGCGCGCACGCGCAATGGTCGCAGCCGCTTCTCTTTAAGAG GACTCCTTTTGCTCCGCCGACCCCTTCGCTTCGCTCCGCTTCCACAATGCAGTGGCGCT GAGCGCTCGGAGCCCGCGGGACGCTGCGGGGGGACCCGTGCTGAgggcggcggcggcagct gggctgcggcgggcccgcggcgctgggcgggtcggtatgcggctgggcggagcagcgcgcgggcaggAGGGCGAC GGGCGCATCTACGTGGGGAACTTCCGACCGACGTGCGCGAGAAGGACTTGGAGGACCTG TTCTACAAGTACGGCCGCATCCGCGAGATCGAGCTCAAGAACCCGGCACGGCCTCGTGCCT TGCCTTCTgacgactgtgcttctagttgccagccatctgttgtttgccctcccccgctcttcttgaacccctggaag ggccactccactgtcctttcctaataaaatgaggaaattgcatcgattgtctgagtaggtgtcattctattcttgggggtg gggggtggggcagcagcaagggggggaggattgggaagacaatagcaggcatctgaggatgcgggtgggctctatgg GGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGA GAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGGGGGTA AACTGGGAAAGTGATGTCTGTACTGGCTCCGCTTTTTCCCGAGGGTGGGGGAGAACCCT ATATAAGTCGAGTAGTCGCGGTGAACGTTCTTTTTCGCAACGGGTTTGCCGCCAGAACA GCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCCGCCCTACCTGAGGCCGC CATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGTCCTCTGAAGTCTGCTGCTC CGCGCTCTAGGTAAGTTTAAAGCTCAGGTGAGACCGGGCTTTGTCCGCGCTCTGCTGCTC AGCTACCTAGACTCAGCGCGCTCTCCAGCTTTCGCTGACCTGCTGCTGCTCAACTCTACGTC</p>	<p>2541</p>

	<p>TTTGTTCGTTTTCTGTTCTGCGCCGTACAGATCCAAGCTGTGACCGGCGCCTACTCTAGAG CTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCCA TCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCG AGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCC CGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAAGTGTTCAGCCGCTACC CCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCCAGGA GCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCGCGCCGAGGTGAAGTTCGAG GGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAAC ATCCTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCTATATCATGGCCGACA AGCAGAAGAACGGCATCAAGGTGAAGTCAAGATCCGCCACAACATCGAGGACGGCAGCG TGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGTGTGCC CGACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGA TCACATGGTCTGTGGAGTTCGTGACCGCCGCGGGATCACTCTCGGCATGGACGAGCTG TACAAtgattgtttattgagcttataatggttacaataaagcaatagcatcacaatttcacaataaagcattttt ttcactgcattctagttgtgtgttgcctcaactcatcaatgtatcttatGTGCGCTTCGAGGACCCCGGTGAG Gccccgcgccccctgcctctcctcctcggtgctgaggccccgccttccctgctgtccccctccccagggtccctctcc ccggcctccccctccccgcctccgcgcagacccctcaCGGCGCCCTCACGGGTGGAGGATGAGGCA GCCTCTCTCGCAGGCCCGGGCGCTCTTCGCGCCGTCGTCACTTCTTTATTTTATTATTC CAATATTCTTACTAGAAACCCAAAGCTGAGCCTTTGGAGGGCCCAAGCCCGCTGCACCG GCCTCGGGGGTCCAATGAGCCTTGTCCGCTCTGCTGGGGCAGCACCGTAGGGGGA AGCGGCGCGGGGACGCGGGGGTGCCTGTCGCCCTCCCGCTCGCCTCTCCCCGGCC CGTGCTCGCGTGGCTGGAGAGCAAGCT</p>	
pARBI- 689: SUB1_1_ Exogenou s_70	<p>GTAAGTACTAGCCTTAGTAGACTGTGGTTCCAGGTTTATTCAGAAGTAGCAAGATCCCTC CAtttttttCTACCAAAGAAATCGTATGTGGGATCCCAAACCACAAAATAACCGTTCCTGTGG TTAATACTACTATAATGCCTGAAGTGCTTTTGGGATCCTGAGAACAGAGTTTGAAAACATT ACTAGACAGAAGGATTGGTTAGATTATAGTTTTGTTGTTGAGTGAAACTTGCTTATGTATA TATTTATGATATTTGGATGTAGTCTTTTGATTGTTTAAATCTTAAAAAGTAATGGGATCTTT TGACACTGGGGTATGTTTTATTTTATGTGTGCAAAATTTAACCATAATCTTTCTAGTTAA GAGGAAAAAGCAAGTTGCTCCAGAAAAACCTGTAAAGAAAAAAGACAGGTGAGACTTC GAGAGCCCTGTCAtgacgactgtgccttctagttgccagccatctgtgttttccccctccccgtgccttcttgacc tgggaagtgccactcccactgtcctttcctaataaaatgaggaaattgcatgcattgtctgagtaggtgctattctattct gggggtgggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgcggtgggc tctatggGATCTGCGATGCTCCGCTGCCGTGCGGTCAGTGGGCAGAGCGCACATCGCCACAGTC CCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGG GGTAACTGGGAAAGTGATGTCGTGTAAGTCTCCGCTTTTCCCGAGGGTGGGGGAGA ACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCAGAA CACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCTACCTGAGG CCGCCATCCACGCGGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCTGAAGCTG CGTCCGCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGTCCC TTGGAGCCTACCTAGACTCAGCCGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAACTCTA CGTCTTTGTTCTGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCT AGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGT GCCCCCTCGGTGAGCTGACGCGGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGA GGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAA GCTGCCCGTGCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAAGTGTTCAGCC GCTACCCCGACCATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCGAAGGCTACGT CCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAA GTTGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGA CGGCAACATCTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCTATATCATG GCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTCAAGATCCGCCACAACATCGAGGAC GGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGC TGCTGCCCCACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAGAA GCGCGATCACATGGTCTGTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCATGGAC GAGCTGTACAAAtgattgtttattgagcttataatggttacaataaagcaatagcatcacaatttcacaataa agcattttttcactgcattctagttgtgtgttgcctcaactcatcaatgtatcttatTCTTCTAAACAGAGCAGCA</p>	2541

	GCAGCAGAGATGATAACATGTTTCAGGTAAGTTGGCTAttttttttttttttttgacatggagtcagtcctgtcaccaggctggagtgagtgccgcatctcggctcactgcaacctcagcctcctgagttcaagcagttctctgctcctcagctcccagtagctaggattacaggcatccgccaccagacctggctaattttgtatttttagtagagatgggtttaccatcttggccaggctggcttgaactcctgaccttgatccaactgcctcagcctccaaaagtctgggtttacaggtgtgagccaccatgccttggccAAAGTTGGCTGTTTCTTTAGATTAGAGGAATTATTATCTGGCTTGATCTGAAGAATGTTAAAAGTACTATGATCTGATAATTGCCTAATATG	
pARBI-690: SUB1_2_ Exogenous_71	ATAAATAAACATATCTCGAAATGGAATAAGTTGGTTATATTCTTTTAAATTAGTATATCTGCTTCGTAAAAATAAGTAACTGACTAGCCTTAGTAGACTGTGGTTTCCAGGTTTATTACAGAAAGTAGCAAGATCCCTCCATTTTTTTTCTACCAAAGAAATCGTATGTGGGATCCCAAACCAAAAAATACCGTTCCGTGGTTAATACTACTATAATGCCTGAAGTGCTTTTGGGATCCTGAGAACAGAGTTTGAAAACATTACTAGACAGAAGGATTGGTTAGATTCATAGTTTTGTTGTTGAGTGAAACCTTGCTTATGTATATTTATGATATTTGGATGTAGTCTTTTGATTGTTTAAATCTTAAAAAGTAATGGGATCTTTGACACTGGGGTATGTTTTATTTTATGTGTGCAAATTTAAACCATATCTTTTCTAGTTAtgacgactgtgccttctagttgccagccatctgtgtttgccccccccctgccttccttgacctggaagggtccactcccactgtcctttcctaataaaatgaggaaattgcatcgcatgtgctgagtaggtgtcattctattctggggggggggggggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctgggggatgcgggtggctctatggGGATCTGCGATCGTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGACTGGCTCCGCTTTTTCCGAGGGTGGGGGAGAACGTATATAAGTGACGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCGCGCCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCTTCTGCCGCTCCGCTGTGGTGCCTCCTGAACTGCGTCCGCGCTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCCTGACCTGCTTGCTCAACTCTACGCTTTGTTTCTGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCTACTCTAGAGCTAGCGAATTgcccaccacATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTGGTGCCATCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACGGCAAGCTGC CCGTCCCTGCCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAAGTCTTCAGCCGCTACCCGACCACATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCGAAGGCTACGTCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCTGGGGACAAGCTGGAGTACAACACAGCCACAACGCTATATCATGGCCGACAAGCAGAAACGGCATCAAGGTGAATTCAGATCCGCCACAACATCGAGGACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGTGCTGTGCCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCTGACCGCCGCGGGATCACTCTGGCATGGACGAGCTGTACAAAtgattgtttattgcagcttataatggttacaaataaagcaatagcatcacaaattcacaaataaagcattttttcactgcattctagttgtgggttgcctcaactcatcaatgtatcttatAAGAGGAAAAAGCAAGTTGCTCCAGAAAACTGTAAAGAAACAAAAGACAGGTGAGACTTCGAGAGCCCTGTCATCTTCTAAACAGAGCAGCAGCAGAGATGATAACATGTTTCAGGTAAGTTGGCTATTTTTTTTTTTTTTTTTTTGACATGGAGTCATGCTCTGTACCCAGGCTGGAGTGAGTGGCGCCATCTCGGCTCCTGCAACCTCAGCCTCCTGAGTTCAAGCAGTTCTCTGCCTCAGCCTCCGAGTAGCTAGGATTACAGGCATCCGCCACCAGACCTGGCTAATTTTTGTATTTTAGTAGAGATGGGGTTTACCATCTTGGCCAGGCTGGTCTTGAACCTCTGACCTTGATCCAACCTGCCTCAGCCTCCAAAAATGTCTGGGTTTACAGGTGTGAGCCACCATGCCTTGCCAAAGTTGGCTGTTTCTT	2541
pARBI-691: SUB1_3_ Exogenous_72	AATTAGTATATCTGCTTCGTAAAAATAAGTAACTGACTAGCCTTAGTAGACTGTGGTTTCCAGGTTATTACAGAAGTAGCAAGATCCCTCCATTTTTTTTCTACCAAAGAAATCGTATGTGGGATCCCAAACCAAAAAATAACCGTTCCTGTGGTTAATACTACTATAATGCCTGAAGTGCTTTTGGATCCTGAGAACAGAGTTTAAAAACATTACTAGACAGAAGGATTGGTTAGATTCATAGTTTGTGTTGAGTGAACTTGCTTATGTATATTTATGATATTTGGATGTAGTCTTTTGATTGTTTAAATCTTAAAAAGTAATGGGATCTTTGACACTGGGGTATGTTTTATTTTATGTGTGCAAAATTTAACCATATTTCTTTCTAGTTAAAGAGGAAAAAGCAAGTTGCTCCAGAAAAACCTGTAAAGAAACAAAAGTgacgactgtgccttctagttgccagccatctgtgtttgccccccccctgccttccttgacctggaagggtccactcccactgtcctttcctaataaaatgaggaaattgcatcgcatgtgctgagtaggtgtcattctatt	2541

	<p>ctggggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgcggtgg gctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCGAGCGCACATCGCCACAG TCCCGGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGGCGC GGGGTAAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCCGAGGGTGGGGGA GAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGCCA GAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCTACCTG AGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTGAA CTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCGCT CCCTTGGAGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGCTCACT CTACGCTCTTTGTTTCGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGCGCTAC TCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGGTG GTGCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGC GAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGC AAGCTGCCCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCA GCCGCTACCCCGACCATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCCGAAGGCTA CGTCCAGGAGCGCACCATTCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTG AAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAG GACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACTACAACAGCCACAACGCTATATCA TGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAGG ACGGCAGCGTGACGTGCGCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCCGT GCTGTGCCGACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACGAG AAGCGCGATCAGATGGTCTGCTGGAGTTCGTGACCGCGCCGGGATCACTCTCGGCATGG ACGAGCTGTACAAatgattgtttatgcagcttataatggttacaataaagcaatagcatcacaattcacaat aaagcattttttcactgcattctagttgtgtttgtccaaactcatcaatgtatcttatACAGGTGAGACTTCGAG AGCCCTGTCTCTTCTAAACAGAGCAGCAGCAGCAGAGATGATAACATGTTTCAGGTAAAG TTGGCTATTTTTTTTTTTTTTTTTTGACATGGAGTCATGCTCTGTACCCAGGCTGGAGTGC AGTGGCGCCATCTCGGCTCACTGCAACCTCAGCCTCCTGAGTTCAGCAGTTCCTGCTCA GCCTCCCGAGTAGCTAGGATTACAGGCATCCGCCACCAGACCTGGCTAATTTTTGTATTTTT AGTAGAGATGGGGTTTACCATCTTGGCCAGGCTGCTTGAACCTCTGACCTTGATGATCA ACTGCTCAGCCTCCAAAAGTGCTGGGTTTACAGGTGTGAGCCACCATGCCTTGCCAAAAGTT GGCTGTTTCTTTAGATTGAGAGGAATTATTATCTGGCTTGATCTGAAGAATGTTAAAAGT</p>	
pARBI- 692: TET2_1_E xogenous _73	<p>CACATTTTAATTTTTGTTCCATGCTCTTGAATCAACTAGAGGGCAGCCTTGTTGGATGGC CCCGAAGCAAGCCTGATGGAACAGGATAGAACCAACCATGTTGAGGGCAACAGACTAAGT CCATTCTGATACCATCACCTCCATTTGCCAGACAGAACCTCTGGCTACAAAGCTCCAGAA TGGAAGCCCACTGCCTGAGAGAGCTCATCCAGAAGTAAATGGAGACCAAGTGGCACTCT TTCAAAAGTTATTATGGAATACCCTGTATGAAGGGAAGCCAGAATAGTCGTGTGAGTCTG ACTTTACACAAGAAAGTAGAGGGTATTCCAAGTGTTTGCAAAATGGAGGAATAAAACGCAC AGTTAGTGAACCTTCTCTCTGGGCTCCTTCAGATCAAGAAATTGAAACAAGACCAAAAAGG CTAATGGAGAAAGACGTAACtgacgactgtgccttctagttgcagccatctgtgtttgccctccccgtgcct tccttgacctggaaggtgccactcccactgtcctttcctaataaaataggaaattgcatcgattgtctgagtaggtgc attctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggat gcggtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCGAGCGCACATCGC CCACAGTCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGG TGCGCGGGGTAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCCGAGGGTG GGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGC CGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCCCT ACCTGAGGCGCCATCCACGCCGTTGAGTCGCGTCTGCGCGCTCCCGCTCGCTGTGCGCTC CTGAATGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCG GCGCTCCCTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGC TCAACTCTACGTCTTTGTTTCTGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGC GCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACC GGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTG TCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC ACGGGCAAGCTGCCCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGT GCTTCAGCCGCTACCCCGACCATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCCGAA</p>	2541

	<p>GGCTACGTCCAGGAGCGCACCATTCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCG AGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCA AGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCT ATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACAT CGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGG CCCCGTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCGGGGATCACTCTCG GCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatt tcacaataaagcattttttcactgcattctagtgtgtgtgttccaaactcatcaatgtatcttatTTCGGGGTAAG CCAAGAAAGAAATCCAGGTGAAAGCAGTCAACCAAATGTCTCCGATTGAGTGATAAGAAA GAATCTGTGAGTTCTGTAGCCCAAGAAAATGCAGTTAAAGATTTACCACTTTTCAACACA TAATGTCAGTGGGCTGAAAATCCAGAGCTTCAGATTCTGAATGAGCAGGAGGGGAAAAAG TGCTAATTACCATGACAAGAACATTGTATTACTTAAAAACAAGGCAGTGCTAATGCCTAATG GTGCTACAGTTTCTGCCTCTTCCGTGGAACACACATGGTGAACCTCTGAAAAAACACTG TCTCAATATTATCCAGATTGTGTTTCCATTGCGGTGCAGAAAACCATCTCACATAAATGCC ATTAACAGTCAGGCTACTAATGAGTTGCTCTGTGAGATCACTACCCATCGCATACCTCAGG GCAGATC</p>	
<p>pARBI- 693: TET2_2_E xogenous _74</p>	<p>AATGGAGAAAGACGTAACTTCGGGGTAAGCCAAGAAAGAAATCCAGGTGAAAGCAGTCAA CCAAATGTCTCCGATTGAGTGATAAGAAAGAAATCTGTGAGTTCTGTAGCCCAAGAAAATG CAGTTAAAGATTTTCAACAGTTTTTCAACACATAACTGCAGTGGGCCTGAAAATCCAGAGCTT CAGATTCTGAATGAGCAGGAGGGGAAAAAGTGCTAATTACCATGACAAGAACATTGTATTAC TTAAAAACAAGGCAGTGCTAATGCCTAATGGTGTCTACAGTTTCTGCCTCTTCCGTGGAACAC ACACATGGTGAACCTCTGAAAAAACACTGTCTCAATATTATCCAGATTGTGTTTCCATTGC GGTGACAGAAAACCATCTCACATAAATGCCATTAACAGTCAGGCTACTAATGAGTTGCTCT GTGAGATCACTACCCATCGtgacgactgtgccttctagtgtccagccatctgtgttggccctccccgtgcctt ccttgaccctggaaggtgccactcccactgtcctttcctaataaaatgaggaaatgcatgcattgtctgagtaggtgc attctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggat gcggtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGC CCACAGTCCCGAGAAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAAG TGCGCGGGGTAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCCGAGGGTG GGGGAGAACCGTATATAAGTGAGTAGTGCCTGTAACGTTCTTTTTCGCAACGGGTTTGC CGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCGCCCT ACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCGCCTCCCGCTGTGGTGCCTC CTGAACTGCGTCCGCCGTCTAGGTAAGTTAAAGCTCAGGTGAGACCGGGCCTTTGTCCG GCGCTCCCTTGAGGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCCTGCTTGC TCAACTCTACGTCTTTGTTTCTGTTTCTGTTCTGCGCCGTACAGATCCAAGCTGTGACCGGC GCCTACTCTAGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTCAAC GGGGTGTTGCCATCCTGGTTCGAGCTGGACGCGACGTAAACGGCCACAAGTTACGCGTG TCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC ACCGGCAAGCTGCCCGTGCCCTGGCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGT GCTTCAGCCGCTACCCCGACCATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAA GGCTACGTCCAGGAGCGCACCATTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCG AGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCA AGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACAGCCACAACGTCT ATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACAT CGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGG CCCGTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCGGGATCACTCTCG GCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatt tcacaataaagcattttttcactgcattctagtgtgtgtgttccaaactcatcaatgtatcttatCATACCTCAGGG CAGATCAATTCGCACAGACCTCTAACTCTGAGCTGCCTCCAAAGCCAGCTGCAGTGGTGA GTGAGGCTGTGATGCTGATGCTGATAATGCCAGTAACTAGCTGCAATGCTAAATAC CTGTTCTTTTCAAGAACGAGAACTACAACAACAAAAATCAGTTTTTGTAGATATGCCCAT CTCTGCAGAAAAAATACATCCAGGGAACCAAAAGCTAGCGTCTGGTGAAGAATTCTGTTT AGGTTCAGCAGCAATTTGCAAGCTCCTGGTGGCAGCTCTGAACGGTATTTAAAAACAAAT</p>	2541

	GAAATGAATGGTGCTTACTTCAAGCAAAGCTCAGTGTTCACTAAGGATTCTTTTCTGCCAC TACCACACCACCACCACCATCACAATTGCTTCTTCTCCCCCTCCTCCTTCCACAGGTTCT CAGCTT	
pARBI- 694: TET2_3_E xogenous _75	GGAAAAAGCACTCTGAATGGTGGAGTTTTAGAAGAACACCACCACTACCCCAACCAAAGTA ACACAACACTTTTAAAGGGAAGTGAATAAGAGGGTAAACCTGAGGCACCACCTTCCAGAG TCCTAATCCATCTACACATGTATGCAGCCCTTCTCCGATGCTTTCTGAAAGGCCTCAGAATAA TTGTGTGAACAGGAATGACATACAGACTGCAGGGACAATGACTGTTCCATTGTGTTCTGAG AAAACAAGACCAATGTCAGAACCTCAAGCATAACCCACCAATTTTTGGTAGCAGTGGAG AGCTACAGGACAACTGCCAGCAGTTGATGAGAAACAAAGAGCAAGAGATTCTGAAGGGTC GAGACAAGGAGCAAACACGAGATCTTGTGCCCCCAACACAGCACTATCTGAAACCAGGAT GGATTGAATTGAAGGCCCTCGTtgacgactgtgccttctagttgccagccatctgtgttggccctccccgt gccttcttgaccctggaaggtgccactcccactgtccttcttaataaaatgaggaaattgcatcgattgtctgagtag gtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctgg ggatgcggtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACAT CGCCACAGTCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGA AGGTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTTCCCGAG GGTGGGGGAGAACCGTATATAAGTGCAAGTAGTCGCCGTGAACGTTCTTTTTCGCAACGGGT TTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTACGCGCCCCGCG CCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGTTG CCTCTGAAGTGCCTGCCCTCTAGGTAAGTTTAAAGCTCAGGTGAGAGCCGGGCTTTGT CCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCCTGACCTGCT TGCTCAACTCTACGCTTTTGTTCGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACC GGCGCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTT ACCGGGGTGGTGCCCATCTGTTGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGC GTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGC ACCACGGCAAGCTGCCCGTGCCCTGGCCACCCTCGTGACCACCTGACCTACGGCGTGC AGTGCTTACGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTCAAGTCCGCCATGCCC GAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCACTACAAGACCCGCG CCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACT TCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAATAACAAGCCACAACG TCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTCAAGATCCGCCACAA CATCGAGGACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGA CGGCCCGGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGAC CCCAACGAGAAGCGCGATCACATGTCCTGCTGGAGTTCTGTGACCGCCGCGGGGATCACTC TCGGCATGGACGAGCTGTACAAatgattgtttattgacgttataatggttacaaataaagcaatagcatcaca aattcacaataaagcattttttcactgcattctagttgtgtgttgcctcaaatcatcaatgtatcttatTTTACCAA GCGGAATCCCATCTAAACGTAATGAGGCATCACTGCCATCAATTCTCAGTATCAACCCAA TCTCTCCAATCAAATGACCTCCAACAATACACTGGAAATTCCAACATGCCTGGGGGGCTCC CAAGGCAAGCTTACCCAGAAAACAACACAGCTGGAGCACAAAGTCACAAATGTACCAAGT TGAAATGAATCAAGGGCAGTCCCAAGGTACAGTGACCAACATCTCCAGTTCAAAAACCC TCACACCAGGTGCACTTCTCCAAAACAGACATTTACCAAAAGCTCATGTGCAGTCACTGTG TGGCACTAGATTTTCAATTTTCAACAAAGAGCAGATTCCCAAACTGAAAACTTATGTCCCCAG TGTTGAAACAGCACTGAATCAACAGGCTTCAGAGACTGAGCCATTTTCAAACTCACACCTT TTGCAACAT	2541
pARBI- 695: TIGIT_1_E xogenous _76	AAAGGGAGGTTGAGATGGGCTGAGGTCTTCTAGGAGGCGGGGAGGGAGTGACGCCTTGA CAAGCTCCCTGTGGGCGAGGTGTAAAGAGGGGCGAGAAGTCAGCTCTGGAAGCATAGGGC AGTGGGTGGGGAGGAGATGGGCTGGGCTGGGCTGAGAGTAGAGATGTGTGGAGAAGGGT GAGAAGACTGGAAGACAACTGAATGGGGGACTGGGAGCCTTGAATAACAGGCATGGA GAGGAGCGTCTTGAATGGAAGAAACAGGAAATAATTACAGCCTCTATGGAGGAGCAA CAGGATGGACTGGAGAACTATCATTCCAAAATCCAGTTGGGGCCTCAAAGGCCCTTAGAA TTTTCTAGGAAGTTGAAGGCCAGCTGCTGACCCAGGACTCACATGTGCTTCGCTCTTTC CCTAGGAATGATGACAGGCACAATAGAAACAtgacgactgtgccttctagttgccagccatctgtgttgc ccctccccgtgccttcttgaccctggaaggtgccactcccactgtccttcttaataaaatgaggaaattgcatcgatt gtctgagtaggtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagca ggcatgtggggatgcgggtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGA	2541

	<p>GCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTCGGCAATTGAACGGGTG CCTAGAGAAGGTGGCGGGGTAAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCTTT TTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCG CAACGGGTTTCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTACGC GCCCCGCCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGC CTGTGGTGCCTCCTGAAGTGCCTCCGCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCG GGCCTTTGTCCGGCGCTCCCTTGGAGCTACCTAGACTCAGCCGGCTCTCCACGCTTTCCT GACCCTGCTTGCTCAACTCTACGTCTTTGTTTCGTTTCTGTTCTGCGCCGTTACAGATCAA GCTGTGACCGGCGCCTACTCTAGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAG GAGCTGTTACCCGGGTGGTGCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCAC AAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAG TTCATCTGCACACCGGCAAGCTGCCGTGCCCTGGCCACCCTCGTGACCACCTGACCTA CGGCGTGCACTGCTTACGCCGTACCCCGACCACATGAAGCAGCAGACTTCTTCAAGTCC GCCATGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACA AGACCCGCGCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGG GCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACATAACA GCCACAACGTCTATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTCAAGAT CCGCCACAACATCGAGGACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACAACCCC ATCGGCGACGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGA GCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCGCCG GGATCACTCTCGGCATGGACGAGCTGTACAAtgattgtttattgcagcttataatggttacaataaagc aatagcatcacaatttcacaataaagcattttttcactgcattctagttgtggtttgtccaaactcatcaatgtatctta tACGGGGAACATTTCTGCAGAGAAAGGTGGCTCTATCATCTTACAATGTCACCTCTCCTCCA CCACGGCACAAGTGACCCAGGTCAACTGGGAGCAGCAGGACCACTTCTGGCCATTGTAA TGCTGACTTGGGGTGGACATCTCCCCATCCTTCAAGGATCGAGTGGCCCCAGGTCCCGGC CTGGGCTCACCTCCAGTCGCTGACCGTGAACGATACAGGGGAGTACTTCTGCATCTATCA CACCTACCTGATGGGACGTACACTGGGAGAATCTTCTGGAGGTCCTAGAAAGCTCAGGT ATTCTGCTGGAGCAAGTTGGTGATAAACCTCTCCCTTAGCATAGAAAATGCAATCCTGA AACATGCAACGAGGGCTTCTCAATTGCGGATCACATTTGAATCACCTGAGGAGATTTAA ATCATACTGATGCCGAGGCC</p>	
pARBI- 696: TIGIT_2_E xogenous _77	<p>GAGGAGATGGGCTGGGCTGGGCTGGAGTAGAGATGTGTGGAGAAGGGTGAGAAGACTG GAAAGACAACCTGAATGGGGGACTGGGAGCCTTGAATAACAGGCATGGAGAGGAGCGTC TCTTGAAATGGAAGAAACAGGAAATAATTACAGCCTCTATGGAGGAGCAACAGGATGGAC TGGAGAAACTATCATTCCAAAATCCAGTTGGGGCTCAAAGGCCCTTAGAATTTTCTAGGA AGGTTGAAGGCCAGCTGTGACCCAGGACTCACATGTGCTTCGTCTCTTCCCTAGGAATG ATGACAGGCACAATAGAAACAACGGGGAAACATTTCTGCAGAGAAAGGTGGCTCTATCATCT TACAATGTCACCTCTCTCCACCACGGCACAAGTGACCCAGGTCAACTGGGAGCAGCAGGA CCAGCTTCTGGCCATTGTATGTAATGCTGACtgacgactgtgcttctagttgcccagccatctgtgttgcctc ccccgtgccttcttgaccctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgattgtctg agtaggtgtcattctattctgggggtgggggtggggcaggacagcaaggggaggattgggaagacaatagcaggcat gtggggatgcggtgggctctatggGGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGC ACATCGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAG AGAAGGTGGCGCGGGTAAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCTTTTCCCG AGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACG GGTTTGGCCGAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCCG CCGCCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTG GTGCCTCTGAAGTGCCTCCGCTAGGTAAGTTTAAAGCTCAGGTCGAGACCCGGCCTG TTGTCCGGCGCTCCCTTGGAGCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCC TGCTTGCTCAACTCTACGTCTTTGTTTCGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGT GACCGGCGCCTACTCTAGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCT GTTACCGGGGTGGTGCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTT CAGCGTGTCCGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCAT CTGACCAACGGCAAGCTGCCGTGCCCTGGCCACCCTCGTGACCACCTGACCTACGGC GTGCACTGCTTACGCCGTACCCGACCACATGAAGCAGCAGACTTCTTCAAGTCCGCCAT CCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACC</p>	2541

	<p>CGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATC GACTTCAAGGAGGACGGCAACATCTGGGGCACAAGCTGGAGTACAACACAAGCCAC AACGCTATATCATGGCCGACAAGCAGAAGAACGGGCATCAAGGTGAAGTCAAGATCCGCC ACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCG GCGACGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAA AGACCCCAACGAGAAGCGCGATCAGTGGTCTGCTGGAGTTCGTGACCGCCGCGGGAT CACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgagcttataatggttacaataaagcaatag catcacaatttcacaataaagcattttttcactgcattctagttgtgtttgtccaaactcatatgtatcttatTTG GGGTGGGCATCTCCCATCCTTCAAGGATCGAGTGGCCCCAGGTCCCGCCTGGGCCTCA CCCTCCAGTCGCTGACCGTGAACGATACAGGGGAGTACTTCTGCATCTATCACACCTACCCCT GATGGGACGTACACTGGGAGAATCTTCTGGAGGTCTAGAAAGCTCAGGTATTCTGCTG GAGCAAGTTGGTGGATAAACCTCTCCCTCTAGCATAGAAAATGCAATCCTGAAACACTGCA CAGCAGGGCTTCTCAATTCGGGATCACATTTGAATCACCTGAGGAGATTTTAAATCATACTG ATGCCGAGGCCTCACCAGACCAATTCAATCAGAATCCCTAATAGCAGAGCTAAACAAGGG TAAGGTCTAAAAGCATTTCCAGGTGATTCTAATGGGCAGCCAATACTGAGAACCACTGTTCT TATGTAAGAAGCACATC</p>	
<p>pARBI- 697: TIGIT_3_E xogenous _78</p>	<p>CCTCCCTGTGGGCGAGGTGTAAAGAGGGGCGAGAAGTCAGCTCTGGAAGCATAGGGCAGT GGGTGGGGAGGAGATGGGCTGGGCTGGGCTGGAGTAGAGATGTGTGGAGAAGGGTGAG AAGACTGGAAAGACAACCTGAATGGGGGACTGGGAGCCTTGAATAACAGGCATGGAGAG GAGCGTCTCTTGAATGGAAGAAACAGGAAATAATTACAGCCTCTATGGAGGAGCAACAG GATGGACTGGAGAACTATCATTTCCAAAATCCAGTTGGGGCCTCAAAGGCCCTTAGAATTT TTCTAGGAAGTTGAAGGCCAGTGTGCTGACCCAGGACTCACATGTGCTTCGCTCTTCCCT AGGAATGATGACAGGCACAATAGAAACAACGGGGAAACATTTCTGAGAGAAAGGTGGCTC TATCATCTTACAATGTACCTCTCCTCCACtgcagactgtgccttctagttgccagccatctgtgtttgccc ctccccgtgccttcttgaccctggaagggtgcactcccactgtccttctcaataaaatgaggaaattgcatcgcatgtt ctgagtaggtgtcatctattctgggggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcagg catgtcgggatgacggtgggctctatggGATCTGCGATCGCTCCGGTGGCCGTGAGTGGGCAGAGC GCACATCGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGGCAATTGAACGGGTGCCT AGAGAAGGTGGCGCGGGGTAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCTTTTTC CCGAGGGTGGGGGAGAACCGTATATAAGTGAGTAGTCGCCGTGAACGTTCTTTTCGCAA CGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCC CGCCGCCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCCTG TGGTGCTCTGAAGTGCCTCGCGCTAGGTAAAGTTAAAGCTCAGGTCGAGACCGGGC CTTTGTCCGGCGCTCCCTTGAGCGCTACCTAGACTCAGCCGGCTCTCCACGCTTGTCTGAC CCTGCTTGCTCAACTCTACGTCTTTGTTTCTGTTTCTGCGCGTTACAGATCCAAGCT GTGACCGGCGCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAG CTGTTACCGGGGTGGTGCCATCCTGGTTCGAGCTGGACGGCGACGTAACGGCCACAAG TTACAGCTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTC ATCTGCACCACCGGAAGCTGCCGTGCCCTGGCCACCTCGTGACCACCTGACCTACGG CGTGCACTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCA TGCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGAC CCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCAT CGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACATAACAGCCA CAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTCAAGATCCGC CACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCATCG GCGACGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAA AGACCCCAACGAGAAGCGCATCAGTGGTCTGCTGGAGTTCGTGACCGCCCGGGAT CACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgagcttataatggttacaataaagcaatag catcacaatttcacaataaagcattttttcactgcattctagttgtgtttgtccaaactcatatgtatcttatACG GCACAAGTGACCCAGGTCAACTGGGAGCAGCAGGACCAGCTTCTGGCCATTTGTAATGCTG ACTTGGGGTGGCACATCTCCCATCCTTCAAGGATCGAGTGGCCCCAGGTCCCGCCTGGG CCTCACCTCCAGTCGCTGACCGTGAACGATACAGGGGAGTACTTCTGCATCTATCACACCT ACCCTGATGGGACGTACACTGGGAGAATCTTCTGGAGGTCTAGAAAGCTCAGGTATTCC TGCTGGAGCAAGTTGGTGGATAAACCTCTCCCTCTAGCATAGAAAATGCAATCCTGAAACA CTGCACAGCAGGGCTTCTCAATTCGGGATCACATTTGAATCACCTGAGGAGATTTTAAATCA</p>	2541

	TACTGATGCCGAGGCCTCACCAGACCAATTCAATCAGAATCCCTAATAGCAGAGCTAAAC AAGGGTAAGGTCTAAAAG	
pARBI- 698: TRAC_1_ Exogenou s_79	TAATGCCCAGCCTAAGTTGGGGAGACCACTCCAGATTCCAAGATGTACAGTTTGCTTTGCTG GGCCTTTTTCCCATGCCTGCCTTTACTCTGCCAGAGTTATATTGCTGGGGTTTTGAAGAAGAT CCTATTAAATAAAAGAATAAGCAGTATTATTAAGTAGCCCTGCATTTACAGTTTCCTTGAGT GGCAGGCCAGGCCTGGCCGTGAACGTTCACTGAAATCATGGCCTCTTGCCCAAGATTGATA GCTTGTGCCTGTCCCTGAGTCCCAGTCCATCACGAGCAGCTGGTTTCTAAGATGCTATTTCC CGTATAAAGCATGAGACCGTGACTTGCCAGCCCCACAGAGCCCCGCCCTTGCCATCACTG GCATCTGGACTCCAGCCTGGGTTGGGGCAAAGAGGGAAATGAGATCATGTCCTAACCCCTG ATCCTCTTGTCACAGATtgacgactgtgccttctagttgccagccatctgtgtttgccctccccgtgccttc ttgacctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgattgtctgagtaggtgcatt ctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctgggatgcg gtgggctctatggGATCTGCGATCGCTCCGGTGCCGTCAGTGGGCAGAGCGCACATCGCCCA CAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAGAGAAGGTGG CGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGTCCGCCTTTTTCCGAGGGTGGG GGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTTCGAACGGGTTTGCCG CCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTACGCGCCCGCCGCCCTACC TGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCCTGTGGTGCCTCCTG AATCGCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGCCCTTTGTCCGCG CTCCTTGAGCCTACCTAGACTAGCCGGCTCTCCACGCTTTGCCGTGACCCCTGCTTGCTCAA CTCTACGTCTTTGTTTCTGTTCTGCGCCGTACAGATCCAAGCTGTGACCGGCGCCT ACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCGGGG TGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCG GCGAGGGCGAGGGCGATGCCACCTACGCGCAAGCTGACCCCTGAAGTTCATCTGCACCACCG GCAAGCTGCCCCTGCCCCTGCCCCACCCCTCGTGACCACCCCTGACCTACGGCGTGCACTGCTT AGCCGTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCT ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGT GAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGA GGACGGCAACATCCTGGGGCAACAAGCTGGAGTACAACACTACAACAGCCACAACGTCTATATC ATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAG GACGGCAGCGTGCACTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCC GTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACG AGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCAT GGACGAGCTGTACAAtgattgtttattgcagcttataatgggttacaataaagcaatagcatcacaatttcaca aataaagcatttttctactgcattctagttgtgtttgtccaaactcatcaatgtatcttatATCCAGAACCTGACC CTGCCGTGTACCAGCTGAGAGACTCTAAATCCAGTGACAAGTCTGTCTGCCTATTACCGAT TTTGATTCTCAAACAAATGTGTCAAAAGTAAGGATTCTGATGTGTATATCACAGACAAAAC TGTGCTAGACATGAGGTCTATGGACTTCAAGAGCAACAGTCTGTGGCCTGGAGCAACAAA TCTGACTTTGCATGTGCAAACGCCTTCAACAACAGCATTATTCCAGAAGACACCTTCTCCCC AGCCCAGGTAAGGGCAGCTTTGGTGCCCTTCGAGGCTGTTTCCTTGCTTCAGGAATGGCCA GGTCTGCCAGAGCTCTGGTCAATGATGTCTAAAACCTCTGATTGGTGGTCTCGGCCTT ATCCATTGCCACAAAACCTCTTTTACTAAGAAACAGTGAGCCTTGTTCTGGCAGTCCAG A	2541
pARBI- 699: TRAC_2_ Exogenou s_80	GATTCCAAGATGTACAGTTTGCTTTGCTGGGCCTTTTTCCCATGCCTGCCTTTACTCTGCCAG AGTTATATTGCTGGGGTTTTGAAGAAGATCCTATTAATAAAAGAATAAGCAGTATTATTA GTAGCCCTGCATTTACAGTTTCCTTGAGTGGCAGGCCAGGCCTGGCCGTGAACGTTCACTG AAATCATGGCCTCTTGCCCAAGATTGATAGCTTGCTGCTGCTCCTGAGTCCAGTCCATCAC GAGCAGCTGGTTTCTAAGATGCTATTTCCCGTATAAAGCATGAGACCGTGACTTGCCAGGCC CACAGAGCCCCGCCCTTGTCATCACTGGCATCTGGACTCCAGCCTGGGTTGGGGCAAAGA GGGAAATGAGATCATGTCCTAACCTGATCCTCTTGTCACAGATATCCAGAACCCTGACC CTGCCGTGTACCAGCTGtgacgactgtgccttctagttgccagccatctgtgtttgccctccccgtgccttcctt gacctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcatcgattgtctgagtaggtgcattc tattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctgggatgcg tgggctctatggGATCTGCGATCGCTCCGGTGCCGTCAGTGGGCAGAGCGCACATCGCCAC AGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAGAGAAGGTGGC	2541

	<p>GCGGGGTAAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCCGAGGGTGGGG GAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCGC CAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCCTACCT GAGGCCCGCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCCTCTG AACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCG CTCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCCTGCTTGCTCAA CTCTACGTCTTTGTTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCT ACTTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCCGGGG TGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCG GCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCG GCAAGCTGCCCGTCCCTGCCCCACCCTCTGACCACCCTGACCTACGGCGTGACGTGCTTC AGCCGTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCGGAAGGCT ACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGT GAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGA GGACGGCAACATCCTGGGGCACAAGCTGGAGTACAATAACAACGCCACAACGTCTATATC ATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACATCGAG GACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCC GTGTGCTGCCCGACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACG AGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCAT GGACGAGCTGTACAAatgattgtttattgcagcttataatgggttacaataaagcaatagcatcacaatttcaca aataaagcattttttcactgcattctagtgtgtgtgtgttgcacaaactcatcaatgtatcttatAGAGACTCTAAATCC AGTGACAAGTCTGTCTGCCTATTCACCGATTTTGATTCTCAAACAAATGTGTCACAAAGTAA GGATTCTGATGTGTATATCACAGACAAAAGTGTCTAGACATGAGGTCTATGGACTTCAAG AGCAACAGTGCTGTGGCCTGGAGCAACAAATCTGACTTTGCATGTGCAAACGCCTTCAACA ACAGCATTATTCCAGAAGACACCTTCTTCCCCAGCCAGGTAAGGGCAGCTTTGGTGCTTC GCAGGCTGTTTCCTTGCTTCAGGAATGGCCAGGTTCTGCCAGAGCTCTGGTCAATGATGTC TAAACTCTCTGATTGGTGGTCTCGGCCTTATCCATTGCCACCAAAACCTCTTTTACTAA GAAACAGTGAGCCTTGTCTGGCAGTCCAGAGAATGACACGGGAAAAAAGCAGATGAAGA GAAG</p>	
pARBI- 700: TRAC_3_ Exogenou s_81	<p>TTCTGTGGTAGCGGAACTACTAAGGGGCCATCTGGACCCGAGGTATTGTGATGATAAA TTCTGAGCACCTACCCATCCCCAGAAGGGCTCAGAAATAAAATAAGAGCCAAGTCTAGTC GGTGTTCCTGTCTTGAACACAATACTGTTGGCCCTGGAAGAATGCACAGAATCTGTTTGT AAGGGGATATGCACAGAAGCTGCAAGGGACAGGAGGTGCAGGAGCTGCAGGCCTCCCC ACCCAGCCTGCTCTGCTTGGGGAAAACCGTGGGTGTGCTCTGCAGGCCATGCAGGCCTGG GACATGCAAGCCATAACCGCTGTGGCCTCTTGGTTTTACAGATACGAACCTAAACTTTCAA AACCTGTCAGTGATTGGGTTCCGAATCCTCCTCTGAAAGTGGCCGGGTTAATCTGCTCAT GACGCTGCGGCTGTGGTCCAGTgacgactgtgcttctagtgtgccagccatctgtgtttgccccccccggtg ccttccttgaccctggaaggtgccactcccactgtcctttcctaataaaatgaggaaattgcacgcattgtctgagttagt gtcattctattctggggggtggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtgggg atgcggtgggctctatggGATCTGCGATCGCTCCGTGCCGTGAGTGGGCGAGAGCGCACATCG CCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCTAGAGAAG GTGGCGCGGGGTAAACTGGGAAAGTGATGTCGTGTAAGTGGCTCCGCCTTTTCCCGAGGGT GGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTG CCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCC TACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCT CCTGAAGTCCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGCCCTTTGTC GCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCTGACCTGTCTG CTCAACTCTACGTCTTTGTTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGG CGCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCC GGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTG TCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC ACCGGCAAGCTGCCCGTCCCTGCCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAAGT GCTTCAGCCGTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAA GGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCG AGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCA</p>	2541

	AGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAACAGCCACAACGTCT ATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGATCCGCCACAACAT CGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGG CCCCGTGCTGCTGCCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCTGTACC GCCCGCCGGGATCACTCTCG GCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaatt tcacaataaagcatttttttactgcattctagttgtggtttgtccaaactcatcaatgtatcttatTGAGGTGAGGG GCCTTGAAGCTGGGAGTGGGGTTTAGGGACGCGGGTCTCTGGGTGCATCCTAAGCTCTGA GAGCAAACTCCCTGCAGGGTCTTGCTTTAAGTCCAAAGCCTGAGCCCAAACTCTCCT ACTTCTTCTGTTACAAAATTCCTCTTGCAATAATAATGGCTGAAACGCTGTAAAATATCC TCATTTAGCCGCCTCAGTTGCACTTCTCCCCTATGAGGTAGGAAGAAGAGTTGTTTAGAAA CGAAGAACTGAGGCCCCACAGCTAATGAGTGAGGAAGAGAGACACTTGTGTACACCAC ATGCCTTGTGTGACTTCTCTACCGTGTAACTCTCTCATGTCTCTCTCCCACTACGGCTC TCTTAGCTCAGTAGAAAGAAGACATTACACTCATATTACACCCAATCCTGGCTAGAGTCTC CGCACC	
pARBI- 701: TRAC_4_ Exogenou s_82	ATTATTAAGTAGCCCTGCATTTAGGTTTCCTTGAGTGGCAGGCCAGGCCTGGCCGTGAAC GTTCACTGAAATCATGGCCTCTTGCCAAAGATTGATAGCTTGTGCCTGTCCCTGAGTCCCAG TCCATCACGAGCAGCTGGTTTCTAAGATGCTATTTCCGTATAAAGCATGAGACCGTGACTT GCCAGCCCCACAGAGCCCCCTTGCCATCACTGGCATCTGGACTCCAGCTGGGTGG GGCAAAAGAGGGAAATGAGATCATGTCTTAACCTGATCCTTGTGCCACAGATATCCAGA ACCTGACCCTGCCGTGTACCAGCTGAGAGACTCTAAATCCAGTGACAAGTCTGTCTGCCTA TTCACCGATTTTGATTCTCAAACAAATGTGTCACAAAGTAAGGATTCTGATGTGTATATCAC AGACAAAAGTGTGCTAGACTgacgactgtgcttctagttgcagccatctgtgtttgccccccccgcttct cttgaccctggaaggtgccactcccactgtccttcttaataaaatgaggaaattgcatcgattgtctgagtaggtgca ttctattctgggggtgggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgc ggtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCC ACAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTG GCGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCTTTTCCCGAGGGTGG GGGAGAACCGTATATAAGTGCAGTAGTCGCGTGAACGTTCTTTTCGCAACGGGTTTGCC GCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTACGCGCCCGCCGCCCTA CCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTCTGCGCCTCCCGCCTGTGGTGCCTCC TGAAGTGCCTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGG CGCTCCCTTGAGGCCTACCTAGACTCAGCCGGCTCTCCACGCTTGCCTGACCCTGCTTGCTC AACTCTACGCTTTGTTTCTGTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGC CTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTACCCGG GGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTG CGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCAC CGGCAAGCTGCCCGTGCCCTGGCCACCCCTCGTGACCACCTGACCTACGCGGTGCAAGTGC TTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAG GCTACGTCCAGGAGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGA GGTGAAGTTGAGGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAA GGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACACAACAGCCACAACGTCTA TATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGATCCGCCACAACATC GAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGC CCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCA ACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGG CATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaattt cacaataaagcatttttttactgcattctagttgtggtttgtccaaactcatcaatgtatcttatATGAGGTCTATG GACTTCAAGAGCAACAGTGCTGTGGCCTGGAGCAACAAATCTGACTTTGCATGTGCAACG CCTTCAACAACAGCATTATTCCAGAAGACACCTTCTTCCCAGCCAGGTAAGGGCAGCTTT GGTGCCTTCGAGGCTGTTTCTTGTCTCAGGAATGGCCAGGTTCTGCCAGAGCTCTGGTC AATGATGTCTAAACTCTCTGATTGGTGGTCTCGGCCTATCCATTGCCACCAAAACCTCT TTTTACTAAGAAACAGTGAGCCTTGTCTGGCAGTCCAGAGAATGACACGGGAAAAAAGCA GATGAAGAGAAGGTGGCAGGAGAGGGCACGTGGCCAGCCTCAGTCTCTCAACTGAGTT	2541

	CCTGCCTGCCTTGTGCTCAGACTGTTTGCCCTTACTGCTCTTCTAGGCCTCATTCTAAGC CCCTT	
pARBI- 702: TRAC_6_ Exogenou s_84	<p>TTCATTTCCATTTGAGTTGTTCTTATTGAGTCATCCTTCCTGTGGTAGCGGAACCTACTAAGG GGCCCATCTGGACCCGAGGTATTGTGATGATAAATTCTGAGCACCTACCCCATCCCCAGAA GGGCTCAGAAATAAATAAGAGCCAAGTCTAGTCGGTGTTCCTGTCTTGAAACACAATAC TGTTGGCCCTGGAAGAATGCACAGAATCTGTTTGTAAAGGGATATGCACAGAAGCTGCAA GGGACAGGAGGTGCAGGAGCTGCAGGCCTCCCCACCCAGCCTGCTCTGCCTTGGGGAAA ACCGTGGGTGTCTCTGCAGGCCATGCAGGCCTGGGACATGCAAGCCCATAACCGCTGTG GCCTCTTGGTTTTACAGATACGAACCTAACTTTCAAACTGTCAAGTATTGGGTTCGAA TCCTCCTCTGAAAGTGGCCGGTgacgactgtgccttctagtgtccagccatctgtgtttgccctccccgt gccttccttgaccctggaaggtgccactcccactgtccttctctaataaaatgaggaaattgcatgcattgtctgagtag gtgtcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctgg ggatgcggtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACAT CGCCACAGTCCCCGAGAAGTTGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGA AGGTGGCGCGGGTAACTGGGAAAGTATGTCGTGTACTGGCTCCGCTTTTCCCGAG GGTGGGGGAGAACCCTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGT TTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACGCGCCCGCG CCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTG CCTCTGAAGTGCCTCGCGCTCTAGTAAGTTAAAGCTCAGGTGAGACCGGGGCTTTGT CCGGCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCAGCTTTGCCTGACCTGTCT TGCTCAACTCTACGTCTTTGTTCTGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACC GGCGCCTACTCTAGAGCTAGCGAATTgccgccaccATGGTGAGCAAGGGCGAGGAGCTGTTT ACCGGGGTGGTGCCCATCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGC GTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGC ACCACCGGCAAGCTGCCCGTGCCCTGGCCACCCCTCGTGACCACTGACCTACGGCGTG AGTGCTTACGCGCTACCCCGACCATGAAGCAGCAGCACTTCTTCAAGTCCGCCATGCCC GAAGGTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCG CCGAGGTGAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACT TCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACCTACAACAGCCACAACG TCTATATCATGGCCGACAAGCAGAAGAAGCGCATCAAGGTGAAGTCAAGATCCGCCACAA CATCGAGGACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGA CGGCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCAAGCTGAGCAAAGAC CCCAACGAGAAGCGCGATCACATGTCCTGCTGGAGTTCGTGACCGCGCGGGGATCACTC TCGGCATGGACGAGCTGTACAAatgattgttattgagcttataatggttacaataaagcaatagcatcaca aattcacaaataaagcattttttcactgcattctagtgtgtgttgcctcaactcatcaatgtatcttatTTAATCTG CTCATGACGCTGCGGCTGTGGTCCAGCTGAGGTGAGGGGCTTGAAGCTGGGAGTGGGGT TTAGGGACGCGGGTCTCTGGGTGCATCCTAAGCTCTGAGAGCAAACTCCCTGCAGGGTCT TGCTTTTAAAGTCCAAAGCCTGAGCCACCAAACTCTCTACTTCTTCTGTTACAAATCTCT TGTGAATAATAATGGCTGAAACGCTGAAAATATCCTCATTTACGCGCCTCAGTTGCAC TTCTCCCTATGAGGTAGGAAGAAGAGTGTGTTAGAAACGAAGAACTGAGGCCCCACAGC TAATGAGTGGAGGAAGAGAGACACTTGTGTACACCACATGCCTGTGTGTACTTCTCTCAC CGTGTAACTCCTCATGTCCTCTCTCCCACTACGGCTCTCTTACTCAGTAGAAAAGAGAC ATTACACTC</p>	2541
pARBI- 703: TRAC_Exo genous_8 3	<p>CAGTCCATCACGAGCAGCTGGTTTCTAAGATGCTATTTCCCGTATAAAGCATGAGACCGTGA CTTGCCAGCCCCACAGAGCCCCGCCCTGTCCATCACTGGCATCTGGACTCCAGCCTGGGTT GGGGCAAAGAGGGGAAATGAGATCATGTCTAACCTGATCCTCTTGCCACAGATATCCA GAACCTGACCCTGCCGTGTACCAGCTGAGAGACTCTAAATCCAGTGACAAGTCTGTCTGC CTATTCACCGATTTTGATTCTCAACAAATGTGTACAAAAGTAAGGATTCTGATGTGTATATC ACAGACAAAATGTGCTAGACATGAGGTCTATGGACTTCAAGAGCAACAGTGCTGTGGCCT GGAGCAACAAATCTGACTTTGCATGTGCAACGCCCTTCAACAACAGCATTATCCAGAAGA CACCTTCTCCCCAGCCAtgacgactgtgccttctagtgtccagccatctgtgtttgccctccccgtgccttc ttgacctggaaggtgccactcccactgtccttctctaataaaatgaggaaattgcatgcattgtctgagtaggtgtcatt ctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgcg gtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAGTGGGCAGAGCGCACATCGCCCA CAGTCCCCGAGAAGTTGGGGGGAGGGGTGCGCAATTGAACGGGTGCCTAGAGAAGGTGG</p>	2541

	<p>CGCGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTTTTCCCGAGGGTGGG GGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGCCG CCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGCGCCCGCCGCCCTACC TGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGCTGTGGTGCCTCCTG AACTGCGTCCGCCGTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCGGCG CTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGTTTGCCTGACCTGCTTGCTCAA CTCTACGCTTTTGTTCGTTTTCTGTTCTGCGCCGTTACAGATCCAAGCTGTGACCGGCGCCT ACTTAGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAGGAGCTGTTACACGGGG TGGTGCCATCCTGGTCGAGCTGGACGGCGACGTAACGGCCACAAGTTCAGCGTGTCCG GCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCTGAAGTTCATCTGCACACCG GCAAGCTGCCGTGCCCTGGCCACCCTCTGACCACTGACCTACGGCGTGACGTGCTTC AGCCGTACCCCGACCACATGAAGCAGCAGACTTCTTCAAGTCCGCCATGCCGAAGGCT ACGTCCAGGAGCGCACCATCTTCTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGT GAAGTTCGAGGGCGACACCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGA GGACGGCAACATCCTGGGGCACAAGCTGGAGTACAATAACAACGCCACAACGTCTATATC ATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAAGTCAAGATCCGCCACAACATCGAG GACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGGCCCC GTGTGCTGCCCGACAACCACTACCTGAGCACCAGTCCAAGCTGAGCAAAGACCCCAACG AGAAGCGCATCACATGGTCTGCTGGAGTTCGTGACCGCCCGGGGATCACTCTCGGCAT GGACGAGCTGTACAAtgattgtttattgagcttataatggttacaataaagcaatagcatcacaatttcaca aataaagcattttttcactgcattctagtgtgtgtgttgcacaaactcatcaatgtatcttatGGTAAGGGCAGCTTT GGTGCCTTCGAGGCTGTTTCTTCTGCTCAGGAATGGCCAGGTTCTGCCAGAGCTCTGGTC AATGATGTCTAAAACCTCTGATTGGTGGTCTCGGCCTTATCCATTGCCACAAAACCTCT TTTTACTAAGAAACAGTGAGCCTTGTCTGGCAGTCCAGAGAATGACACGGGAAAAAAGCA GATGAAGAGAAGGTGGCAGGAGAGGGCAGTGGCCAGCCTCAGTCTCTCAAAGTGAAGT CCTGCCTGCCTGCTTTGCTCAGACTGTTGCCCTTACTGCTCTTAGGCCTCATTTAAGC CCCTTCTCAAAGTTGCTCTCTTATTTCTCCCTGTCTGCCAAAAATCTTTCCAGCTCACTA AGTCAGTCTACGCGAGTCACTATTAACCCCAATCACTGATTGTGCCGGCAGATGAATG</p>	
pARBI- 704: TRIM28_ 1_Exogen ous_85	<p>TGAGGAAGAAGCGCGGGCGGCGCTTCGGGAGGCGAGCAGGCAGTGTGGCGTGCCG TAGCAGCGTCCCGCGCGCGGGCAGCGGCCAGGAGGCGCGTGCGCGCTCGGCCT CGCGGCGGCGGGCGGCGAGCGGCCAGCAGTTGGCGGCGAGCGCGTCTGCGCTGCGC GGCGGGCCCCCGCCCCCTCTCCCCCTGGGCGCCCCGGCGGCGTGTGAATGGCGGCT CCGCGGCGGCGAGCTCGGCAGCAGCGGCTCGGCCGCTCTGGCAGCCCGGGCCGGCG AGGGCTCCGCTGGCGGCGAAAAGCGCTCCACCGCCCCCTCGGCCGAGCCTCGGCCTCTGC CTCAGCCGCGGCGTCTGTCGCCCGCGGGGGGCGGCGCGAGGCGCTGGAGCTGTGGAGC ACTGCGGCGTGTGCAGAGAGCGCTCGCACCTgacgactgtgcttctagtgtccagccatctgttgtt gccccccccgtgcttcttgaccctggaaggtgcccactcccactgtccttctcaataaaatgaggaaattgcatgc attgtctgagtaggtgtcattctattctgggggtggggcgaggacagcaagggggaggattgggaagacaatag caggcatgctggggatgcggtgggctctatggGATCTGCGATCGCTCCGCTGCCGTGAGTGGGCGAG AGCGCACATCGCCACAGTCCCCGAGAAGTTGGGGGGAGGGGTGGCAATTGAACGGGT GCCTAGAGAAGGTGGCGGGGGTAAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCCTT TTTCCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTC GCAACGGGTTTGCCGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCCTTCACG CGCCCGCCGCCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTCTGCGCCTCCCG CCTGTGGTGCCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTGAGACC GGGCCTTTGTCCGGCGCTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCG TGACCTGCTTGCTCAACTCTACGCTTTTGTTCGTTTTCTGTTCTGCGCGTTACAGATCCAA GCTGTGACCGGCGCCTACTCTAGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAG GAGCTGTTACCGGGGTGGTGCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCAC AAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAG TTCATCTGCACACCGGCAAGCTGCCGTGCCCTGGCCACCCTCGTGACCACTGACCTA CGGCGTGCAAGTCTTACGCCGTACCCCGACCATGAAGCAGCAGACTTCTTCAAGTCC GCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACA AGACCCGCGCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGG GCATCGACTTCAAGGAGGACGGCAACATCTGGGGCAAGCTGGAGTACAATAACAACA</p>	2541

	<p>GCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGAT CCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCC ATCGGCGACGGCCCCGCTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGA GCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCG GGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagc aatagcatcacaaatttcacaataaagcattttttcactgcattctagttgtggtttgtccaactcatcaatgtatctta tGAGAGGGAGCCCCGCTGCTGCCCTGTTGCACTCGGCCTGTAGTGCCTGCTTAGGGCCCC GCGGCCCCCGCCGCCCAACAGCTCGGGGACGGCGGGGGCGGGCGGGGACGGCACCGG TAAGTACGAAGTGATCGGTGCCACCCCTCCCCCTACTCTGCTCTTGTGATTCCGATGGGTG CAGAGATGAGGATGCCACCTGGGCGAGAGGATGGGGGCCCGACAGGGCAGGGGAAATA CTTCTGGGTCTGCATACGAACGTGGGTTTGTGCTGGCCGCTGAGATGGGACATCTGACT AAAGTTGGAGAAAAGAAGGCTCGGGGAGGGGAGGGGCTGGTTCGCTGCGGGATAATGGT CGGGGGCCCAACCAGCAGGGGAATGGTGGGGGCCATAACCTGGGTGGGAACCTGTAACA GTCTCCACATCCCTGCTTCTCGAAGTGGTG</p>	
pARBI- 705: TRIM28_ 2_Exogen ous_86	<p>TCGAAGTGGTGGACTGTCCCGTGTGCAAGCAACAGTGCTTCTCCAAAGACATCGTGGAGAA TTATTTTCATGCGTGATAGTGGCAGCAAGGCTGCCACCGACGCCAGGATGCGAACCAAGGTG CGTCTATCTCAGCAACCACAAGGAGGTTTCTGGGGAGGGGGCATCTGCGCAGGAGGAGC TTGGCACCAGCTCCAGGCTGTTACTCCATTTCCCAAGGCTCTGGGTGGGCTGCCTAGGTTG GCTCAAGGGACCAATCTTAAATCTCCGTTGTATTTTCTGGGATGTAAACGTGGATCTATCA AGTTGTCTTGCTTCTCTGACCTGCTTTGTCTGGCAGTGCTGCACTAGCTGTGAGGATAA TGCCCCAGCCACCAGCTACTGTGTGGAGTGCTCGGAGCCTCTGTGTGAGACCTGTGTAGAG GCGCACCAGCGGGTGAAGTACTgacgactgtgcttctagttgccagcatctgtgtttgccctccccgtgc cttcttgacctggaaggtgccactcccactgtcttcttaataaaataggaaattgcatgcattgtctgagtaggtg tcattctattctgggggtgggggtggggcaggacagcaagggggaggattgggaagacaatagcaggcatgtgggga tgcggtgggctctatggGATCTGCGATCGCTCCGGTGCCCGTCAAGTGGGCGAGAGCGCACATCGC CCACAGTCCCCGAGAAGTTGGGGGGAGGGGTCGGCAATTGAACGGGTGCCTAGAGAAGG TGGCGCGGGGTAACTGGGAAAGTGATGTCGTGACTGGCTCCGCCTTTTCCCGAGGGTG GGGGAGAACCGTATATAAGTGCAGTAGTCGCCGTGAACGTTCTTTTCGCAACGGGTTTGC CGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCAACGCGCCCGCCCT ACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCGCCTGTGGTGCCTC CTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCGGGCCTTTGTCCG GCGCTCCCTTGGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCTGACCTGCTTGC TCAACTCTACGTCTTTGTTTCTGTTTCTGTTCTGCGCGTTACAGATCCAAGCTGTGACCGGC GCCTACTCTAGAGCTAGCGAATTgcccaccacATGGTGAGCAAGGGCGAGGAGCTGTTACC GGGGTGGTGCCCATCCTGGTTCGAGCTGGACGGCGACGTAAACGGGCCACAAGTTCAGCGTG TCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACC ACGGCAAGCTGCCGTGCCCTGGCCACCCCTCGTGACCACCTGACCTACGGCGTGCAGT GCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAA GGCTACGTCCAGGAGCGACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCGG AGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCA AGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTAACTACAACAGCCACAACGTCT ATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGATCCGCCACAACAT CGAGGACGGCAGCGTGACGCTCGCCGACCACTACCAGCAGAACACCCCATCGGCGACGG CCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCC AACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCTGTGACCGCCCGCGGGATCACTCTCG GCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagcaatagcatcacaaatt tcacaataaagcattttttcactgcattctagttgtggtttgtccaactcatcaatgtatcttatACCAAGGACCA TACTGTGCGCTCTACTGGTACATGAGGCTGAGGGGGGCTGTTGGAGTTGTTCTCCCATGTG TGCCCTCAGTTGCTTTATGATGTTGGTTGCATCTGGTGGATGGGTCTAGAGTTCTTAGG GGGTGCCGCCCGAAGGGCCGAGGGCAGAACTCCAGAAGCAGAAAACTGGGGTTGTGG TGTGTAGTCTTAGGGCCTAGGTGGGAGAGGGTGGGAAGGGGAAATAAGGGAGACCTTA ATGTGCTGCAGGAGGTACAAAGGGTTTGAGAAGGCTTATCAGGGAGTTGTGAGACCTGG TGGTGAAGGGCTCAGCATATGCAACAGGGAAAGGCATGGTGTGAAGGGCTTTCTGGGTT TGTGTTCCCTGGCACACATCTGGTATAAGATGCTGCTAGGGAAAGTAGACTGTGGGTCCA TGGATTATAAGTGATGA</p>	2541

pARBI-706: TRIM28_3_ Exogenous_87	GGCGCCAATGCGCTGCGCGGCGGCGTGGCGCCAGTTATTTCTGTCCCGCCCCCGGCC TCGGCTCTTTCTGCGAGCGGGCGCGGGCGAGCGGTTGTGCTTGTGCTTGTGGCGCTG GTGCGGTTTTCGGCGGCGGCTGAGGAAGAAGCGCGGGCGGCGCCTTCGGGAGGCGAGCA GGCAGCAGTTGGCGGTGCGTAGCAGCGTCCCGCGCGGCGGGCAGCGGCCAGGAGG CGCGTGGCGGCGCTCGGCCTCGCGGCGGCGGCGGCGGCGAGCGGCCAGCAGTTGGCGGC GAGCGCTCTGCGCTGCGGCGGCGGCCCCGCGCCCCCTCTCCCCCCTGGGCGCCCCCGG CGGCGTGTGAATGGCGGCTCCGCGGCGGCGAGCTCGGCAGCAGCGGCTCGGCCGCTC TGGCAGCCCCGGGCGGCGAGGGCTCCGCTgacgactgtgcttctagtgtccagccatctgtgttg ccctccccgtgcttcttgacctggaaggtgccactcccactgtccttccataaaaatgaggaaattgcatgcat tgtctgagtaggtgtcattctattctgggggtggggcaggacagcaaggggaggattgggaagacaatagc aggcatgctgggatgctgggtgctctatggGATCTGCGATCGCTCCGTTGCCGTCACTGGGCGAG GCGCACATCGCCACAGTCCCGGAGAAGTTGGGGGAGGGGTGGCAATTGAACGGGTG CCTAGAGAAGGTGGCGGGGTAACTGGGAAAGTGATGTCGTGTACTGGCTCCGCTTT TTCCGAGGGTGGGGGAGAACCGTATATAAGTGCAGTAGTCGCGTGAACGTTCTTTTTCG CAACGGGTTTGC CGCCAGAACACAGCTGAAGCTTCGAGGGGCTCGCATCTCTCTTCACGC GCCCCGCCCTACCTGAGGCCGCCATCCACGCCGTTGAGTCGCGTTCTGCCGCTCCCGC CTGTGGTGCTCTGAACTGCGTCCGCCGTCTAGGTAAGTTTAAAGCTCAGGTCGAGACCG GGCCTTTGTCCGGCGTCCCTTGAGCCTACCTAGACTCAGCCGGCTCTCCACGCTTTGCCT GACCCTGCTTGTCAACTCTACGCTCTTTGTTTCTGTTTCTGTTCTGCGCCGTTACAGATCCAA GCTGTGACCGGCGCCTACTCTAGAGCTAGCGAATTgcccaccATGGTGAGCAAGGGCGAG GAGCTGTTACCGGGTGGTGCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCAC AAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAG TTCATCTGACACCGGCAAGCTGCCGTGCCCTGGCCACCCTCGTGACCACCTGACCTA CGGCGTGCACTGCTTACCGCGTACCCCGACCATGAAGCAGCAGCACTTCTTCAAGTCC GCCATGCCCCAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACA AGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGG GCATCGACTTCAAGGAGGACGGCAACATCTGGGGCACAAGCTGGAGTACAACCTACAACA GCCACAACGTCTATATCATGCGCGACAAGCAGAAGAACGGCATCAAGGTGAACCTCAAGAT CCGCCACAACATCGAGGACGGCAGCGTGAGCTCGCCGACCACTACCAGCAGAACACCCCC ATCGGCGACGGCCCCGTGCTGCTGCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGA GCAAAGACCCCAACGAGAAGCGCGATCACATGGTCTGCTGGAGTTCGTGACCGCCGCCG GGATCACTCTCGGCATGGACGAGCTGTACAAatgattgtttattgcagcttataatggttacaataaagc aatagcatcacaatttcacaataaagcattttttcactgcattctagtgtgtgttgcctaaactcatcaatgtatctta tGGCGGCGAAAAGCGCTCCACCGCCCCCTTCGGCCGACGCTCGGCCCTCTGCCTCAGCCGCG GCGTCGTGCCCCGCGGGGGCGGCGCCGAGGCGCTGGAGCTGCTGGAGCACTGCGGCGT GTGAGAGAGCGCTGCGACCCGAGAGGGAGCCCCGCTGCTGCCCTGTTGCACTCGGC CTGTAGTGCCTGCTTAGGGCCCGCGCCCCCGCCGCCAACAGCTCGGGGACGGCGG GGCGGCGGCGACGGCACCGGTAAGTACGAAGTGATCGGTGCCACCCCTCCCCCTACTCTC TGCTTTGATTCCGACTGGGTGCGAGAGATGAGGATGCCACCTGGGCGAGAGGATGGGGGC CCGACAGGGCACGGGAAATACTTTCTGGGTCCTGCATACGAACGTGGGTTTGTGCTGGCC GCTGAGATGGGACATCTGACTAAAGTTGG	2541
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CLAIMS

1. An engineered cell, comprising at least one sequence encoding a transgene, wherein the at least one sequence is inserted within a safe harbor locus, the safe harbor locus is at any one or more of an sgRNA target loci provided in Table 4; and wherein expression of the at least one sequence encoding the transgene is operatively linked to an endogenous promoter.
2. An engineered cell, comprising at least one sequence encoding a transgene, wherein the at least one sequence is inserted within a safe harbor locus, the safe harbor locus is at any one or more of an sgRNA target loci provided in Table 4; and wherein expression of the at least one sequence encoding the transgene is operatively linked to an exogenous promoter.
3. The engineered cell of claim 1 or 2, wherein the sgRNA target locus is selected from: chr11:128340000-128350000, chr10:33130000-33140000, chr10:72290000-72300000, chr11:65425000-65427000 (NEAT1), chr15:92830000-92840000, chr16:11220000-11230000, chr2:87460000-87470000, chr3:186510000-186520000, chr3:59450000-59460000, chr8:127980000-128000000, or chr9:7970000-7980000.
4. The engineered cell of any one of claims 1-3, wherein the sgRNA target locus is selected from: chr11:128340000-128350000, chr10:72290000-72300000, chr15:92830000-92840000, or chr16:11220000-11230000.
5. The engineered cell of any one of claims 1-4, wherein the sgRNA target locus is chr11:128340000-128350000.
6. The engineered cell of any one of claims 1-4, wherein the sgRNA target locus is chr15:92830000-92840000.
7. The engineered cell of claim 1 or 2, wherein the sgRNA target locus is a gene selected from: *APRT*, *B2M*, *CAPNS1*, *CBLB*, *CD2*, *CD3E*, *CD3G*, *CD5*, *EDF1*, *FTL*, *PTEN*, *PTPN2*, *PTPN6*, *PTPRC*, *PTPRCAP*, *RPS23*, *RTRAF*, *SERF2*, *SLC38A1*, *SMAD2*, *SOC31*, *SRP14*, *SRSF9*, *SUB1*, *TET2*, *TIGIT*, *TRAC*, or *TRIM28*.
8. The engineered cell of any one of claims 1-3, wherein the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS94, GS88, GS89, GS90, GS91, GS92, GS93, GS95, GS96, GS97, GS98, GS99, GS100, GS101, GS102, GS103, GS104, GS105, GS106, GS107, GS108, GS109, GS110, GS111, GS112, GS113, GS114, GS115, GS116, GS117, GS118, GS119, or GS120.
9. The engineered cell of any one of claims 1-4, wherein the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS94, GS91, GS92, GS93, GS95, GS96, GS100, GS101, GS102, GS103, GS104, and GS105.

10. The engineered cell of claim 8 or 9, wherein the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS103, GS104, or GS105.
11. The engineered cell of claim 8 or 9, wherein the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS94, GS95, or GS96.
12. The engineered cell of claim 8 or 9, wherein the safe harbor locus is an GS94 integration site in Table 4.
13. The engineered cell of claim 8 or 9, wherein the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS100, GS101, or GS102.
14. The engineered cell of claim 8 or 9, wherein the safe harbor locus is an GS102 integration site in Table 4.
15. The engineered cell of claim 8 or 9, wherein the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS91, GS92, or GS93.
16. The engineered cell of any one of claims 2-15, wherein the exogenous promoter is an EF1a promoter.
17. The engineered cell of any one of claims 1-16, wherein the engineered cell is a stem cell, a human cell, a primary cell, an hematopoietic cell, an adaptive immune cell, an innate immune cell, a T cell or a T cell progenitor.
18. The engineered cell of claim 17, wherein the cell is a T cell or a T cell progenitor.
19. The engineered cell of any one of claims 1-18, wherein the engineered cell is undifferentiated.
20. The engineered cell of any one of claims 1-18, wherein the engineered cell is CD45RA⁺ and CCR7⁺.
21. The engineered cell of any one of claims 1-20, wherein the transgene encodes a recombinant protein, optionally a therapeutic agent.
22. The engineered cell of any one of claims 1-21, wherein the transgene encodes a chimeric antigen receptor (CAR).
23. A composition comprising the engineered cell of any one of claims 1-22 and a pharmaceutical excipient.
24. A guide ribonucleic acids (gRNA) for editing a cell at a safe harbor locus, wherein gRNA comprises any one of the sgRNA sequences in Table 4.
25. The gRNA of claim 24, wherein the gRNA comprises any one of SEQ ID NOS:1-120.
26. The gRNA of claim 24 or 25, wherein the gRNA comprises any one of SEQ ID NOS: 91-96 and 100-105.

27. The gRNA of any one of claims 24-26, wherein the gRNA comprises SEQ ID NO:94 or SEQ ID NO:102.
28. The gRNA of any one of claims 24-26, wherein the gRNA comprises SEQ ID NO:94.
29. The gRNA of any one of claims 24-26, wherein the gRNA comprises SEQ ID NO:102.
30. The gRNA of any one of claims 24-29, wherein the cell is a stem cell, a human cell, a primary cell, an hematopoietic cell, an adaptive immune cell, an innate immune cell, a T cell or a T cell progenitor.
31. A method of editing a cell having chromosomal DNA, comprising inserting at least one sequence encoding a transgene within a safe harbor locus in the chromosomal DNA of the cell, wherein the safe harbor locus is any one or more of the sgRNA target loci provided in Table 4.
32. The method of claim 31, wherein the sgRNA target locus is selected from: chr11:128340000-128350000, chr10:33130000-33140000, chr10:72290000-72300000, chr11:65425000-65427000 (NEAT1), chr15:92830000-92840000, chr16:11220000-11230000, chr2:87460000-87470000, chr3:186510000-186520000, chr3:59450000-59460000, chr8:127980000-128000000, or chr9:7970000-7980000.
33. The method of claim 31 or 32, wherein the sgRNA target locus is selected from: chr11:128340000-128350000, chr10:72290000-72300000, chr15:92830000-92840000, or chr16:11220000-11230000.
34. The method of any one of claims 31-33, wherein the sgRNA target locus is chr11:128340000-128350000.
35. The method of any one of claims 31-33, wherein the sgRNA target locus is chr15:92830000-92840000.
36. The method of claim 31, wherein the sgRNA target locus is a gene selected from: *APRT*, *B2M*, *CAPNS1*, *CBLB*, *CD2*, *CD3E*, *CD3G*, *CD5*, *EDF1*, *FTL*, *PTEN*, *PTPN2*, *PTPN6*, *PTPRC*, *PTPRCAP*, *RPS23*, *RTRAF*, *SERF2*, *SLC38A1*, *SMAD2*, *SOCS1*, *SRP14*, *SRSF9*, *SUB1*, *TET2*, *TIGIT*, *TRAC*, or *TRIM28*.
37. The method of claim 31 or 32, wherein the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS94, GS88, GS89, GS90, GS91, GS92, GS93, GS95, GS96, GS97, GS98, GS99, GS100, GS101, GS102, GS103, GS104, GS105, GS106, GS107, GS108, GS109, GS110, GS111, GS112, GS113, GS114, GS115, GS116, GS117, GS118, GS119, or GS120.

- 38.** The method of any one of claims 31-33, wherein the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS94, GS91, GS92, GS93, GS95, GS96, GS100, GS101, GS102, GS103, GS104, or GS105.
- 39.** The method of any one of claims 31-33, wherein the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS103, GS104, or GS105.
- 40.** The method of any one of claims 31-33, wherein the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS94, GS95, or GS96.
- 41.** The method of any one of claims 31-33, wherein the safe harbor locus is the GS94 integration site in Table 4.
- 42.** The method of any one of claims 31-33, wherein the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS100, GS101, or GS102.
- 43.** The method of any one of claims 31-33, wherein the safe harbor locus is the GS102 integration site in Table 4.
- 44.** The method of any one of claims 31-33, wherein the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS91, GS92, or GS93.
- 45.** The method of any one of claims 31-44, wherein the transgene encodes a recombinant protein, optionally a therapeutic agent.
- 46.** The method of any one of claims 31-45, wherein the transgene encodes a chimeric antigen receptor (CAR).
- 47.** The method of any one of claims 31-46, wherein the at least one sequence comprises an exogenous promoter and the exogenous promoter is operably linked to the transgene.
- 48.** The method of claim 47, wherein the exogenous promoter is an EF1a promoter.
- 49.** The method of any one of claims 31-48, wherein the cell is a stem cell, a human cell, a primary cell, an hematopoietic cell, an adaptive immune cell, an innate immune cell, a T cell or T cell progenitor.
- 50.** The method of claim 49, wherein the cell is a T cell or a T cell progenitor.
- 51.** The method of any one of claims 31-50, wherein the engineered cell is undifferentiated.
- 52.** The method of any one of claims 31-51, wherein the engineered cell is CD45RA⁺ and CCR7⁺.
- 53.** The method of any one of claims 31-52, wherein the at least one sequence is inserted using a homology-directed repair.

- 54.** The method of any one of claims 31-52, wherein the at least one sequence is inserted using a homology independent targeted insertion.
- 55.** The method of any one of claims 31-54, wherein the at least one sequence is inserted using one or more guide ribonucleic acids (gRNAs) and one or more Cas9 endonucleases.
- 56.** The method of claim 55, wherein the one or more gRNAs comprises any one of SEQ ID NOS: 1-120.
- 57.** The method of claim 55 or 56, wherein the one or more gRNAs comprises any one of SEQ ID NOS: 91-96 and 100-105.
- 58.** The method of any one of claims 55-57, wherein the gRNA comprises SEQ ID NO:94 or SEQ ID NO:102.
- 59.** The method of any one of claims 55-58, wherein the gRNA comprises SEQ ID NO:94.
- 60.** The method of any one of claims 55-58, wherein the gRNA comprises SEQ ID NO:102.
- 61.** A method of editing a T cell, comprising contacting a T cell with one or more guide ribonucleic acids (gRNAs), at least one sequence encoding a transgene, and one or more Cas9 endonucleases, wherein the one or more gRNAs and Cas9 endonucleases facilitate the insertion of the at least one sequence into chromosomal DNA within a safe harbor locus, wherein the safe harbor locus is selected from any one or more of an sgRNA target loci in Table 4.
- 62.** The method of claim 61, wherein the one or more gRNAs comprises a sequence selected from any one of the sgRNA sequences in Table 4.
- 63.** The method of claim 61 or 62, wherein the one or more gRNAs comprises any one of SEQ ID NOS: 1-120.
- 64.** The method of any one of claims 61-63, wherein the one or more gRNAs comprises any one of SEQ ID NOS: 91-96 and 100-105.
- 65.** The method of any one of claims 61-64, wherein the gRNA comprises SEQ ID NO:94 or SEQ ID NO:102.
- 66.** The method of any one of claims 61-65, wherein the gRNA comprises SEQ ID NO:94.
- 67.** The method of any one of claims 61-65, wherein the gRNA comprises SEQ ID NO:102.

- 68.** The method of any one of claims 61-67, wherein the sgRNA target locus is selected from: chr11:128340000-128350000, chr10:33130000-33140000, chr10:72290000-72300000, chr11:65425000-65427000 (NEAT1), chr15:92830000-92840000, chr16:11220000-11230000, chr2:87460000-87470000, chr3:186510000-186520000, chr3:59450000-59460000, chr8:127980000-128000000, or chr9:7970000-7980000.
- 69.** The method of any one of claims 61-68, wherein the sgRNA target locus is selected from: chr11:128340000-128350000, chr10:72290000-72300000, chr15:92830000-92840000, or chr16:11220000-11230000.
- 70.** The method of any one of claims 61-69, wherein the sgRNA target locus is chr11:128340000-128350000.
- 71.** The method of any one of claims 61-69, wherein the sgRNA target locus is chr15:92830000-92840000.
- 72.** The method of claim 61-67, wherein the sgRNA target locus is a gene selected from: *APRT*, *B2M*, *CAPNS1*, *CBLB*, *CD2*, *CD3E*, *CD3G*, *CD5*, *EDF1*, *FTL*, *PTEN*, *PTPN2*, *PTPN6*, *PTPRC*, *PTPRCAP*, *RPS23*, *RTRAF*, *SERF2*, *SLC38A1*, *SMAD2*, *SOC31*, *SRP14*, *SRSF9*, *SUB1*, *TET2*, *TIGIT*, *TRAC*, or *TRIM28*.
- 73.** The method of any one of claims 61-68, wherein the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS94, GS88, GS89, GS90, GS91, GS92, GS93, GS95, GS96, GS97, GS98, GS99, GS100, GS101, GS102, GS103, GS104, GS105, GS106, GS107, GS108, GS109, GS110, GS111, GS112, GS113, GS114, GS115, GS116, GS117, GS118, GS119, or GS120.
- 74.** The method of any one of claims 61-68 and 73, wherein the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS94, GS91, GS92, GS93, GS95, GS96, GS100, GS101, GS102, GS103, GS104, or GS105.
- 75.** The method of any one of claims 61-68 and 73-74, wherein the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS103, GS104, or GS105.
- 76.** The method of any one of claims 61-68 and 73-74, wherein the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS94, GS95, and GS96.
- 77.** The method of claim 76, wherein the safe harbor locus is the GS94 integration site in Table 4.

- 78.** The method of any one of claims 61-68 and 73-74, wherein the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS100, GS101, or GS102.
- 79.** The method of claim 78, wherein the safe harbor locus is the GS102 integration site in Table 4.
- 80.** The method of any one of claims 61-68 and 73-74, wherein the safe harbor locus is selected from any one of the integration sites in Table 4 designated: GS91, GS92, or GS93.
- 81.** The method of any one of claims 61-80, wherein the engineered cell is undifferentiated.
- 82.** The method of any one of claims 61-81, wherein the engineered cell is CD45RA⁺ and CCR7⁺.
- 83.** An *ex vivo* method of obtaining an engineered cell or population thereof, comprising:
- a. obtaining a cell;
 - b. genetically modifying the cell by inserting at least one sequence encoding a transgene within a safe harbor locus, wherein the safe harbor locus is selected from any one of an sgRNA target loci in Table 4.
- 84.** The method of claim 83, wherein obtaining the cell comprises: (i) collecting a tissue sample from a subject, (ii) isolating the cells from the tissue samples, and (iii) culturing the cells in vitro.
- 85.** The method of claim 84, wherein the tissue sample is a blood sample.
- 86.** The method of any one of claims 83-85, wherein the cell is a stem cell, a human cell, a primary cell, an hematopoietic cell, an adaptive immune cell, an innate immune cell, a T cell, or T cell progenitor.
- 87.** The method of claim 86, wherein the cell is a T cell or a T cell progenitor.
- 88.** The method of any one of claims 83-87, wherein the engineered cell is undifferentiated.
- 89.** The method of any one of claims 83-88, wherein the engineered cell is CD45RA⁺ and CCR7⁺.
- 90.** The method of any one of claims 83-89, wherein the at least one sequence is inserted using a homology-directed repair.
- 91.** The method of any one of claims 83-89, wherein the at least one sequence is inserted using a homology independent targeted insertion.

- 92.** The method of any one of claims 83-91, wherein the genetically modifying in step (b) comprises contacting the cell with one or more guide ribonucleic acids (gRNAs), the at least one sequence, and one or more Cas9 endonucleases, wherein the one or more gRNAs and Cas9 endonucleases facilitate the insertion of the at least one sequence into chromosomal DNA within the safe harbor locus.
- 93.** The method of claim 92, wherein the one or more gRNAs comprises a sequence selected from any one of the sgRNA sequences in Table 4.
- 94.** The method of any one of claims 83-93, wherein the transgene encodes a recombinant protein, optionally a therapeutic agent.
- 95.** The method of any one of claims 83-93, wherein the transgene encodes a chimeric antigen receptor (CAR).
- 96.** The method of claim 83-95, wherein the at least one sequence comprises an exogenous promoter and the exogenous promoter is operably linked to the transgene.
- 97.** The method of claim 96, wherein the exogenous promoter is an EF1a promoter.
- 98.** A method of treating a subject having or at risk of having a disease, comprising administering to the subject an effective amount of the cell of any one of claims 1-22, a population thereof, or the composition of claim 23.
- 99.** The method of claim 98, wherein the cell, the population thereof, or the composition is administered to the subject by infusion.
- 100.** A method of treating a subject having or at risk of having a disease, comprising:
- a. conducting the method of any one of claims 83-97; and
 - b. administering to the subject an effective amount of a composition comprising the cell or a population thereof.
- 101.** The method of claim 100, wherein the composition is administered to the subject by infusion.
- 102.** The method of claim 100 or 101, wherein the disease is cancer.
- 103.** The method of any one of claims 100-102 or , wherein the disease is blood cancer.
- 104.** A method of identifying a safe harbor locus, comprising:
- a. identifying genes or non-coding regions in a chromosome that are above a threshold level for expression across developmental cell states and/or a threshold level for accessibility of chromatin;

- b. generating a linear model that correlates the gene or non-coding region from step (a) with knock-in (KI) efficiency and estimates the KI efficiency of any gene or coding region on the chromosome; and
- c. selecting the safe harbor locus based on threshold parameters;
wherein the safe harbor locus is selected for insertion of at least one sequence encoding a transgene within a cell.

105. The method of claim 104, wherein the threshold parameters include one or more of: stable expression of a transgene, knockout of the gene confers benefit to the function of the cell, no known function within the cell, stable transgene expression *in vitro* with or without CD3/CD28 stimulation, negligible off-target cleavage as detected by iGuide-Seq or CRISPR-Seq, less off-target cleavage relative to other loci as detected by iGuide-Seq or CRISPR-Seq, negligible transgene-independent cytotoxicity, negligible transgene-independent cytokine expression, negligible transgene-independent chimeric antigen receptor expression, negligible deregulation or silencing of nearby genes, and positioned outside of a cancer-related gene.

106. The method of claim 105, wherein the stable expression of a transgene at the safe harbor locus is less than or equal to 2-fold expression change over the course of at least 1, 2, 3, 4, 5, 6, or 7 days, and wherein expression change is measured by mean fluorescence intensity of a reporter gene encoded by the at least one sequence.

107. The method of any one of claims 104-106, wherein the accessibility of chromatin is measured using an assay for transposase-accessible chromatin using sequencing (ATAC-seq).

108. The method of any one of claims 104-107, wherein the level of expression across developmental cell states is measured using RNA sequencing (RNA-seq).

109. The method of any one of claims 104-108, wherein the cell is a stem cell, a human cell, a primary cell, an hematopoietic cell, an adaptive immune cell, an innate immune cell, a T cell or T cell progenitor.

110. The method of any one of claims 104-109, wherein the linear model has a coefficient of determination (R^2 value) of at least 30%.

111. The engineered cell, composition, gRNA or method of any one of the preceding claims, wherein insertion within the safe harbor locus increase cell cytotoxicity of diseased cells.

- 112.** The engineered cell, composition, gRNA or method of any one of the preceding claims wherein knock-in efficiency at the safe harbor locus is increased relative to other locations along the chromosome.
- 113.** An engineered cell, comprising at least one sequence encoding a transgene, wherein the at least one sequence is inserted within a safe harbor locus, wherein the safe harbor locus is at any one or more of an sgRNA target loci; and wherein expression of the at least one sequence encoding the transgene is operatively linked to an endogenous promoter or an exogenous promoter, and wherein the engineered cell is undifferentiated.
- 114.** The engineered cell of claim 113, wherein the safe harbor locus is selected any one of the integration sites designated: GS94, GS88, GS89, GS90, GS91, GS92, GS93, GS95, GS96, GS97, GS98, GS99, GS100, GS101, GS102, GS103, GS104, GS105, GS106, GS107, GS108, GS109, GS110, GS111, GS112, GS113, GS114, GS115, GS116, GS117, GS118, GS119, or GS120.
- 115.** The engineered cell of claim 113 or 114, wherein the safe harbor locus is the GS94 integration site.
- 116.** The engineered cell of claim 113, wherein the sgRNA target locus is selected from: chr11:128340000-128350000, chr10:33130000-33140000, chr10:72290000-72300000, chr11:65425000-65427000 (NEAT1), chr15:92830000-92840000, chr16:11220000-11230000, chr2:87460000-87470000, chr3:186510000-186520000, chr3:59450000-59460000, chr8:127980000-128000000, or chr9:7970000-7980000.
- 117.** The engineered cell of claim 113, wherein the sgRNA target locus is a gene selected from: *APRT*, *B2M*, *CAPNS1*, *CBLB*, *CD2*, *CD3E*, *CD3G*, *CD5*, *EDF1*, *FTL*, *PTEN*, *PTPN2*, *PTPN6*, *PTPRC*, *PTPRCAP*, *RPS23*, *RTRAF*, *SERF2*, *SLC38A1*, *SMAD2*, *SOC1*, *SRP14*, *SRSF9*, *SUB1*, *TET2*, *TIGIT*, *TRAC*, or *TRIM28*.
- 118.** The engineered cell of any one of claims 113-117, wherein the one or more gRNAs comprises any one of SEQ ID NOS: 1-120.
- 119.** The engineered cell of any one of claims 113-118, wherein the engineered cell is a stem cell, a human cell, a primary cell, an hematopoietic cell, an adaptive immune cell, an innate immune cell, a T cell or a T cell progenitor.
- 120.** The engineered cell of claim 119, wherein the cell is a T cell or a T cell progenitor.
- 121.** The engineered cell of any one of claims 113-120, wherein the engineered cell is CD45RA⁺ and CCR7⁺.

- 122.** The engineered cell of any one of claims 113-121, wherein the transgene encodes a recombinant protein, optionally a therapeutic agent.
- 123.** The engineered cell of any one of claims 113-122, wherein the transgene encodes a chimeric antigen receptor (CAR).
- 124.** A composition comprising the engineered cell of any one of claims 113-123 and a pharmaceutical excipient.
- 125.** A method of editing a cell having chromosomal DNA, comprising inserting at least one sequence encoding a transgene within a safe harbor locus in the chromosomal DNA of the cell, wherein the safe harbor locus is at any one or more of an sgRNA target loci; and wherein the engineered cell is undifferentiated.
- 126.** The method of claim 125, wherein the engineered cell is a stem cell, a human cell, a primary cell, an hematopoietic cell, an adaptive immune cell, an innate immune cell, a T cell or a T cell progenitor.
- 127.** The method of claim 125 or 126, wherein the cell is a T cell or a T cell progenitor.
- 128.** A method of editing a T cell, comprising contacting a T cell with one or more guide ribonucleic acids (gRNAs), at least one sequence encoding a transgene, and one or more Cas9 endonucleases, wherein the one or more gRNAs and Cas9 endonucleases facilitate the insertion of the at least one sequence into chromosomal DNA within a safe harbor locus.
- 129.** The method of any one of claims 125-128, wherein the safe harbor locus is selected from any one of the integration sites designated: GS88, GS89, GS90, GS91, GS92, GS93, GS94, GS95, GS96, GS97, GS98, GS99, GS100, GS101, GS102, GS103, GS104, GS105, GS106, GS107, GS108, GS109, GS110, GS111, GS112, GS113, GS114, GS115, GS116, GS117, GS118, GS119, or GS120.
- 130.** The method of any one of claims 125-128, wherein the safe harbor locus is the GS94 integration site.
- 131.** The method of any one of claims 125-128, wherein the sgRNA target locus is selected from: chr11:128340000-128350000, chr10:33130000-33140000, chr10:72290000-72300000, chr11:65425000-65427000 (NEAT1), chr15:92830000-92840000, chr16:11220000-11230000, chr2:87460000-87470000, chr3:186510000-186520000, chr3:59450000-59460000, chr8:127980000-128000000, or chr9:7970000-7980000.
- 132.** The method of any one of claims 125-128, wherein the sgRNA target locus is a gene selected from: *APRT*, *B2M*, *CAPNS1*, *CBLB*, *CD2*, *CD3E*, *CD3G*, *CD5*, *EDF1*, *FTL*, *PTEN*,

PTPN2, *PTPN6*, *PTPRC*, *PTPRCAP*, *RPS23*, *RTRAF*, *SERF2*, *SLC38A1*, *SMAD2*, *SOCS1*, *SRP14*, *SRSF9*, *SUB1*, *TET2*, *TIGIT*, *TRAC*, or *TRIM28*.

133. The method of any one of claims 125-132, wherein the one or more gRNAs comprises any one of SEQ ID NOS: 1-120.

134. The method of any one of claims 125-133, wherein the engineered cell is CD45RA⁺ and CCR7⁺ after insertion of the at least one sequence into the safe harbor locus.

135. The method of any one of claims 125-134, wherein the transgene encodes a recombinant protein, optionally a therapeutic agent.

136. The method of any one of claims 125-135, wherein the transgene encodes a chimeric antigen receptor (CAR).

137. An *ex vivo* method of obtaining an undifferentiated engineered cell or population thereof, comprising:

- c. obtaining a cell;
- d. genetically modifying the cell by inserting at least one sequence encoding a transgene within a safe harbor locus, wherein the engineered cell is undifferentiated.

138. The method of claim 137, wherein obtaining the cell comprises: (i) collecting a tissue sample from a subject, (ii) isolating the cells from the tissue samples, and (iii) culturing the cells *in vitro*.

139. The method of claim 138, wherein the tissue sample is a blood sample.

140. The method of any one of claims 137-139, wherein the cell is a stem cell, a human cell, a primary cell, an hematopoietic cell, an adaptive immune cell, an innate immune cell, a T cell or T cell progenitor.

141. The method of claim 140, wherein the cell is a T cell or a T cell progenitor.

142. The method of any one of claims 137-142, wherein the engineered cell is CD45RA⁺ and CCR7⁺.

143. The method of any one of claims 137-143, wherein the transgene encodes a recombinant protein, optionally a therapeutic agent.

144. The method of any one of claims 137-143, wherein the transgene encodes a chimeric antigen receptor (CAR).

- 145.** A method of treating a subject having or at risk of having a disease, comprising administering to the subject an effective amount of the cell of any one of claims 113-123, a population thereof, or the composition of claim 124.
- 146.** A method of treating a subject having or at risk of having a disease, comprising:
- c. conducting the method of any one of claims 125-144; and
 - d. administering to the subject an effective amount of a composition comprising the cell or a population thereof.
- 147.** The method of claim 146, wherein the composition is administered to the subject by infusion.
- 148.** The method of claim 146 or 147, wherein the disease is cancer.