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(54) METHODS FOR SCREENING GENETIC PERTURBATIONS

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A61K 35/44	(2006.01)

(52) **U.S. Cl.**

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(57) **ABSTRACT**

Understanding the complex effects of genetic perturbations on cellular state and fitness in human pluripotent stem cells (hPSCs) has been challenging using traditional pooled screening techniques which typically rely on unidimensional phenotypic readouts. Here, Applicants use barcoded open reading frame (ORF) overexpression libraries with a coupled single-cell RNA sequencing (scRNA-seq) and fitness screening approach, a technique we call SEUSS (ScalablE fUnctional Screening by Sequencing), to establish a comprehensive assaying platform. Using this system, Applicants perturbed hPSCs with a library of developmentally critical transcription factors (TFs), and assayed the impact of TF overexpression on fitness and transcriptomic cell state across multiple media conditions. Applicants further leveraged the versatility of the ORF library approach to systematically assay mutant gene libraries and also whole gene families. From the transcriptomic responses, Applicants built genetic co-perturbation networks to identify key altered gene modules. Strikingly, we found that KLF4 and SNAI2 have opposing effects on the pluripotency gene module, highlighting the power of this method to characterize the effects of genetic perturbations. From the fitness responses, Applicants identified ETV2 as a driver of reprogramming towards an endothelial-like state.

Specification includes a Sequence Listing.

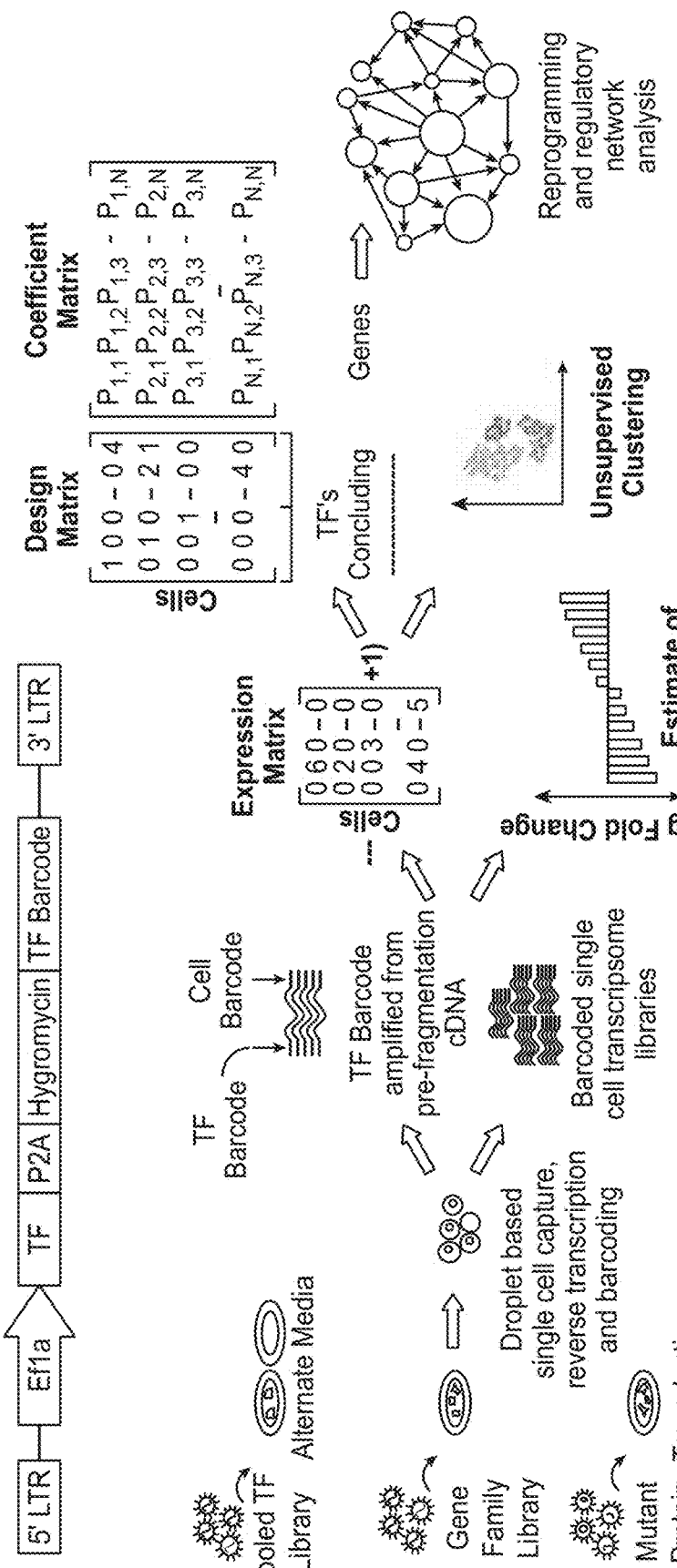

5' LTR
Ef1a
TF
P2A
Hygromycin
TF Barcode
3' LTR
Pooled TF Library
Alternate Media
Gene Family Library
Mutant Protein Library
Transduction and selection
Droplet based single cell capture, reverse transcription and barcoding
TF Barcode
Cell Barcode
Barcoded single cell transcripsome libraries
TF Barcode amplified from pre-fragmentation cDNA
Cells
Expression Matrix
Log Fold Change
Estimate of Fitness
TF's Concluding
Design Matrix
Coefficient Matrix
Genes
Unsupervised Clustering
Reprogramming and regulatory network analysis

FIG. 1A

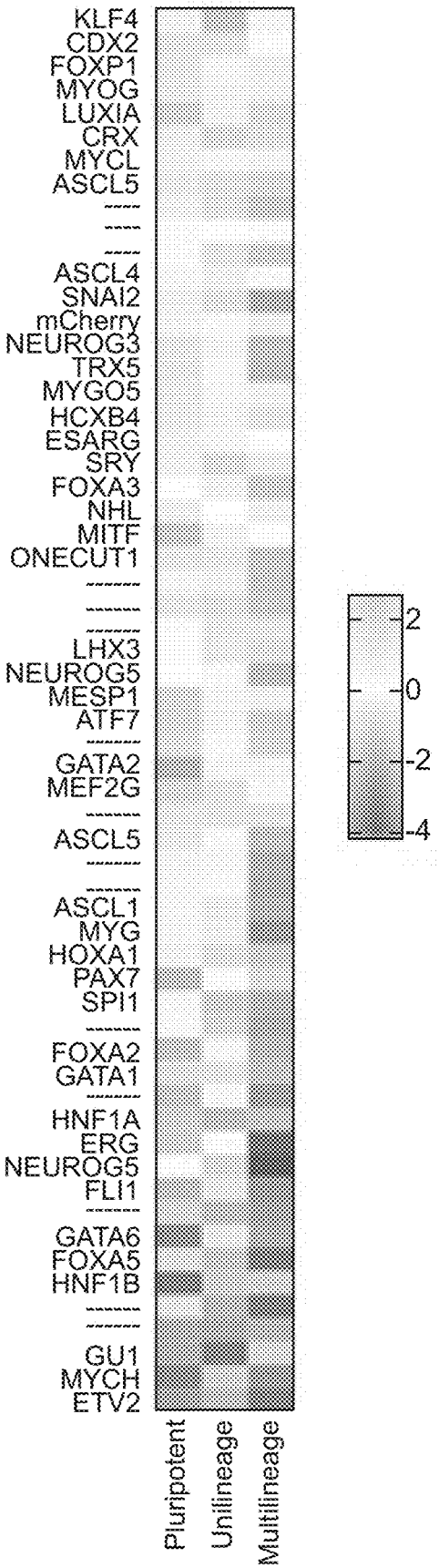

KLF4
CDX2
FOXP1
MYOG
LUXIA
CRX
MYCL
ASCL5
ASCL4
SNAI2
mCherry
NEUROG3
TRX5
MYGO5
HCXB4
ESARG
SRY
FOXA3
NHL
MITF
ONECUT1
LHX3
NEUROG5
MESP1
ATF7
GATA2
MEF2G
ASCL5
ASCL1
MYG
HOXA1
PAX7
SPI1
FOXA2
GATA1
HNF1A
ERG
NEUROG5
FLI1
GATA6
FOXA5
HNF1B
GU1
MYCH
ETV2
2
0
-2
-4
Pluripotent
Unilineage
Multilineage

FIG. 1B

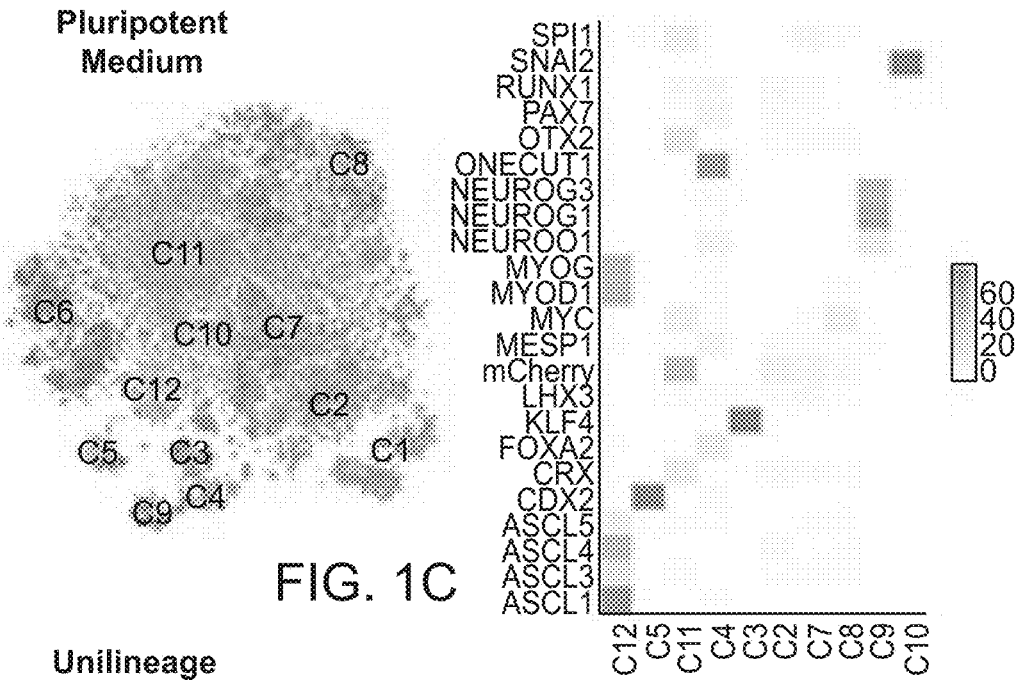


FIG. 1C

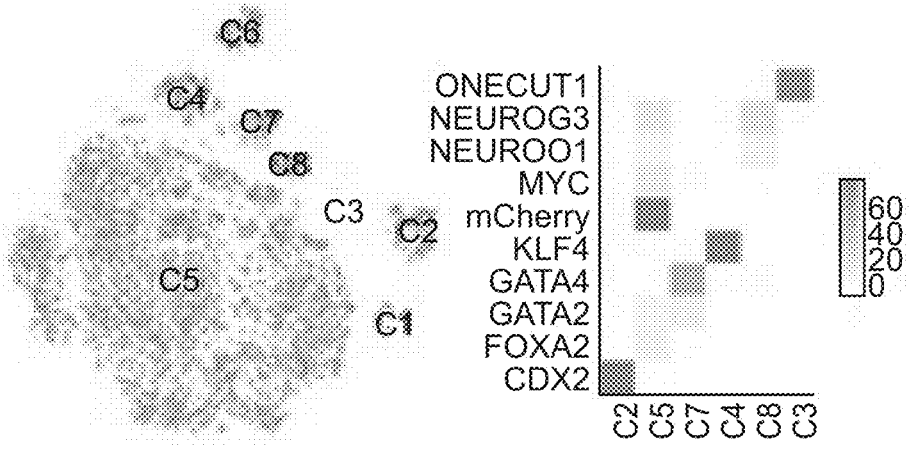


FIG. 1D

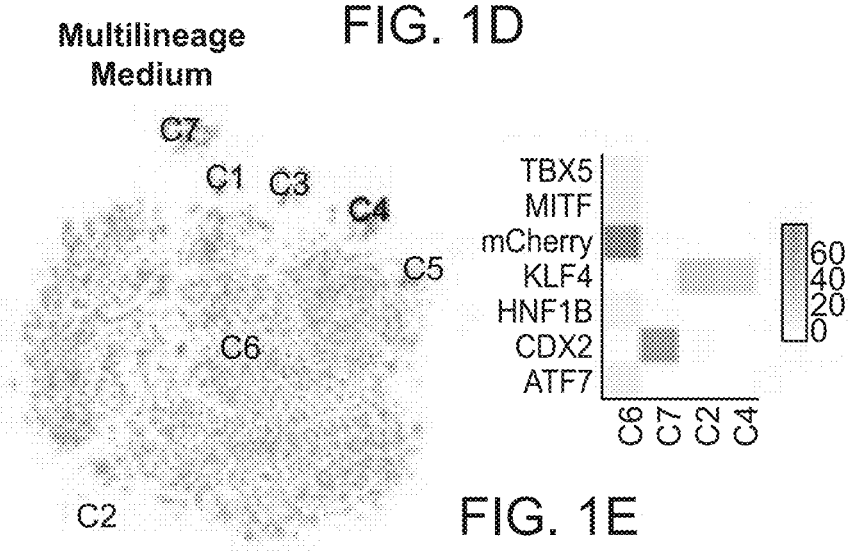


FIG. 1E

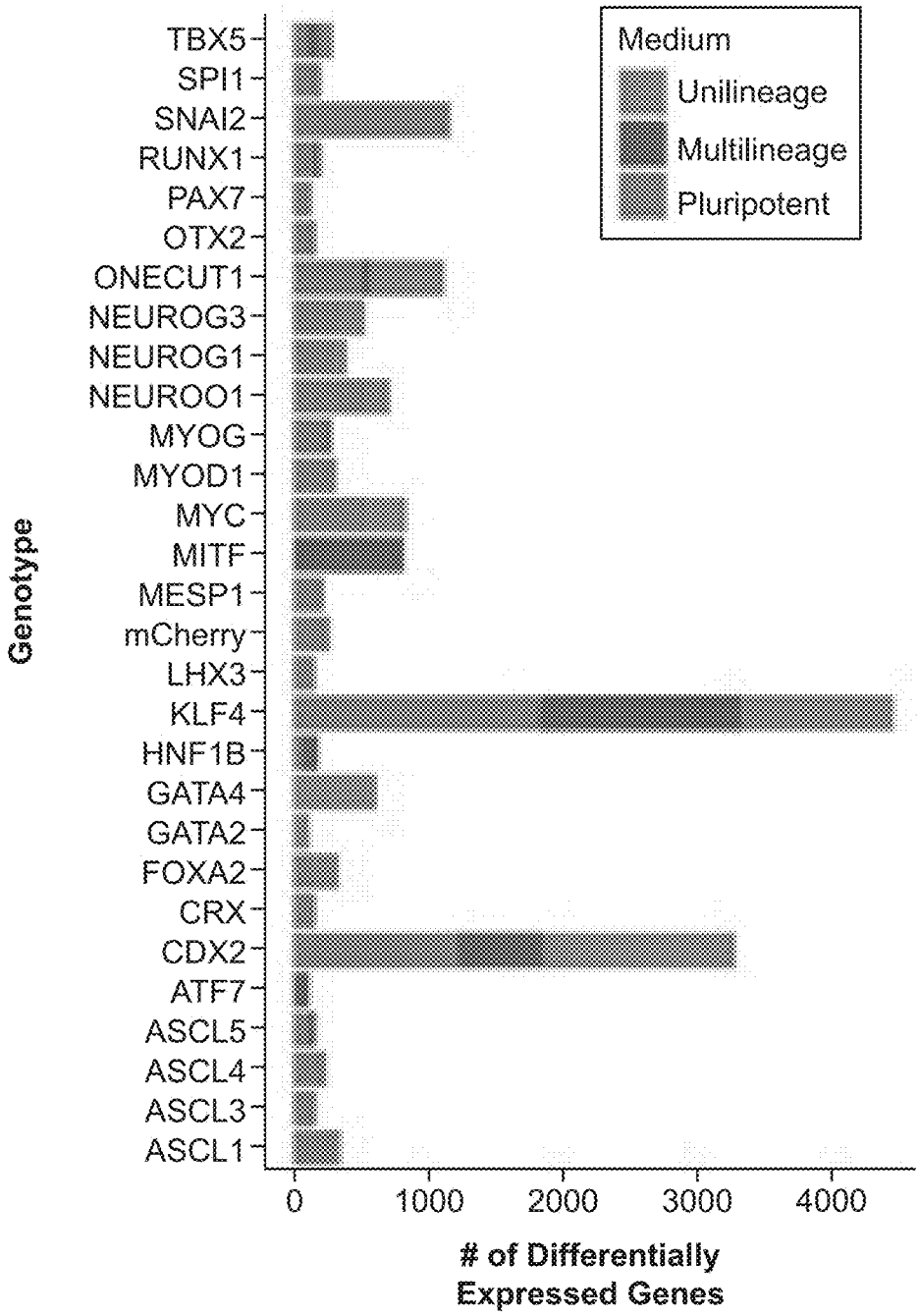

Medium
Unilineage
Multilineage
Pluripotent
Genotype
TBX5
SPI1
SNAI2
RUNX1
PAX7
OTX2
ONECUT1
NEUROG3
NEUROG1
NEUROO1
MYOG
MYOD1
MYC
MITF
MESP1
mCherry
LHX3
KLF4
HNF1B
GATA4
GATA2
FOXA2
CRX
CDX2
ATF7
ASCL5
ASCL4
ASCL3
ASCL1
0
1000
2000
3000
4000
# of Differentially Expressed Genes

FIG. 1F

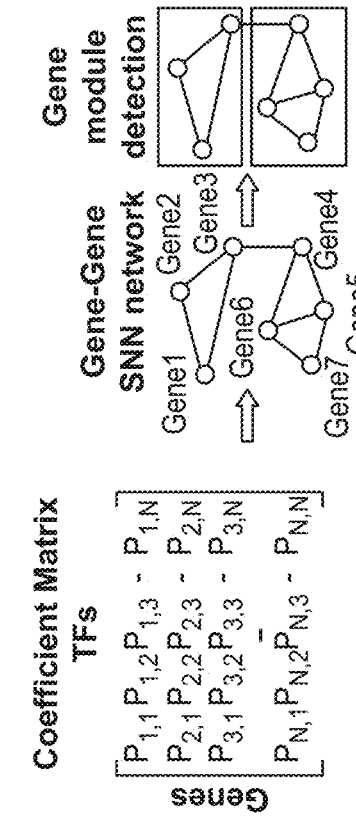


FIG. 2A

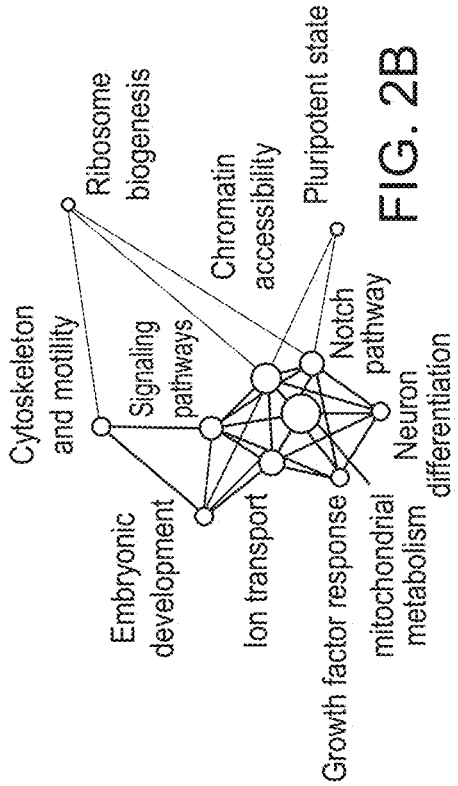


FIG. 2B

FIG. 2C

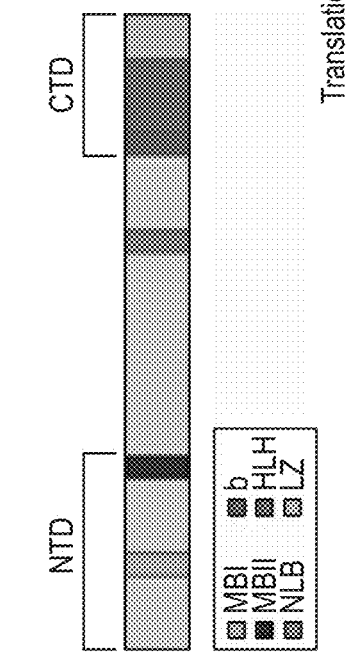


FIG. 2D

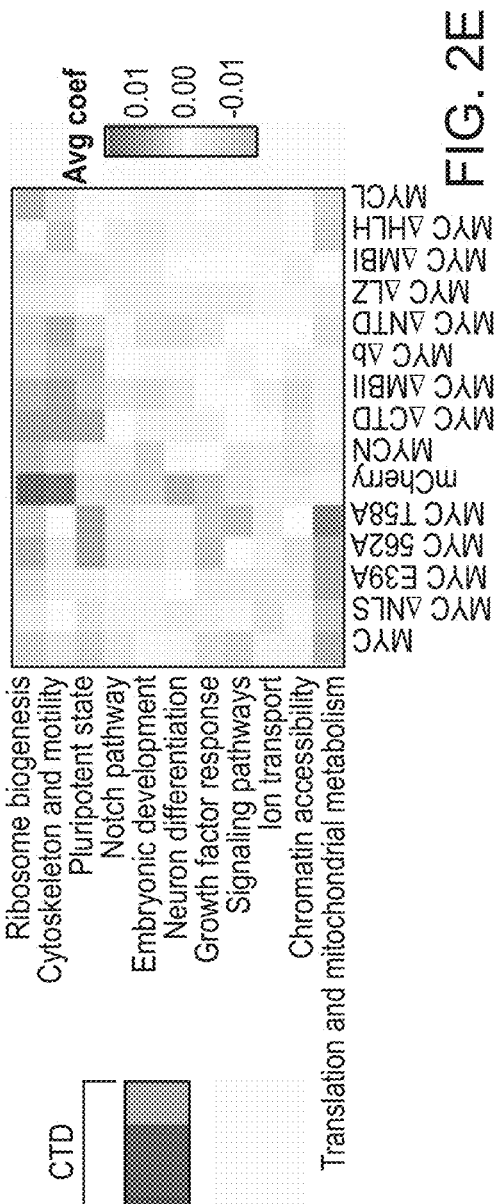


FIG. 2E

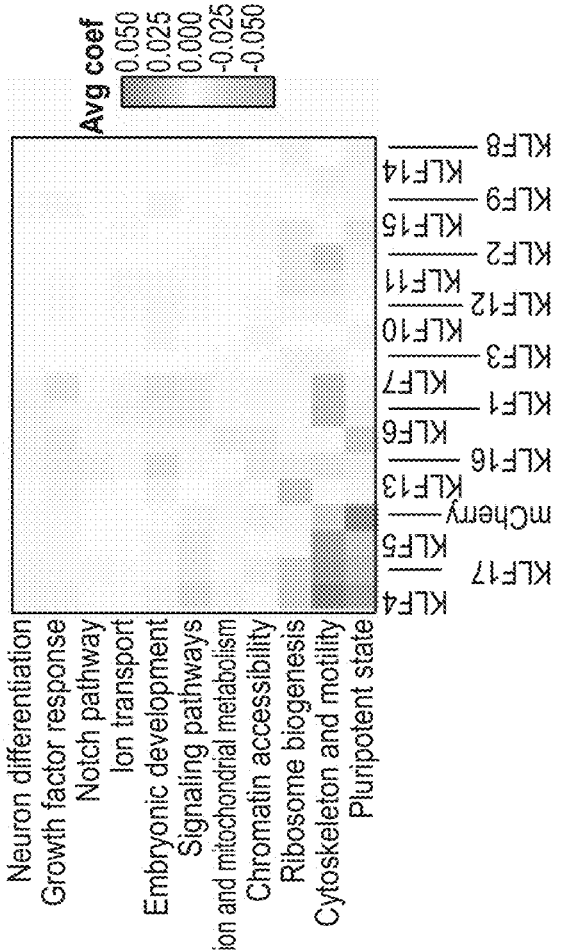
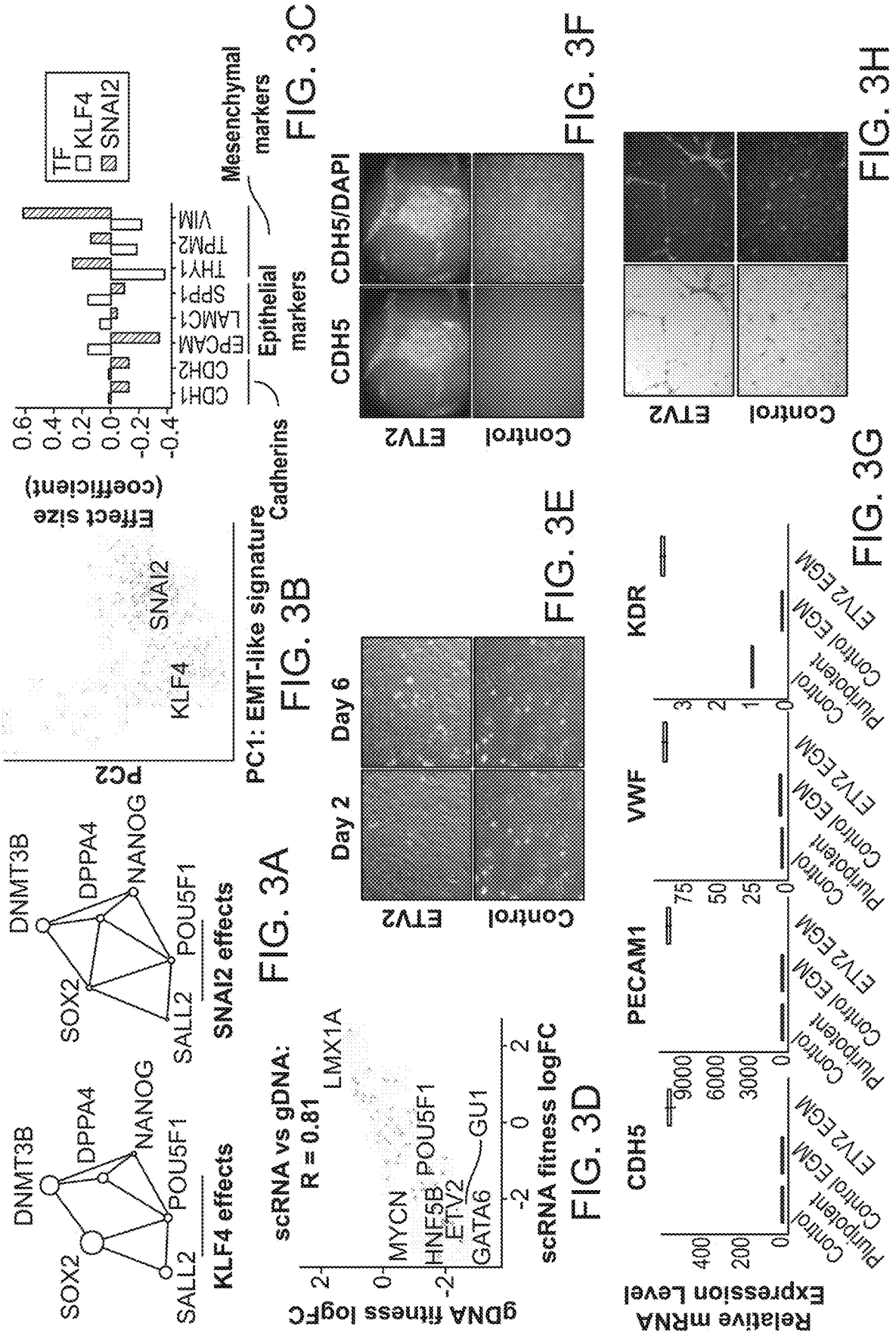


FIG. 2G

FIG. 2F


KLF4 effects
SOX2
DNMT3B
DPPA4
NANOG
POU5F1
SALL2
SNAI2 effects
SOX2
DNMT3B
DPPA4
NANOG
POU5F1
SALL2
FIG. 3A
PC2
KLF4
SNAI2
PC1: EMT-like signature
Cadherins
Epithelial markers
Mesenchymal markers
Effect size (coefficient)
0.6
0.4
0.2
0.0
-0.2
-0.4
CDH1
CDH2
EPCAM
LAMC1
SPP1
THY1
TPM2
VIM
TF
KLF4
SNAI2
FIG. 3B
Day 2
Day 6
Control
ETV2
FIG. 3E
CDH5
CDH5/DAPI
Control
ETV2
FIG. 3F
Control
ETV2
FIG. 3H
scRNA vs gDNA:
R = 0.81
LMX1A
MYCN
HNF5B
POU5F1
ETV2
GATA6
GU1
gDNA fitness logFC
scRNA fitness logFC
2
0
-2
FIG. 3D
CDH5
PECAM1
VWF
KDR
Relative mRNA Expression Level
9000
6000
3000
0
400
200
0
75
50
25
0
3
2
1
0
Control
Pluripotent
Control EGM
ETV2 EGM
FIG. 3G

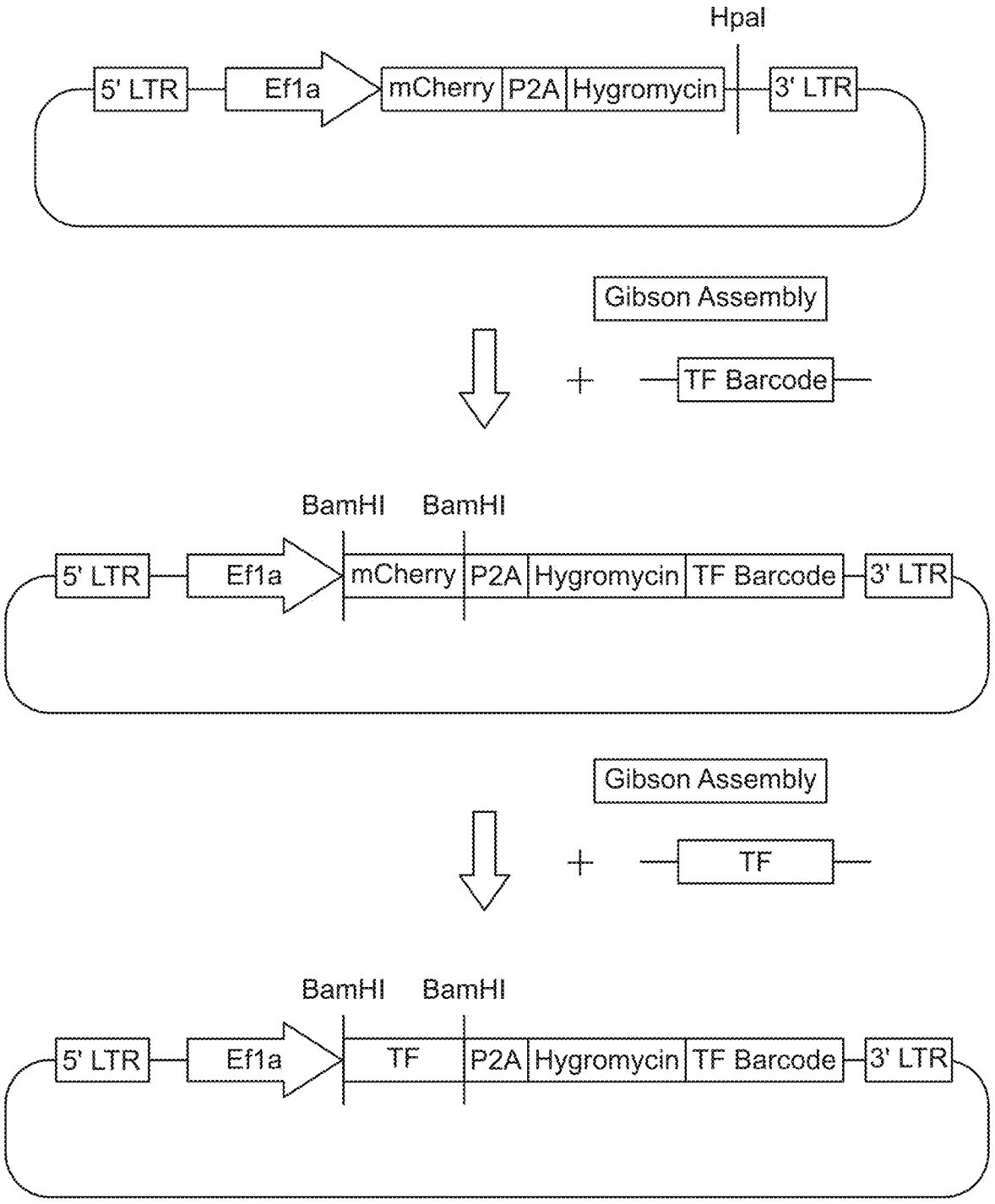

HpaI
5' LTR
Ef1a
mCherry
P2A
Hygromycin
3' LTR
Gibson Assembly
TF Barcode
BamHI
BamHI
5' LTR
Ef1a
mCherry
P2A
Hygromycin
TF Barcode
3' LTR
Gibson Assembly
TF
BamHI
BamHI
5' LTR
Ef1a
TF
P2A
Hygromycin
TF Barcode
3' LTR

FIG. 4

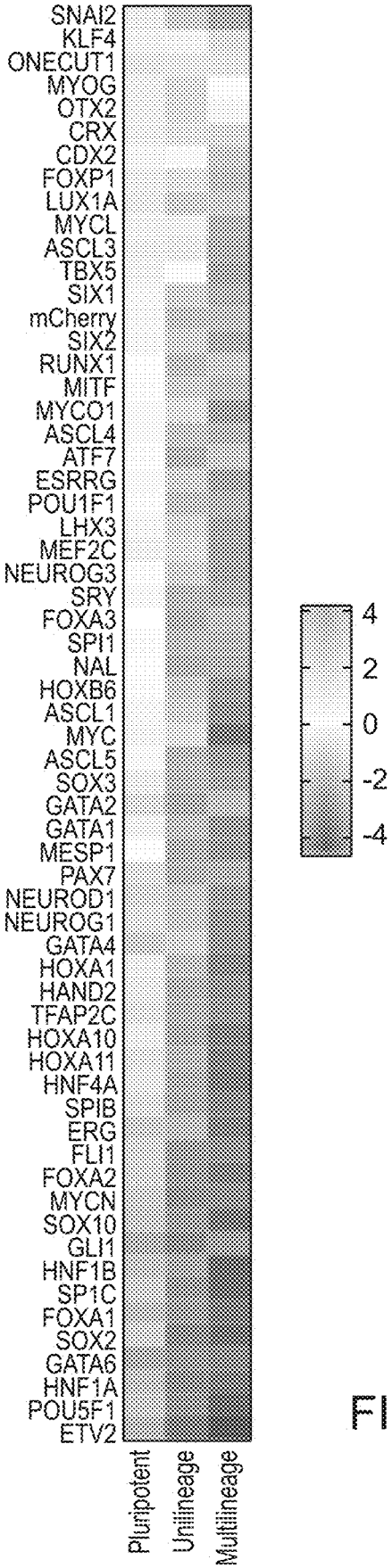


FIG. 5A

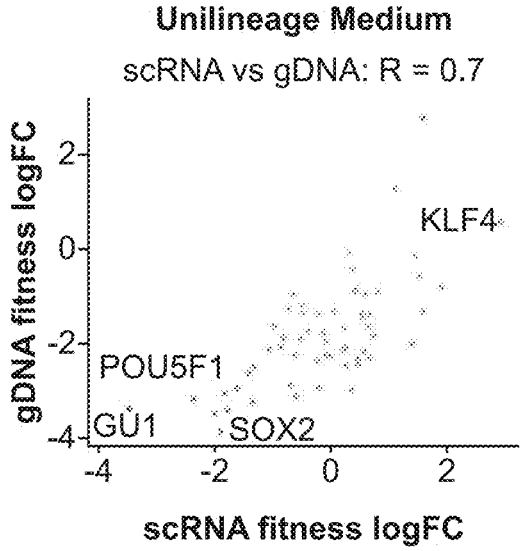


FIG. 5B

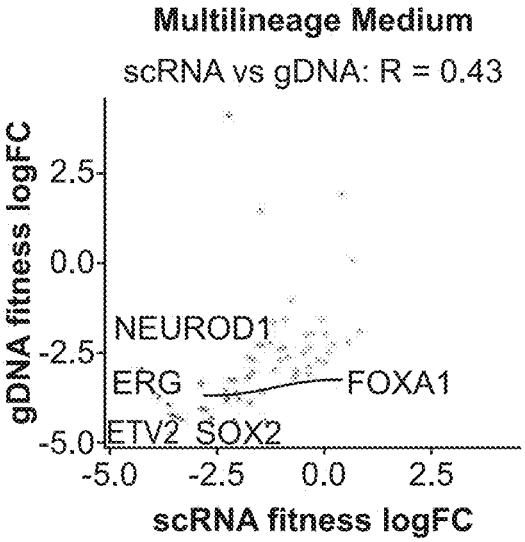


FIG. 5C

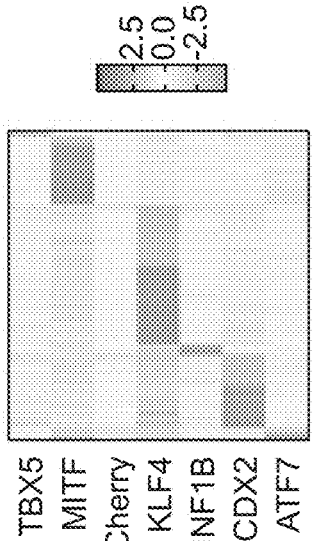


FIG. 6C

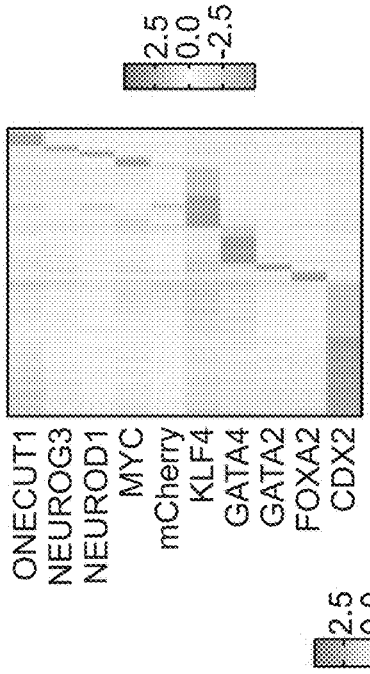


FIG. 6B

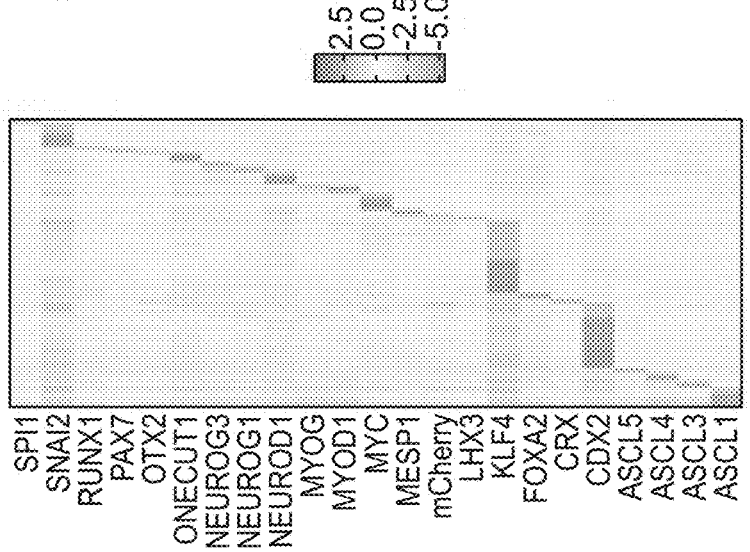


FIG. 6A

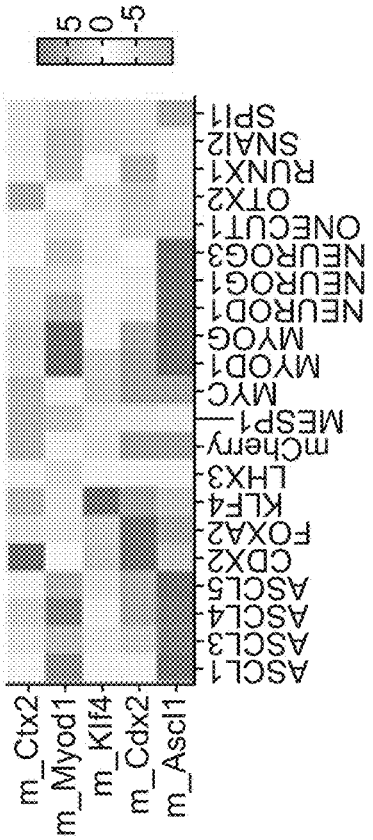


FIG. 6D

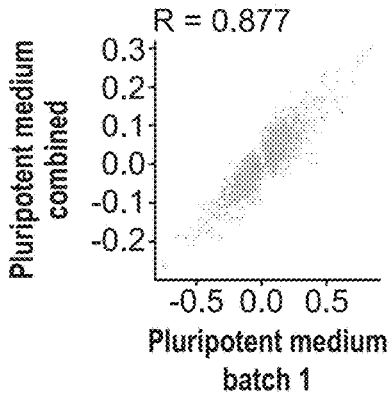


FIG. 7A

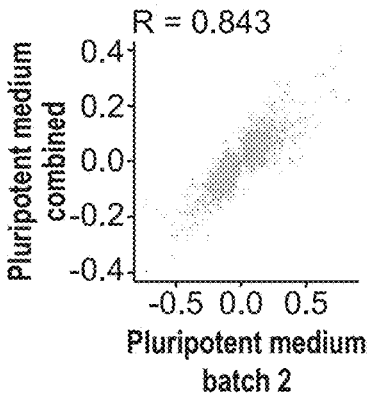


FIG. 7B

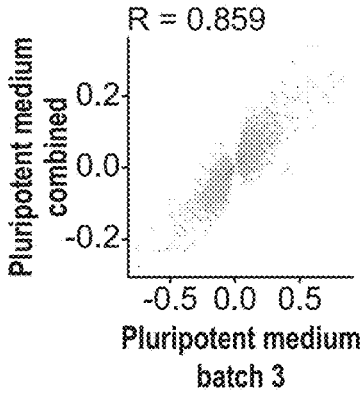


FIG. 7C

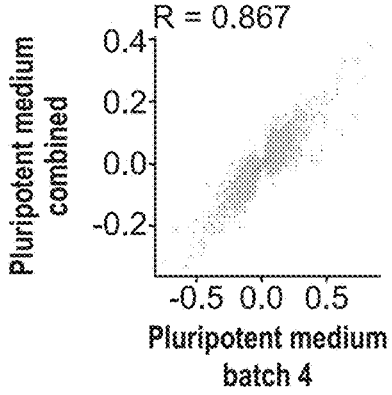


FIG. 7D

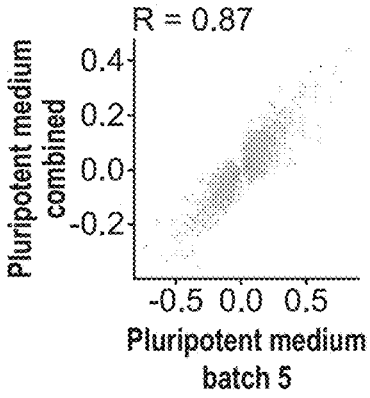


FIG. 7E

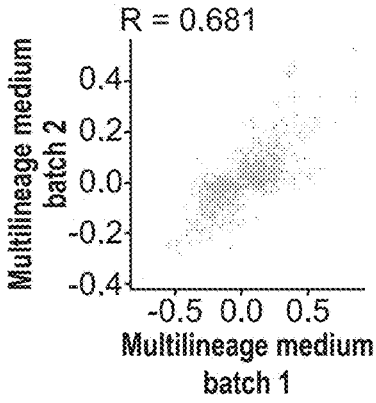


FIG. 7F

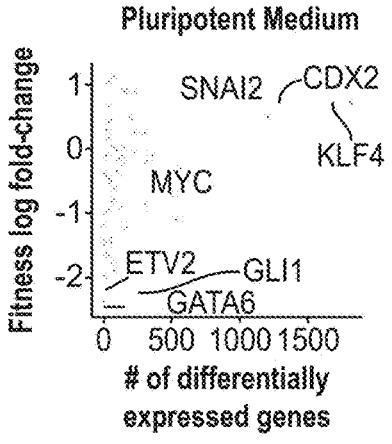


FIG. 8A

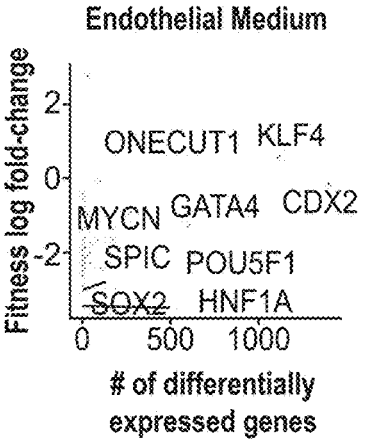


FIG. 8B

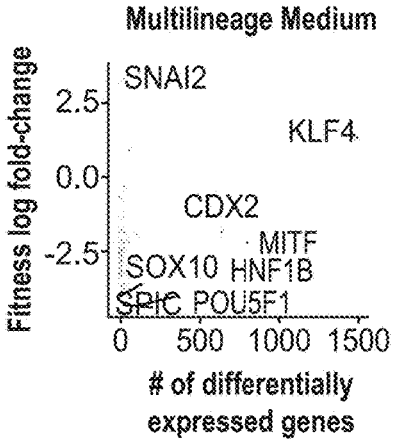


FIG. 8C

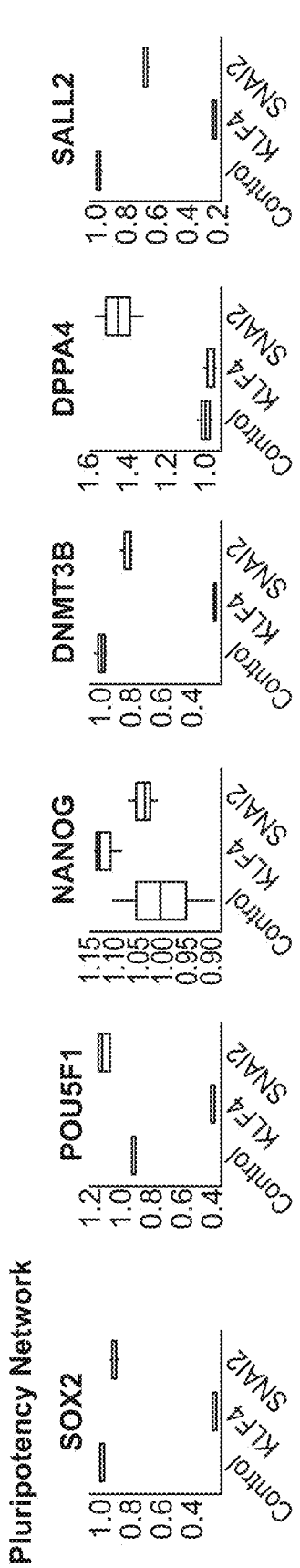


FIG. 9A

FIG. 9B

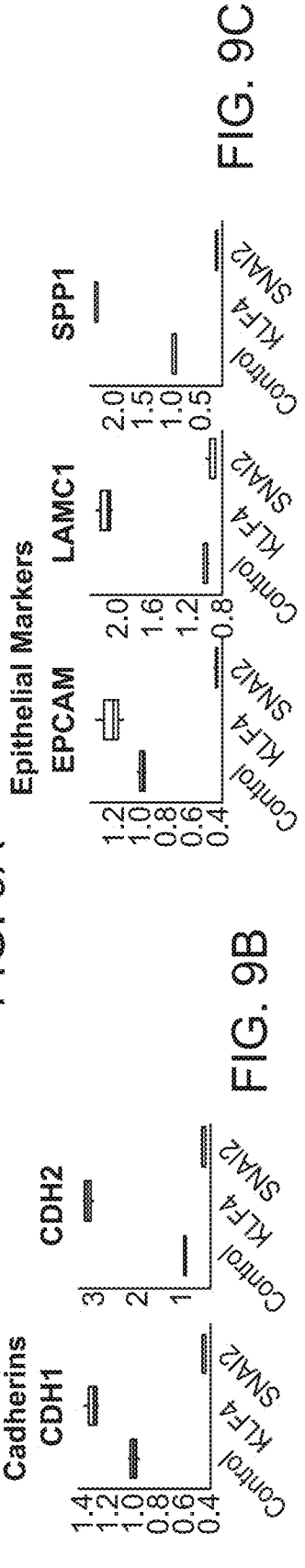


FIG. 9C

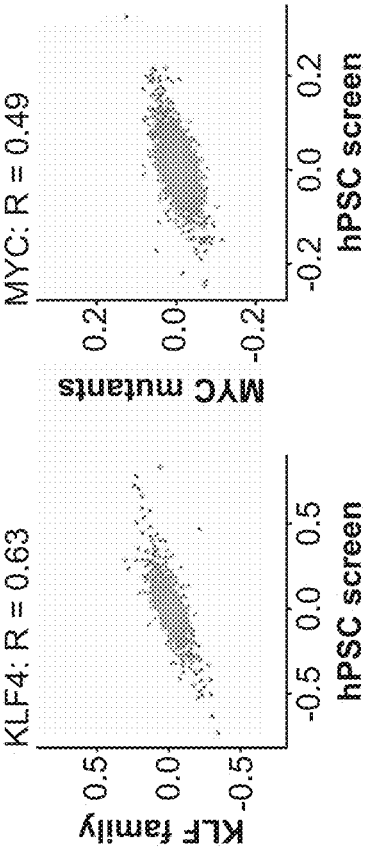


FIG. 10A

FIG. 10B

FIG. 9D

METHODS FOR SCREENING GENETIC PERTURBATIONS

CROSS-REFERENCE TO RELATED APPLICATION

[0001] This application claims priority to 35 U.S.C. § 119(e) of U.S. Provisional Application Ser. No. 62/904,614, filed Sep. 23, 2019, the content of which is hereby incorporated by reference its entirety.

[0002] This invention was made with government support under HG009285 awarded by the National Institutes of Health. The government has certain rights in the invention.

SEQUENCE LISTING

[0003] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on Dec. 14, 2020, is named 114198-0152_SL.txt and is 155,507 bytes in size.

BACKGROUND

[0004] Cellular reprogramming by the overexpression of transcription factors (TF), has widely impacted biological research, from the direct conversion of adult somatic cells to the induction of pluripotent stem cells, and the differentiation of hPSCs. To date, the choice of TFs that drive such reprogramming has been through a combination of the knowledge of their role in development and cellular transformation, and systematic trial-and-error. These challenges highlight the need for the development of a scalable screening method to assess the effects of TF overexpression. Such a screening method would have broad applicability in advancing a fundamental understanding of reprogramming, and as a means for the discovery of novel reprogramming factors. This disclosure addresses this need and provides related advantages as well.

SUMMARY

[0005] Described herein is a comprehensive high-throughput platform to determine an optimal method to drive the differentiation of pluripotent cells to specific somatic lineages. In some aspects, the platform utilizes a novel open reading frame (ORF) gene overexpression vector library of developmentally critical transcription factors. The platform builds genetic co-perturbation networks to identified key altered gene modules and identifies key reprogramming/differentiation drivers from transcriptomic responses. The platform enabled identification of the key role of (previously not recognized) transcription factor ETV2 in reprogramming towards an endothelial state.

[0006] Thus, in one aspect, provided herein are isolated nucleic acids comprising, consisting of, or consisting essentially of (a) a nucleic acid encoding a transcription factor (TF) open reading frame (ORF); (b) a nucleic acid barcode, and (c) an optional vector comprising (a) and (b); wherein the nucleic acid barcode is located 3' to the TF ORF. In some embodiments, the TF ORF encodes a developmentally critical TF.

[0007] In another aspect, provided herein is a TF screening library comprising, consisting of, or consisting essentially of at least one isolated nucleic acid comprising, consisting of, or consisting essentially of (a) a nucleic acid encoding a transcription factor (TF) open reading frame (ORF); (b) a nucleic acid barcode, and (c) an optional vector comprising (a) and (b); wherein the nucleic acid barcode is located 3' to the TF ORF. In some embodiments, the TF ORF encodes a developmentally critical TF, optionally selected from the TFs listed in Table 1.

[0008] In some embodiments, the TF screening library comprises, consists of, or consists essentially of at least 10, at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, or at least 100 nucleic acids or vectors, wherein each nucleic acid or vector comprises, consists of, or consists essentially of a distinct nucleic acid encoding a TF ORF.

[0009] In some embodiments, the TF screening library further comprises, consists of, or consists essentially of a nucleic acid encoding a selectable marker. In some embodiments, the TF screening library further comprises, consists of, or consists essentially of a nucleic acid encoding an expression control element. In some embodiments, the expression control element is a promoter or a long terminal repeat (LTR). In some embodiments, the TF screening library further comprises, consists of, or consists essentially of a nucleic acid encoding a translation elongation factor, optionally wherein the translation elongation factor is Ef1a.

[0010] In some embodiments, the vector is a retroviral vector, optionally a lentiviral vector.

[0011] In another aspect, provided herein is a viral packaging system comprising, consisting of, or consisting essentially of at least one isolated nucleic acid comprising, consisting of, or consisting essentially of (a) a nucleic acid encoding a transcription factor (TF) open reading frame (ORF); (b) a nucleic acid barcode, and (c) an optional vector comprising (a) and (b); wherein the nucleic acid barcode is located 3' to the TF ORF; or aTF screening library; and a packaging plasmid.

[0012] In another aspect, provided herein is a method for producing a viral particle, the method comprising, consisting of, or consisting essentially of transfecting a packaging cell line with a viral packaging system comprising, consisting of, or consisting essentially of at least one isolated nucleic acid comprising, consisting of, or consisting essentially of (a) a nucleic acid encoding a transcription factor (TF) open reading frame (ORF); (b) a nucleic acid barcode, and (c) an optional vector comprising (a) and (b); wherein the nucleic acid barcode is located 3' to the TF ORF; or aTF screening library; and a packaging plasmid under conditions suitable to package the vector or the TF screening library into a viral particle. In another aspect, also provided herein is a viral particle produced by this method, and optionally a carrier. In another aspect, also provided herein is an isolated cell comprising a nucleic acid, vector, or particle as described herein, and optionally a carrier.

[0013] In another aspect, provided herein is a kit comprising, consisting of, or consisting essentially of at least one of (a) a nucleic acid or vector according to any of the embodiments described herein; and/or (b) a TF screening library according to any of the embodiments described herein; and/or (c) a viral packaging system according to any of the embodiments described herein; and/or (d) a viral particle according to any of the embodiments described herein; and/or (e) an isolated cell according to any of the embodiments described herein, and optionally instructions for use.

[0014] In another aspect, provided herein is a method of performing a high throughput gene activation screen, the method comprising, consisting of, or consisting essentially

of: (a) transducing a target cell with the viral particle according to any of the embodiments described herein; and (b) performing scRNA-seq on the transduced target cell to identify the nucleic acid barcode. In some embodiments, the method further comprises or consists of determining a fitness effect in the transduced target cell. In some embodiments, the method further comprises or consists of identifying a co-perturbation network. In some embodiments, the method further comprises or consists of identifying a functional gene module. In some embodiments, the target cell is a stem cell. In some embodiments, the stem cell is an embryonic stem cell (ESC) or an induced pluripotent stem cell (iPSC). In some embodiments, the target cell is a mammalian cell, optionally wherein the mammalian cell is an equine, bovine, canine, murine, porcine, feline, or human cell. In a particular embodiment, the target cell is a human cell.

[0015] In other aspects, also provided herein is a method driving differentiation of a stem cell into an endothelial cell, the method comprising, consisting of, or consisting essentially of inducing ectopic expression of ETV2 in a stem cell under conditions suitable to support differentiation of the stem cell into an endothelial cell. In some embodiments, ectopic expression of ETV2 is induced by transducing the stem cell with a vector comprising a nucleic acid encoding ETV2 and a nucleic acid encoding an expression control element. In some embodiments, the stem cell is an ESC or an iPSC. In some embodiments, the stem cell is a mammalian cell, optionally wherein the mammalian cell is an equine, bovine, canine, murine, porcine, feline, or human cell. In some embodiments, the stem cell is a human cell. In some embodiments, the stem cell has been genetically modified. In some embodiments, the method further comprises or consists of genetically modifying the stem cell or the endothelial cell.

[0016] In further aspect, also provided herein is an endothelial cell produced by a method driving differentiation of a stem cell into an endothelial cell, the method comprising, consisting of, or consisting essentially of inducing ectopic expression of ETV2 in a stem cell under conditions suitable to support differentiation of the stem cell into an endothelial cell, and optionally a carrier. In some embodiments, the endothelial cell expresses at least one of CDH5, PECAM1, or VWF.

[0017] In another aspect, also provided herein is a population of endothelial cells produced by a method driving differentiation of a stem cell into an endothelial cell, the method comprising, consisting of, or consisting essentially of inducing ectopic expression of ETV2 in a stem cell under conditions suitable to support differentiation of the stem cell into an endothelial cell, and optionally a carrier.

[0018] In some aspects, provided herein is a composition comprising, consisting of, or consisting essentially of an endothelial cell produced by a method driving differentiation of a stem cell into an endothelial cell, the method comprising, consisting of, or consisting essentially of inducing ectopic expression of ETV2 in a stem cell under conditions suitable to support differentiation of the stem cell into an endothelial cell, or a population of endothelial cells produced according to a method described herein, and one or more of: a pharmaceutically acceptable carrier, a cryopreservative or a preservative. In some embodiments, the carrier is a pharmaceutically acceptable carrier. In some embodiments, the cryopreservative is suitable for long term storage of the composition at a temperature ranging from −200° C. to 0° C., from −80° C. to 0° C., from −20° C. to 0° C., or from 0° C. to 10° C.

[0019] In some aspects, provided herein is a method of treating a subject in need thereof, the method comprising, consisting of, or consisting essentially of administering an endothelial cell produced by a method driving differentiation of a stem cell into an endothelial cell, the method comprising, consisting of, or consisting essentially of inducing ectopic expression of ETV2 in a stem cell under conditions suitable to support differentiation of the stem cell into an endothelial cell, or a population of endothelial cells produced according to a method described herein, or a composition comprising, consisting of, or consisting essentially of the endothelial cell or population and a carrier to the subject. In some embodiments of the method, an effective amount of the endothelial cell, population, or composition is administered to the subject. In some embodiments, the endothelial cell or population is allogenic or autologous to the subject being treated.

[0020] In some embodiments of the method, the subject has a wound, a corneal disease or condition, a myocardial infarction, or a vascular disease or condition. In some embodiments, the subject has a corneal disease or condition. In some embodiments, the administration is local or systemic. In some embodiments, the endothelial cell, population, or composition is administered to the subject's eye.

[0021] In some embodiments of the method, the subject is a mammal and the mammal is an equine, bovine, canine, murine, porcine, feline, or human. In some embodiments, the mammal is a human. In some embodiments, the endothelial cells are autologous or allogeneic to the subject being treated.

BRIEF DESCRIPTION OF THE FIGURES

[0022] FIGS. **1**A-**1**F: SEUSS workflow and identification of significant TFs from fitness and scRNA-seq analysis. (FIG. **1**A) Schematic of experimental and analytical framework for evaluation of effects of transcription factor (TF) overexpression in hPSCs: Individual TFs are cloned into the barcoded ORF overexpression vector, pooled and packaged into lentiviral libraries for transduction of hPSCs. Transduced cells are harvested at a fixed time point to be assayed as single cells using droplet based scRNA-seq to evaluate transcriptomic changes. Cells are genotyped by amplifying the overexpression transcript from scRNA-seq cDNA prior to fragmentation and library construction, and identifying the overexpressed TF barcode for each cell. The cell count for each genotype is used to estimate fitness. Gene expression matrices from scRNA-seq are used to obtain differential gene expression and clustering signatures which in turn are used for evaluation of cell state reprogramming and gene regulatory network analysis. (FIG. **1**B) Fitness effect of TFs: log fold change of individual TFs, calculated as cell counts normalized against plasmid library read counts. (FIG. **1**C) t-SNE projection (left panel), and cluster enrichment of significant TFs in clusters (right panel) from screens in pluripotent stem cell medium. (FIG. **1**D) t-SNE projection (left panel), and cluster enrichment of significant TFs in clusters (right panel) from screens in unilineage (endothelial) growth medium. (FIG. **1**E) t-SNE projection (left panel), and enrichment of significant TFs in clusters (right panel) from screens in multilineage differentiation medium. (FIG. **1**F) Number of differentially expressed genes for TFs

across different growth media. The TFs in (FIG. **1**C), (FIG. **1**D), (FIG. **1**E) and (FIG. **1**F) were chosen as significant with the following criteria: cluster enrichment with a false discovery rate (FDR) of less than 10^{-6} and a cluster enrichment profile different from control (mCherry) with a FDR less than 10^{-6}, or if the TF drove differential expression of more than 100 genes.

[0023] FIGS. **2**A-**2**G: Effect of TF overexpression on gene-to-gene co-perturbation network (FIG. **2**A) Schematic for gene-gene co-perturbation network analysis: A SNN network is built from the linear model coefficients and the network is then segmented into gene modules. Genes have a highly weighted edge between them if they respond similarly to TF overexpression. (FIG. **2**B) Gene module network: Node size indicates the number of genes in the module; Edge size indicates distance between modules. (FIG. **2**C) Effect of TF overexpression on gene modules: (FIG. **2**D) Schematic of functional domains of c-MYC: MYC Box I (MBI) and MYC Box II (II) which are essential for transactivation of target genes are housed in the amino-terminal domain (NTD); the basic (b) helix-loop-helix (HLH) leucine zipper (LZ) motif, which is required for heterodimerization with the MAX protein is housed in the carboxy-terminal domain (CTD); the nuclear localization signal domain (NLS) is located in the central region of the protein. (FIG. **2**E) Effect of MYC mutant overexpression on gene modules. (FIG. **2**F) Schematic of KLF gene family protein structure grouped by common structural and functional features (FIG. **2**G) Effect of KLF family overexpression on gene modules. For heatmaps in (FIG. **2**C), (FIG. **2**E), (FIG. **2**F), effect size was calculated as the average of the linear model coefficients for a given TF perturbation across all genes within a module.

[0024] FIGS. **3**A-**3**H: Elucidating effects of KLF4, SNAI2 and ETV2 (FIG. **3**A) Effect of KLF4 and SNAI2 on a subnetwork of the pluripotent state module, encompassing key pluripotency regulators. Node size indicates the effect size; blue nodes are downregulated, red nodes are upregulated. (FIG. **3**B) PC plot of performing PCA on 200 genes from the Hallmark Epithelial Mesenchymal Transition gene-set from MSigDB[42]. PC1 corresponds to an EMT-like signature. (FIG. **3**C) Effect of KLF4 and SNAI2 on selected epithelial and mesenchymal markers, including key Cadherin genes. (FIG. **3**D) Correlation between fitness estimate from scRNA-seq genotype counts and bulk fitness estimate from gDNA in hPSC medium. (FIG. **3**E) Morphology change for cells transduced with either ETV2 or mCherry in EGM. (FIG. **3**F) Immunofluorescence micrograph of CDH5 labelled day 6 ETV2- or mCherry-transduced cells. (FIG. **3**G) qRT-PCR analysis of signature endothelial genes CDH5, PECAM1, VWF and KDR, at day 6 post-transduction. Data were normalized to GAPDH and expressed relative to control cells in pluripotent stem cell medium. (FIG. **3**H) Tube formation assay for day 6 ETV2- or mCherry-transduced cells

[0025] FIG. **4**: Schematic of cloning strategy for synthesis of barcoded ORF vectors. The construction involved two steps: (i) insertion of a pool of barcodes into the backbone after digestion with HpaI, (ii) individually substituting mCherry with TFs after digestion with BamHI.

[0026] FIGS. **5**A-**5**C: Fitness analysis from genomic DNA and correlation with fitness from scRNA-seq genotyped cell counts (FIG. **5**A) Log fold-change of TF read counts amplified from genomic DNA vs plasmid library control (FIG. **5**B) Log fold change of TF counts vs plasmid library control for genomic DNA reads vs cell counts fitness for: (FIG. **5**B) Unilineage medium (endothelial growth medium) (FIG. **5**C) Multilineage medium.

[0027] FIGS. **6**A-**6**D: Differential gene expression analysis of significant TFs (FIG. **6**A) Heatmap of differentially expressed genes for significant TFs in hPSC medium. (FIG. **6**B) Heatmap of differentially expressed genes for significant TFs in endothelial growth medium. (FIG. **6**C) Heatmap of differentially expressed genes for significant TFs in multilineage medium (FIG. **6**D) Heatmap showing signed log p-values of enrichment for differentially expressed homologous genes in mESCs upon overexpression of TFs[25]. ASCL1, CDX2, KLF4, MYOD1, and OTX2 display a high degree of overlap with overexpression of their homologs in mESCs.

[0028] FIGS. **7**A-**7**F: Correlation between aggregated samples. For all plots, correlation was between the coefficients of significant hits, with a hit being defined as a gene—TF pair with the following significance criteria: (FDR<0.05, |coef|>0.025). (FIGS. **7**A-**7**E) Correlation between significant hits in the combined hPSC dataset with hits in each individual dataset. (FIG. **7**F) Correlation of hits between the two multilineage datasets.

[0029] FIGS. **8**A-**8**C: Correlation between fitness and transcriptomic effects. (FIG. **8**A) Correlation of the number of differentially expressed genes for each TF vs the fitness effect (log-FC) for hPSC medium (FIG. **8**B) Correlation of the number of differentially expressed genes for each TF vs the fitness effect (log-FC) for endothelial medium (FIG. **8**C) Correlation of the number of differentially expressed genes for each TF vs the fitness effect (log-FC) for multilineage medium.

[0030] FIGS. **9**A-**9**D: Confirmatory assays for effects of KLF4 and SNAI2 on key genes in the pluripotency network and involved in EMT (FIG. **9**A) qRT-PCR analysis of signature pluripotency network genes SOX2, POU5F1, NANOG, DNMT3B, DPPA4 and SALL2 at day 5 post-transduction in in pluripotent stem cell medium. (FIG. **9**B) qRT-PCR analysis of signature cadherins during EMT: CDH1 and CDH2 at day 5 post-transduction in pluripotent stem cell medium. (FIG. **9**C) qRT-PCR analysis of signature epithelial marker genes during EMT: EPCAM, LAMC1 and SPP1 at day 5 post-transduction in pluripotent stem cell medium. (FIG. **9**D) qRT-PCR analysis of signature mesenchymal marker genes during EMT: TPM2, THY1 and VIM at day 5 post-transduction in pluripotent stem cell medium. Data for all assays were normalized to GAPDH and expressed relative to control cells.

[0031] FIGS. **10**A-**10**B: Correlation of KLF4 and MYC effects across samples. (FIG. **10**A) Correlation of KLF4 effects in the KLF family screen with KLF4 effects in the hPSC screen. (FIG. **10**B) Correlation of MYC effects in the MYC mutants screen with KLF4 effects in the hPSC screen.

DETAILED DESCRIPTION

[0032] Unless defined otherwise, all technical and scientific terms used herein have the same meanings as commonly understood by one of ordinary skill in the art to which this invention belongs. Although any methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, the preferred methods, devices, and materials are now described. All technical and patent publications cited herein

are incorporated herein by reference in their entirety. Nothing herein is to be construed as an admission that the invention is not entitled to antedate such disclosure by virtue of prior invention.

[0033] The practice of the present invention will employ, unless otherwise indicated, conventional techniques of tissue culture, immunology, molecular biology, microbiology, cell biology and recombinant DNA, which are within the skill of the art. See, e.g., Sambrook and Russell eds. (2001) Molecular Cloning: A Laboratory Manual, 3rd edition; the series Ausubel et al. eds. (2007) Current Protocols in Molecular Biology; the series Methods in Enzymology (Academic Press, Inc., N.Y.); MacPherson et al. (1991) PCR 1: A Practical Approach (IRL Press at Oxford University Press); MacPherson et al. (1995) PCR 2: A Practical Approach; Harlow and Lane eds. (1999) Antibodies, A Laboratory Manual; Freshney (2005) Culture of Animal Cells: A Manual of Basic Technique, 5th edition; Gait ed. (1984) Oligonucleotide Synthesis; U.S. Pat. No. 4,683,195; Hames and Higgins eds. (1984) Nucleic Acid Hybridization; Anderson (1999) Nucleic Acid Hybridization; Hames and Higgins eds. (1984) Transcription and Translation; Immobilized Cells and Enzymes (IRL Press (1986)); Perbal (1984) A Practical Guide to Molecular Cloning; Miller and Calos eds. (1987) Gene Transfer Vectors for Mammalian Cells (Cold Spring Harbor Laboratory); Makrides ed. (2003) Gene Transfer and Expression in Mammalian Cells; Mayer and Walker eds. (1987) Immunochemical Methods in Cell and Molecular Biology (Academic Press, London); Herzenberg et al. eds (1996) Weir's Handbook of Experimental Immunology; Manipulating the Mouse Embryo: A Laboratory Manual, 3rd edition (Cold Spring Harbor Laboratory Press (2002)); Sohail (ed.) (2004) Gene Silencing by RNA Interference: Technology and Application (CRC Press).

[0034] All numerical designations, e.g., pH, temperature, time, concentration, and molecular weight, including ranges, are approximations which are varied (+) or (−) by increments of 0.1 or 1.0, where appropriate. It is to be understood, although not always explicitly stated that all numerical designations are preceded by the term "about." It also is to be understood, although not always explicitly stated, that the reagents described herein are merely exemplary and that equivalents of such are known in the art.

Definitions

[0035] As used in the specification and claims, the singular form "a", "an" and "the" include plural references unless the context clearly dictates otherwise. For example, the term "a cell" includes a plurality of cells, including mixtures thereof.

[0036] As used herein, the term "comprising" or "comprises" is intended to mean that the compositions and methods include the recited elements, but not excluding others. "Consisting essentially of" when used to define compositions and methods, shall mean excluding other elements of any essential significance to the combination for the stated purpose. Thus, a composition consisting essentially of the elements as defined herein would not exclude trace contaminants from the isolation and purification method and pharmaceutically acceptable carriers, such as phosphate buffered saline, preservatives and the like. "Consisting of" shall mean excluding more than trace elements of other ingredients and substantial method steps for administering the compositions of this disclosure or process steps to produce a composition or achieve an intended result. Embodiments defined by each of these transition terms are within the scope of this disclosure.

[0037] As is known to those of skill in the art, there are 6 classes of viruses. The DNA viruses constitute classes I and II. The RNA viruses and retroviruses make up the remaining classes. Class III viruses have a double-stranded RNA genome. Class IV viruses have a positive single-stranded RNA genome, the genome itself acting as mRNA Class V viruses have a negative single-stranded RNA genome used as a template for mRNA synthesis. Class VI viruses have a positive single-stranded RNA genome but with a DNA intermediate not only in replication but also in mRNA synthesis. Retroviruses carry their genetic information in the form of RNA; however, once the virus infects a cell, the RNA is reverse-transcribed into the DNA form which integrates into the genomic DNA of the infected cell. The integrated DNA form is called a provirus.

[0038] A "viral vector" is defined as a recombinantly produced virus or viral particle that comprises a nucleic acid to be delivered into a host cell, either in vivo, ex vivo or in vitro. Examples of viral vectors include retroviral vectors, lentiviral vectors, adenovirus vectors, adeno-associated virus vectors, alphavirus vectors and the like. Alphavirus vectors, such as Semliki Forest virus-based vectors and Sindbis virus-based vectors, have also been developed for use in gene therapy and immunotherapy. See, Schlesinger and Dubensky (1999) Curr. Opin. Biotechnol. 5:434-439 and Ying, et al. (1999) Nat. Med. 5(7):823-827.

[0039] In aspects where gene transfer is mediated by a lentiviral vector, a vector construct refers to the polynucleotide comprising the lentiviral genome or part thereof, and a therapeutic gene. As used herein, "lentiviral mediated gene transfer" or "lentiviral transduction" carries the same meaning and refers to the process by which a gene or nucleic acid sequences are stably transferred into the host cell by virtue of the virus entering the cell and integrating its genome into the host cell genome. The virus can enter the host cell via its normal mechanism of infection or be modified such that it binds to a different host cell surface receptor or ligand to enter the cell. Retroviruses carry their genetic information in the form of RNA; however, once the virus infects a cell, the RNA is reverse-transcribed into the DNA form which integrates into the genomic DNA of the infected cell. The integrated DNA form is called a provirus. As used herein, lentiviral vector refers to a viral particle capable of introducing exogenous nucleic acid into a cell through a viral or viral-like entry mechanism. A "lentiviral vector" is a type of retroviral vector well-known in the art that has certain advantages in transducing nondividing cells as compared to other retroviral vectors. See, Trono D. (2002) Lentiviral vectors, New York: Spring-Verlag Berlin Heidelberg.

[0040] Lentiviral vectors of this disclosure include vectors based on or derived from oncoretroviruses (the sub-group of retroviruses containing MLV), and lentiviruses (the sub-group of retroviruses containing HIV). Examples include ASLV, SNV and RSV all of which have been split into packaging and vector components for lentiviral vector particle production systems. The lentiviral vector particle according to this disclosure may be based on a genetically or otherwise (e.g. by specific choice of packaging cell system) altered version of a particular retrovirus.

[0041] That the vector particle according to the disclosure is "based on" a particular retrovirus means that the vector is

derived from that particular retrovirus. The genome of the vector particle comprises components from that retrovirus as a backbone. The vector particle contains essential vector components compatible with the RNA genome, including reverse transcription and integration systems. Usually these will include gag and pol proteins derived from the particular retrovirus. Thus, the majority of the structural components of the vector particle will normally be derived from that retrovirus, although they may have been altered genetically or otherwise so as to provide desired useful properties. However, certain structural components and in particular the env proteins, may originate from a different virus. The vector host range and cell types infected or transduced can be altered by using different env genes in the vector particle production system to give the vector particle a different specificity.

[0042] The term "an expression control element" as used herein, intends a polynucleotide that is operatively linked to a target polynucleotide to be transcribed, and facilitates the expression of the target polynucleotide. A promoter is an example of an expression control element.

[0043] The term "promoter" refers to a nucleic acid sequence (e.g., a region of genomic DNA) that initiates transcription of a particular gene. The promoter includes the core promoter, which is the minimal portion of the promoter required to properly initiate transcription and can also include regulatory elements such as transcription factor binding sites. The regulatory elements may promote transcription or inhibit transcription. Regulatory elements in the promoter can be binding sites for transcriptional activators or transcriptional repressors. A promoter can be constitutive or inducible. A constitutive promoter refers to one that is always active and/or constantly directs transcription of a gene above a basal level of transcription. An inducible promoter is one which is capable of being induced by a molecule or a factor added to the cell or expressed in the cell. An inducible promoter may still produce a basal level of transcription in the absence of induction, but induction typically leads to significantly more production of the protein. Non-tissue specific promoters include but are not limited to human cytomegalovirus (CMV), CMV enhancer/chicken (3-actin (CBA) promoter, Rous sarcoma virus (RSV), simian virus 40 (SV40) and mammalian elongation factor 1α (EF1α), are non-specific promoters and are commonly used in gene therapy vectors. Promoters can also be tissue specific. A tissue specific promoter allows for the production of a protein in a certain population of cells that have the appropriate transcriptional factors to activate the promoter.

[0044] A "target cell" as used herein, shall intend a cell containing the genome into which polynucleotides that are operatively linked to an expression control element are to be integrated. Cells that are infected with a lentivirus or susceptible to lentiviral infection are non-limiting examples of target cells.

[0045] "Host cell" refers not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

[0046] The terms "polynucleotide," "nucleic acid," and "oligonucleotide" are used interchangeably and refer to a polymeric form of nucleotides of any length, either deoxyribonucleotides or ribonucleotides or analogs thereof. Polynucleotides can have any three-dimensional structure and may perform any function, known or unknown. The following are non-limiting examples of polynucleotides: a gene or gene fragment (for example, a probe, primer, EST or SAGE tag), exons, introns, messenger RNA (mRNA), transfer RNA, ribosomal RNA, ribozymes, cDNA, recombinant polynucleotides, branched polynucleotides, plasmids, vectors, isolated DNA of any sequence, isolated RNA of any sequence, nucleic acid probes and primers. A polynucleotide can comprise modified nucleotides, such as methylated nucleotides and nucleotide analogs. If present, modifications to the nucleotide structure can be imparted before or after assembly of the polynucleotide. The sequence of nucleotides can be interrupted by non-nucleotide components. A polynucleotide can be further modified after polymerization, such as by conjugation with a labeling component. The term also refers to both double- and single-stranded molecules. Unless otherwise specified or required, any embodiment of this this disclosure that is a polynucleotide encompasses both the double-stranded form and each of two complementary single-stranded forms known or predicted to make up the double-stranded form.

[0047] A polynucleotide is composed of a specific sequence of four nucleotide bases: adenine (A); cytosine (C); guanine (G); thymine (T); and uracil (U) for thymine when the polynucleotide is RNA. Thus, the term "polynucleotide sequence" is the alphabetical representation of a polynucleotide molecule. This alphabetical representation can be input into databases in a computer having a central processing unit and used for bioinformatics applications such as functional genomics and homology searching.

[0048] The term "isolated" as used herein refers to molecules or biological or cellular materials being substantially free from other materials, e.g., greater than 70%, or 80%, or 85%, or 90%, or 95%, or 98%. In one aspect, the term "isolated" refers to nucleic acid, such as DNA or RNA, or protein or polypeptide, or cell or cellular organelle, or tissue or organ, separated from other DNAs or RNAs, or proteins or polypeptides, or cells or cellular organelles, or tissues or organs, respectively, that are present in the natural source and which allow the manipulation of the material to achieve results not achievable where present in its native or natural state, e.g., recombinant replication or manipulation by mutation. The term "isolated" also refers to a nucleic acid or peptide that is substantially free of cellular material, viral material, or culture medium when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. Moreover, an "isolated nucleic acid" is meant to include nucleic acid fragments which are not naturally occurring as fragments and would not be found in the natural state. The term "isolated" is also used herein to refer to polypeptides which are isolated from other cellular proteins and is meant to encompass both purified and recombinant polypeptides, e.g., with a purity greater than 70%, or 80%, or 85%, or 90%, or 95%, or 98%. The term "isolated" is also used herein to refer to cells or tissues that are isolated from other cells or tissues and is meant to encompass both cultured and engineered cells or tissues.

[0049] As used herein, "stem cell" defines a cell with the ability to divide for indefinite periods in culture and give rise to specialized cells. At this time and for convenience, stem

cells are categorized as somatic (adult), embryonic or induced pluripotent stem cells. A somatic stem cell is an undifferentiated cell found in a differentiated tissue that can renew itself (clonal) and (with certain limitations) differentiate to yield all the specialized cell types of the tissue from which it originated. An embryonic stem cell is a primitive (undifferentiated) cell from the embryo that has the potential to become a wide variety of specialized cell types. Pluripotent embryonic stem cells can be distinguished from other types of cells by the use of markers including, but not limited to, Oct-4, alkaline phosphatase, CD30, TDGF-1, GCTM-2, Genesis, Germ cell nuclear factor, SSEA1, SSEA3, and SSEA4.

[0050] The term "culturing" refers to the in vitro propagation of cells or organisms on or in synthetic culture conditions such as culture media of various kinds. In some aspects, the medium is changed daily. It is understood that the descendants of a cell grown in culture may not be completely identical (i.e., morphologically, genetically, or phenotypically) to the parent cell. By "expanded" is meant any proliferation, growth, or division of cells. Disclosed herein are culture methods that support differentiation by in inclusion of nutrients and effector molecules necessary to promote or support the differentiation of stem cells into differentiated cells.

[0051] "Differentiation" describes the process whereby an unspecialized cell acquires the features of a specialized cell such as a heart, liver, pancreas, or muscle cell. "Directed differentiation" refers to the manipulation of stem cell culture conditions to induce differentiation into a particular cell type. "Dedifferentiated" defines a cell that reverts to a less committed position within the lineage of a cell. As used herein, the term "differentiates or differentiated" defines a cell that takes on a more committed ("differentiated") position within the lineage of a cell and may also include maturation or development of the cell. As used herein, "a cell that differentiates into pancreatic beta cell" defines any cell that can become a committed pancreatic cells that produces insulin. Non-limiting examples of cells that are capable of differentiating into endothelial cells include embryonic stem cells, pluripotent stem cells, induced pluripotent stem cells (iPSCs), mesenchymal stem cell, hematopoietic stem cells, and adipose stem cells.

[0052] As used herein, a "pluripotent cell" defines a less differentiated cell that can give rise to at least two distinct (genotypically and/or phenotypically) further differentiated progeny cells. In another aspect, a "pluripotent cell" includes an Induced Pluripotent Stem Cell (iPSC) which is an artificially derived stem cell from a non-pluripotent cell, typically an adult somatic cell, produced by inducing expression of one or more stem cell specific genes.

[0053] A "composition" is intended to encompass a combination of active agent and another "carrier," e.g., compound or composition, inert (for example, a detectable agent or label) or active, such as an adjuvant, diluent, binder, stabilizer, buffers, salts, lipophilic solvents, preservative, adjuvant or the like. Compositions may include stabilizers and preservatives. As used herein, the term "pharmaceutically acceptable carrier" encompasses any of the standard pharmaceutical carriers, such as a phosphate buffered saline solution, water, and emulsions, such as an oil/water or water/oil emulsion, and various types of wetting agents. For examples of carriers, stabilizers and adjuvants, see Martin (1975) Remington's Pharm. Sci., 15th Ed. (Mack Publ. Co., Easton). Carriers also include biocompatible scaffolds, pharmaceutical excipients and additives proteins, peptides, amino acids, lipids, and carbohydrates (e.g., sugars, including monosaccharides, di-, tri-, tetra-, and oligosaccharides; derivatized sugars such as alditols, aldonic acids, esterified sugars and the like; and polysaccharides or sugar polymers), which can be present singly or in combination, comprising alone or in combination 1-99.99% by weight or volume. Exemplary protein excipients include serum albumin such as human serum albumin (HSA), recombinant human albumin (rHA), gelatin, casein, and the like. Representative amino acid/antibody components, which can also function in a buffering capacity, include alanine, glycine, arginine, betaine, histidine, glutamic acid, aspartic acid, cysteine, lysine, leucine, isoleucine, valine, methionine, phenylalanine, aspartame, and the like. Carbohydrate excipients are also intended within the scope of this this disclosure, examples of which include but are not limited to monosaccharides such as fructose, maltose, galactose, glucose, D-mannose, sorbose, and the like; disaccharides, such as lactose, sucrose, trehalose, cellobiose, and the like; polysaccharides, such as raffinose, melezitose, maltodextrins, dextrans, starches, and the like; and alditols, such as mannitol, xylitol, maltitol, lactitol, xylitol sorbitol (glucitol) and myo-inositol.

[0054] A population of cells intends a collection of more than one cell that is identical (clonal) or non-identical in phenotype and/or genotype.

[0055] "Substantially homogeneous" describes a population of cells in which more than about 50%, or alternatively more than about 60%, or alternatively more than 70%, or alternatively more than 75%, or alternatively more than 80%, or alternatively more than 85%, or alternatively more than 90%, or alternatively, more than 95%, of the cells are of the same or similar phenotype. Phenotype can be determined by assaying for expression of a pre-selected cell surface marker or other marker.

[0056] An "effective amount" is an amount sufficient to effect beneficial or desired results. In the context of a therapeutic cell, population, or composition, the term "effective amount" as used herein refers to the amount to alleviate at least one or more symptom of a disease, disorder, or condition (e.g., corneal condition), and relates to a sufficient amount of the cell, population, or composition to provide the desired effect (e.g., repair of the cornea). An effective amount as used herein would also include an amount sufficient to delay the development of a disease, disorder, or condition symptom, alter the course of disease, disorder, or condition symptom (for example but not limited to, slow the progression of corneal degradation), or reverse a symptom of a disease, disorder, or condition. Thus, it is not possible to specify the exact "effective amount." However, for any given case, an appropriate "effective amount" can be determined by one of ordinary skill in the art using only routine experimentation.

[0057] An effective amount can be administered in one or more administrations, applications or dosages. Such delivery is dependent on a number of variables including the time period for which the individual dosage unit is to be used, the bioavailability of the therapeutic agent, the route of administration, etc. It is understood, however, that specific dose levels of the therapeutic agents of the present disclosure for any particular subject depends upon a variety of factors including the activity of the specific compound employed,

the age, body weight, general health, sex, and diet of the subject, the time of administration, the rate of excretion, the drug combination, and the severity of the particular disorder being treated and form of administration. Treatment dosages generally may be titrated to optimize safety and efficacy. The dosage can be determined by a physician and adjusted, as necessary, to suit observed effects of the treatment. Typically, dosage-effect relationships from in vitro and/or in vivo tests initially can provide useful guidance on the proper doses for patient administration. In general, one will desire to administer an amount of the compound that is effective to achieve a serum level commensurate with the concentrations found to be effective in vitro. Determination of these parameters is well within the skill of the art. These considerations, as well as effective formulations and administration procedures are well known in the art and are described in standard textbooks. Consistent with this definition, as used herein, the term "therapeutically effective amount" is an amount sufficient to inhibit RNA virus replication ex vivo, in vitro or in vivo. Consistent with this definition, as used herein, the term "therapeutically effective amount" is an amount sufficient to achieve the result of the method.

[0058] The term "administration" shall include without limitation, administration by oral, parenteral (e.g., intramuscular, intraperitoneal, intravenous, ICV, intracisternal injection or infusion, subcutaneous injection, or implant), by inhalation spray nasal, vaginal, rectal, sublingual, urethral (e.g., urethral suppository) or topical routes of administration (e.g., gel, ointment, cream, aerosol, etc.) and can be formulated, alone or together, in suitable dosage unit formulations containing conventional non-toxic pharmaceutically acceptable carriers, adjuvants, excipients, and vehicles appropriate for each route of administration. The invention is not limited by the route of administration, the formulation or dosing schedule.

[0059] An "enriched population" of cells intends a substantially homogenous population of cells having certain defined characteristics. The cells are greater than 60%, or alternatively greater than 65%, or alternatively greater than 70%, or alternatively greater than 75%, or alternatively greater than 80%, or alternatively greater than 85%, or alternatively greater than 90%, or alternatively greater than 95%, or alternatively greater than 98% identical in the defined characteristics. In one aspect, the substantially homogenous population of cells express markers that correlate with pluripotent cell identity such as expression of stem-cell specific genes like OCT4 and NANOG. In another aspect, the substantially homogenous population of cells express markers that are correlated with definitive endoderm cell identity such SOX17, CXCR4, FOXA2, and GATA4. In another aspect, the substantially homogenous population of cells express markers that are correlated with posterior foregut cell identity such as HNF1β, HNF4A while suppressing expression of HHEX, HOXA3, CDX2, OCT4, and NANOG. In another aspect, the substantially homogenous population of cells express markers that are correlated with pancreatic progenitor cell identity such as PDX1 (pancreatic duodenal homeobox gene 1). In another aspect, the substantially homogenous population of cells express markers that are correlated with endocrine pancreas cell identity such as NKX6.1, NEURO-D1, and NGN3. In yet another aspect, the substantially homogenous population of cells express markers that are correlated with islet precursor cell identity such as INS. This population may further be identified by its ability to secrete C-peptide.

[0060] A "gene" refers to a polynucleotide containing at least one open reading frame that is capable of encoding a particular RNA, polypeptide, or protein after being transcribed and/or translated. The term "express" refers to the production of a gene product. As used herein, "expression" refers to the process by which polynucleotides are transcribed into RNA and/or the process by which the transcribed RNA such as mRNA is subsequently being translated into peptides, polypeptides, or proteins. If the polynucleotide is derived from genomic DNA, expression may include splicing of the mRNA in a eukaryotic cell. A "gene product" or alternatively a "gene expression product" refers to the amino acid (e.g., peptide or polypeptide) or functional RNA (e.g. a tRNA, miRNA, rRNA, or shRNA) generated when a gene is transcribed and translated.

[0061] The term "treating" (or "treatment") of a pancreatic or immune disorder or condition refers to ameliorating the effects of, or delaying, halting or reversing the progress of, or delaying or preventing the onset of, a pancreatic or immune condition such as diabetes, pre-diabetes, juvenile onset (Type I) diabetes mellitus, including pediatric insulin-dependent diabetes mellitus (IDDM), and adult onset diabetes mellitus (Type II diabetes). Treatment includes preventing the disease or condition (i.e., causing the clinical symptoms of the disease not to develop in a patient that may be predisposed to the disease but does not yet experience or display symptoms of the disease), inhibiting the disease or condition (i.e., arresting or reducing the development of the disease or its clinical symptoms), or relieving the disease or condition (i.e., causing regression of the disease or its clinical symptoms).

[0062] A mammalian stem cell, as used herein, intends a stem cell having an origin from a mammal. Non-limiting examples include, e.g., a murine, a canine, an equine, a simian and a human. An animal stem cell intends a stem cell having an origin from an animal, e.g., a mammalian stem cell.

[0063] A "subject," "individual" or "patient" is used interchangeably herein, and refers to a vertebrate, preferably a mammal, more preferably a human. Mammals include, but are not limited to, murines, rats, rabbit, simians, bovines, ovine, porcine, canines, feline, farm animals, sport animals, pets, equine, and primate, particularly human. Besides being useful for human treatment, the methods and compositions disclosed herein are also useful for veterinary treatment of companion mammals, exotic animals and domesticated animals, including mammals, rodents, and the like which is susceptible to diabetes or other immune or pancreatic diseases or conditions. In one embodiment, the mammals include horses, dogs, and cats. In another embodiment of the present disclosure, the human is an adolescent or infant under the age of eighteen years.

[0064] An immature stem cell, as compared to a mature stem cell, intends a phenotype wherein the cell expresses or fails to express one or more markers of a mature phenotype. Examples of such are known in the art, e.g., telomerase length or the expression of actin for mature cardiomyocytes derived or differentiated from a less mature phenotype such as an embryonic stem cell. An immature beta cell intends a pancreatic cell that has insulin secretory granules but lacks

GSIS. In contrast, mature beta cells typically are positive for GSIS and have low lactate dehydrogenase (LDH).

Descriptive Embodiments

[0065] Understanding the complex effects of genetic perturbations on cellular state and fitness in human pluripotent stem cells (hPSCs) has been challenging using traditional pooled screening techniques which typically rely on unidimensional phenotypic readouts. Here, Applicants use barcoded open reading frame (ORF) overexpression libraries with a coupled single-cell RNA sequencing (scRNA-seq) and fitness screening approach, a technique Applicants call SEUSS (ScalablE fUnctional Screening by Sequencing), to establish a comprehensive assaying platform. Using this system, Applicants perturbed hPSCs with a library of developmentally critical transcription factors (TFs), and assayed the impact of TF overexpression on fitness and transcriptomic cell state across multiple media conditions. Applicants further leveraged the versatility of the ORF library approach to systematically assay mutant gene libraries and also whole gene families. From the transcriptomic responses, Applicants built genetic co-perturbation networks to identify key altered gene modules. Strikingly, Applicants found that KLF4 and SNAI2 have opposing effects on the pluripotency gene module, highlighting the power of Applicants' method to characterize the effects of genetic perturbations. From the fitness responses, Applicants identified ETV2 as a driver of reprogramming towards an endothelial-like state.

Isolated Nucleic Acids and Transcription Factor Screening Libraries

[0066] This disclosure provides isolated polynucleotides or nucleic acids comprising, consisting of, or consisting essentially of (a) a polynucleotide or nucleic acid encoding a transcription factor (TF) open reading frame (ORF); (b) a nucleic acid barcode, and (c) an optional vector comprising (a) and (b); wherein the nucleic acid barcode is located 3' to the TF ORF.

[0067] Transcription factors are proteins that bind (directly or indirectly through recruitment factors) to enhancer or promoter regions of DNA (e.g. a genome) and interact to activate, repress, or maintain the current level of transcription of a particular gene or genetic locus. Many transcription factors can bind to specific DNA sequences. Non-limiting examples of TFs can be found at TFCat (Genome Biol. 2009; 10(3): R29).

[0068] An ORF refers to the part of a gene or polynucleotide that has the potential to be transcribed and/or translated. ORFs span intron/exon regions, which in some embodiments can be spliced together after transcription of the ORF to yield a final mRNA for protein translation. Thus, ORFs include both introns and exons, when applicable. In some embodiments, an ORF is a continuous stretch of codons that contain a start codon and a stop codon. In some embodiments, the transcription termination site is located after the ORF, beyond the translation stop codon.

[0069] In some embodiments, the TF ORF encodes a developmentally critical TF. As used herein, "developmentally critical" refers to a transcription factor that regulates development and/or differentiation by modulating transcription. Regulation may include, for example, suppression of one or more specific developmental or differentiation gene expression programs, activation of one or more specific developmental or differentiation gene expression programs, and/or maintenance of a specific level of activation or suppression of a specific developmental or differentiation program. For example, a developmentally critical transcription factor may function upstream of a lineage-specific gene network and direct a stem or progenitor cell to differentiate into that specific cell lineage. Examples of developmentally critical TFs include but are not limited to ASCL1, ASCL3, ASCL4, ASCL5, ATF7, CDX2, CRX, ERG, ESRRG, ETV2, FLI1, FOXA1, FOXA2, FOXA3, FOXP1, GATA1, GATA2, GATA4, GATA6, GLI1, HAND2, HNF1A, HNF1B, HNF4A, HOXA1, HOXA10, HOXA11, HOXB6, KLF4, LHX3, LMX1A, MEF2C, MESP1, MITF, MYC, MYCL, MYCN, MYOD1, MYOG, NEUROD1, NEUROG1, NEUROG3, NRL, ONECUT1, OTX2, PAX7, POU1F1, POU5F1, RUNX, SIX1, SIX2, SNAI2, SOX10, SOX2, SOX3, SPI1, SPIB, SPIC, SRY, TBX5, and TFAP2C.

[0070] In some embodiments, the vector is a retroviral vector, optionally a lentiviral vector.

[0071] This disclosure provides a vector comprising, or alternatively consisting essentially of, or yet further consisting of a viral backbone. In one aspect, the viral backbone contains essential nucleic acids or sequences for integration into a target cell's genome. In one aspect, the essential nucleic acids necessary for integration of the genome of the target cell include at the 5' and 3' ends the minimal LTR regions required for integration of the vector.

[0072] In one aspect, the term "vector" intends a recombinant vector that retains the ability to infect and transduce non-dividing and/or slowly-dividing cells and integrate into the target cell's genome. In several aspects, the vector is derived from or based on a wild-type virus. In further aspects, the vector is derived from or based on a wild-type lentivirus. Examples of such, include without limitation, equine infectious anaemia virus (EIAV), simian immunodeficiency virus (SIV), feline immunodeficiency virus (FIV), and human immunodeficiency virus (HIV). Alternatively, it is contemplated that other retrovirus can be used as a basis for a vector backbone such murine leukemia virus (MLV). It will be evident that a viral vector need not be confined to the components of a particular virus. The viral vector may comprise components derived from two or more different viruses, and may also comprise synthetic components. Vector components can be manipulated to obtain desired characteristics, such as target cell specificity.

[0073] The recombinant vectors of this disclosure are derived from primates and non-primates. Examples of primate lentiviruses include the human immunodeficiency virus (HIV), the causative agent of human acquired immunodeficiency syndrome (AIDS), and the simian immunodeficiency virus (SIV). The non-primate lentiviral group includes the prototype "slow virus" visna/maedi virus (VMV), as well as the related caprine arthritis-encephalitis virus (CAEV), equine infectious anaemia virus (EIAV) and the more recently described feline immunodeficiency virus (FIV) and bovine immunodeficiency virus (BIV). Prior art recombinant lentiviral vectors are known in the art, e.g., see U.S. Pat. Nos. 6,924,123; 7,056,699; 7,07,993; 7,419,829 and 7,442,551, incorporated herein by reference.

[0074] U.S. Pat. No. 6,924,123 discloses that certain retroviral sequence facilitate integration into the target cell genome. This patent teaches that each retroviral genome comprises genes called gag, pol and env which code for virion proteins and enzymes. These genes are flanked at both

ends by regions called long terminal repeats (LTRs). The LTRs are responsible for proviral integration, and transcription. They also serve as enhancer-promoter sequences. In other words, the LTRs can control the expression of the viral genes. Encapsidation of the retroviral RNAs occurs by virtue of a psi sequence located at the 5' end of the viral genome. The LTRs themselves are identical sequences that can be divided into three elements, which are called U3, R and U5. U3 is derived from the sequence unique to the 3' end of the RNA. R is derived from a sequence repeated at both ends of the RNA, and U5 is derived from the sequence unique to the 5'end of the RNA. The sizes of the three elements can vary considerably among different retroviruses. For the viral genome and the site of poly (A) addition (termination) is at the boundary between R and U5 in the right hand side LTR. U3 contains most of the transcriptional control elements of the provirus, which include the promoter and multiple enhancer sequences responsive to cellular and in some cases, viral transcriptional activator proteins.

[0075] With regard to the structural genes gag, pol and env themselves, gag encodes the internal structural protein of the virus. Gag protein is proteolytically processed into the mature proteins MA (matrix), CA (capsid) and NC (nucleocapsid). The pol gene encodes the reverse transcriptase (RT), which contains DNA polymerase, associated RNase H and integrase (IN), which mediate replication of the genome.

[0076] In another aspect, provided herein is a TF screening library comprising, consisting of, or consisting essentially of at least one isolated nucleic acid comprising, consisting of, or consisting essentially of (a) a nucleic acid encoding a transcription factor (TF) open reading frame (ORF); (b) a nucleic acid barcode, and (c) an optional vector comprising (a) and (b); wherein the nucleic acid barcode is located 3' to the TF ORF. In some embodiments, the TF ORF encodes a developmentally critical TF, optionally selected from the TFs listed in Table 1.

[0077] In some embodiments, the TF screening library comprises, consists of, or consists essentially of at least 10, at least 20, at least 30, at least 40, at least 50, at least 60, at least 70, at least 80, at least 90, or at least 100 nucleic acids or vectors, wherein each nucleic acid or vector comprises, consists of, or consists essentially of a distinct nucleic acid encoding a TF ORF.

[0078] In some embodiments, the TF screening library further comprises, consists of, or consists essentially of a nucleic acid encoding a selectable marker (e.g., hygromycin). In some embodiments, the TF screening library further comprises, consists of, or consists essentially of a nucleic acid encoding an expression control element. In some embodiments, the expression control element is a promoter or a long terminal repeat (LTR). In some embodiments, the TF screening library further comprises, consists of, or consists essentially of a nucleic acid encoding a translation elongation factor, optionally wherein the translation elongation factor is Ef1a.

[0079] For the production of viral vector particles, the vector RNA genome is expressed from a DNA construct encoding it, in a host cell. The components of the particles not encoded by the vector genome are provided in trans by additional nucleic acid sequences (the "packaging system", which usually includes either or both of the gag/pol and env genes) expressed in the host cell. The set of sequences required for the production of the viral vector particles may be introduced into the host cell by transient transfection, or they may be integrated into the host cell genome, or they may be provided in a mixture of ways. The techniques involved are known to those skilled in the art.

[0080] In another aspect, provided herein is a viral packaging system comprising, consisting of, or consisting essentially of at least one isolated nucleic acid comprising, consisting of, or consisting essentially of (a) a nucleic acid encoding a transcription factor (TF) open reading frame (ORF); (b) a nucleic acid barcode, and (c) an optional vector comprising (a) and (b); wherein the nucleic acid barcode is located 3' to the TF ORF; or aTF screening library; and a packaging plasmid.

[0081] In another aspect, provided herein is a method for producing a viral particle, the method comprising, consisting of, or consisting essentially of transfecting a packaging cell line with a viral packaging system comprising, consisting of, or consisting essentially of at least one isolated nucleic acid comprising, consisting of, or consisting essentially of (a) a nucleic acid encoding a transcription factor (TF) open reading frame (ORF); (b) a nucleic acid barcode, and (c) an optional vector comprising (a) and (b); wherein the nucleic acid barcode is located 3' to the TF ORF; or aTF screening library; and a packaging plasmid under conditions suitable to package the vector or the TF screening library into a viral particle. In another aspect, also provided herein is a viral particle produced by this method, and optionally a carrier. In another aspect, also provided herein is an isolated cell comprising a nucleic acid, vector, or particle as described herein, and optionally a carrier.

[0082] Retroviral vectors for use in the methods and compositions described herein include, but are not limited to Invitrogen's pLenti series versions 4, 6, and 6.2 "ViraPower" system. Manufactured by Lentigen Corp.; pHIV-7-GFP, lab generated and used by the City of Hope Research Institute; "Lenti-X" lentiviral vector, pLVX, manufactured by Clontech; pLKO.1-puro, manufactured by Sigma-Aldrich; pLemi®, manufactured by Open Biosystems; and pLV, lab generated and used by Charité Medical School, Institute of Virology (CBF), Berlin, Germany.

[0083] This invention also provides the suitable packaging cell line. In one aspect, the packaging cell line is the HEK-293 cell line. Other suitable cell lines are known in the art, for example, described in the patent literature within U.S. Pat. Nos. 7,070,994; 6,995,919; 6,475,786; 6,372,502; 6,365,150 and 5,591,624, each incorporated herein by reference.

[0084] Yet further provided is an isolated cell or population of cells, comprising, or alternatively consisting essentially of, or yet further consisting of, a retroviral particle of this invention, which in one aspect, is a viral particle. In one aspect, the isolated host cell is a packaging cell line.

Kits

[0085] In another aspect, provided herein is a kit comprising, consisting of, or consisting essentially of at least one of (a) a nucleic acid or vector according to any of the embodiments described herein; and/or (b) a TF screening library according to any of the embodiments described herein; and/or (c) a viral packaging system according to any of the embodiments described herein; and/or (d) a viral particle according to any of the embodiments described herein; and/or (e) an isolated cell according to any of the embodiments described herein, and optionally instructions for use.

High Throughput Gene Activation Screens

[0086] In another aspect, provided herein is a method of performing a high throughput gene activation screen, the method comprising, consisting of, or consisting essentially of: (a) transducing a target cell with the viral particle according to any of the embodiments described herein; and (b) performing single cell RNA sequencing (scRNA-seq) on the transduced target cell to identify the nucleic acid barcode.

[0087] In some embodiments, scRNA-seq methods comprise the following steps: isolation of single cell and RNA, reverse transcription (RT), optional amplification, library generation, and sequencing. Several scRNA-seq protocols appropriate for use with the disclosed methods have been published: Tang et al. (Nat Methods. 6 (5): 377-82) STRT (Islam, S. et al. (2011). Genome Res. 21 (7): 1160-7), SMART-seq (Ramskold, D. et al. (2012). Nat. Biotechnol. 30 (8): 777-82) CEL-seq (Hashimshony, T. et al. (2012) Cell Rep. 2 (3): 666-73), and Quartz-seq (Sasagawa, Y. et al. (2013) Genome Biol. 14 (4): R31).

[0088] In some embodiments, the method further comprises or consists of determining a fitness effect in the transduced target cell. Fitness effects include but are not limited to effects on cell proliferation, effects on cell viability, effects on rate of senescence, effects on apoptosis, effects on DNA repair mechanisms, effects on genome stability, effects on gene transcription, and effects on stress response. In some embodiments, fitness effects are calculated from genomic DNA or mRNA reads,

[0089] In some embodiments, the method further comprises or consists of identifying a co-perturbation network. In some embodiments, the method further comprises or consists of identifying a functional gene module. In some embodiments, the target cell is a stem cell. In some embodiments, the stem cell is an embryonic stem cell (ESC) or an induced pluripotent stem cell (iPSC). In some embodiments, the target cell is a mammalian cell, optionally wherein the mammalian cell is an equine, bovine, canine, murine, porcine, feline, or human cell. In a particular embodiment, the target cell is a human cell.

Endothelial Differentiation Methods and Compositions

[0090] Also provided herein is a method driving or directing differentiation of a stem cell into an endothelial cell, the method comprising, consisting of, or consisting essentially of inducing ectopic expression of ETV2 (Ets variant 2, Entrez gene: 2116) in a stem cell under conditions suitable to support differentiation of the stem cell into an endothelial cell.

[0091] In some embodiments, ectopic expression of ETV2 is induced by transducing the stem cell with a vector (e.g., AAV) comprising a nucleic acid encoding ETV2 and a nucleic acid encoding an expression control element. In other embodiments, the vector encodes an open reading frame of ETV2. In other embodiments, the vector encodes a cDNA of ETV2 (RefSeq: NM 001300974; NM 001304549; NM 014209). A non-limiting example of the sequence of an ETV2 cDNA is provided:

(SEQ ID NO: 1)

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   1  ttcctgttgc agataagccc agcttagccc agctgacccc agaccctctc ccctcactcc
  61  ccccatgtcg caggatcgag accctgaggc agacagcccg ttcaccaagc cccccgcccc
 121  gcccccatca ccccgtaaac ttctcccagc ctccgccctg ccctcaccca gcccgctgtt
 181  ccccaagcct cgctccaagc ccacgccacc cctgcagcag ggcagcccca gaggccagca
 241  cctatccccg aggctggggt cgaggctcgg ccccgccccc gcctctgcaa cttgagcctg
 301  gctgcgaccc ctgctctgac gtctcggaaa attccccctt gcccaggccc ttgggggagg
 361  gggtgcatgg tatgaaatgg ggctgagacc cccggctggg ggcagaggaa cccgccagag
 421  aaggagccaa attaggcttc tgtttccctg atctggcact ccaaggggac acgccgacag
 481  cgacagcaga gacatgctgg aaaggtacaa gctcatccct ggcaagcttc ccacagctgg
 541  actggggctc cgcgttactg cacccagaag ttccatgggg ggcggagccc gactctcagg
 601  ctcttccgtg gtccggggac tggacagaca tggcgtgcac agcctgggac tcttggagcg
 661  gcgcctcgca gaccctgggc cccgcccctc tcggcccggg ccccatcccc gccgccggct
 721  ccgaaggcgc cgcgggccag aactgcgtcc ccgtggcggg agaggccacc tcgtggtcgc
 781  gcgcccaggc cgccgggagc aacaccagct gggactgttc tgtggggccc gacggcgata
 841  cctactgggg cagtggcctg ggcggggagc cgcgcacgga ctgtaccatt tcgtggggcg
 901  ggcccgcggg cccggactgt accacctcct ggaacccggg gctgcatgcg ggtggcacca
 961  cctctttgaa gcggtaccag agctcagctc tcaccgtttg ctccgaaccg agcccgcagt
1021  cggaccgtgc cagtttggct cgatgcccca aaactaacca ccgaggtccc attcagctgt
1081  ggcagttcct cctggagctg ctccacgacg gggcgcgtag cagctgcatc cgttggactg
1141  gcaacagccg cgagttccag ctgtgcgacc ccaaagaggt ggctcggctg tggggcgagc
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1201  gcaagagaaa gccgggcatg aattacgaga agctgagccg gggccttcgc tactactatc

1261  gccgcgacat cgtgcgcaag agcgggggggc gaaagtacac gtaccgcttc gggggccgcg

1321  tgcccagcct agcctatccg gactgtgcgg gaggcggacg gggagcagag acacaataaa

1381  aattcccggt caaacctcaa aaaaaaaaaa aaa
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[0092] In some embodiments, the stem cell is an ESC or an iPSC. In some embodiments, the stem cell is a mammalian cell, optionally wherein the mammalian cell is an equine, bovine, canine, murine, porcine, feline, or human cell. In some embodiments, the stem cell is a human cell. In some embodiments, the stem cell has been genetically modified. In some embodiments, the method further comprises or consists of genetically modifying the stem cell or the endothelial cell.

[0093] In further aspect, also provided herein is an endothelial cell produced by a method driving differentiation of a stem cell into an endothelial cell, the method comprising, consisting of, or consisting essentially of inducing ectopic expression of ETV2 in a stem cell under conditions suitable to support differentiation of the stem cell into an endothelial cell, and optionally a carrier. In some embodiments, the endothelial cell expresses at least one of CDH5 (VE-Cadherin, Entrez gene: 1003; RefSeq: NM 001114117, NM 00179, PECAM1 (Platelet endothelial cell adhesion molecule, Entrez gene: 5175; RefSeq: NM 000442), or VWF (Von Willebrand Factor, Entrez gene: 7450, RefSeq: NM 000552).

[0094] In another aspect, also provided herein is a population of endothelial cells produced by a method driving differentiation of a stem cell into an endothelial cell, the method comprising, consisting of, or consisting essentially of inducing ectopic expression of ETV2 in a stem cell under conditions suitable to support differentiation of the stem cell into an endothelial cell, and optionally a carrier.

[0095] In some aspects, provided herein is a composition comprising, consisting of, or consisting essentially of an endothelial cell produced by a method driving differentiation of a stem cell into an endothelial cell, the method comprising, consisting of, or consisting essentially of inducing ectopic expression of ETV2 in a stem cell under conditions suitable to support differentiation of the stem cell into an endothelial cell, or a population of endothelial cells produced according to a method described herein, and one or more of: a pharmaceutically acceptable carrier, a cryopreservative or a preservative. In some embodiments, the carrier is a pharmaceutically acceptable carrier. In some embodiments, the cryopreservative is suitable for long term storage of the composition at a temperature ranging from −200° C. to 0° C., from −80° C. to 0° C., from −20° C. to 0° C., or from 0° C. to 10° C.

Methods of Treatment

[0096] In some aspects, provided herein is a method of treating a subject in need thereof, the method comprising, consisting of, or consisting essentially of administering an endothelial cell produced by a method driving differentiation of a stem cell into an endothelial cell, the method comprising, consisting of, or consisting essentially of inducing ectopic expression of ETV2 in a stem cell under conditions suitable to support differentiation of the stem cell into an endothelial cell, or a population of endothelial cells produced according to a method described herein, or a composition comprising, consisting of, or consisting essentially of the endothelial cell or population and a carrier to the subject. In some embodiments of the method, an effective amount of the endothelial cell, population, or composition is administered to the subject. In some embodiments, the endothelial cell or population is allogenic or autologous to the subject being treated. In one aspect, the treatment excludes prevention.

[0097] In some embodiments of the method, the subject has a wound, a corneal disease or condition, a myocardial infarction, or a vascular disease or condition. In some embodiments, the subject has a corneal disease or condition. In some embodiments, the administration is local or systemic. In some embodiments, the endothelial cell, population, or composition is administered to the subject's eye.

[0098] An effective amount can be administered in one or more administrations, applications or dosages. Such delivery is dependent on a number of variables including the time period for which the individual dosage unit is to be used, the bioavailability of the therapeutic agent, the route of administration, etc. It is understood, however, that specific dose levels of the therapeutic agents of the present disclosure for any particular subject depends upon a variety of factors including the activity of the specific compound employed, the age, body weight, general health, sex, and diet of the subject, the time of administration, the rate of excretion, the drug combination, and the severity of the particular disorder being treated and form of administration. Treatment dosages generally may be titrated to optimize safety and efficacy. The dosage can be determined by a physician and adjusted, as necessary, to suit observed effects of the treatment. Typically, dosage-effect relationships from in vitro and/or in vivo tests initially can provide useful guidance on the proper doses for patient administration. In general, one will desire to administer an amount of the compound that is effective to achieve a serum level commensurate with the concentrations found to be effective in vitro. Determination of these parameters is well within the skill of the art. These considerations, as well as effective formulations and administration procedures are well known in the art and are described in standard textbooks. Consistent with this definition, as used herein, the term "therapeutically effective amount" is an amount sufficient to achieve the result of the method.

[0099] The term "administration" shall include without limitation, administration by oral, parenteral (e.g., intramuscular, intraperitoneal, intravenous, ICV, intracisternal injection or infusion, subcutaneous injection, or implant), by inhalation spray nasal, vaginal, rectal, sublingual, urethral (e.g., urethral suppository) or topical routes of administration (e.g., gel, ointment, cream, aerosol, etc.) and can be formulated, alone or together, in suitable dosage unit formulations containing conventional non-toxic pharmaceutically acceptable carriers, adjuvants, excipients, and vehicles

appropriate for each route of administration. The invention is not limited by the route of administration, the formulation or dosing schedule.

[0100] In some embodiments of the method, the subject is a mammal and the mammal is an equine, bovine, canine, murine, porcine, feline, or human. In some embodiments, the mammal is a human. In some embodiments, the endothelial cells are autologous or allogeneic to the subject being treated.

[0101] Having been generally described herein, the follow examples are provided to further illustrate this invention.

Example 1

[0102] Recently, screens combining genetic perturbations with scRNA-seq readouts have emerged as promising alternatives to traditional screens, enabling high-throughput, high-content screening by profiling the transcriptomes of tens of thousands of individual cells simultaneously. Unlike array-based methods scRNA-seq screens are scalable, while unlike traditional pooled screening techniques, they enable direct readout of cell state changes. In addition, they also enable the evaluation of heterogeneous cellular response to perturbations. While several groups have demonstrated CRISPR-Cas9 based knock-out and knock-down scRNA-seq screens, to Applicants' knowledge, gene activation screens have yet to be demonstrated.

[0103] Here, Applicants use barcoded ORF overexpression libraries with a coupled scRNA-seq and fitness screen, a technique Applicants call SEUSS, to systematically overexpress TFs and assay both, the transcriptomic and fitness effects on hPSCs. Applicants chose open-reading frame (ORF) constructs for several reasons, namely that ORF constructs yield strong, stable expression of the gene of interest, enable the ability to express a targeted isoform of the gene, and allow for the ability to express engineered or mutant forms of the gene, aspects otherwise not accessible through endogenous gene activation. Applicants screened a pooled library of TFs that are either developmentally critical, specific to key lineages, or are pioneer factors capable of binding closed chromatin (Table 1). From the transcriptomic readouts, Applicants built a gene-gene co-perturbation network, segmented the network genes into functional gene modules, and used these gene modules to also elucidate the impact of TF overexpression on the pluripotent cell state. Notably, Applicants also leveraged the versatility of the ORF library approach and SEUSS to systematically assay mutant gene libraries (MYC) and whole gene families (KLF). Finally, Applicants also leveraged the complementary fitness information via SEUSS to ascertain that ETV2 is a novel reprogramming factor for hPSCs, whose overexpression yields rapid differentiation towards the endothelial lineage.

[0104] Applicants designed Applicants' ORF overexpression vector such that each TF was paired with a unique 20 bp barcode sequence located downstream of the 3' end of a hygromycin resistance transgene (FIG. **1**A, FIG. **4**), and 200 bp upstream of the lentiviral 3'-long terminal repeat (LTR) region. This yields a polyadenylated transcript bearing the barcode proximal to the 3' end, thereby facilitating efficient capture and detection in scRNA-seq. To construct the ORF library, transcription factors were amplified out of a multi-tissue human cDNA pool or directly synthesized as double-stranded DNA fragments, and individually cloned into the backbone vector (FIG. **4**). The final library consisted of 61 developmentally critical or pioneer TFs (Table 1). Applicants chose this library size to ensure that within a single scRNA-seq run of up to 10,000 cells, each perturbation was represented by at least 50-100 cells. However, SEUSS can be scaled up to include all known TFs.

[0105] Applicants conducted the overexpression screens by transducing lentiviral ORF libraries into human embryonic stem cells (hESCs), maintaining them under antibiotic selection for 5 days after transduction, for screens in hPSC medium, and 6 days after transduction, for screens in unlineage (endothelial) and multilineage (high serum) medium, and then performing scRNA-seq on the transduced and selected cells. TF barcodes were recovered and associated with scRNA-seq cell barcodes by targeted amplification from the unfragmented cDNA, allowing genotyping of each cell for downstream analysis (FIG. **1**A). Genotyped cell counts, although an under-sampling of the bulk population, also allowed Applicants to obtain an estimate of fitness, which was strongly correlated with bulk fitness obtained from genomic DNA (FIG. **1**A, FIG. **3**D, FIGS. **5**A-**5**C).

[0106] To analyze the effect of the TF perturbations, Applicants used the Seurat computational pipeline to cluster the cells from the scRNA-seq expression matrix (FIG. **1**C, FIG. **1**D, FIG. **1**E). In parallel, a linear model was used to identify genes whose expression levels are appreciably changed by the perturbation. To select TFs for downstream analysis, Applicants calculated over-enrichment of TFs in clusters using Fisher's exact test (FIG. **1**C, FIG. **1**D, FIG. **1**E). Subsequently, Applicants focused Applicants' analysis on TFs that were either significantly enriched for at least one cluster (FDR<10^{-6}), or had at least 100 significant differentially expressed genes. For TFs that had significant over-enrichment in a cluster, Applicants repeated the linear regression analysis, only including cells that fell into enriched clusters (FIG. **1**F).

[0107] This framework was used to conduct screens in hPSC medium, aggregating 12,873 cells across five samples. Applicants found that these independent experiments were well correlated with the combined dataset (Pearson R>0.84), implying overall reproducibility and the absence of strong batch effects (FIGS. **7**A-**7**E). To study the interplay of ORF overexpression with growth media conditions, Applicants also conducted screens in a unilineage medium, specifically endothelial growth medium, on 5,646 cells and in a multilineage (ML) differentiation medium, specifically a high serum growth medium, on 3476 cells (Table 3). Two samples were aggregated for analysis in the ML medium, again showing good correlation (FIG. **7**F; Pearson R=0.68).

[0108] From Applicants' screen in hPSC medium, Applicants found that transcriptomic changes do not necessarily correlate with changes in fitness (FIG. **5**), thus Applicants' coupled screening method enables a more comprehensive profiling of impacts on both fitness and cell state. Among the most significantly depleted TFs, was the haemato-endothelial master regulator ETV2, (FIG. **3**D, FIG. **5**), which guided Applicants' choice of EGM for a unilineage medium screen.

[0109] Applicants find that certain TFs show consistent effects across all media conditions (CDX2, KLF4), while some TFs have medium-specific effects. For instance, SNAI2 effects were specific to hPSC medium, MITF to ML medium, and GATA4 to EGM (FIG. **1**F). To benchmark Applicants' results, Applicants compared expression profiles for significant TFs in hPSC medium with a previously reported bulk RNA-seq screen of TF perturbations in mESCs. For TFs present in both datasets, Applicants found

a strong overlap, suggesting the effectiveness of Applicants' screen for studying perturbations (FIG. **6**D).

[0110] To interpret the effects of the significant TFs, Applicants used the regression coefficients of the linear model to build a weighted gene-to-gene co-perturbation network, where genes with a highly weighted edge between them respond to TF perturbations in a similar manner (FIG. **2**A). Using this network, Applicants identified 11 altered gene modules via a modularity optimization graph clustering algorithm. Many of these gene modules showed a strong enrichment for Gene Ontology (GO) terms, and gene module identity was assigned using GO enrichment paired with manual inspection of genes in each module. In this network, Applicants found that the pluripotency gene module and the chromatin accessibility module are highly interconnected, reflecting the relationship between those two biological processes (FIG. **2**B), and suggesting that this network may serve as a resource to understand the cascading effects of genetic perturbations (FIG. **2**B, Table 5).

[0111] Applicants next calculated the effect of each significant TF on the gene modules (FIG. **2**C). Applicants found that the annotated neural specifiers NEUROD1, NEUROG1, and NEUROG3, which show similar cluster enrichment and differential expression patterns, upregulate the neuron differentiation module, consistent with their known effects. ASCL1 and MYOD1, which also show similarity in clustering and expression patterns, upregulate the Notch pathway module (FIG. **2**C). This similarity between ASCL1 and MYOD1 may be due to a myogenic program initiated by ASCL1. Notably, for the TFs with consistent effects across medium conditions, Applicants find that both CDX2 and KLF4 strongly downregulate the pluripotency gene module, while CDX2 also upregulates the embryonic development gene module, potentially reflecting its role in trophectoderm development, and KLF4 tends to upregulate the cytoskeleton and motility gene modules.

[0112] Next, since in Applicants' screens MYC was found to drive significant transcriptomic changes in hPSC medium in its wild type form (FIG. **1**F), Applicants chose to focus on it in demonstrating the ability of Applicants' platform to also systematically screen mutant forms of proteins. Specifically, Applicants constructed a library of mutant MYC proteins, where functional domains were systematically deleted (FIG. **2**D), or mutations at known hotspots were incorporated (Glu-39, Thr-58 and Ser-62). Screening this library in pluripotent stem cell medium, Applicants found that while some variants, such as known hotspot mutations, as well as deletion of the nuclear localization signal (NLS) sequence maintain an effect similar to the wild type MYC, a majority of the other mutant forms show a greater overlap with the control mCherry-transduced cells, suggesting the essential requirement of the mapped domains for function of MYC in hPSCs (FIG. **2**E).

MYC Mutants Library:

[0113]

GENE	SEQUENCE	SEQ ID NO:	MUTATION
MYC ΔMBI	ATGCCCCTCAACGTTAGCTTCACCAACAGGAACTATGACC TCGACTACGACTCGGTGCAGCCGTATTTCTACTGCGACGA GGAGGAGAACTTCTACCAGCAGCAGCAGCAGAGCGAGCT GCAGCCCCCGGCGGGATCAGGTAGCGGTAGCCGCCGCTC CGGGCTCTGCTCGCCCTCCTACGTTGCGGTCACACCCTTCT CCCTTCGGGGAGACAACGACGGCGGTGGCGGGAGCTTCT CCACGGCCGACCAGCTGGAGATGGTGACCGAGCTGCTGG GAGGAGACATGGTGAACCAGAGTTTCATCTGCGACCCGG ACGACGAGACCTTCATCAAAAACATCATCATCCAGGACTG TATGTGGAGCGGCTTCTCGGCCGCCGCCAAGCTCGTCTCA GAGAAGCTGGCCTCCTACCAGGCTGCGCGCAAAGACAGC GGCAGCCCGAACCCCGCCCGCGGCCACAGCGTCTGCTCCA CCTCCAGCTTGTACCTGCAGGATCTGAGCGCCGCCGCCTC AGAGTGCATCGACCCCTCGGTGGTCTTCCCCTACCCTCTC AACGACAGCAGCTCGCCCAAGTCCTGCGCCTCGCAAGACT CCAGCGCCTTCTCTCCGTCCTCGGATTCTCTGCTCTCCTCG ACGGAGTCCTCCCCGCAGGGCAGCCCCGAGCCCCTGGTGC TCCATGAGGAGACACCGCCCACCACCAGCAGCGACTCTG AGGAGGAACAAGAAGATGAGGAAGAAATCGATGTTGTTT CTGTGGAAAAGAGGCAGGCTCCTGGCAAAAGGTCAGAGT CTGGATCACCTTCTGCTGGAGGCCACAGCAAACCTCCTCA CAGCCCACTGGTCCTCAAGAGGTGCCACGTCTCCACACAT CAGCACAACTACGCAGCGCCTCCCTCCACTCGGAAGGACT ATCCTGCTGCCAAGAGGGTCAAGTTGGACAGTGTCAGAGT CCTGAGACAGATCAGCAACAACCGAAAATGCACCAGCCC CAGGTCCTCGGACACCGAGGAGAATGTCAAGAGGCGAAC ACACAACGTCTTGGAGCGCCAGAGGAGGAACGAGCTAAA ACGGAGCTTTTTTGCCCTGCGTGACCAGATCCCGGAGTTG GAAAACAATGAAAAGGCCCCCAAGGTAGTTATCCTTAAA AAAGCCACAGCATACATCCTGTCCGTCCAAGCAGAGGAG CAAAAGCTCATTTCTGAAGAGGACTTGTTGCGGAAACGAC GAGAACAGTTGAAACACAAACTTGAACAGCTACGGAACT CTTGTGCG	2	Deletion of MYC Box I
c-MYC ΔMBII	ATGCCCCTCAACGTTAGCTTCACCAACAGGAACTATGACC TCGACTACGACTCGGTGCAGCCGTATTTCTACTGCGACGA GGAGGAGAACTTCTACCAGCAGCAGCAGCAGAGCGAGCT GCAGCCCCCGGCGCCCAGCGAGGATATCTGGAAGAAATT CGAGCTGCTGCCCACCCCGCCCCTGTCCCCTAGCCGCCGC	3	Deletion of MYC Box II

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GENE	SEQUENCE	SEQ ID NO:	MUTATION
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	GGAGGAGACATGGTGAACCAGAGTTTCATCTGCGACCCG		
	GACGACGAGACCTTCATCAAAAACATCGGATCAGGTAGC		
	GGTCTCGTCTCAGAGAAGCTGGCCTCCTACCAGGCTGCGC		
	GCAAAGACAGCGGCAGCCCGAACCCCGCCCGCGGCCACA		
	GCGTCTGCTCCACCTCCAGCTTGTACCTGCAGGATCTGAG		
	CGCCGCCGCCTCAGAGTGCATCGACCCCTCGGTGGTCTTC		
	CCCTACCCTCTCAACGACAGCAGCTCGCCCAAGTCCTGCG		
	CCTCGCAAGACTCCAGCGCCTTCTCTCCGTCCTCGGATTCT		
	CTGCTCTCCTCGACGGAGTCCTCCCCGCAGGGCAGCCCCG		
	AGCCCCTGGTGCTCCATGAGGAGACACCGCCCACCACCAG		
	CAGCGACTCTGAGGAGGAACAAGAAGATGAGGAAGAAAT		
	CGATGTTGTTTCTGTGGAAAAGAGGCAGGCTCCTGGCAAA		
	AGGTCAGAGTCTGGATCACCTTCTGCTGGAGGCCACAGCA		
	AACCTCCTCACAGCCCACTGGTCCTCAAGAGGTGCCACGT		
	CTCCACACATCAGCACAACTACGCAGCGCCTCCCTCCACT		
	CGGAAGGACTATCCTGCTGCCAAGAGGGTCAAGTTGGAC		
	AGTGTCAGAGTCCTGAGACAGATCAGCAACAACCGAAAA		
	TGCACCAGCCCCAGGTCCTCGGACACCGAGGAGAATGTC		
	AAGAGGCGAACACACAACGTCTTGGAGCGCCAGAGGAGG		
	AACGAGCTAAAACGGAGCTTTTTTGCCCTGCGTGACCAGA		
	TCCCGGAGTTGGAAAACAATGAAAAGGCCCCCAAGGTAG		
	TTATCCTTAAAAAAGCCACAGCATACATCCTGTCCGTCCA		
	AGCAGAGGAGCAAAAGCTCATTTCTGAAGAGGACTTGTT		
	GCGGAAACGACGAGAACAGTTGAAACACAAACTTGAACA		
	GCTACGGAACTCTTGTGCG		
MYC ΔNLS	ATGCCCCTCAACGTTAGCTTCACCAACAGGAACTATGACC TCGACTACGACTCGGTGCAGCCGTATTTCTACTGCGACGA GGAGGAGAACTTCTACCAGCAGCAGCAGCAGAGCGAGCT GCAGCCCCCGGCGCCCAGCGAGGATATCTGGAAGAAATT CGAGCTGCTGCCCACCCCGCCCCTGTCCCCTAGCCGCCGC TCCGGGCTCTGCTCGCCCTCCTACGTTGCGGTCACACCCTT CTCCCTTCGGGGAGACAACGACGGCGGTGGCGGGAGCTT CTCCACGGCCGACCAGCTGGAGATGGTGACCGAGCTGCTG GGAGGAGACATGGTGAACCAGAGTTTCATCTGCGACCCG GACGACGAGACCTTCATCAAAAACATCATCATCCAGGACT GTATGTGGAGCGGCTTCTCGGCCGCCGCCAAGCTCGTCTC AGAGAAGCTGGCCTCCTACCAGGCTGCGCGCAAAGACAG CGGCAGCCCGAACCCCGCCCGCGGCCACAGCGTCTGCTCC ACCTCCAGCTTGTACCTGCAGGATCTGAGCGCCGCCGCCT CAGAGTGCATCGACCCCTCGGTGGTCTTCCCCTACCCTCTC AACGACAGCAGCTCGCCCAAGTCCTGCGCCTCGCAAGACT CCAGCGCCTTCTCTCCGTCCTCGGATTCTCTGCTCTCCTCG ACGGAGTCCTCCCCGCAGGGCAGCCCCGAGCCCCTGGTGC TCCATGAGGAGACACCGCCCACCACCAGCAGCGACTCTG AGGAGGAACAAGAAGATGAGGAAGAAATCGATGTTGTTT CTGTGGAAAAGAGGCAGGCTCCTGGCAAAAGGTCAGAGT CTGGATCACCTTCTGCTGGAGGCCACAGCAAACCTCCTCA CAGCCCACTGGTCCTCAAGAGGTGCCACGTCTCCACACAT CAGCACAACTACGCAGCGCCTCCCTCCACTCGGAAGGACT ATGGATCAGGTAGCGGTAGTGTCAGAGTCCTGAGACAGA TCAGCAACAACCGAAAATGCACCAGCCCCAGGTCCTCGG ACACCGAGGAGAATGTCAAGAGGCGAACACACAACGTCT TGGAGCGCCAGAGGAGGAACGAGCTAAAACGGAGCTTTT TTGCCCTGCGTGACCAGATCCCGGAGTTGGAAAACAATGA AAAGGCCCCCAAGGTAGTTATCCTTAAAAAAGCCACAGC ATACATCCTGTCCGTCCAAGCAGAGGAGCAAAAGCTCATT TCTGAAGAGGACTTGTTGCGGAAACGACGAGAACAGTTG AAACACAAACTTGAACAGCTACGGAACTCTTGTGCG	4	Deletion of nuclear localization signal sequence
MYC Δb	ATGCCCCTCAACGTTAGCTTCACCAACAGGAACTATGACC TCGACTACGACTCGGTGCAGCCGTATTTCTACTGCGACGA GGAGGAGAACTTCTACCAGCAGCAGCAGCAGAGCGAGCT GCAGCCCCCGGCGCCCAGCGAGGATATCTGGAAGAAATT CGAGCTGCTGCCCACCCCGCCCCTGTCCCCTAGCCGCCGC TCCGGGCTCTGCTCGCCCTCCTACGTTGCGGTCACACCCTT CTCCCTTCGGGGAGACAACGACGGCGGTGGCGGGAGCTT CTCCACGGCCGACCAGCTGGAGATGGTGACCGAGCTGCTG GGAGGAGACATGGTGAACCAGAGTTTCATCTGCGACCCG GACGACGAGACCTTCATCAAAAACATCATCATCCAGGACT	5	Deletion of basic motif

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	CAGAGTGCATCGACCCCTCGGTGGTCTTCCCCTACCCTCTC		
	AACGACAGCAGCTCGCCCAAGTCCTGCGCCTCGCAAGACT		
	CCAGCGCCTTCTCTCCGTCCTCGGATTCTCTGCTCTCCTCG		
	ACGGAGTCCTCCCCGCAGGGCAGCCCCGAGCCCCTGGTGC		
	TCCATGAGGAGACACCGCCCACCACCAGCAGCGACTCTG		
	AGGAGGAACAAGAAGATGAGGAAGAAATCGATGTTGTTT		
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	CTGGATCACCTTCTGCTGGAGGCCACAGCAAACCTCCTCA		
	CAGCCCACTGGTCCTCAAGAGGTGCCACGTCTCCACACAT		
	CAGCACAACTACGCAGCGCCTCCCTCCACTCGGAAGGACT		
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	CCTGAGACAGATCAGCAACAACCGAAAATGCACCAGCCC		
	CAGGTCCTCGGACACCGAGGAGAATGTCGGATCAGGTAG		
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	ATCCCGGAGTTGGAAAACAATGAAAAGGCCCCCAAGGTA		
	GTTATCCTTAAAAAAGCCACAGCATACATCCTGTCCGTCC		
	AAGCAGAGGAGCAAAAGCTCATTTCTGAAGAGGACTTGT		
	TGCGGAAACGACGAGAACAGTTGAAACACAAACTTGAAC		
	AGCTACGGAACTCTTGTGCG		
MYC ΔHLH	ATGCCCCTCAACGTTAGCTTCACCAACAGGAACTATGACC	6	Deletion of helix-loop-helix motif
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	CAGGTCCTCGGACACCGAGGAGAATGTCAAGAGGCGAAC		
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MYC ΔLZ	ATGCCCCTCAACGTTAGCTTCACCAACAGGAACTATGACC	7	Deletion of leucine zipper motif
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	GCAGCCCCCGGCGCCCAGCGAGGATATCTGGAAGAAATT		
	CGAGCTGCTGCCCACCCCGCCCCTGTCCCCTAGCCGCCGC		
	TCCGGGCTCTGCTCGCCCTCCTACGTTGCGGTCACACCCTT		
	CTCCCTTCGGGGAGACAACGACGGCGGTGGCGGGAGCTT		
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	CGGCAGCCCGAACCCCGCCCGCGGCCACAGCGTCTGCTCC		
	ACCTCCAGCTTGTACCTGCAGGATCTGAGCGCCGCCGCCT		
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GENE	SEQUENCE	SEQ ID NO:	MUTATION
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MYC ΔCTD	ATGCCCCTCAACGTTAGCTTCACCAACAGGAACTATGACC TCGACTACGACTCGGTGCAGCCGTATTTCTACTGCGACGA GGAGGAGAACTTCTACCAGCAGCAGCAGCAGAGCGAGCT GCAGCCCCCGGCGCCCAGCGAGGATATCTGGAAGAAATT CGAGCTGCTGCCCACCCCGCCCCTGTCCCCTAGCCGCCGC TCCGGGCTCTGCTCGCCCTCCTACGTTGCGGTCACACCCTT CTCCCTTCGGGGAGACAACGACGGCGGTGGCGGGAGCTT CTCCACGGCCGACCAGCTGGAGATGGTGACCGAGCTGCTG GGAGGAGACATGGTGAACCAGAGTTTCATCTGCGACCCG GACGACGAGACCTTCATCAAAAACATCATCATCCAGGACT GTATGTGGAGCGGCTTCTCGGCCGCCGCCAAGCTCGTCTC AGAGAAGCTGGCCTCCTACCAGGCTGCGCGCAAAGACAG CGGCAGCCCGAACCCCGCCCGCGGCCACAGCGTCTGCTCC ACCTCCAGCTTGTACCTGCAGGATCTGAGCGCCGCCGCCT CAGAGTGCATCGACCCCTCGGTGGTCTTCCCCTACCCTCTC AACGACAGCAGCTCGCCCAAGTCCTGCGCCTCGCAAGACT CCAGCGCCTTCTCTCCGTCCTCGGATTCTCTGCTCTCCTCG ACGGAGTCCTCCCCGCAGGGCAGCCCCGAGCCCCTGGTGC TCCATGAGGAGACACCGCCCACCACCAGCAGCGACTCTG AGGAGGAACAAGAAGATGAGGAAGAAATCGATGTTGTTT CTGTGGAAAAGAGGCAGGCTCCTGGCAAAAGGTCAGAGT CTGGATCACCTTCTGCTGGAGGCCACAGCAAACCTCCTCA CAGCCCACTGGTCCTCAAGAGGTGCCACGTCTCCACACAT CAGCACAACTACGCAGCGCCTCCCTCCACTCGGAAGGACT ATCCTGCTGCCAAGAGGGTCAAGTTGGACAGTGTCAGAGT CCTGAGACAGATCAGCAACAACCGAAAATGCACCAGCCC CAGGTCCTCGGACACCGAGGAGAATGTC	9	Deletion of carboxy-terminal domain: Housing basic helix-loop-helix leucine zipper motif, governing heterodimerization with MAX protein
MYC Glu39Ala	ATGCCCCTCAACGTTAGCTTCACCAACAGGAACTATGACC TCGACTACGACTCGGTGCAGCCGTATTTCTACTGCGACGA GGAGGAGAACTTCTACCAGCAGCAGCAGCAGAGCGcGCT GCAGCCCCCGGCGCCCAGCGAGGATATCTGGAAGAAATT CGAGCTGCTGCCCACCCCGCCCCTGTCCCCTAGCCGCCGC TCCGGGCTCTGCTCGCCCTCCTACGTTGCGGTCACACCCTT	10	Point mutation changing Glutamic Acid to Alanine at amino acid 39

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GENE	SEQUENCE	SEQ ID NO:	MUTATION
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	CGGCAGCCCGAACCCCGCCCGCGGCCACAGCGTCTGCTCC		
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	GAGAACAGTTGAAACACAAACTTGAACAGCTACGGAACT		
	CTTGTGCG		
MYC Thr58Ala	ATGCCCCTCAACGTTAGCTTCACCAACAGGAACTATGACC TCGACTACGACTCGGTGCAGCCGTATTTCTACTGCGACGA GGAGGAGAACTTCTACCAGCAGCAGCAGCAGAGCGAGCT GCAGCCCCCGGCGCCCAGCGAGGATATCTGGAAGAAATT CGAGCTGCTGCCCGCCCCGCCCCTGTCCCCTAGCCGCCGC TCCGGGCTCTGCTCGCCCTCCTACGTTGCGGTCACACCCTT CTCCCTTCGGGGAGACAACGACGGCGGTGGCGGGAGCTT CTCCACGGCCGACCAGCTGGAGATGGTGACCGAGCTGCTG GGAGGAGACATGGTGAACCAGAGTTTCATCTGCGACCCG GACGACGAGACCTTCATCAAAAACATCATCATCCAGGACT GTATGTGGAGCGGCTTCTCGGCCGCCGCCAAGCTCGTCTC AGAGAAGCTGGCCTCCTACCAGGCTGCGCGCAAAGACAG CGGCAGCCCGAACCCCGCCCGCGGCCACAGCGTCTGCTCC ACCTCCAGCTTGTACCTGCAGGATCTGAGCGCCGCCGCCT CAGAGTGCATCGACCCCTCGGTGGTCTTCCCCTACCCTCTC AACGACAGCAGCTCGCCCAAGTCCTGCGCCTCGCAAGACT CCAGCGCCTTCTCTCCGTCCTCGGATTCTCTGCTCTCCTCG ACGGAGTCCTCCCCGCAGGGCAGCCCCGAGCCCCTGGTGC TCCATGAGGAGACACCGCCCACCACCAGCAGCGACTCTG AGGAGGAACAAGAAGATGAGGAAGAAATCGATGTTGTTT CTGTGGAAAAGAGGCAGGCTCCTGGCAAAAGGTCAGAGT CTGGATCACCTTCTGCTGGAGGCCACAGCAAACCTCCTCA CAGCCCACTGGTCCTCAAGAGGTGCCACGTCTCCACACAT CAGCACAACTACGCAGCGCCTCCCTCCACTCGGAAGGACT ATCCTGCTGCCAAGAGGGTCAAGTTGGACAGTGTCAGAGT CCTGAGACAGATCAGCAACAACCGAAAATGCACCAGCCC CAGGTCCTCGGACACCGAGGAGAATGTCAAGAGGCGAAC ACACAACGTCTTGGAGCGCCAGAGGAGGAACGAGCTAAA ACGGAGCTTTTTTGCCCTGCGTGACCAGATCCCGGAGTTG GAAAACAATGAAAAGGCCCCCAAGGTAGTTATCCTTAAA AAAGCCACAGCATACATCCTGTCCGTCCAAGCAGAGGAG CAAAAGCTCATTTCTGAAGAGGACTTGTTGCGGAAACGAC GAGAACAGTTGAAACACAAACTTGAACAGCTACGGAACT CTTGTGCG	11	Point mutation changing Threonine to Alanine at amino acid 58
MYC Ser62Ala	ATGCCCCTCAACGTTAGCTTCACCAACAGGAACTATGACC TCGACTACGACTCGGTGCAGCCGTATTTCTACTGCGACGA GGAGGAGAACTTCTACCAGCAGCAGCAGCAGAGCGAGCT GCAGCCCCCGGCGCCCAGCGAGGATATCTGGAAGAAATT CGAGCTGCTGCCCACCCCGCCCCTGGCCCCTAGCCGCCGC TCCGGGCTCTGCTCGCCCTCCTACGTTGCGGTCACACCCTT CTCCCTTCGGGGAGACAACGACGGCGGTGGCGGGAGCTT CTCCACGGCCGACCAGCTGGAGATGGTGACCGAGCTGCTG GGAGGAGACATGGTGAACCAGAGTTTCATCTGCGACCCG	12	Point mutation changing Serine to Alanine at amino acid 58

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GENE	SEQUENCE	SEQ ID NO:	MUTATION
	GACGACGAGACCTTCATCAAAAACATCATCATCCAGGACT		
	GTATGTGGAGCGGCTTCTCGGCCGCCGCCAAGCTCGTCTC		
	AGAGAAGCTGGCCTCCTACCAGGCTGCGCGCAAAGACAG		
	CGGCAGCCCGAACCCCGCCCGCGGCCACAGCGTCTGCTCC		
	ACCTCCAGCTTGTACCTGCAGGATCTGAGCGCCGCCGCCT		
	CAGAGTGCATCGACCCCTCGGTGGTCTTCCCCTACCCTCTC		
	AACGACAGCAGCTCGCCCAAGTCCTGCGCCTCGCAAGACT		
	CCAGCGCCTTCTCTCCGTCCTCGGATTCTCTGCTCTCCTCG		
	ACGGAGTCCTCCCCGCAGGGCAGCCCCGAGCCCCTGGTGC		
	TCCATGAGGAGACACCGCCCACCACCAGCAGCGACTCTG		
	AGGAGGAACAAGAAGATGAGGAAGAAATCGATGTTGTTT		
	CTGTGGAAAAGAGGCAGGCTCCTGGCAAAAGGTCAGAGT		
	CTGGATCACCTTCTGCTGGAGGCCACAGCAAACCTCCTCA		
	CAGCCCACTGGTCCTCAAGAGGTGCCACGTCTCCACACAT		
	CAGCACAACTACGCAGCGCCTCCCTCCACTCGGAAGGACT		
	ATCCTGCTGCCAAGAGGGTCAAGTTGGACAGTGTCAGAGT		
	CCTGAGACAGATCAGCAACAACCGAAAATGCACCAGCCC		
	CAGGTCCTCGGACACCGAGGAGAATGTCAAGAGGCGAAC		
	ACACAACGTCTTGGAGCGCCAGAGGAGGAACGAGCTAAA		
	ACGGAGCTTTTTTGCCCTGCGTGACCAGATCCCGGAGTTG		
	GAAAACAATGAAAAGGCCCCCAAGGTAGTTATCCTTAAA		
	AAAGCCACAGCATACATCCTGTCCGTCCAAGCAGAGGAG		
	CAAAAGCTCATTTCTGAAGAGGACTTGTTGCGGAAACGAC		
	GAGAACAGTTGAAACACAAACTTGAACAGCTACGGAACT		
	CTTGTGCG		

[0114] Additionally, the consistent and strong effects of KLF4 overexpression motivated the investigation of the full KLF zinc finger transcription factor family (FIG. **2**F) as a demonstration of the utility of Applicants' technique in studying patterns of perturbation effects across gene families. A screen including all 17 members of the KLF family was conducted in pluripotent stem cell medium. Gene module analysis showed that KLF5 and KLF17 also have similar effects as KLF4 (FIG. **2**G), which may reflect their similar role in promoting or maintaining epithelial cell states. On the other hand, unlike most of the KLF family, KLF13 and KLF16 fail to activate the cytoskeleton and motility module (FIG. **2**G).

KLF Family Library

[0115]

GENE	SEQUENCE	SEQ ID NO:
KLF1	ATGGCGACTGCGGAGACAGCACTTCCATCAATCTCAACACTCACTGCACTG	13
	GGGCCATTTCCAGATACCCAGGACGATTTCCTTAAGTGGTGGCGGTCCGAA	
	GAGGCTCAAGACATGGGACCTGGTCCGCCGGATCCCACCGAACCTCCTCTG	
	CATGTCAAAAGTGAAGATCAGCCTGGCGAGGAAGAGGATGACGAAAGGG	
	GTGCCGACGCCACTTGGGACTTGGATCTTCTCCTTACCAATTTCTCTGGTCC	
	GGAACCTGGCGGGGCACCACACAGACGTGCGCTCTCGCTCCCTCAGAAGCGA	
	GCGGGGCTCAGTACCCACCCCCTCCCGAAACTCTGGGAGCCTATGCTGGGG	
	GTCCTGGACTGGTGGCTGGGTTGCTTGGTAGTGAGGACCATTCTGGCTGGG	
	TACGCCCCGCTTTGAGGGCCCGCGCTCCGGACGCCTTTGTGGGACCGGCGC	
	TCGCTCCTGCACCGGCTCCGGAACCAAAAGCCCTCGCGCTGCAGCCCGTGT	
	ACCCCGGACCCGGAGCCGGATCCTCAGGGGGATACTTCCCACGGACCGGA	
	CTCAGCGTTCCAGCGGCTTCCGGGGCGCCATACGGATTGTTGAGCGGCTAC	
	CCGGCTATGTATCCCGCTCCCCAGTACCAAGGACACTTCCAATTGTTCCGG	
	GGTCTTCAAGGGCCTGCGCCCGGGCCTGCTACCAGTCCCAGTTTCCTCAGT	
	TGTCTGGGACCGGGAACTGTTGGCACTGGACTTGGCGGGACTGCAGAGGA	
	CCCAGGCGTTATAGCAGAGACAGCGCCAAGTAAAAGGGGCCGACGAAGCT	
	GGGCCAGGAAACGCCAAGCTGCGCACACTTGTGCCCATCCAGGTTGCGGT	
	AAATCCTACACGAAGAGCAGTCATCTTAAAGCACATCTTCGCACACACAC	
	GGGCGAGAAGCCCTACGCCTGTACTTGGGAAGGTTGCGGCTGGAGATTCG	
	CTAGATCTGACGAGCTCACCCGGCATTATCGAAAACACACTGGCCAGCGA	
	CCGTTCCGGTGCCAACTCTGCCCAAGGGCGTTCAGTCGCTCAGATCATCTG	
	GCTTTGCATATGAAGCGACACCTT	
KLF2	ATGGCCCTTAGTGAACCCATTCTTCCCAGCTTTTCCACGTTCGCGTCTCCTT	14
	GCCGAGAGAGAGGCCTTCAGGAAAGGTGGCCGAGGGCTGAACCCGAGTCT	
	GGAGGTACGGATGATGATCTTAACAGTGTGCTCGATTTCATACTCTCAATG	
	GGACTGGACGGGCTGGGAGCGGAGGCAGCTCCTGAACCACCACCACCCCC	
	TCCGCCCCCAGCGTTTTACTACCCGGAGCCAGGTGCGCCGCCGCCATATTC	
	AGCCCCGGCGGGTGGCTTGGTGTCCGAGCTCCTCCGGCCTGAATTGGATGC	

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GENE	SEQUENCE	SEQ ID NO:
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	CCTGGCCCGGCTGCAAGCTGTATGCGGGGGCCCGGTGGGAGGCCTCCCCC	
	GCCCCCTGATACACCCCCCCTTAGTCCAGATGGACCAGCTCGACTTCCCGC	
	ACCTGGCCCCAGAGCGAGTTTCCCCCCTCCATTTGGAGGACCGGGGTTTGG	
	CGCCCCAGGTCCTGGACTTCACTACGCCCCTCCTGCCCCCCCCAGCTTTTGGT	
	CTTTTCGACGATGCTGCTGCTGCCGCAGCAGCCTTGGGCCTTGCGCCGCCC	
	GCAGCCAGGGGACTGCTCACGCCACCGGCAAGCCCCCTGGAGCTCCTTGA	
	AGCCAAGCCGAAGCGAGGACGCAGATCATGGCCGCGCAAGCGGACAGCT	
	ACGCATACCTGCTCATATGCGGGCTGCGGAAAAACCTACACAAAGAGTTC	
	ACACCTTAAAGCGCACCTTCGCACACACACAGGCGAGAAACCATATCATT	
	GTAACTGGGACGGATGTGGATGGAAATTTGCTCGGTCTGATGAGCTTACGA	
	GACATTATCGAAAGCATACCGGACATCGGCCCTTTCAATGCCATCTTTGTG	
	ACAGAGCTTTTTCCCGGTCTGACCACCTCGCTCTGCACATGAAGAGGCACA	
	TG	
KLF3	ATGCTCATGTTTGACCCAGTTCCTGTCAAGCAAGAGGCCATGGACCCTGTC	15
	TCAGTGTCATACCCATCTAATTACATGGAATCCATGAAGCCTAACAAGTAT	
	GGGGTCATCTACTCCACACCATTGCCTGAGAAGTTCTTTCAGACCCCAGAA	
	GGTCTGTCGCACGGAATACAGATGGAGCCAGTGGACCTCACGGTGAACAA	
	GCGGAGTTCACCCCCTTCGGCTGGGAATTCGCCCTCCTCTCTGAAGTTCCC	
	GTCCTCACACCGGAGAGCCTCGCCTGGGTTGAGCATGCCTTCTTCCAGCCC	
	ACCGATAAAAAAATACTCACCCCCTTCTCCAGGCGTGCAGCCCTTCGGCGT	
	GCCGCTGTCCATGCCACCAGTGATGGCAGCTGCCCTCTCGCGGCATGGAAT	
	ACGGAGCCCGGGGATCCTGCCCGTCATCCAGCCGGTGGTGGTGCAGCCCG	
	TCCCCTTTATGTACACAAGTCACCTCCAGCAGCCTCTCATGGTCTCCTTATC	
	GGAGGAGATGGAAAATTCCAGTAGTAGCATGCAAGTACCTGTAATTGAAT	
	CATATGAGAAGCCTATATCACAGAAAAAAATTAAAATAGAACCTGGGATC	
	GAACCACAGAGGACAGATTATTATCCTGAAGAAATGTCACCCCCCTTAATG	
	AACTCAGTGTCCCCCCCGCAAGCATTGTTGCAAGAGAATCACCCTTCGGTC	
	ATCGTGCAGCCTGGGAAGAGACCTTTACCTGTGGAATCCCCGGATACTCAA	
	AGGAAGCGGAGGATACACAGATGTGATTATGATGGATGCAACAAAGTGTA	
	CACTAAAAGCTCCCACTTGAAAGCACACAGAAGAACACACACAGGAGAAA	
	AACCCTACAAATGTACATGGGAAGGGTGCACATGGAAGTTTGCTCGGTCT	
	GATGAACTAACAAGACATTTCCGAAAACATACTGGAATCAAACCTTTCCA	
	GTGCCCGGACTGTGACCGCAGCTTCTCCCGTTCTGACCATCTTGCCCTCCAT	
	AGGAAACGCCACATGCTAGTC	
KLF5	ATGGCTACAAGGGTGCTGAGCATGAGCGCCCGCCTGGGACCCGTGCCCCA	16
	GCCGCCGGCGCCGCAGGACGAGCCGGTGTTCGCGCAGCTCAAGCCGGTGC	
	TGGGCGCCGCGAATCCGGCCCGCGACGCGGCGCTCTTCCCCGGCGAGGAG	
	CTGAAGCACGCGCACCACCGCCCGCAGGCGCAGCCCGCGCCCGCGCAGGC	
	CCCGCAGCCGGCCCAGCCGCCCGCCACCGGCCCGCGGCTGCCTCCAGAGG	
	ACCTGGTCCAGACAAGATGTGAAATGGAGAAGTATCTGACACCTCAGCTT	
	CCTCCAGTTCCTATAATTCCAGAGCATAAAAAGTATAGACGAGACAGTGCC	
	TCAGTCGTAGACCAGTTCTTCACTGACACTGAAGGGTTACCTTACAGTATC	
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	AAATCCCAGAGACCGTGCGTAACACACATCAAGACAGAACCTGTTGCCAT	
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	CCTCCCTGAGTTCACCAGTATATTCAGCTCACACCAGACCGCAGCTCCAGA	
	GGTGAACAATATTTTCATCAAACAAGAACTTCCTACACCAGATCTTCATCT	
	TTCTGTCCCTACCCAGCAGGGCCACCTGTACCAGCTACTGAATACACCGGA	
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	TGTTTCTATGTCAGCTGCCATGGCAGGCCTTAACACACACACCTCTGCTGTT	
	CCGCAGACTGCAGTGAAACAATTCCAGGGCATGCCCCCTTGCACATACAC	
	AATGCCAAGTCAGTTTCTTCCACAACAGGCCACTTACTTTCCCCCGTCACC	
	ACCAAGCTCAGAGCCTGGAAGTCCAGATAGACAAGCAGAGATGCTCCAGA	
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	ACCTGTCAGATACAATAGAAGGAGTAACCCCGATTTGGAGAAACGACGCA	
	TCCACTACTGCGATTACCCTGGTTGCACAAAAGTTTATACCAAGTCTTCTC	
	ATTTAAAAGCTCACCTGAGGACTCACACTGGTGAAAAGCCATACAAGTGT	
	ACCTGGGAAGGCTGCGACTGGAGGTTCGCGCGATCGGATGAGCTGACCCG	
	CCACTACCGGAAGCACACAGGCGCCAAGCCCTTCCAGTGCGGGGTGTGCA	
	ACCGCAGCTTCTCGCGCTCTGACCACCTGGCCCTGCATATGAAGAGGCACC	
	AGAAC	
KLF6	ATGGACGTGCTCCCCATGTGCAGCATCTTCCAGGAGCTCCAGATCGTGCAC	17
	GAGACCGGCTACTTCTCGGCGCTGCCGTCTCTGGAGGAGTACTGGCAACAG	
	ACCTGCCTAGAGCTGGAACGTTACCTCCAGAGCGAGCCCTGCTATGTTTCA	
	GCCTCAGAAATCAAATTTGACAGCCAGGAAGATCTGTGGACCAAAATCAT	
	TCTGGCTCGGGAGAAAAAGGAGGAATCCGAACTGAAGATATCTTCCAGTC	

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GENE	SEQUENCE	SEQ ID NO:
	CTCCAGAGGACACTCTCATCAGCCCGAGCTTTTGTTACAACTTAGAGACCA	
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	GCTCGGGAAAATTGAGCTCCTCTGTCACCTCCACGCCTCCATCTTCTCCGG	
	AACTGAGCAGGGAACCTTCTCAACTGTGGGGTTGCGTGCCCGGGGAGCTG	
	CCCTCGCCAGGGAAGGTGCGCAGCGGGACTTCGGGGAAGCCAGGTGACAA	
	GGGAAATGGCGATGCCTCCCCCGACGGCAGGAGGAGGGTGCACCGGTGCC	
	ACTTTAACGGCTGCAGGAAAGTTTACACCAAAAGCTCCCACTTGAAAGCA	
	CACCAGCGGACGCACACAGGAGAAAAGCCTTACAGATGCTCATGGGAAGG	
	GTGTGAGTGGCGTTTTGCAAGAAGTGATGAGTTAACCAGGCACTTCCGAA	
	AGCACACCGGGGCCAAGCCTTTTAAATGCTCCCACTGTGACAGGTGTTTTT	
	CCAGGTCTGACCACCTGGCCCTGCACATGAAGAGGCACCTC	
KLF7	ATGGACGTGTTGGCTAGTTATAGTATATTCCAGGAGCTACAACTTGTCCAC	18
	GACACCGGCTACTTCTCAGCTTTACCATCCCTGGAGGAGACCTGGCAGCAG	
	ACATGCCTTGAATTGGAACGCTACCTACAGACGGAGCCCCGGAGGATCTC	
	AGAGACCTTTGGTGAGGACTTGGACTGTTTCCTCCACGCTTCCCCTCCCCC	
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	CAAGTTGCTATCTGAGACCTGCCTCAGCCTCCAGCCGGCCAGCTCTTCTCT	
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	TAACGCCCCCATCGTCCCCTGAGCTCAGCCGCCATCTGGTCAAAACCTCAC	
	AAACTCTCTCTGCCGTGGATGGCACGGTGACGTTGAAACTGGTGGCCAAG	
	AAGGCTGCTCTCAGCTCCGTAAAGGTGGGAGGGGTCGCAACAGCTGCAGC	
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	CCGCTGTCAGTTTAACGGGTGCCGGAAAGTTTATACAAAAAGCTCCCACTT	
	AAAGGCCCACCAGAGGACTCACACAGGTGAGAAGCCTTATAAGTGCTCAT	
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	TACAGGAAACACACAGGTGCAAAGCCCTTCAAATGCAACCACTGCGACAG	
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KLF8	ATGGTCGATATGGATAAACTCATAAACAACTTGGAGGTCCAACTTAATTCA	19
	GAAGGTGGCTCAATGCAGGTATTCAAGCAGGTCACTGCTTCTGTTCGGAAC	
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	GAGTGGATCCTCAGCCTTGCAGAGTCTGCAGGGACTACAGCAAGAACCAG	
	CAGCAATGGCCCAAATGCAGGGAGAAGAGTCGCTTGACTTGAAGAGAAGA	
	CGGATTCACCAATGTGACTTTGCAGGATGCAGCAAAGTGTACACCAAAAG	
	CTCTCACCTGAAAGCTCACCGCAGAATCCATACAGGAGAGAAGCCTTATA	
	AATGCACCTGGGATGGCTGCTCCTGGAAATTTGCTCGCTCAGATGAGCTCA	
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	TGACACCATG	
KLF9	ATGTCCGCGGCCGCCTACATGGACTTCGTGGCTGCCCAGTGTCTGGTTTCC	20
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	AGTCTGGAAAGTCCAGATGAGGATATGGGATCCGACAGCGACGTGACCAC	
	CGAATCTGGGTCGAGTCCTTCCCACAGCCCGGAGGAGAGACAGGATCCTG	
	GCAGCGCGCCCAGCCCGCTCTCCCTCCTCCATCCTGGAGTGGCTGCGAAGG	
	GGAAACACGCCTCCGAAAAGAGGCACAAGTGCCCCTACAGTGGCTGTGGG	
	AAAGTCTATGGAAAATCCTCCCATCTCAAAGCCCATTACAGAGTGCATACA	
	GGTGAACGGCCCTTTCCCTGCACGTGGCCAGACTGCCTTAAAAAGTTCTCC	
	CGCTCAGACGAGCTGACCCGCCACTACCGGACCCACACTGGGGAAAAGCA	
	GTTCCGCTGTCCGCTGTGTGAGAAGCGCTTCATGAGGAGTGACCACCTCAC	
	AAAGCACGCCCGGCGGCACACCGAGTTCCACCCCAGCATGATCAAGCGAT	
	CGAAAAAGGCGCTGGCCAACGCTTTG	

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GENE	SEQUENCE	SEQ ID NO:
KLF10	ATGCTCAACTTCGGTGCCTCTCTCCAGCAGACTGCGGAGGAAAGAATGGA AATGATTTCTGAAAGGCCAAAAGAGAGTATGTATTCCTGGAACAAAACTG CAGAGAAAAGTGATTTTGAAGCTGTAGAAGCACTTATGTCAATGAGCTGC AGTTGGAAGTCTGATTTTAAGAAATACGTTGAAAACAGACCTGTTACACCA GTATCTGATTTGTCAGAGGAAGAGAATCTGCTTCCGGGAACACCTGATTTT CATACAATCCCAGCATTTTGTTTGACTCCACCTTACAGTCCTTCTGACTTTG AACCCTCTCAAGTGTCAAATCTGATGGCACCAGCGCCATCTACTGTACACT TCAAGTCACTCTCAGATACTGCCAAACCTCACATTGCCGCACCTTTCAAAG AGGAAGAAAAGAGCCCAGTATCTGCCCCCAAACTCCCCAAAGCTCAGGCA ACAAGTGTGATTCGTCATACAGCTGATGCCCAGCTATGTAACCACCAGACC TGCCCAATGAAAGCAGCCAGCATCCTCAACTATCAGAACAATTCTTTTAGA AGAAGAACCCACCTAAATGTTGAGGCTGCAAGAAAGAACATACCATGTGC CGCTGTGTCACCAAACAGATCCAAATGTGAGAGAAACACAGTGGCAGATG TTGATGAGAAAGCAAGTGCTGCACTTTATGACTTTTCTGTGCCTTCCTCAG AGACGGTCATCTGCAGGTCTCAGCCAGCCCCTGTGTCCCCACAACAGAAGT CAGTGTTGGTCTCTCCACCTGCAGTATCTGCAGGGGGAGTGCCACCTATGC CGGTCATCTGCCAGATGGTTCCCCTTCCTGCCAACAACCCTGTTGTGACAA CAGTCGTTCCCAGCACTCCTCCCAGCCAGCCACCAGCCGTTTGCCCCCCTG TTGTGTTCATGGGCACACAAGTCCCCAAAGGCGCTGTCATGTTTGTGGTAC CCCAGCCCGTTGTGCAGAGTTCAAAGCCTCCGGTGGTGAGCCCGAATGGC ACCAGACTCTCTCCCATTGCCCCTGCTCCTGGGTTTTCCCCTTCAGCAGCAA AAGTCACTCCTCAGATTGATTCATCAAGGATAAGGAGTCACATCTGTAGCC ACCCAGGATGTGGCAAGACATACTTTAAAAGTTCCCATCTGAAGGCCCAC ACGAGGACGCACACAGGAGAAAAGCCTTTCAGCTGTAGCTGGAAAGGTTG TGAAAGGAGGTTTGCCCGTTCTGATGAACTGTCCAGACACAGGCGAACCC ACACGGGTGAGAAGAAATTTGCGTGCCCCATGTGTGACCGGCGGTTCATG AGGAGTGACCATTTGACCAAGCATGCCCGGCGCCATCTATCAGCCAAGAA GCTACCAAACTGGCAGATGGAAGTGAGCAAGCTAAATGACATTGCTCTAC CTCCAACCCCTGCTCCCACACAG	21
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KLF12	ATGAACATTCACATGAAGCGCAAGACGATAAAGAACATCAATACATTCGA GAACCGAATGTTGATGTTGGATGGCATGCCCGCTGTACGGGTAAAAACCG AGCTCCTGGAGTCTGAACAAGGATCCCCAAACGTCCACAACTACCCGGAT ATGGAGGCAGTGCCGCTCTTGCTCAACAATGTGAAGGGAGAGCCGCCTGA GGACTCTCTCTCCGTAGATCATTTCCAGACACAGACTGAGCCCGTAGATCT TTCAATTAACAAAGCCAGAACATCTCCTACTGCGGTAAGTTCTTCTCCCGT AAGTATGACAGCAAGTGCATCTAGTCCAAGTTCTACGAGCACTAGCAGTTC TTCATCTAGTAGACTTGCTAGTTCACCAACGGTGATCACAAGTGTTTCTAG CGCCAGCAGCAGCTCAACGGTACTGACTCCCGGTCCACTCGTGGCAAGCG CTAGTGGCGTGGGTGGCCAACAATTTCTCCATATTATTCACCCCGTGCCTC	23

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GENE	SEQUENCE	SEQ ID NO:
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	CCATGGGAAAGCACAGATGGACCCCCGCGGCTTGTCACCGAGACAGTCTA	
	AATCCGATAGTGACGACGATGATTTGCCTAACGTAACACTGGACTCTGTGA	
	ACGAGACCGGGAGTACCGCTCTGTCAATCGCTAGGGCCGTACAGGAGGTC	
	CACCCAAGCCCTGTGTCACGAGTCCGAGGTAACAGGATGAATAATCAGAA	
	ATTTCCCTGTAGCATCAGCCCATTTTCTATAGAGTCCACTCGGAGACAGCG	
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	ATACGGGCGTAAAGCCGTTTAAATGCGCTGATTGCGACAGGAGTTTTAGCC	
	GCTCTGATCACCTTGCTCTTCACCGGAGGCGACACATGCTTGTT	
KLF13	ATGGCTGCGGCTGCATATGTGGATCATTTTGCGGCTGAGTGCCTGGTGTCA	24
	ATGTCTAGTAGAGCGGTGGTACACGGTCCCAGAGAAGGCCCAGAATCACG	
	CCCAGAGGGCGCCGCCGTCGCTGCAACACCGACGCTGCCTCGGGTCGAGG	
	AGCGCCGCGACGGGAAGGACAGTGCGTCACTTTTCGTAGTAGCGAGAATA	
	TTGGCAGATCTGAATCAACAGGCTCCAGCACCTGCGCCCGCTGAACGCCG	
	GGAGGGCGCCGCTGCCAGAAAGGCCAGAACACCATGCCGCTTGCCGCCAC	
	CTGCGCCAGAACCCACAAGTCCAGGTGCCGAAGGTGCGGCGGCTGCCCCT	
	CCTTCACCGGCCTGGTCTGAACCAGAACCAGAGGCAGGTCTTGAACCTGA	
	GCGCGAACCCGGCCCTGCAGGCTCTGGGGAACCTGGCCTGAGGCAGCGGG	
	TGAGGCGCGGCCGGAGCAGGGCCGACCTGGAATCACCGCAAAGGAAACAT	
	AAATGCCATTATGCTGGTTGCGAAAAGGTTTATGGAAAGTCATCCCACCTG	
	AAAGCACACCTCCGCACTCACACGGGTGAGCGACCTTTTGCGTGTTCCTGG	
	CAAGACTGCAATAAAAAGTTTGCTAGATCTGATGAACTTGCACGGCATTAT	
	CGAACTCATACCGGTGAAAAGAAGTTCTCATGCCCTATATGTGAGAAACG	
	GTTCATGCGCTCTGACCACTTGACGAAACATGCAAGACGACATGCTAATTT	
	TCATCCGGGGATGTTGCAGAGACGGGGAGGGGGAAGTAGGACTGGAAGTC	
	TCTCCGACTATTCCCGATCCGACGCTTCCTCACCAACGATTAGCCCCGCAA	
	GCAGTCCC	
KLF14	ATGTCAGCCGCAGTCGCATGCCTTGATTACTTCGCGGCCGAGTGTCTTGTTT	25
	CCATGTCAGCGGGGGCTGTCGTTCACAGAAGACCACCAGACCCGGAGGGA	
	GCGGGAGGGGCAGCTGGATCTGAAGTCGGCGCGGCTCCACCTGAATCAGC	
	GCTTCCCGGCCCTGGTCCTCCAGGTCCCGCTAGCGTGCCCCAACTCCCACA	
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	AGCATCAGTGTGGGCCGATCTTCGCGGAAGCTCCGGGGAGGGCTCCTGGG	
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	GCGGCAGTGTGCGCACCTGAAAGCTCATCCGATGCGCCGGCCGTTCCATCT	
	GCGCCAGCTGCTCCCGGTGCACCCGCAGCATCTGGCGGCTTTAGTGGTGGA	
	GCTCTTGGGGCGGGTCCCGCCCCTGCGGCGGATCAAGCTCCTCGCAGGCGC	
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	AAAGCATACTATAAGTCATCCCATCTCAAGAGTCACCAGAGGACGCATAC	
	AGGTGAGAGACCTTTTAGCTGTGACTGGCTCGATTGCGACAAGAAATTTAC	
	GCGGAGCGACGAACTTGCGCGGCACTACCGCACTCACACTGGAGAAAAGA	
	GGTTCTCTTGTCCCCTGTGTCCCAAGCAGTTCTCACGCAGTGATCACTTGAC	
	AAAACATGCTAGGAGACATCCAACATACCATCCCGACATGATAGAGTATC	
	GAGGTAGGCGACGCACACCTAGAATTGATCCTCCGCTGACTAGTGAAGTC	
	GAGTCAAGTGCCAGTGGAAGCGGACCGGGTCCCGCGCCCTCATTTACAAC	
	CTGTCTT	
KLF15	ATGGTGGACCACTTACTTCCAGTGGACGAGAACTTCTCGTCGCCAAAATGC	26
	CCAGTTGGGTATCTGGGTGATAGGCTGGTTGGCCGGCGGGCATATCACATG	
	CTGCCCTCACCCGTCTCTGAAGATGACAGCGATGCCTCCAGCCCCTGCTCC	
	TGTTCCAGTCCCGACTCTCAAGCCCTCTGCTCCTGCTATGGTGGAGGCCTG	
	GGCACCGAGAGCCAGGACAGCATCTTGGACTTCCTATTGTCCCAGGCCACG	
	CTGGGCAGTGGCGGGGGCAGCGGCAGTAGCATTGGGGCCAGCAGTGGCCC	
	CGTGGCCTGGGGGCCCTGGCGAAGGGCAGCGGCCCCTGTGAAGGGGGAGC	
	ATTTCTGCTTGCCCGAGTTTCCTTTGGGTGATCCTGATGACGTCCCACGGCC	
	CTTCCAGCCTACCCTGGAGGAGATTGAAGAGTTTCTGGAGGAGAACATGG	
	AGCCTGGAGTCAAGGAGGTCCCTGAGGGCAACAGCAAGGACTTGGATGCC	
	TGCAGCCAGCTCTCAGCTGGGCCACACAAGAGCCACCTCCATCCTGGGTCC	
	AGCGGGAGAGAGCGCTGTTCCCCTCCACCAGGTGGTGCCAGTGCAGGAGG	
	TGCCCAGGGCCCAGGTGGGGGCCCCACGCCTGATGGCCCCATCCCAGTGTT	
	GCTGCAGATCCAGCCCGTGCCTGTGAAGCAGGAATCGGGCACAGGGCCTG	
	CCTCCCCTGGGCAAGCCCCAGAGAATGTCAAGGTTGCCCAGCTCCTGGTCA	
	ACATCCAGGGGCAGACCTTCGCACTCGTGCCCCAGGTGGTACCCTCCTCCA	
	ACTTGAACCTGCCCTCCAAGTTTGTGCGCATTGCCCCTGTGCCCATTGCCGC	
	CAAGCCTGTTGGATCGGGACCCCTGGGGCCTGGCCCTGCCGGTCTCCTCAT	

-continued

GENE	SEQUENCE	SEQ ID NO:
	GGGCCAGAAGTTCCCCAAGAACCCAGCCGCAGAACTCATCAAAATGCACA	
	AATGTACTTTCCCTGGCTGCAGCAAGATGTACACCAAAAGCAGCCACCTCA	
	AGGCCCACCTGCGCCGGCACACGGGTGAGAAGCCCTTCGCCTGCACCTGG	
	CCAGGCTGCGGCTGGAGGTTCTCGCGCTCTGACGAGCTGTCGCGGCACAG	
	GCGCTCGCACTCAGGTGTGAAGCCGTACCAGTGTCCTGTGTGCGAGAAGA	
	AGTTCGCGCGGAGCGACCACCTCTCCAAGCACATCAAGGTGCACCGCTTCC	
	CGCGGAGCAGCCGCTCCGTGCGCTCCGTGAAC	
KLF16	ATGTCAGCCGCGGTCGCGTGCGTGGATTATTTTGCAGCAGATGTGCTGATG	27
	GCAATTTCATCCGGTGCAGTAGTTCATCGCGGAAGACCAGGTCCTGAGGGT	
	GCGGGGCCTGCGGCCGGGTTGGATGTTCGCGCCGCGCGCAGGGAAGCCGC	
	TTCTCCCGGAACACCTGGCCCTCCTCCTCCTCCGCCGGCGGCATCAGGCCC	
	GGGTCCTGGTGCAGCTGCGGCTCCTCACCTGTTGGCAGCCTCCATACTGGC	
	TGACCTGCGAGGGGGGCCAGGCGCTGCACCTGGTGGCGCGAGTCCAGCAA	
	GTTCCAGCTCCGCGGCGTCCTCCCCGAGTAGTGGGCGAGCTCCGGGCGCGG	
	CACCTTCTGCTGCCGCTAAATCACACCGATGCCCTTTCCCAGACTGCGCGA	
	AGGCGTATTATAAGTCCAGTCATTTGAAATCACACTTGAGGACACATACCG	
	GCGAGAGACCTTTTGCGTGCGACTGGCAGGGTTGTGATAAGAAATTTGCG	
	AGAAGCGACGAACTGGCCCGCCATCACCGCACCCACACAGGGGAAAAAA	
	GATTCTCATGCCCACTCTGTTCTAAGCGCTTCACGCGAAGCGACCATCTTG	
	CAAAGCACGCTAGGAGACACCCTGGGTTCCACCCCGACCTCTTGCGACGA	
	CCTGGCGCCCGGTCTACTAGCCCGTCTGACTCATTGCCGTGCTCTCTCGCA	
	GGGTCCCCTGCTCCGAGCCCCGCACCGTCCCCAGCTCCTGCCGGGCTT	
KLF17	ATGTACGGCCGACCGCAGGCTGAGATGGAACAGGAGGCTGGGGAGCTGAG	28
	CCGGTGGCAGGCGGCGCACCAGGCTGCCCAGGATAACGAGAACTCAGCGC	
	CCATCTTGAACATGTCTTCATCTTCTGGAAGCTCTGGAGTGCACACCTCTTG	
	GAACCAAGGCCTACCAAGCATTCAGCACTTTCCTCACAGCGCAGAGATGCT	
	GGGGTCCCCTTTGGTGTCTGTTGAGGCGCCGGGGCAGAATGTGAATGAAG	
	GGGGGCCACAGTTCAGTATGCCACTGCCTGAGCGTGGTATGAGCTACTGCC	
	CCCAAGCGACTCTCACTCCTTCCCGGATGATTTACTGTCAGAGAATGTCTC	
	CCCCTCAGCAAGAGATGACGATTTTCAGTGGGCCCCAACTAATGCCCGTAG	
	GAGAGCCCAATATTCCAAGGGTAGCCAGGCCCTTCGGTGGGAATCTAAGG	
	ATGCCCCCCAATGGGCTGCCAGTCTCGGCTTCCACTGGAATCCCAATAATG	
	TCCCACACTGGGAACCCTCCAGTGCCTTACCCTGGCCTCTCGACAGTACCT	
	TCTGACGAAACATTGTTGGGCCCGACTGTGCCTTCCACTGAGGCCCAGGCA	
	GTGCTCCCCTCCATGGCTCAGATGTTGCCCCCGCAAGATGCCCATGACCTT	
	GGGATGCCCCCAGCTGAGTCCCAGTCATTGCTGGTTTTAGGATCTCAGGAC	
	TCTCTTGTCAGTCAGCCAGACTCTCAAGAAGGCCCATTTCTACCAGAGCAG	
	CCCGGACCTGCTCCACAGACAGTAGAGAAGAACTCCAGGCCTCAGGAAGG	
	GACTGGTAGAAGGGGCTCCTCAGAGGCAAGGCCTTACTGCTGCAACTACG	
	AGAACTGCGGAAAAGCTTATACCAAACGCTCCCACCTCGTGAGCCACCAG	
	CGCAAGCACACAGGTGAGAGGCCATATTCTTGCAACTGGGAAAGTTGTTC	
	ATGGTCTTTCTTCCGTTCTGATGAGCTTAGACGACATATGCGGGTACACAC	
	CAGATATCGACCATATAAATGTGATCAGTGCAGCCGGGAGTTCATGAGGT	
	CTGACCATCTCAAGCAACACCAGAAGACTCATCGGCCGGGACCCTCAGAC	
	CCACAGGCCAACAACAACAATGGAGAGCAGGACAGTCCTCCTGCTGCTGG	
	TCCT	

[0116] To further demonstrate the applicability of the network analysis to uncover novel phenomena, Applicants focused on two TFs, SNAI2 and KLF4, which seemed to have opposite effects on the pluripotency module. Since KLF4 and SNAI2 are known to play critical and opposing roles in epithelial-mesenchymal transition (EMT) Applicants assessed whether they cause changes along an EMT-like axis in hPSCs as well. A PCA analysis using 200 genes from a consensus EMT geneset from MSigDB demonstrated a distinct stratification of KLF4-transduced cells towards an epithelial-like state and SNAI2-transduced cells towards a mesenchymal-like state. The scRNA-seq data also demonstrates expression level changes in signature genes consistent with EMT (FIG. **3**C), which Applicants confirmed with qRT-PCR (FIG. **9**).

[0117] Finally, Applicants chose to focus on ETV2, which has the greatest average fitness loss across all medium conditions (FIG. **1**B), as an exemplary case for investigation of a TF showing markedly reduced fitness in all medium conditions. Applicants hypothesized that the reduced fitness could be due to a proliferation disadvantage if ETV2-transduced cells are undergoing massive reprogramming without division. Focused experiments revealed that while ETV2-transduced cells undergo extensive cell death in pluripotent medium, there is a morphology change, indicative of an endothelial phenotype, in endothelial medium (FIG. **3**E). Confirmatory qRT-PCR assays demonstrated a strong upregulation of the key endothelial markers CDH5, PECAM1 and VWF (FIG. **3**F). Immunofluorescence revealed a distinct distribution of CDH5, with greater localization at cell-cell junctions (FIG. **3**G), consistent with known results. In addition, functional testing confirmed tube formation (FIG. **3**H), suggesting that a single TF, ETV2, may be able to drive reprogramming from a pluripotent to an endothelial-like state.

[0118] To Applicants' knowledge, this is the first demonstration of a high-throughput gene over-expression screening approach that can simultaneously assay both fitness and

transcriptome-wide effects. Applicants' use of ORF overexpression drove strong phenotypic effects, allowing Applicants to capture subtle transcriptomic signals. Additionally, Applicants demonstrated the versatility of the SEUSS screening platform, by assaying mutant forms of a single TF, and assaying all the TFs in a gene family to uncover patterns and differences. Applicants note that the effects of gene overexpression are context dependent. In Applicants' assays, since hPSCs were transduced with pooled libraries, transcriptomic changes driven by cell-cell interactions could increase variability, even supporting the survival of certain cells or disrupting the pluripotent state of control cells. Applicants also assume, in aggregating multiple batches from independent experiments, that each batch is relatively similar. Additionally, while Applicants believe the gene co-perturbation network is a valuable resource, it is dependent on the set of perturbations and conditions used in the experiment.

[0119] Taken together, SEUSS has broad applicability to study the effects of overexpression in diverse cell types and contexts; it may be extended to novel applications such as high-throughput screening of large-scale protein mutagenesis, and is amenable to scale-up. In combination with other methods of genetic and epigenetic perturbation it may allow Applicants to generate a comprehensive understanding of the pluripotent and differentiation landscape.

Example 1 Methods

Cell Culture

[0120] H1 hESC cell line was maintained under feeder-free conditions in mTeSR1 medium (Stem Cell Technologies). Prior to passaging, tissue-culture plates were coated with growth factor-reduced Matrigel (Corning) diluted in DMEM/F-12 medium (Thermo Fisher Scientific) and incubated for 30 minutes at 37° C., 5% CO_2. Cells were dissociated and passaged using the dissociation reagent Versene (Thermo Fisher Scientific).

Library Preparation

[0121] A lentiviral backbone plasmid was constructed containing the EF1α promoter, mCherry transgene flanked by BamHI restriction sites, followed by a P2A peptide and hygromycin resistance enzyme gene immediately downstream. Each transcription factor in the library was individually inserted in place of the mCherry transgene. Since the ectopically expressed transcription factor would lack a poly-adenylation tail due to the presence of the 2A peptide immediately downstream of it, the transcript will not be captured during single-cell transcriptome sequencing which relies on binding the poly-adenylation tail of mRNA. Thus, a barcode sequence was introduced to allow for identification of the ectopically expressed transcription factor. The backbone was digested with HpaI, and a pool of 20 bp long barcodes with flanking sequences compatible with the HpaI site, was inserted immediately downstream of the hygromycin resistance gene by Gibson assembly. The vector was constructed such that the barcodes were located only 200 bp upstream of the 3'-LTR region. This design enabled the barcodes to be transcribed near the poly-adenylation tail of the transcripts and a high fraction of barcodes to be captured during sample processing for scRNA-seq.

[0122] To create the transcription factor library, individual transcription factors were PCR amplified out of a human cDNA pool (Promega Corporation) or obtained as synthesized double-stranded DNA fragments (gBlocks, IDT Inc) with flanking sequences compatible with the BamHI restriction sites. MYC mutants were obtained as gBlocks with a 6-amino acid GSGSGS linker (SEQ ID NO: 29) substituted in place of deleted domains (Table 1). The lentiviral backbone was digested with BamHI HF (New England Biolabs) at 37° C. for 3 hours in a reaction consisting of: lentiviral backbone, 4 μg, CutSmart buffer, 5 μl, BamHI, 0.625 μl, H_20 up to 50 μl. After digestion, the vector was purified using a QIAquick PCR Purification Kit (Qiagen). Each transcription factor vector was then individually assembled via Gibson assembly. The Gibson assembly reactions were set up as follows: 100 ng digested lentiviral backbone, 3:10 molar ratio of transcription factor insert, 2× Gibson assembly master mix (New England Biolabs), H_20 up to 20 μl. After incubation at 50° C. for 1 h, the product was transformed into One Shot Stb13 chemically competent *Escherichia coli* (Invitrogen). A fraction (150 μL) of cultures was spread on carbenicillin (50 μg/ml) LB plates and incubated overnight at 37° C. Individual colonies were picked, introduced into 5 ml of carbenicillin (50 μg/ml) LB medium and incubated overnight in a shaker at 37° C. The plasmid DNA was then extracted with a QIAprep Spin Miniprep Kit (Qiagen), and Sanger sequenced to verify correct assembly of the vector and to extract barcode sequences.

[0123] To assemble the library, individual transcription factor vectors were pooled together in an equal mass ratio along with a control vector containing the mCherry transgene which constituted 10% of the final pool.

Viral Production

[0124] HEK 293T cells were maintained in high glucose DMEM supplemented with 10% fetal bovine serum (FBS). In order to produce lentivirus particles, cells were seeded in a 15 cm dish 1 day prior to transfection, such that they were 60-70% confluent at the time of transfection. For each 15 cm dish 36 μl of Lipofectamine 2000 (Life Technologies) was added to 1.5 ml of Opti-MEM (Life Technologies). Separately 3 μg of pMD2.G (Addgene no. 12259), 12 μg of pCMV delta R8.2 (Addgene no. 12263) and 9 μg of an individual vector or pooled vector library was added to 1.5 ml of Opti-MEM. After 5 minutes of incubation at room temperature, the Lipofectamine 2000 and DNA solutions were mixed and incubated at room temperature for 30 minutes. During the incubation period, medium in each 15 cm dish was replaced with 25 ml of fresh, pre-warmed medium. After the incubation period, the mixture was added dropwise to each dish of HEK 293T cells. Supernatant containing the viral particles was harvested after 48 and 72 hours, filtered with 0.45 μm filters (Steriflip, Millipore), and further concentrated using Amicon Ultra-15 centrifugal ultrafilters with a 100,000 NMWL cutoff (Millipore) to a final volume of 600-800 μl, divided into aliquots and frozen at −80° C.

Viral Transduction

[0125] For viral transduction, on day −1, H1 cells were dissociated to a single cell suspension using Accutase (Innovative Cell Technologies) and seeded into Matrigel-coated plates in mTeSR containing ROCK inhibitor, Y-27632 (10

μM, Sigma-Aldrich). For transduction with the TF library, cells were seeded into 10 cm dishes at a density of 6×10^6 cells for screens conducted in mTeSR or 4.5×10^6 cells for screens conducted in endothelial growth medium (EGM) or multilineage (ML) medium (DMEM+20% FBS.) For transduction with individual transcription factors cells were seeded at a density of 4×10^5 cells per well of a 12 well plate for experiments conducted in mTeSR or 3×10^5 cells per well for experiments conducted in the alternate media.

[0126] On day 0, medium was replaced with fresh mTeSR to allow cells to recover for 6-8 hours. Recovered cells were then transduced with lentivirus added to fresh mTeSR containing polybrene (5 μg/ml, Millipore). On day 1, medium was replaced with the appropriate fresh medium: mTeSR, endothelial growth medium or high glucose DMEM+20% FBS. Hygromycin (Thermo Fisher Scientific) selection was started from day 2 onward at a selection dose of 50 μg/ml, medium containing hygromycin was replaced daily.

Single Cell Library Preparation

[0127] For screens conducted in mTeSR cells were harvested 5 days after transduction while for alternate media, EGM or ML, cells were harvested 6 days after transduction with the TF library. Cells were dissociated to single cell suspensions using Accutase (Innovative Cell Technologies). For samples sorted with magnetically assisted cell sorting (MACS), cells were labelled with anti-TRA-1-60 antibodies or with dead cell removal microbeads and sorted as per manufacturer's instructions (Miltenyi Biotec). Samples were then resuspended in 1×PBS with 0.04% BSA at a concentration between 600-2000 per μl. Samples were loaded on the 10× Chromium system and processed as per manufacturer's instructions (10× Genomics). Unused cells were centrifuged at 300 rcf for 5 minutes and stored as pellets at −80° C. until extraction of genomic DNA.

[0128] Single cell libraries were prepared as per the manufacturer's instructions using the Single Cell 3' Reagent Kit v2 (10× Genomics). Prior to fragmentation, a fraction of the sample post-cDNA amplification was used to amplify the transcripts containing both the TF barcode and cell barcode.

Barcode Amplification

[0129] Barcodes were amplified from cDNA generated by the single cell system as well as from genomic DNA from cells not used for single cell sequencing. Barcodes were amplified from both types of samples and prepared for deep sequencing through a two-step PCR process.

[0130] For amplification of barcodes from cDNA, the first step was performed as three separate 50 μl reactions for each sample. 2 μl of the cDNA was input per reaction with Kapa Hifi Hotstart ReadyMix (Kapa Biosystems). The PCR primers used were, Nexterai7_TF_Barcode_F: GTCTCGTGGGCTCGGAGATGTGTATAAGAGACAGAGAACTATTTCCTGGCTGTTACG CG (SEQ ID NO: 30) and NEBNext Universal PCR Primer for Illumina (New England Biolabs). The thermocycling parameters were 95° C. for 3 min; 26-28 cycles of 98° C. for 20 s; 65° C. for 15 s; and 72° C. for 30 s; and a final extension of 72° C. for 5 min. The numbers of cycles were tested to ensure that they fell within the linear phase of amplification. Amplicons (~500 bp) of 3 reactions for each sample were pooled, size-selected and purified with Agencourt AMPure XP beads at a 0.8 ratio. The second step of PCR was performed with two separate 50 μl reactions with 50 ng of first step purified PCR product per reaction. Nextera XT Index primers were used to attach Illumina adapters and indices to the samples. The thermocycling parameters were: 95° C. for 3 min; 6-8 cycles of (98° C. for 20 s; 65° C. for 15 s; 72° C. for 30 s); and 72° C. for 5 min. The amplicons from these two reactions for each sample were pooled, size-selected and purified with Agencourt AMPure XP beads at a 0.8 ratio. The purified second-step PCR library was quantified by Qubit dsDNA HS assay (Thermo Fisher Scientific) and used for downstream sequencing on an Illumina HiSeq platform.

[0131] For amplification of barcodes from genomic DNA, genomic DNA was extracted from stored cell pellets with a DNeasy Blood and Tissue Kit (Qiagen). The first step PCR was performed as three separate 50 μl reactions for each sample. 2 μg of genomic DNA was input per reaction with Kapa Hifi Hotstart ReadyMix. The PCR primers used were, NGS_TF-Barcode_F: ACACTCTTTCCCTACACGACGCTCTTCCGATCTAGAACTATTTCCTGGCTGTTACGCG (SEQ ID NO: 31) and NGS_TF-Barcode_R: GACTGGAGTTCAGACGTGTGCTCTTCCGATCTTGTCTTCGTTGGGAGTGAATTAGC (SEQ ID NO: 32). The thermocycling parameters were: 95° C. for 3 min; 26-28 cycles of 98° C. for 20 s; 55° C. for 15 s; and 72° C. for 30 s; and a final extension of 72° C. for 5 min. The numbers of cycles were tested to ensure that they fell within the linear phase of amplification. Amplicons (200 bp) of 3 reactions for each sample were pooled, size-selected with Agencourt AMPure XP beads (Beckman Coulter, Inc.) at a ratio of 0.8, and the supernatant from this was further size-selected and purified at a ratio of 1.6. The second step of PCR was performed as two separate 50 μl reactions with 50 ng of first step purified PCR product per reaction. Next Multiplex Oligos for Illumina (New England Biolabs) Index primers were used to attach Illumina adapters and indices to the samples. The thermocycling parameters were: 95° C. for 3 min; 6 cycles of (98° C. for 20 s; 65° C. for 20 s; 72° C. for 30 s); and 72° C. for 2 min. The amplicons from these two reactions for each sample were pooled, size-selected with Agencourt AMPure XP beads at a ratio of 0.8, and the supernatant from this was further size-selected and purified at a ratio of 1.6. The purified second-step PCR library was quantified by Qubit dsDNA HS assay (Thermo Fisher Scientific) and used for downstream sequencing on an Illumina MiSeq platform.

Single Cell RNA-Seq Processing and Genotype Deconvolution

[0132] Using the 10× genomics CellRanger pipeline [citation], Applicants aligned Fastq files to hg38, counted UMIs to generate counts matrices, and aggregated samples across 10× runs with cellranger aggr. All cellranger commands were run using default settings.

[0133] To assign one or more transcription factor genotypes to each cell, Applicants aligned the plasmid barcode reads to hg38 using BWA, and then labeled each read with its corresponding cell and UMI tags. To remove potential chimeric reads, Applicants used a two-step filtering process. First, Applicants only kept UMIs that made up at least 0.5% of the total amount of reads for each cell. Applicants then counted the number of UMIs and reads for each plasmid barcode within each cell, and only assigned that cell any

barcode that contained at least 10% of the cell's read and UMI counts. Barcodes were mapped to transcription factors within one edit distance of the expected barcode. The code for assigning genotypes to each cell can be found on github at: github.com/yanwu2014/genotyping-matrices

Clustering and Cluster Enrichment

[0134] Clustering was performed on the aggregated counts matrices using the Seurat pipeline. Applicants first filtered the counts matrix for genes that are expressed in at least 2% of cells, and cells that express at least 500 genes. Applicants then normalized the counts matrix, found overdispersed genes, and used a negative binomial linear model to regress away library depth, batch effects, and mitochondrial gene fraction. Applicants performed PCA on the overdispersed genes, keeping the first 20 principal components. Applicants then used the PCs to generate a K Nearest Neighbors graph, with K=30, used the KNN graph to calculate a shared nearest neighbors graph, and used a modularity optimization algorithm on the SNN graph to find clusters. Clusters were recursively merged until all clusters could be distinguished from every other cluster with an out of the box error (oobe) of less than 5% using a random forest classifier trained on the top 15 genes by loading magnitude for the first 20 PCs. Applicants used tSNE on the first 20 PCs to visualize the results.

[0135] Cluster enrichment was performed using Fisher's exact test, testing each genotype for over-enrichment in each cluster. The p-value from the Fisher test for each genotype and cluster combination was corrected using the Benjamini-Hochberg method.

Differential Expression, Identification of Significant Genotypes, and Genotype Trimming

[0136] Applicants used a modified version of the MIMOSCA linear model to analyze the differentially expressed genes for each genotype. In this model, Applicants used the R glmnet package with the multigaussian family, with alpha (the lasso vs ridge parameter) set to 0.5. Lambda (the coefficient magnitude regularization parameter) was set using 5-fold cross validation.

[0137] In order to account for unperturbed cells, Applicants "trimmed" the cells in each transcription factor genotype to only include cells that belonged to a cluster that the genotype was enriched for. Specifically, Applicants first obtained a set of transcription factor genotypes with strong cluster enrichment, such that each significantly enriched genotype was enriched for a cluster with an FDR>1e-6, and whose cluster enrichment profile was different from the control mCherry profile with an adjusted chi-squared p-value of less than 1e-6. For each significantly enriched genotype, Applicants only kept cells that were part of a cluster that the genotype was enriched for at FDR<0.01 level. Each genotype can be enriched for more than one cluster. After trimming the significantly enriched genotypes, Applicants repeated the differential expression.

[0138] TFs were chosen as significant for downstream analysis if they were enriched for one or more clusters as described, or if the TF drove statistically significant differential expression of greater than 100 genes.

Gene Co Perturbation Network and Module Detection

[0139] Applicants took the genes by genotypes coefficients matrix from the regression analysis with trimmed genotypes and used it to calculate the Euclidean distance between genes, using the significant genotypes as features. Applicants then built a k-nearest neighbors graph from the Euclidean distances between genes, with k=30. From this kNN graph, Applicants calculated the fraction of shared nearest neighbors (SNN) for each pair of genes to build and SNN graph. For example, if two genes share 23/30 neighbors, Applicants create an edge between them in the SNN graph with a weight of 23/30=0.767.

[0140] To identify gene modules, Applicants used the Louvain modularity optimization algorithm. For each gene module, Applicants identified enriched Gene Ontology terms using Fisher's exact test (Table 5). Applicants also ranked genes in each gene module by the number of enriched Gene Ontology terms the gene is part of, to identify the most biologically significant genes in each module (Table 5). Gene module identities were assigned based on manual inspection of enriched GO terms and the genes within each module. The effect of each genotype on a gene module was calculated by taking the average of the regression coefficients for the genotype and the genes within the module.

Dataset Correlation

[0141] To compare how the combined hPSC medium dataset correlated with the five individual datasets, Applicants correlated the regression coefficients of the combined dataset with the coefficients for each individual dataset, subsetting for coefficients that were statistically significant in either the individual dataset, or the combined dataset. Each coefficient represents the effect of a single TF on a single gene. The two datasets for the multilineage lineage screens were correlated in the same manner.

Fitness Effect Analysis

[0142] To calculate fitness effects from genomic DNA reads, Applicants first used MagECK to align reads to genotype barcodes and count the number of reads for each genotype in each sample, resulting in a genotypes by samples read counts matrix. Applicants normalized the read counts matrix by dividing each column by the sum of that column, and then calculated log fold-change by dividing each sample by the normalized plasmid library counts, and then taking a log 2 transform. For the stem cell media, Applicants averaged the log fold change across the non MACS sorted samples.

[0143] To calculate fitness effects from genotype counts identified from single cell RNA-seq, Applicants used a cell counts matrix instead of a read counts matrix, and repeated the above protocol.

Epithelial Mesenchymal Transition Analysis

[0144] Applicants took 200 genes from the Hallmark Epithelial Mesenchymal Transition geneset from MSigDB and ran PCA on those genes with the stem cell medium dataset, visualizing the first two principal components. The first principal component was an EMT-like signature and Applicants used the gene loadings, along with literature research to identify a relevant panel of EMT related genes to display. All analysis code can be found at github.com/yanwu2014/SEUS S-Analysis.

RNA Extraction, and qRT-PCR

[0145] RNA was extracted from cells using the RNeasy Mini Kit (Qiagen) as per the manufacturer's instructions. The quality and concentration of the RNA samples was measured using a spectrophotometer (Nanodrop 2000, Thermo Fisher Scientific). cDNA was prepared using the Protoscript II First Strand cDNA synthesis kit (New England Biolabs) in a 20 μl reaction and diluted up to 1:5 with nuclease-free water. qRT-PCR reactions were setup as: 2 μl cDNA, 400 nM of each primer, 2× Kapa SYBR Fast Master Mix (Kapa Biosystems), H_2O up to 20 μl. qRT-PCR was performed using a CFX Connect Real Time PCR Detection System (Bio-Rad) with the thermocycling parameters: 95° C. for 3 min; 95° C. for 3 s; 60° C. for 20 s, for 40 cycles. All experiments were performed in triplicate and results were normalized against a housekeeping gene, GAPDH. Relative mRNA expression levels, compared with GAPDH, were determined by the comparative cycle threshold ($\Delta\Delta C_T$) method. Primers used for qRT-PCR are listed in Table 6.

Immunofluorescence

[0146] Cells were fixed with 4% (wt/vol) paraformaldehyde in PBS at room temperature for 30 minutes. Cells were then incubated with a blocking buffer: 5% donkey serum, 0.2% Triton X-100 in PBS for 1 hour at room temperature followed by incubation with primary antibodies diluted in the blocking buffer at 4° C. overnight. Primary antibodies used were: VE-Cadherin (D87F2, Cell Signaling Technology; 1:400). Secondary antibodies used were: DyLight 488 labelled donkey anti-rabbit IgG (ab96891, Abcam; 1:250).

[0147] After overnight incubation with primary antibodies, cells were labelled with secondary antibodies diluted in 1% BSA in PBS for 1 hour at 37° C. Nuclear staining was done by incubating cells with DAPI for 5 minutes at room temperature. All imaging was conducted on a Leica DMi8 inverted microscope equipped with an Andor Zyla sCMOS camera and a Lumencor Spectra X multi-wavelength fluorescence light source.

Endothelial Tube Formation Assay

[0148] A mCherry expressing H1 cell line was created by transducing H1 cells with a lentivirus containing the EF1α promoter driving expression of the mCherry transgene, internal ribosome entry site (IRES) and a puromycin resistance gene. Cells were then maintained under constant puromycin selection at a dose of 0.75 μg/ml. mCherry labelled H1 cells were transduced with either ETV2 lentivirus or control mCherry lentivirus, hygromycin selection was started on day 2 and cells were used for tube formation assay on day 6.

[0149] Growth-factor reduced Matrigel (Corning) was thawed on ice and 250 μl was deposited cold per well of a 24-well plate. The deposited Matrigel was incubated for 60 minutes at 37° C., 5% CO_2, to allow for complete gelation and the ETV2-transduced or control cells were then seeded on it at a density of 3.2×10^5 cells per well in a volume of 500 μl EGM. Imaging was conducted 24 hours after deposition of the cells.

Example 2

Corneal Endothelial Stem Cell Transplant

[0150] Skin fibroblasts are isolated from a patient with a corneal eye disease. iPSCs are generated from the fibroblasts using techniques known in the art. Briefly, the isolated fibroblasts are reprogrammed by forced expression of one or more pluripotency genes selected from: OCT3/4, SOX1, SOX2, SOX15, SOX18, KLF1, KLF2, KLF4, KLF5, n-MYC, c-MYC, L-MYC, NANOG, LIN28, and GLIS1.

[0151] Next, the iPSCs are directed to differentiate into endothelial cells by introducing expression of ETV2. Expression is introduced by infecting the cells with an AAV virus encoding ETV2. After the cells differentiate into endothelial cells, they are expanded ex vivo and harvested.

[0152] The cells are administered to the patient by transplant to the cornea following removal of the diseased corneal tissue. After corneal transplant with the endothelial cells, repair of the cornea is identified by achieving full or partial restoration of corneal function in the patient.

TABLE 1

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
mCherry Control	ATGGTGAGCAAGGGCGAGGAGGAT AACATGGCCATCATCAAGGAGTTC ATGCGCTTCAAGGTGCACATGGAG GGCTCCGTGAACGGCCACGAGTTC GAGATCGAGGGCGAGGGCGAGGGC CGCCCCTACGAGGGCACCCAGACC GCCAAGCTGAAGGTGACCAAGGGT GGCCCCCTGCCCTTCGCCTGGGACA TCCTGTCCCCTCAGTTCATGTACGG CTCCAAGGCCTACGTGAAGCACCC CGCCGACATCCCCGACTACTTGAAG CTGTCCTTCCCCGAGGGCTTCAAGT GGGAGCGCGTGATGAACTTCGAGG ACGGCGGCGTGGTGACCGTGACCC AGGACTCCTCCCTGCAGGACGGCG AGTTCATCTACAAGGTGAAGCTGC GCGGCACCAACTTCCCCTCCGACGG CCCCGTAATGCAGAAGAAGACCAT GGGCTGGGAGGCCTCCTCCGAGCG GATGTACCCCGAGGACGGCGCCCT GAAGGGCGAGATCAAGCAGAGGCT GAAGCTGAAGGACGGCGGCCACTA CGACGCTGAGGTCAAGACCACCTA	33	Non-functional control vector	

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	CAAGGCCAAGAAGCCCGTGCAGCT GCCCGGCGCCTACAACGTCAACAT CAAGTTGGACATCACCTCCCACAAC GAGGACTACACCATCGTGGAACAG TACGAACGCGCCGAGGGCCGCCAC TCCACCGGCGGCATGGACGAGCTG TACAAG			
ASCL1	ATGGAGTCTTCTGCTAAAATGGAGT CCGGAGGCGCGGGACAACAACCAC AACCGCAACCACAACAACCCTTCCT GCCGCCGGCCGCATGTTTTTTCGCG ACCGCTGCTGCTGCTGCAGCGGCG GCGGCTGCTGCCGCCGCGCAATCC GCCCAACAGCAACAACAACAACAG CAGCAGCAGCAACAAGCGCCTCAA CTTCGACCCGCTGCAGACGGGCAG CCCTCAGGGGGAGGGCACAAGAGC GCTCCGAAGCAGGTTAAAAGGCAG AGGAGCAGTAGTCCCGAACTGATG CGATGTAAGAGGCGCCTCAATTTTA GCGGTTTTGGTTACTCTTTGCCCCA GCAGCAGCCGGCTGCCGTAGCTCG CCGAAATGAGCGGGAAAGGAACCG CGTTAAACTTGTGAATCTCGGTTTC GCGACACTTCGAGAGCACGTACCA AATGGGGCAGCTAACAAGAAAATG AGTAAAGTTGAGACACTGCGGTCT GCAGTGGAGTATATTAGAGCTCTTC AACAATTGCTTGACGAGCACGATG CCGTATCAGCCGCATTTCAAGCCGG GGTGCTGTCCCCAACAATATCTCCG AACTACAGCAATGATCTTAATAGC ATGGCGGGAAGTCCCGTTTCCTCCT ACTCCTCTGATGAGGGCAGCTACG ACCCTCTCAGTCCCGAGGAGCAAG AGCTTCTTGACTTCACTAACTGGTT C	34	Involved in neuronal specification and differentiation. Demonstrated to drive neuronal differentiation from hPSCs	Wilkinson, G. et al. Proneural genes in neocortical development. Neuroscience 253, 256-273 (2013). Chanda, S. et al. Generation of induced neuronal cells by the single reprogramming factor ASCL1. Stem cell reports 3, 282-96 (2014).
ASCL3	ATGATGGACAACAGAGGCAACTCT AGTCTACCTGACAAACTTCCTATCT TCCCTGATTCTGCCCGCTTGCCACT TACCAGGTCCTTCTATCTGGAGCCC ATGGTCACTTTCCACGTGCACCCAG AGGCCCCGGTGTCATCTCCTTACTC TGAGGAGCTGCCACGGCTGCCTTTT CCCAGCGACTCTCTTATCCTGGGAA ATTACAGTGAACCCTGCCCCTTCTC TTTCCCGATGCCTTATCCAAATTAC AGAGGGTGCGAGTACTCCTACGGG CCAGCCTTCACCCGGAAAAGGAAT GAGCGGGAAAGGCAGCGGGTGAAA TGTGTCAATGAAGGCTACGCCCAG CTCCGACATCATCTGCCAGAGGAGT ATTTGGAGAAGCGACTCAGCAAAG TGGAAACCCTCAGAGCTGCGATCA AGTACATTAACTACCTGCAGTCTCT TCTGTACCCTGATAAAGCTGAGACA AAGAATAACCCTGGAAAAGTTTCC TCCATGATAGCAACCACCAGCCAC CATGCTGACCCTATGTTCAGAATTG TTTGCCCAACTTTCTTGTACAAAGT TGTCCCC	35	Involved in salivary gland cell development	Bullard, T. et al. Ascl3 expression marks a progenitor population of both acinar and ductal cells in mouse salivary glands. Dev. Biol. 320, 72-78(2008)

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
ASCL4	ATGGAGACGCGTAAACCGGCGGAA CGGCTGGCCTTGCCATACTCGCTGC GCACCGCGCCCCTGGGCGTTCCGG GGACCCTGCCCGGACTCCCGCGGA GGGACCCCCTCAGGGTCGCCCTGC GTCTGGACGCCGCGTGCTGGGAGT GGGCGCGCAGCGGCTGCGCACGGG GATGGCAGTACTTGCCCGTGCCGCT GGACAGCGCCTTCGAGCCCGCCTTC CTCCGCAAGCGCAACGAGCGCGAG CGGCAGCGGGTGCGCTGCGTGAAC GAGGGCTATGCGCGCCTCCGAGAC CACCTGCCCCGGGAGCTGGCAGAC AAGCGCCTCAGCAAAGTGGAGACG CTCCGCGCTGCCATCGACTACATCA AGCACCTGCAGGAGCTGCTGGAGC GCCAGGCCTGGGGGCTCGAGGGCG CGGCCGGCGCCGTCCCCCAGCGCA GGGCGGAATGCAACAGCGACGGGG AGTCCAAGGCCTCTTCGGCGCCTTC GCCCAGCAGCGAGCCCGAGGAGGG GGGCAGC	36	Involved in development of skin	Jonsson, M. et al. Hash4, a novel human achaete-scute homologue found in fetal skin. Genomics 84, 859-866 (2004)
ASCL5	ATGCCGATGGGGGCAGCAGAAAGA GGTGCTGGGCCCCAATCATCTGCAG CACCATGGGCTGGTTCAGAAAAGG CGGCAAAGAGAGGGCCATCAAAAA GCTGGTACCCAAGAGCTGCTGCATC TGATGTCACGTGCCCGACTGGTGGT GATGGAGCTGACCCAAAACCTGGA CCTTTTGGAGGTGGTTTAGCTTTAG GGCCTGCGCCCAGAGGAACAATGA ATAATAATTTCTGCAGGGCCCTTGT TGACAGAAGGCCTTTAGGACCCCCT TCATGTATGCAATTAGGTGTAATGC CACCGCCAAGACAAGCGCCCCTCC CGCCGGCTGAACCCCTTGGAAATGT ACCTTTCCTCCTATACCCTGGCCCA GCTGAACCACCATATTATGATGCAT ATGCTGGTGTTTTCCCATATGTGCC TTTCCCTGGTGCTTTTGGTGTATAT GAATACCCTTTTGAGCCGGCTTTTA TCCAAAAGAGGAATGAAAGAGAGA GACAGAGAGTGAAGTGTGTGAATG AAGGATACGCCAGATTGAGAGGCC ATTTGCCTGGTGCCCTGGCAGAAAA GAGATTATCAAAAGTTGAAACCCT GAGGGCGGCAATCAGATATATAAA ATACCTCCAAGAACTCCTTTCATCA GCACCTGATGGATCGACACCACCG GCTTCAAGAGGTTTACCTGGAACTG GACCATGCCCTGCACCGCCTGCTAC ACCAAGGCCAGACAGACCTGGAGA TGGAGAAGCAAGAGCACCTTCTTC CCTTGTCCCTGAATCTTCTGAATCA TCATGTTTTTCGCCTTCCCCTTTTTT AGAAAGTGAAGAATCCTGGCA	37	Paralog of ASCL4	Wang, C. et al. Systematic analysis of the achaete-scute complex-like gene signature in clinical cancer patients. Molecular and Clinical Oncology 6, (Spandidos Publications, 2017).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
ATF7	ATGGGAGACGACAGACCGTTTGTG TGCAATGCCCCGGGCTGTGGACAG AGATTTACAAACGAGGACCACCTG GCAGTTCATAAACACAAGCATGAG ATGACATTGAAATTTGGCCCAGCCC GAACTGACTCAGTCATCATTGCAGA TCAAACGCCTACTCCAACTAGATTC CTGAAGAACTGTGAGGAGGTGGGA CTCTTCAATGAACTAGCTAGCTCCT TTGAACATGAATTCAAGAAAGCTG CAGATGAGGATGAGAAAAAGGCAA GAAGCAGGACTGTTGCCAAAAAAC TGGTGGCTGCTGCTGGGCCCCTTGA CATGTCTCTGCCTTCCACACCAGAC ATCAAAATCAAAGAAGAAGAGCCA GTGGAGGTAGACTCATCCCCACCTG ATAGCCCTGCCTCTAGTCCCTGTTC CCCACCACTGAAGGAGAAGGAGGT TACCCCAAAGCCTGTTCTGATCTCT ACCCCCACACCCACCATTGTACGTC CTGGCTCCCTGCCTCTCCACTTGGG CTATGATCCACTTCATCCAACCCTT CCCTCCCCAACCTCTGTCATCACAC AGGCTCCACCATCCAACAGGCAAA TGGGGTCTCCCACTGGCTCCCTCCC TCTTGTCATGCATCTTGCTAATGGA CAGACCATGCCTGTGTTGCCAGGGC CTCCAGTACAGATGCCGTCTGTTAT ATCGCTGGCCAGACCTGTGTCCATG GTGCCCAACATTCCTGGTATCCCTG GCCCACCAGTTAACAGTAGTGGCTC CATTTCTCCCTCTGGCCACCCTATA CCATCAGAAGCCAAGATGAGACTG AAAGCCACCCTAACTCACCAAGTCT CCTCAATCAATGGTGGTTGTGGAAT GGTGGTGGGTACTGCCAGCACCAT GGTGACAGCCCGCCCAGAGCAGAG CCAGATTCTCATCCAGCACCCTGAT GCCCCATCCCCTGCCCAGCCACAG GTCTCACCAGCTCAGCCCACCCCTA GTACTGGGGGGCGACGGCGGCGCA CAGTAGATGAAGATCCAGATGAGC GACGGCAGCGCTTTCTGGAGCGCA ACCGGGCTGCAGCCTCCCGCTGCCG CCAAAAGCGAAAGCTGTGGGTGTC CTCCCTAGAGAAGAAGGCCGAAGA ACTCACTTCTCAGAACATTCAGCTG AGTAATGAAGTCACATTACTACGC AATGAGGTGGCCCAGTTGAAACAG CTACTGTTAGCTCATAAAGACTGCC CAGTCACTGCACTACAGAAAAAGA CTCAAGGCTATTTAGAAAGCCCCA AGGAAAGCTCAGAGCCAACGGGTT CTCCAGCCCCTGTGATTCAGCACAG CTCAGCAACAGCCCCTAGCAATGG CCTCAGTGTTCGCTCTGCAGCTGAA GCTGTGGCCACCTCGGTCCTCACTC AGATGGCCAGCCAAAGGACAGAAC TGAGCATGCCGATACAATCGCATGT AATCATGACCCCACAGTCCCAGTCT GCGGGCAGA	38	Involved in early cell signaling, binds cAMP response element	Peters, C. S. et al. ATF-7, a novel bZIP protein, interacts with the PRL-1 protein-tyrosine phosphatase. J. Biol. Chem. 276, 13718-26 (2001). Hamard, P.-J. et al. A functional interaction between ATF7 and TAF12 that is modulated by TAF4. Oncogene 24, 3472-3483 (2005).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
CDX2	ATGTACGTGAGCTACCTCCTGGACA AGGACGTGAGCATGTACCCTAGCT CCGTGCGCCACTCTGGCGGCCTCAA CCTGGCGCCGCAGAACTTCGTCAGC CCCCCGCAGTACCCGGACTACGGC GGTTACCACGTGGCGGCCGCAGCT GCAGCGGCAGCGAACTTGGACAGC GCGCAGTCCCCGGGGCCATCCTGG CCGGCAGCGTATGGCGCCCCACTCC GGGAGGACTGGAATGGCTACGCGC CCGGAGGCGCCGCGGCCGCCGCCA ACGCCGTGGCTCACGGCCTCAACG GTGGCTCCCCGGCCGCAGCCATGG GCTACAGCAGCCCCGCAGACTACC ATCCGCACCACCACCCGCATCACC ACCCGCACCACCCGGCCGCCGCGC CTTCCTGCGCTTCTGGGCTGCTGCA AACGCTCAACCCCGGCCCTCCTGGG CCCGCCGCCACCGCTGCCGCCGAG CAGCTGTCTCCCGGCGGCCAGCGG CGGAACCTGTGCGAGTGGATGCGG AAGCCGGCGCAGCAGTCCCTCGGC AGCCAAGTGAAAACCAGGACGAAA GACAAATATCGAGTGGTGTACACG GACCACCAGCGGCTGGAGCTGGAG AAGGAGTTTCACTACAGTCGCTACA TCACCATCCGGAGGAAAGCCGAGC TAGCCGCCACGCTGGGGCTCTCTGA GAGGCAGGTTAAAATCTGGTTTCA GAACCGCAGAGCAAAGGAGAGGA AAATCAACAAGAAGAAGTTGCAGC AGCAACAGCAGCAGCAGCCACCAC AGCCGCCTCCGCCGCCACCACAGC CTCCCCAGCCTCAGCCAGGTCCTCT GAGAAGTGTCCCAGAGCCCTTGAG TCCGGTGTCTTCCCTGCAAGCCTCA GTGTCTGGCTCTGTCCCTGGGGTTC TGGGGCCAACTGGGGGGGTGCTAA ACCCCACCGTCACCCAG	39	Involved in trophectoderm specification and differentiation	Strumpf, D. et al. Cdx2 is required for correct cell fate specification and differentiation of trophectoderm in the mouse blastocyst. Development 132, 2093-102 (2005).
CRX	ATGATGGCGTATATGAACCCGGGG CCCCACTATTCTGTCAACGCCTTGG CCCTAAGTGGCCCCAGTGTGGATCT GATGCACCAGGCTGTGCCCTACCCA AGCGCCCCCAGGAAGCAGCGGCGG GAGCGCACCACCTTCACCCGGAGC CAACTGGAGGAGCTGGAGGCACTG TTTGCCAAGACCCAGTACCCAGAC GTCTATGCCCGTGAGGAGGTGGCTC TGAAGATCAATCTGCCTGAGTCCAG GGTTCAGGTTTGGTTCAAGAACCGG AGGGCTAAATGCAGGCAGCAGCGA CAGCAGCAGAAACAGCAGCAGCAG CCCCCAGGGGGCCAGGCCAAGGCC CGGCCTGCCAAGAGGAAGGCGGGC ACGTCCCCAAGACCCTCCACAGAT GTGTGTCCAGACCCTCTGGGCATCT CAGATTCCTACAGTCCCCCTCTGCC CGGCCCCTCAGGCTCCCCAACCAC GGCAGTGGCCACTGTGTCCATCTGG AGCCCAGCCTCAGAGTCCCCTTTGC CTGAGGCGCAGCGGGCTGGGCTGG TGGCCTCAGGGCCGTCTCTGACCTC CGCCCCCTATGCCATGACCTACGCC CCGGCCTCCGCTTTCTGCTCTTCCC CCTCCGCCTATGGGTCTCCGAGCTC CTATTTCAGCGGCCTAGACCCCTAC CTTTCTCCCATGGTGCCCCAGCTAG GGGGCCCGGCTCTTAGCCCCCTCTC TGGCCCCTCCGTGGGACCTTCCCTG GCCCAGTCCCCCACCTCCCTATCAG GCCAGAGCTATGGCGCCTACAGCC CCGTGGATAGCTTGGAATTCAAGG	40	Involved in photoreceptor differentiation	Furukawa, T., Morrow, E. M. & Cepko, C. L. Crx, a novel otx-like homeobox gene, shows photoreceptor-specific expression and regulates photoreceptor differentiation. Cell 91, 531-541 (1997).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	ACCCCACGGGCACCTGGAAATTCA CCTACAATCCCATGGACCCTCTGGA CTACAAGGATCAGAGTGCCTGGAA GTTTCAGATCTTG			
ERG	ATGGCCAGCACTATTAAGGAAGCC TTATCAGTTGTGAGTGAGGACCAGT CGTTGTTTGAGTGTGCCTACGGAAC GCCACACCTGGCTAAGACAGAGAT GACCGCGTCCTCCTCCAGCGACTAT GGACAGACTTCCAAGATGAGCCCA CGCGTCCCTCAGCAGGATTGGCTGT CTCAACCCCCAGCCAGGGTCACCAT CAAAATGGAATGTAACCCTAGCCA GGTGAATGGCTCAAGGAACTCTCCT GATGAATGCAGTGTGGCCAAAGGC GGGAAGATGGTGGGCAGCCCAGAC ACCGTTGGGATGAACTACGGCAGC TACATGGAGGAGAAGCACATGCCA CCCCCAAACATGACCACGAACGAG CGCAGAGTTATCGTGCCAGCAGAT CCTACGCTATGGAGTACAGACCAT GTGCGGCAGTGGCTGGAGTGGGCG GTGAAAGAATATGGCCTTCCAGAC GTCAACATCTTGTTATTCCAGAACA TCGATGGGAAGGAACTGTGCAAGA TGACCAAGGACGACTTCCAGAGGC TCACCCCCAGCTACAATGCCGACAT CCTTCTCTCACATCTCCACTACCTC AGAGAGACTCCTCTTCCACATTTGA CTTCAGATGATGTTGATAAAGCCTT ACAAAACTCTCCACGGTTAATGCAT GCTAGAAACACAGGGGGTGCAGCT TTTATTTTCCCAAATACTTCAGTAT ATCCTGAAGCTACGCAAAGAATTA CAACTAGGCCAGATTTACCATATGA GCCCCCCAGGAGATCAGCCTGGAC CGGTCACGGCCACCCCACGCCCCA GTCGAAAGCTGCTCAACCATCTCCT TCCACAGTGCCCAAAACTGAAGAC CAGCGTCCTCAGTTAGATCCTTATC AGATTCTTGGACCAACAAGTAGCC GCCTTGCAAATCCAGGCAGTGGCC AGATCCAGCTTTGGCAGTTCCTCCT GGAGCTCCTGTCGGACAGCTCCAA CTCCAGCTGCATCACCTGGGAAGG CACCAACGGGGAGTTCAAGATGAC GGATCCCGACGAGGTGGCCCGGCG CTGGGGAGAGCGGAAGAGCAAACC CAACATGAACTACGATAAGCTCAG CCGCGCCCTCCGTTACTACTATGAC AAGAACATCATGACCAAGGTCCAT GGGAAGCGCTACGCCTACAAGTTC GACTTCCACGGGATCGCCCAGGCC CTCCAGCCCCACCCCCCGGAGTCAT CTCTGTACAAGTACCCCTCAGACCT CCCGTACATGGGCTCCTATCACGCC CACCCACAGAAGATGAACTTTGTG GCGCCCCACCCTCCAGCCCTCCCCG TGACATCTTCCAGTTTTTTTGCTGCC CCAAACCCATACTGGAATTCACCA ACTGGGGGTATATACCCCAACACT AGGCTCCCCACCAGCCATATGCCTT CTCATCTGGGCACTTACTAC	41	Involved in endothelial cell specification and differentiation	Mclaughlin, F. et al. Combined genomic and antisense analysis reveals that the transcription factor Erg is implicated in endothelial cell differentiation. Blood 98, 3332-3339 (2001).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
ESRRG	ATGTCAAACAAAGATCGACACATT GATTCCAGCTGTTCGTCCTTCATCA AGACGGAACCTTCCAGCCCAGCCT CCCTGACGGACAGCGTCAACCACC ACAGCCCTGGTGGCTCTTCAGACGC CAGTGGGAGCTACAGTTCAACCAT GAATGGCCATCAGAACGGACTTGA CTCGCCACCTCTCTACCCTTCTGCT CCTATCCTGGGAGGTAGTGGGCCTG TCAGGAAACTGTATGATGACTGCTC CAGCACCATTGTTGAAGATCCCCAG ACCAAGTGTGAATACATGCTCAACT CGATGCCCAAGAGACTGTGTTTAGT GTGTGGTGACATCGCTTCTGGGTAC CACTATGGGGTAGCATCATGTGAA GCCTGCAAGGCATTCTTCAAGAGG ACAATTCAAGGCAATATAGAATAC AGCTGCCCTGCCACGAATGAATGT GAAATCACAAAGCGCAGACGTAAA TCCTGCCAGGCTTGCCGCTTCATGA AGTGTTTAAAAGTGGGCATGCTGA AAGAAGGGGTGCGTCTTGACAGAG TACGTGGAGGTCGGCAGAAGTACA AGCGCAGGATAGATGCGGAGAACA GCCCATACCTGAACCCTCAGCTGGT TCAGCCAGCCAAAAAGCCATTGCT CTGGTCTGATCCTGCAGATAACAAG ATTGTCTCACATTTGTTGGTGGCTG AACCGGAGAAGATCTATGCCATGC CTGACCCTACTGTCCCCGACAGTGA CATCAAAGCCCTCACTACACTGTGT GACTTGGCCGACCGAGAGTTGGTG GTTATCATTGGATGGGCGAAGCAT ATTCCAGGCTTCTCCACGCTGTCCC TGGCGGACCAGATGAGCCTTCTGC AGAGTGCTTGGATGGAAATTTTGAT CCTTGGTGTCGTATACCGGTCTCTT TCGTTTGAGGATGAACTTGTCTATG CAGACGATTATATAATGGACGAAG ACCAGTCCAAATTAGCAGGCCTTCT TGATCTAAATAATGCTATCCTGCAG CTGGTAAAGAAATACAAGAGCATG AAGCTGGAAAAAGAAGAATTTGTC ACCCTCAAAGCTATAGCTCTTGCTA ATTCAGACTCCATGCACATAGAAG ATGTTGAAGCCGTTCAGAAGCTTCA GGATGTCTTACATGAAGCGCTGCA GGATTATGAAGCTGGCCAGCACAT GGAAGACCCTCGTCGAGCTGGCAA GATGCTGATGACACTGCCACTCCTG AGGCAGACCTCTACCAAGGCCGTG CAGCATTTCTACAACATCAAACTAG AAGGCAAAGTCCCAATGCACAAAC TTTTTTTGGAAATGTTGGAGGCCAA GGTC	42	Involved in cardiac development	Alaynick, W. A. et al. ERRγ Directs and Maintains the Transition to Oxidative Metabolism in the Postnatal Heart. Cell Metab. 6, 13-24 (2007).
ETV2	ATGGATCTTTGGAACTGGGATGAA GCTTCCCCTCAAGAAGTTCCCCCCG GAAATAAACTCGCGGGGCTTGGAA GACTCCCTCGCCTTCCGCAACGCGT CTGGGGCGGATGCCCTGGTGGAGC CTCAGCGGACCCAAACCCTTTGTCT CCAGCGGAGGGGGCAAAGTTGGGT TTCTGCTTCCCGGATCTTGCTTTGC AAGGCGATACTCCAACGGCGACGG CAGAGACCTGTTGGAAAGGCACCA GTAGCTCCCTGGCCAGCTTTCCGCA GCTCGATTGGGGGTCAGCCCTTCTC CATCCCGAAGTTCCCTGGGGGGCG GAACCCGACTCCCAAGCCCTTCCCT GGAGTGGTGATTGGACAGATATGG CATGCACAGCCTGGGACAGTTGGT CCGGGGCGTCACAGACATTGGGAC	43	Involved in haemato-endothelial specification and differentiation, and in vasculogenesis	Lee, D. et al. ER71 acts downstream of BMP, Notch, and Wnt signaling in blood and vessel progenitor specification. Cell Stem Cell 2, 49-507 (2008).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	CAGCCCCACTTGGACCGGGGCCTAT CCCCGCAGCAGGAAGCGAAGGAGC TGCTGGTCAGAACTGTGTGCCCGTG GCTGGTGAGGCTACCAGTTGGTCCA GGGCCCAGGCAGCAGGCAGTAACA CCAGCTGGGATTGCTCAGTGGGGC CTGACGGGGATACTTATTGGGGCTC TGGTCTTGGTGGAGAACCGAGAAC GGACTGTACGATAAGTTGGGGCGG TCCAGCTGGGCCTGATTGTACTACG TCATGGAATCCTGGCTTGCACGCCG GCGGCACGACAAGCCTTAAGAGAT ATCAAAGTTCAGCCCTTACAGTTTG CTCAGAACCTTCCCCGCAAAGTGAC CGAGCGTCACTGGCGCGATGTCCTA AAACTAATCATCGAGGGCCGATCC AGTTGTGGCAGTTTTTGCTTGAACT CCTTCACGATGGCGCGAGGAGCAG TTGCATCAGATGGACCGGTAACAG CAGGGAGTTCCAATTGTGTGACCCC AAGGAAGTGGCTCGACTGTGGGGT GAGCGCAAACGGAAGCCTGGTATG AATTACGAAAAGTTGAGTAGGGGT TTGCGATATTACTATAGGCGCGACA TCGTTCGAAAGTCCGGTGGTCGAA AGTACACATACAGATTCGGCGGTC GCGTACCATCTCTTGCATACCCTGA TTGCGCAGGCGGGGGTAGGGGTGC GGAAACACAA			
FLI1	ATGGACGGGACTATTAAGGAGGCT CTGTCGGTGGTGAGCGACGACCAG TCCCTCTTTGACTCAGCGTACGGAG CGGCAGCCCATCTCCCCAAGGCCG ACATGACTGCCTCGGGGAGTCCTG ACTACGGGCAGCCCCACAAGATCA ACCCCCTCCCACCACAGCAGGAGT GGATCAATCAGCCAGTGAGGGTCA ACGTCAAGCGGGAGTATGACCACA TGAATGGATCCAGGGAGTCTCCGG TGGACTGCAGCGTTAGCAAATGCA GCAAGCTGGTGGGCGGAGGCGAGT CCAACCCCATGAACTACAACAGCT ATATGGACGAGAAGAATGGCCCCC CTCCTCCCAACATGACCACCAACGA GAGGAGAGTCATCGTCCCCGCAGA CCCCACACTGTGGACACAGGAGCA TGTGAGGCAATGGCTGGAGTGGGC CATAAAGGAGTACAGCTTGATGGA GATCGACACATCCTTTTTCCAGAAC ATGGATGGCAAGGAACTGTGTAAA ATGAACAAGGAGGACTTCCTCCGC GCCACCACCCTCTACAACACGGAA GTGCTGTTGTCACACCTCAGTTACC TCAGGGAAAGTTCACTGCTGGCCTA TAATACAACCTCCCACACCGACCA ATCCTCACGATTGAGTGTCAAAGA AGACCCTTCTTATGACTCAGTCAGA AGAGGAGCTTGGGGCAATAACATG AATTCTGGCCTCAACAAAAGTCCTC CCCTTGGAGGGGCACAAACGATCA GTAAGAATACAGAGCAACGGCCCC AGCCAGATCCGTATCAGATCCTGG GCCCGACCAGCAGTCGCCTAGCCA ACCCTGGAAGCGGGCAGATCCAGC TGTGGCAATTCCTCCTGGAGCTGCT CTCCGACAGCGCCAACGCCAGCTG TATCACCTGGGAGGGGACCAACGG GGAGTTCAAAATGACGGACCCCGA TGAGGTGGCCAGGCGCTGGGGCGA GCGGAAAAGCAAGCCCAACATGAA TTACGACAAGCTGAGCCGGGCCCT CCGTTATTACTATGATAAAAACATT ATGACCAAAGTGCACGGCAAAAGA	44	Involved in haemato-endothelial specification and differentiation	Liu, F. et al. Fli1 Acts at the Top of the Transcriptional Network Driving Blood and Endothelial Development. Curr. Biol. 18, 1234-1240 (2008).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	TATGCTTACAAATTTGACTTCCACG GCATTGCCCAGGCTCTGCAGCCACA TCCGACCGAGTCGTCCATGTACAAG TACCCTTCTGACATCTCCTACATGC CTTCCTACCATGCCCACCAGCAGAA GGTGAACTTTGTCCCTCCCCATCCA TCCTCCATGCCTGTCACTTCCTCCA GCTTCTTTGGAGCCGCATCACAATA CTGGACCTCCCCCACGGGGGGAAT CTACCCCAACCCCAACGTCCCCCGC CATCCTAACACCCACGTGCCTTCAC ACTTAGGCAGCTACTAC			
FOXA1	ATGTTGGGCACCGTGAGATGGAG GGGCATGAGACAAGCGACTGGAAT TCCTACTACGCGGATACCCAAGAA GCGTATTCTTCAGTTCCCGTAAGCA ATATGAACTCCGGATTGGGGAGCA TGAATAGTATGAACACGTATATGA CAATGAATACGATGACCACCAGCG GCAACATGACACCGGCCTCCTTTAA TATGTCATATGCGAACCCTGGTCTT GGCGCTGGCCTCTCACCAGGTGCG GTCGCTGGAATGCCCGGGGGGAGC GCCGGAGCGATGAACTCCATGACC GCTGCGGGCGTGACGGCCATGGGT ACGGCCCTTGTCACCCAGTGGAATG GGCGCTGGCCTCTCACCAGGTGCG GTCGCTGGAATGCCCGGGGGGAGC GCCGGAGCGATGAACTCCATGACC GCTGCGGGCGTGACGGCCATGGGT ACGGCCCTGTCACCCAGTGGAATG GGAGCTATGGGGGCCCAGCAAGCC GCCTCAATGAATGGATTGGGGCCCT ATGCCGCGGCGATGAATCCCTGCAT GTCCCCTATGGCTTATGCCCCCAGC AATTTGGGTCGCAGTAGAGCCGGC GGTGGTGGCGATGCCAAAACCTTC AAGCGAAGTTATCCTCATGCGAAG CCTCCTTATTCATATATATCCTTGAT TACGATGGCGATACAGCAGGCCCC GTCTAAGATGCTGACTCTGAGTGAG ATATACCAGTGGATCATGGACCTTT TTCCTTACTACCGGCAAAACCAACA GAGATGGCAAAACTCAATACGCCA TAGCCTTTCCTTCAATGATTGCTTT GTCAAAGTCGCTCGGAGCCCTGAC AAGCCCGGTAAAGGGTCCTATTGG ACCCTTCATCCAGATAGCGGCAATA TGTTCGAGAATGGTTGTTATCTTAG ACGGCAGAAACGATTCAAATGTGA GAAACAGCCAGGTGCCGGCGGTGG TGGCGGCAGCGGTTCAGGCGGAAG TGGTGCCAAGGGTGGGCCTGAGTC TAGAAAAGACCCCAGCGGAGCAAG CAATCCAAGCGCGGACTCTCCCCTG CACCGCGGTGTTCATGGTAAGACA GGTCAGCTTGAGGGGGCGCCTGCT CCAGGCCCGGCTGCGTCACCGCAA ACACTGGACCATAGTGGAGCTACA GCGACCGGAGGTGCTTCAGAACTC AAGACGCCTGCGTCCTCCACTGCGC CTCCGATCTCCAGTGGTCCCGGTGC ACTTGCCTCTGTTCCTGCATCTCAT CCAGCACACGGACTCGCGCCGCAC GAGTCCCAGCTCCATTTGAAAGGG GACCCACACTACAGCTTTAACCACC CATTCTCTATTAACAATTTGATGTC ATCCTCAGAACAGCAGCATAAACT CGACTTCAAAGCCTATGAACAGGC	45	Involved in branching morphogenesis, development of lung, liver, prostate, and pancreas	Friedman, J. R. et al. The Foxa family of transcription factors in development and metabolism. Cell. Mol. Life Sci. 63, 2317-2328 (2006).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	CCTGCAGTATTCTCCATATGGCTCT ACACTTCCTGCTTCTCTTCCATTGG GGTCTGCAAGTGTGACAACGCGCT CCCCAATCGAGCCAAGTGCCCTCG AGCCTGCTTATTATCAAGGAGTATA TTCCCGACCAGTTTTGAATACAAGT			
FOXA2	ATGCTGGGAGCGGTGAAGATGGAA GGGCACGAGCCGTCCGACTGGAGC AGCTACTATGCAGAGCCCGAGGGC TACTCCTCCGTGAGCAACATGAACG CCGGCCTGGGGATGAACGGCATGA ACACGTACATGAGCATGTCGGCGG CCGCCATGGGCAGCGGCTCGGGCA ACATGAGCGCGGGCTCCATGAACA TGTCGTCGTACGTGGGCGCTGGCAT GAGCCCGTCCCTGGCGGGGATGTC CCCCGGCGCGGGCGCCATGGCGGG CATGGGCGGCTCGGCCGGGGCGGC TGGCGTGGCGGGCATGGGGCCGCA CTTGAGTCCCAGCCTGAGCCCGCTC GGGGGGCAGGCGGCCGGGGCCATG GGCGGCCTGGCCCCCTACGCCAAC ATGAACTCCATGAGCCCCATGTACG GGCAGGCGGGCCTGAGCCGCGCCC GCGACCCCAAGACCTACAGGCGCA GCTACACGCACGCAAAGCCGCCCT ACTCGTACATCTCGCTCATCACCAT GGCCATCCAGCAGAGCCCCAACAA GATGCTGACGCTGAGCGAGATCTA CCAGTGGATCATGGACCTCTTCCCC TTCTACCGGCAGAACCAGCAGCGC TGGCAGAACTCCATCCGCCACTCGC TCTCCTTCAACGACTGTTTCCTGAA GGTGCCCCGCTCGCCCGACAAGCC CGGCAAGGGCTCCTTCTGGACCCTG CACCCTGACTCGGGCAACATGTTCG AGAACGGCTGCTACCTGCGCCGCC AGAAGCGCTTCAAGTGCGAGAAGC AGCTGGCGCTGAAGGAGGCCGCAG GCGCCGCCGGCAGCGGCAAGAAGG CGGCCGCCGGGGCCCAGGCCTCAC AGGCTCAACTCGGGGAGGCCGCCG GGCCGGCCTCCGAGACTCCGGCGG GCACCGAGTCGCCTCACTCGAGCG CCTCCCCGTGCCAGGAGCACAAGC GAGGGGGCCTGGGAGAGCTGAAGG GGACGCCGGCTGCGGCGCTGAGCC CCCCAGAGCCGGCGCCCTCTCCCG GGCAGCAGCAGCAGGCCGCGGCCC ACCTGCTGGGCCCGCCCCACCACCC GGGCCTGCCGCCTGAGGCCCACCT GAAGCCGGAACACCACTACGCCTT CAACCACCCGTTCTCCATCAACAAC CTCATGTCCTCGGAGCAGCAGCACC ACCACAGCCACCACCACCACCAGC CCCACAAAATGGACCTCAAGGCCT ACGAACAGGTGATGCACTACCCCG GCTACGGTTCCCCCATGCCTGGCAG CTTGGCCATGGGCCCGGTCACGAA CAAAACGGGCCTGGACGCCTCGCC CCTGGCCGCAGATACCTCCTACTAC CAGGGGGTGTACTCCCGGCCCATTA TGAACTCCTCTTTG	46	Involved in branching morphogenesis, development of notochord, lung, liver, prostate, and pancreas.	Friedman, J. R. et al. The Foxa family of transcription factors in development and metabolism. Cell. Mol. Life Sci. 63, 2317-2328 (2006).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
FOXA3	ATGCTGGGCTCAGTGAAGATGGAG GCCCATGACCTGGCCGAGTGGAGC TACTACCCGGAGGCGGGCGAGGTC TACTCGCCGGTGACCCCAGTGCCCA CCATGGCCCCCCTCAACTCCTACAT GACCCTGAATCCTCTAAGCTCTCCC TATCCCCCTGGGGGGCTCCCTGCCT CCCCACTGCCCTCAGGACCCCTGGC ACCCCCAGCACCTGCAGCCCCCCTG GGGCCCACTTTCCCAGGCCTGGGTG TCAGCGGTGGCAGCAGCAGCTCCG GGTACGGGGCCCCGGGTCCTGGGC TGGTGCACGGGAAGGAGATGCCGA AGGGGTATCGGCGGCCCCTGGCAC ACGCCAAGCCACCGTATTCCTATAT CTCACTCATCACCATGGCCATCCAG CAGGCGCCGGGCAAGATGCTGACC TTGAGTGAAATCTACCAGTGGATCA TGGACCTCTTCCCTTACTACCGGGA GAATCAGCAGCGCTGGCAGAACTC CATTCGCCACTCGCTGTCTTTCAAC GACTGCTTCGTCAAGGTGGCGCGTT CCCCAGACAAGCCTGGCAAGGGCT CCTACTGGGCCCTACACCCCAGCTC AGGGAACATGTTTGAGAATGGCTG CTACCTGCGCCGCCAGAAACGCTTC AAGCTGGAGGAGAAGGTGAAAAAA GGGGGCAGCGGGGCTGCCACCACC ACCAGGAACGGGACAGGGTCTGCT GCCTCGACCACCACCCCCGCGGCC ACAGTCACCTCCCCGCCCCAGCCCC CGCCTCCAGCCCCTGAGCCTGAGGC CCAGGGCGGGGAAGATGTGGGGGC TCTGGACTGTGGCTCACCCGCTTCC TCCACACCCTATTTCACTGGCCTGG AGCTCCCAGGGGAGCTGAAGCTGG ACGCGCCCTACAACTTCAACCACCC TTTCTCCATCAACAACCTAATGTCA GAACAGACACCAGCACCTCCCAAA CTGGACGTGGGGTTTGGGGGCTAC GGGGCTGAAGGTGGGGAGCCTGGA GTCTACTACCAGGGCCTCTATTCCC GCTCTTTGCTTAATGCATCC	47	Involved in cell glucose homeostasis	Friedman, J. R. et al. The Foxa family of transcription factors in development and metabolism. Cell. Mol. Life Sci. 63, 2317-2328 (2006).
FOXP1	ATGATGCAAGAATCTGGGACTGAG ACAAAAAGTAACGGTTCAGCCATC CAGAATGGGTCGGGCGGCAGCAAC CACTTACTAGAGTGCGGCGGTCTTC GGGAGGGGCGGTCCAACGGAGAGA CGCCGGCCGTGGACATCGGGGCAG CTGACCTCGCCCACGCCCAGCAGC AGCAGCAACAGTGGCATCTCATAA ACCATCAGCCCTCTAGGAGTCCCAG CAGTTGGCTTAAGAGACTAATTTCA AGCCCTTGGGAGTTGGAAGTCCTGC AGGTCCCCTTGTGGGGAGCAGTTGC TGAGACGAAGATGAGTGGACCTGT GTGTCAGCCTAACCCTTCCCCATTT	48	Involved in development of haematopoetic cells, lung and oesophagus, and neuronal development	Hu, H. et al. Foxp1 is an essential transcriptional regulator of B cell development. Nat. Immunol. 7, 819-826 (2006). Shu, W. et al. Foxp2 and Foxp1 cooperatively regulate lung and esophagus development. Development 134, 1991-2000 (2007). Bacon, C. et al. Brain-specific Foxp1 deletion impairs neuronal

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
				development and causes autistic-like behaviour. Mol. Psychiatry 20, 632-639 (2015).
GATA1	ATGGAGTTCCCTGGCCTGGGGTCCC TGGGGACCTCAGAGCCCCTCCCCCA GTTTGTGGATCCTGCTCTGGTGTCC TCCACACCAGAATCAGGGGTTTTCT TCCCCTCTGGGCCTGAGGGCTTGGA TGCAGCAGCTTCCTCCACTGCCCCG AGCACAGCCACCGCTGCAGCTGCG GCACTGGCCTACTACAGGGACGCT GAGGCCTACAGACACTCCCCAGTCT TTCAGGTGTACCCATTGCTCAACTG TATGGAGGGGATCCCAGGGGGCTC ACCATATGCCGGCTGGGCCTACGG CAAGACGGGGCTCTACCCTGCCTCA ACTGTGTGTCCCACCCGCGAGGACT CTCCTCCCCAGGCCGTGGAAGATCT GGATGGAAAAGGCAGCACCAGCTT CCTGGAGACTTTGAAGACAGAGCG GCTGAGCCCAGACCTCCTGACCCTG GGACCTGCACTGCCTTCATCACTCC CTGTCCCCAATAGTGCTTATGGGGG CCCTGACTTTTCCAGTACCTTCTTTT CTCCCACCGGGAGCCCCCTCAATTC AGCAGCCTATTCCTCTCCCAAGCTT CGTGGAACTCTCCCCCTGCCTCCCT GTGAGGCCAGGGAGTGTGTGAACT GCGGAGCAACAGCCACTCCACTGT GGCGGAGGGACAGGACAGGCCACT ACCTATGCAACGCCTGCGGCCTCTA TCACAAGATGAATGGGCAGAACAG GCCCCTCATCCGGCCCAAGAAGCG CCTGATTGTCAGTAAACGGGCAGG TACTCAGTGCACCAACTGCCAGAC GACCACCACGACACTGTGGCGGAG AAATGCCAGTGGGGATCCCGTGTG CAATGCCTGCGGCCTCTACTACAAG CTACACCACCAGCACTACTGTGGTG GCTCCGCTCAGCTCATGAGGGCAC AGAGCATGGCCTCCAGAGGAGGGG TGGTGTCCTTCTCCTCTTGTAGCCA GAATTCTGGACAACCCAAGTCTCTG GGCCCCAGGCACCCCCTGGCT	49	Involved in erythroid development	Fujiwara, Y., Browne, C. P., Cunniff, K., Goff, S. C. & Orkin, S. H. Arrested development of embryonic red cell precursors in mouse embryos lacking transcription factor GATA-1. PNAS 93, 12355-12358 (1996).
GATA2	ATGGAGGTGGCGCCGGAGCAGCCG CGCTGGATGGCGCACCCGGCCGTG CTGAATGCGCAGCACCCCGACTCA CACCACCCGGGCCTGGCGCACAAC TACATGGAACCCGCGCAGCTGCTG CCTCCAGACGAGGTGGACGTCTTCT TCAATCACCTCGACTCGCAGGGCA ACCCCTACTATGCCAACCCCGCTCA CGCGCGGGCGCGCGTCTCCTACAG CCCCGCGCACGCCCGCCTGACCGG AGGCCAGATGTGCCGCCCACACTT GTTGCACAGCCCGGGTTTGCCCTGG CTGGACGGGGGCAAAGCAGCCCTC TCTGCCGCTGCGGCCCACCACCACA ACCCCTGGACCGTGAGCCCCTTCTC CAAGACGCCACTGCACCCCTCAGCT GCTGGAGGCCCTGGAGGCCCACTC TCTGTGTACCCAGGGGCTGGGGGT GGGAGCGGGGGAGGCAGCGGGAG CTCAGTGGCCTCCCTCACCCCTACA GCAACCCACTCTGGCTCCCACCTTT TCGGCTTCCCACCCACGCCACCCAA AGAAGTGTCTCCTGACCCTAGCACC	50	Involved in haematopoetic development	Pimanda, J. E. et al. Gata2, Fli1, and Scl form a recursively wired gene-regulatory circuit during early hematopoietic development. Proc. Natl. Acad. Sci. U. S. A. 104, 17692-7 (2007). Lugus, J. J. et al. GATA2 functions at multiple steps in hemangioblast development

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	ACGGGGGCTGCGTCTCCAGCCTCAT CTTCCGCGGGGGGTAGTGCAGCCC GAGGAGAGGACAAGGACGGCGTCA AGTACCAGGTGTCACTGACGGAGA GCATGAAGATGGAAAGTGGCAGTC CCCTGCGCCCAGGCCTAGCTACTAT GGGCACCCAGCCTGCTACACACCA CCCCATCCCCACCTACCCCTCCTAT GTGCCGGCGGCTGCCCACGACTAC AGCAGCGGACTCTTCCACCCCGGA GGCTTCCTGGGGGGACCGGCCTCC AGCTTCACCCCTAAGCAGCGCAGC AAGGCTCGTTCCTGTTCAGAAGGCC GGGAGTGTGTCAACTGTGGGGCCA CAGCCACCCCTCTCTGGCGGCGGG ACGGCACCGGCCACTACCTGTGCA ATGCCTGTGGCCTCTACCACAAGAT GAATGGGCAGAACCGACCACTCAT CAAGCCCAAGCGAAGACTGTCGGC CGCCAGAAGAGCCGGCACCTGTTG TGCAAATTGTCAGACGACAACCAC CACCTTATGGCGCCGAAACGCCAA CGGGGACCCTGTCTGCAACGCCTGT GGCCTCTACTACAAGCTGCACAATG TTAACAGGCCACTGACCATGAAGA AGGAAGGGATCCAGACTCGGAACC GGAAGATGTCCAACAAGTCCAAGA AGAGCAAGAAAGGGGCGGAGTGCT TCGAGGAGCTGTCAAAGTGCATGC AGGAGAAGTCATCCCCCTTCAGTGC AGCTGCCCTGGCTGGACACATGGC ACCTGTGGGCCACCTCCCGCCCTTC AGCCACTCCGGACACATCCTGCCCA CTCCGACGCCCATCCACCCCTCCTC CAGCCTCTCCTTCGGCCACCCCCAC CCGTCCAGCATGGTGACCGCCATG GGC			and differentiation. Development 134,393-405 (2007).
GATA4	ATGTACCAGAGCCTGGCTATGGCTG CTAATCATGGACCTCCCCCTGGAGC CTATGAAGCCGGAGGACCTGGCGC TTTTATGCATGGAGCTGGCGCCGCT TCTTCTCCCGTGTATGTGCCTACAC CTAGAGTGCCCAGCAGCGTGCTGG GCCTTTCTTATCTTCAGGGAGGAGG AGCAGGATCTGCTTCTGGCGGAGCT TCAGGCGGATCTTCTGGAGGCGCTG CTTCAGGTGCTGGACCTGGAACTCA ACAGGGATCTCCTGGATGGTCACA GGCAGGAGCTGATGGAGCCGCTTA TACCCCTCCTCCTGTGAGCCCCAGG TTTAGCTTTCCTGGCACAACAGGCT CTTTAGCTGCCGCTGCTGCTGCAGC CGCAGCTAGAGAAGCAGCTGCATA TTCTAGTGGCGGAGGAGCTGCTGG AGCCGGCTTAGCTGGAAGAGAGCA GTACGGAAGAGCCGGATTTGCCGG AAGCTATAGCAGCCCTTACCCTGCC TATATGGCCGATGTTGGCGCATCTT GGGCAGCCGCCGCAGCAGCTTCTG CAGGACCTTTTGACTCACCTGTGCT TCACTCTCTGCCTGGCAGAGCTAAT CCTGCCGCCAGACATCCCAACCTGG ACATGTTCGACGACTTCAGCGAGG GCAGAGAATGCGTGAACTGCGGAG CCATGAGCACCCCCCTTTGGAGAA GAGACGGCACCGGCCACTACCTTT GCAATGCCTGTGGCCTGTACCACAA GATGAACGGCATCAACAGACCCCT GATCAAGCCCCAGAGAAGACTGAG CGCTAGCAGAAGAGTGGGCCTGTC CTGCGCCAATTGCCAGACCACAAC CACCACACTGTGGAGGAGAAATGC CGAGGGCGAGCCTGTGTGTAACGC	51	Involved in cardiovascular development	Xin, M. et al. A threshold of GATA4 and GATA6 expression is required for cardiovascular development. Proc. Natl. Acad. Sci. U. S. A. 103, 11189-94 (2006). Rivera-Feliciano, J. et al. Development of heart valves requires Gata4 expression in endothelial-derived cells. Development 133, 3607-18 (2006).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	CTGTGGACTGTACATGAAGCTGCAC GGCGTGCCCAGACCTCTGGCCATG AGAAAGGAGGGCATCCAGACCAGA AAGAGAAAGCCCAAGAACCTGAAC AAGAGCAAGACCCCCGCTGCTCCTT CTGGAAGCGAGAGCCTGCCTCCAG CCTCTGGAGCCAGCAGCAATAGCT CTAACGCCACCACATCTTCTTCTGA GGAGATGAGGCCCATCAAAACCGA GCCAGGCCTGAGCAGCCACTACGG CCACAGCTCTAGCGTGAGCCAGAC TTTTAGCGTGTCTGCCATGTCAGGC CACGGACCTAGCATTCACCCTGTGC TGAGCGCCCTGAAGTTGAGCCCAC AGGGCTATGCTTCTCCTGTGTCTCA GAGCCCTCAGACCTCCAGCAAGCA GGACTCCTGGAATTCTCTGGTGCTG GCCGACAGCCACGGCGATATCATC ACCGCC			
GATA6	ATGGCCCTGACCGACGGCGGATGG TGTCTCCCTAAAAGATTCGGCGCCG CTGGCGCTGATGCTTCTGACAGCAG AGCCTTCCCCGCTAGGGAACCCAG CACACCACCTAGCCCCATCAGCAG CTCAAGCTCTAGCTGTAGCAGAGG CGGAGAGAGAGGACCTGGAGGCGC TTCTAACTGCGGCACACCTCAGCTG GATACAGAAGCCGCCGCCGGACCA CCAGCCAGATCTCTTTTACTTAGCA GCTACGCCAGCCACCCTTTTGGCGC TCCTCATGGACCCTCTGCTCCTGGT GTGGCCGGACCTGGCGGAAACCTG AGCTCTTGGGAGGACCTTCTGCTGT TTACCGACCTGGACCAGGCTGCCAC CGCTAGCAAGCTTCTGTGGAGCAG CAGGGGCGCTAAGCTGAGCCCTTTT GCCCCTGAGCAGCCCGAGGAGATG TACCAGACCCTGGCTGCTTTAAGCT CTCAGGGACCTGCCGCTTATGACGG AGCCCCTGGTGGATTTGTTCACTCA GCGGCAGCAGCCGCAGCTGCTGCA GCCGCTGCCAGCTCACCTGTGTATG TGCCTACCACAAGAGTGGGCAGCA TGTTACCTGGACTTCCTTACCATCT GCAGGGCAGCGGAAGCGGCCCTGC TAACCATGCCGGAGGAGCTGGAGC TCACCCCGGATGGCCTCAGGCTTCT GCAGATTCTCCTCCTTATGGATCTG GAGGAGGAGCAGCTGGAGGGGGA GCTGCAGGACCAGGTGGAGCCGGA AGCGCAGCAGCACATGTGTCTGCC AGATTTCCCTATAGCCCTAGCCCTC CTATGGCCAATGGCGCTGCTAGAG AACCCGGAGGATATGCTGCGGCAG GCTCTGGCGGCGCTGGCGGAGTTTC TGGAGGTGGATCTTCACTGGCCGCT ATGGGAGGAAGAGAGCCTCAGTAC TCTTCTCTGAGCGCCGCTAGACCAC TGAACGGCACCTATCATCACCACCA CCATCACCATCATCATCACCCCAGC CCTTACTCCCCTTATGTGGGAGCCC CCCTTACACCCGCTTGGCCTGCCGG CCCTTTCGAGACACCTGTGCTGCAC AGCCTTCAGTCTAGAGCTGGCGCAC CTTTACCAGTGCCTAGAGGCCCCTC TGCCGACTTGCTGGAGGATCTGAGC GAGAGCAGAGAGTGCGTGAACTGT GGCAGCATCCAGACACCCCTGTGG AGAAGAGACGGCACCGGCCACTAC CTGTGCAACGCTTGCGGCCTGTACA GCAAGATGAATGGGCTGAGCAGAC CCCTGATCAAGCCCCAGAAGAGGG TGCCCAGCAGCAGACGGCTGGGAC	52	Involved in cardiac, lung, endoderm and extraembryonic development	Xin, M. et al. A threshold of GATA4 and GATA6 expression is required for cardiovascular development. Proc. Natl. Acad. Sci. U. S. A. 103, 11189-94 (2006). Morrisey, E. E. et al. GATA6 regulates HNF4 and is required for differentiation of visceral endoderm in the mouse embryo. Genes Dev. 12, 3579-3590 (1998). Koutsourakis, M.; Langeveld, A.; Patient, R.; Beddington, R.; Grosveld, F. The transcription factor GATA6 is essential for early extraembryonic development. Development 126, 723-732 (1999). Zhang, Y. et al. A Gata6-Wnt pathway required for epithelial stem cell development and airway regeneration.

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	TGAGCTGCGCCAACTGTCATACCAC AACAACCACACTGTGGCGGAGAAA CGCCGAGGGCGAGCCCGTGTGTAA CGCCTGCGGCCTTTACATGAAGCTG CACGGCGTGCCCAGACCTCTGGCC ATGAAGAAGGAGGGAATCCAGACC AGAAAGAGAAAGCCCAAGAACATC AACAAGAGCAAGACCTGCAGCGGC AACAGCAACAACAGCATCCCCATG ACCCCCACCAGCACATCTAGCAAC AGCGACGACTGTAGCAAGAACACA TCACCTACCACCCAGCCCACAGCTA GCGGAGCCGGCGCCCCCGTGATGA CAGGCGCCGGAGAGTCCACAAATC CCGAGAATAGCGAACTGAAGTACT CTGGACAGGACGGACTGTATATCG GCGTGAGCCTGGCTTCTCCCGCCGA GGTGACCAGCTCTGTCAGACCTGAC TCTTGGTGTGCCCTCGCCCTGGCC			Nat. Genet. 40, 862-870 (2008).
GLI1	ATGTTCAACTCGATGACCCCACCAC CAATCAGTAGCTATGGCGAGCCCT GCTGTCTCCGGCCCCTCCCCAGTCA GGGGGCCCCCAGTGTGGGGACAGA AGGACTGTCTGGCCCGCCCTTCTGC CACCAAGCTAACCTCATGTCCGGCC CCCACAGTTATGGGCCAGCCAGAG AGACCAACAGCTGCACCGAGGGCC CACTCTTTTCTTCTCCCCGGAGTGC AGTCAAGTTGACCAAGAAGCGGGC ACTGTCCATCTCACCTCTGTCGGAT GCCAGCCTGGACCTGCAGACGGTT ATCCGCACCTCACCCAGCTCCCTCG TAGCTTTCATCAACTCGCGATGCAC ATCTCCAGGAGGCTCCTACGGTCAT CTCTCCATTGGCACCATGAGCCCAT CTCTGGGATTCCCAGCCCAGATGAA TCACCAAAAAGGGCCCTCGCCTTCC TTTGGGGTCCAGCCTTGTGGTCCCC ATGACTCTGCCCGGGGTGGGATGA TCCCACATCCTCAGTCCCGGGGACC CTTCCCAACTTGCCAGCTGAAGTCT GAGCTGGACATGCTGGTTGGCAAG TGCCGGGAGGAACCCTTGGAAGGT GATATGTCCAGCCCCAACTCCACAG GCATACAGGATCCCCTGTTGGGGAT GCTGGATGGGCGGGAGGACCTCGA GAGAGAGGAGAAGCGTGAGCCTGA ATCTGTGTATGAAACTGACTGCCGT TGGGATGGCTGCAGCCAGGAATTT GACTCCCAAGAGCAGCTGGTGCAC CACATCAACAGCGAGCACATCCAC GGGGAGCGGAAGGAGTTCGTGTGC CACTGGGGGGGCTGCTCCAGGGAG CTGAGGCCCTTCAAAGCCCAGTAC ATGCTGGTGGTTCACATGCGCAGAC ACACTGGCGAGAAGCCACACAAGT GCACGTTTGAAGGGTGCCGGAAGT CATACTCACGCCTCGAAAACCTGA AGACGCACCTGCGGTCACACACGG GTGAGAAGCCATACATGTGTGAGC ACGAGGGCTGCAGTAAAGCCTTCA GCAATGCCAGTGACCGAGCCAAGC ACCAGAATCGGACCCATTCCAATG AGAAGCCGTATGTATGTAAGCTCCC TGGCTGCACCAAACGCTATACAGA TCCTAGCTCGCTGCGAAAACATGTC AAGACAGTGCATGGTCCTGACGCC CATGTGACCAAACGGCACCGTGGG GATGGCCCCCTGCCTCGGGCACCAT CCATTTCTACAGTGGAGCCCAAGA GGGAGCGGGAAGGAGGTCCCATCA GGGAGGAAAGCAGACTGACTGTGC CAGAGGGTGCCATGAAGCCACAGC	53	Involved in neural stem cell proliferation and neural tube development	Lee, J. et al. Gli1 is a target of Sonic hedgehog that induces ventral neural tube development. Development 124, 2537-2552 (1997). Palma, V. et al. Sonic hedgehog controls stem cell behavior in the postnatal and adult brain. Development 132, 335-44 (2005).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	CAAGCCCTGGGGCCCAGTCATCCTG			
	CAGCAGTGACCACTCCCCGGCAGG			
	GAGTGCAGCCAATACAGACAGTGG			
	TGTGGAAATGACTGGCAATGCAGG			
	GGGCAGCACTGAAGACCTCTCCAG			
	CTTGGACGAGGGACCTTGCATTGCT			
	GGCACTGGTCTGTCCACTCTTCGCC			
	GCCTTGAGAACCTCAGGCTGGACC			
	AGCTACATCAACTCCGGCCAATAG			
	GGACCCGGGGTCTCAAACTGCCCA			
	GCTTGTCCCACACCGGTACCACTGT			
	GTCCCGCCGCGTGGGCCCCCCAGTC			
	TCTCTTGAACGCCGCAGCAGCAGCT			
	CCAGCAGCATCAGCTCTGCCTATAC			
	TGTCAGCCGCCGCTCCTCCCTGGCC			
	TCTCCTTTCCCCCCTGGCTCCCCAC			
	CAGAGAATGGAGCATCCTCCCTGC			
	CTGGCCTTATGCCTGCCCAGCACTA			
	CCTGCTTCGGGCAAGATATGCTTCA			
	GCCAGAGGGGGTGGTACTTCGCCC			
	ACTGCAGCATCCAGCCTGGATCGG			
	ATAGGTGGTCTTCCCATGCCTCCTT			
	GGAGAAGCCGAGCCGAGTATCCAG			
	GATACAACCCCAATGCAGGGGTCA			
	CCCGGAGGGCCAGTGACCCAGCCC			
	AGGCTGCTGACCGTCCTGCTCCAGC			
	TAGAGTCCAGAGGTTCAAGAGCCT			
	GGGCTGTGTCCATACCCCACCCACT			
	GTGGCAGGGGGAGGACAGAACTTT			
	GATCCTTACCTCCCAACCTCTGTCT			
	ACTCACCACAGCCCCCCAGCATCA			
	CTGAGAATGCTGCCATGGATGCTA			
	GAGGGCTACAGGAAGAGCCAGAAG			
	TTGGGACCTCCATGGTGGGCAGTG			
	GTCTGAACCCCTATATGGACTTCCC			
	ACCTACTGATACTCTGGGATATGGG			
	GGACCTGAAGGGGCAGCAGCTGAG			
	CCTTATGGAGCGAGGGGTCCAGGC			
	TCTCTGCCTCTTGGGCCTGGTCCAC			
	CCACCAACTATGGCCCCAACCCCTG			
	TCCCCAGCAGGCCTCATATCCTGAC			
	CCCACCCAAGAAACATGGGGTGAG			
	TTCCCTTCCCACTCTGGGCTGTACC			
	CAGGCCCCAAGGCTCTAGGTGGAA			
	CCTACAGCCAGTGTCCTCGACTTGA			
	ACATTATGGACAAGTGCAAGTCAA			
	GCCAGAACAGGGGTGCCCAGTGGG			
	GTCTGACTCCACAGGACTGGCACCC			
	TGCCTCAATGCCCACCCCAGTGAGG			
	GGCCCCCACATCCACAGCCTCTCTT			
	TTCCCATTACCCCCAGCCCTCTCCT			
	CCCCAATATCTCCAGTCAGGCCCCT			
	ATACCCAGCCACCCCCTGATTATCT			
	TCCTTCAGAACCCAGGCCTTGCCTG			
	GACTTTGATTCCCCCACCCATTCCA			
	CAGGGCAGCTCAAGGCTCAGCTTG			
	TGTGTAATTATGTTCAATCTCAACA			
	GGAGCTACTGTGGGAGGGTGGGGG			
	CAGGGAAGATGCCCCCGCCCAGGA			
	ACCTTCCTACCAGAGTCCCAAGTTT			
	CTGGGGGGTTCCCAGGTTAGCCCA			
	AGCCGTGCTAAAGCTCCAGTGAAC			
	ACATATGGACCTGGCTTTGGACCCA			
	ACTTGCCCAATCACAAGTCAGGTTC			
	CTATCCCACCCCTTCACCATGCCAT			
	GAAAATTTTGTAGTGGGGGCAAAT			
	AGGGCTTCACATAGGGCAGCAGCA			
	CCACCTCGACTTCTGCCCCCATTGC			
	CCACTTGCTATGGGCCTCTCAAAGT			
	GGGAGGCACAAACCCCAGCTGTGG			
	TCATCCTGAGGTGGGCAGGCTAGG			
	AGGGGGTCCTGCCTTGTACCCTCCT			
	CCCGAAGGACAGGTATGTAACCCC			
	CTGGACTCTCTTGATCTTGACAACA			

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	CTCAGCTGGACTTTGTGGCTATTCT GGATGAGCCCCAGGGGCTGAGTCC TCCTCCTTCCCATGATCAGCGGGGC AGCTCTGGACATACCCCACCTCCCT CTGGGCCCCCCAACATGGCTGTGG GCAACATGAGTGTCTTACTGAGATC CCTACCTGGGGAAACAGAATTCCTC AACTCTAGTGCC			
HAND2	ATGAGTCTGGTAGGTGGTTTTCCCC ACCACCCGGTGGTGCACCACGAGG GCTACCCGTTTGCCGCCGCCGCGC CGCCAGCCGCTGCAGCCATGAGGA GAACCCCTACTTCCATGGCTGGCTC ATCGGCCACCCCGAGATGTCGCCCC CCGACTACAGCATGGCCCTGTCCTA CAGCCCCGAGTATGCCAGCGGCAC CGCCAACCGCAAGGAGCGGCGCAG GACTCAGAGCATCAACAGCGCCTT CGCCGAACTGCGCGAGTGCATCCC CAACGTACCCGCCGACACCAAACT CTCCAAAATCAAGACCCTGCGCCTG GCCACCAGCTACATCGCCTACCTCA TGGACCTGCTGGCCAAGGACGACC AGAATGGCGAGGCGGAGGCCTTCA AGGCAGAGATCAAGAAGACCGACG TGAAAGAGGAGAAGAGGAAGAAG GAGCTGAACGAAATCTTGAAAAGC ACAGTGAGCAGCAACGACAAGAAA ACCAAAGGCCGGACGGGCTGGCCG CAGCACGTCTGGGCCCTGGAGCTC AAGCAG	54	Involved in cardiac development	Srivastava, D. et al. Regulation of cardiac mesodermal and neural crest development by the bHLH transcription factor, dHAND. Nat. Genet. 16, 154-160 (1997).
HNF1A	ATGGTTTCTAAACTGAGCCAGCTGC AGACGGAGCTCCTGGCGGCCCTGC TGGAGTCAGGGCTGAGCAAAGAGG CACTGCTCCAGGCACTGGGTGAGC CGGGGCCCTACCTCCTGGCTGGAG AAGGCCCCCTGGACAAGGGGGAGT CCTGCGGCGGCGGTCGAGGGGAGC TGGCTGAGCTGCCCAATGGGCTGG GGGAGACTCGGGGCTCCGAGGACG AGACGGACGACGATGGGGAAGACT TCACGCCACCCATCCTCAAAGAGCT GGAGAACCTCAGCCCTGAGGAGGC GGCCCACCAGAAAGCCGTGGTGGA GACCCTTCTGCAGGAGGACCCGTG GCGTGTGGCGAAGATGGTCAAGTC CTACCTGCAGCAGCACAACATCCC ACAGCGGGAGGTGGTCGATACCAC TGGCCTCAACCAGTCCCACCTGTCC CAACACCTCAACAAGGGCACTCCC ATGAAGACGCAGAAGCGGGCCGCC CTGTACACCTGGTACGTCCGCAAGC AGCGAGAGGTGGCGCAGCAGTTCA CCCATGCAGGGCAGGGAGGGCTGA TTGAAGAGCCCACAGGTGATGAGC TACCAACCAAGAAGGGGCGGAGGA ACCGTTTCAAGTGGGGCCCAGCATC CCAGCAGATCCTGTTCCAGGCCTAT GAGAGGCAGAAGAACCCTAGCAAG GAGGAGCGAGAGACGCTAGTGGAG GAGTGCAATAGGGCGGAATGCATC CAGAGAGGGGTGTCCCCATCACAG GCACAGGGGCTGGGCTCCAACCTC GTCACGGAGGTGCGTGTCTACAACT GGTTTGCCAACCGGCGCAAAGAAG AAGCCTTCCGGCACAAGCTGGCCA TGGACACGTACAGCGGGCCCCCCC CAGGGCCAGGCCCGGGACCTGCGC TGCCCGCTCACAGCTCCCCTGGCCT GCCTCCACCTGCCCTCTCCCCCAGT AAGGTCCACGGTGTGCGCTATGGA CAGCCTGCGACCAGTGAGACTGCA	55	Involved in liver, kidney, pancreatic and gut development	D' Angelo, A. et al. Hepatocyte nuclear factor 1alpha and beta control terminal differentiation and cell fate commitment in the gut epithelium. Development 137,1573-82 (2010). Servitj a, J.-M. et al. Hnf1 alpha (MODY3) controls tissue-specific transcriptional programs and exerts opposed effects on cell growth in pancreatic islets and liver. Mol. Cell. Biol. 29, 2945-59 (2009). Si-Tayeb, K.; Lemaigre, F. P.; Duncan, S. A. Organogenesis and Development of the Liver.

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	GAAGTACCCTCAAGCAGCGGCGGT CCCTTAGTGACAGTGTCTACACCCC TCCACCAAGTGTCCCCCACGGGCCT GGAGCCCAGCCACAGCCTGCTGAG TACAGAAGCCAAGCTGGTCTCAGC AGCTGGGGGCCCCCTCCCCCCTGTC AGCACCCTGACAGCACTGCACAGC TTGGAGCAGACATCCCCAGGCCTC AACCAGCAGCCCCAGAACCTCATC ATGGCCTCACTTCCTGGGGTCATGA CCATCGGGCCTGGTGAGCCTGCCTC CCTGGGTCCTACGTTCACCAACACA GGTGCCTCCACCCTGGTCATCGGCC TGGCCTCCACGCAGGCACAGAGTG TGCCGGTCATCAACAGCATGGGCA GCAGCCTGACCACCCTGCAGCCCGT CCAGTTCTCCCAGCCGCTGCACCCC TCCTACCAGCAGCCGCTCATGCCAC CTGTGCAGAGCCATGTGACCCAGA GCCCCTTCATGGCCACCATGGCTCA GCTGCAGAGCCCCCACGCCCTCTAC AGCCACAAGCCCGAGGTGGCCCAG TACACCCACACAGGCCTGCTCCCGC AGACTATGCTCATCACCGACACCAC CAACCTGAGCGCCCTGGCCAGCCTC ACGCCCACCAAGCAGGTCTTCACCT CAGACACTGAGGCCTCCAGTGAGT CCGGGCTTCACACGCCGGCATCTCA GGCCACCACCCTCCACGTCCCCAGC CAGGACCCTGCCGGCATCCAGCAC CTGCAGCCGGCCCACCGGCTCAGC GCCAGCCCCACAGTGTCCTCCAGCA GCCTGGTGCTGTACCAGAGCTCAG ACTCCAGCAATGGCCAGAGCCACC TGCTGCCATCCAACCACAGCGTCAT CGAGACCTTCATCTCCACCCAGATG GCCTCTTCCTCCCAGTTG			Dev. Cell 18, 175-189 (2010). Martovetsky, G., Tee, J. B. & Nigam, S. K. Hepatocyte nuclear factors 4α and 1α regulate kidney developmenta 1 expression of drug-metabolizing enzymes and drug transporters. Mol. Pharmacol. 84,808-23 (2013).
HNF1B	ATGGTTAGCAAACTGACATCCCTCC AGCAGGAACTTCTTTCTGCCCTCCT CTCCAGTGGGGTAACCAAAGAGGT ACTGGTCCAGGCTTTGGAGGAGTTG CTCCCCTCACCGAATTTTGGTGTAA AGTTGGAGACTCTCCCCCTCTCCCC TGGTTCTGGAGCAGAGCCGGATAC TAAACCGGTATTTCATACGCTTACA AACGGACACGCAAAGGGTCGGCTT TCAGGTGACGAAGGGTCTGAGGAC GGCGATGATTATGACACCCCGCCC ATCCTCAAAGAACTGCAGGCCCTTA ATACAGAGGAAGCGGCGGAGCAGC GAGCTGAAGTTGACAGAATGCTCT CAGAAGATCCGTGGAGAGCTGCGA AAATGATTAAGGGATATATGCAGC AACATAACATTCCCCAGAGAGAGG TAGTTGATGTTACCGGCCTTAACCA GAGCCACCTGTCTCAGCATCTCAAT AAGGGTACTCCTATGAAAACACAG AAGCGAGCGGCCCTTTACACATGG TACGTGCGGAAGCAACGAGAAATT CTCCGACAGTTCAATCAGACAGTAC AATCTTCAGGGAACATGACGGATA AAAGCTCACAGGATCAGCTCTTGTT TCTCTTCCCCGAGTTCAGCCAACAG TCCCACGGTCCAGGTCAATCTGATG ATGCTTGCAGTGAACCTACAAACA AAAAAATGAGGAGGAACAGGTTTA AATGGGGACCGGCCTCTCAGCAGA TACTGTACCAAGCGTACGATCGGC AGAAAAACCCAAGCAAAGAGGAGC GCGAGGCATTGGTCGAGGAGTGTA ATCGGGCCGAGTGCTTGCAACGGG GTGTAAGTCCTAGCAAAGCCCATG GTCTCGGCTCAAACTTGGTCACGGA	56	Involved in liver, kidney, pancreatic and gut development	D' Angelo, A. et al. Hepatocyte nuclear factor 1alpha and beta control terminal differentiation and cell fate commitment in the gut epithelium. Development 137,1573-82 (2010). Si-Tayeb, K.; Lemaigre, F. P.; Duncan, S. A. Organogenesis and Development of the Liver. Dev. Cell 18, 175-189 (2010). Clissold, R. L., Hamilton, A. J., Hattersley, A. T., Ellard, S. & Bingham, C. HNF1B-associated renal and extra-renal

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	GGTGAGGGTATATAATTGGTTTGCC AACAGGCGGAAGGAGGAAGCATTC CGGCAAAAGCTGGCGATGGATGCC TACTCAAGCAACCAGACACATAGC CTCAACCCTCTGTTGTCACACGGGT CCCCTCATCACCAACCTTCTTCCTC TCCACCCAACAAACTTTCTGGTGTC CGATATTCCCAGCAGGGGAACAAC GAGATAACATCTTCCTCTACTATAA GTCATCACGGAAATTCTGCAATGGT AACGTCACAGAGTGTGTTGCAACA GGTATCACCCGCGTCTCTTGATCCA GGCCACAATCTGTTGAGCCCTGACG GAAAGATGATCTCTGTTTCTGGTGG CGGACTCCCGCCGGTCTCCACACTT ACCAACATACATAGTCTCAGTCATC ATAATCCTCAGCAGAGCCAAAACC TGATTATGACTCCTCTTAGCGGAGT GATGGCTATTGCGCAATCTTTGAAC ACCTCACAAGCACAATCTGTACCCG TCATAAACAGCGTAGCGGGCTCATT GGCGGCGCTCCAACCAGTGCAGTT CTCCCAGCAGCTCCATTCACCCCAT CAACAGCCTCTGATGCAGCAGAGC CCTGGTAGTCACATGGCTCAACAGC CGTTCATGGCAGCTGTCACTCAGCT CCAGAACTCCCATATGTATGCCCAC AAGCAAGAACCACCACAATACAGT CACACATCAAGATTCCCCAGTGCTA TGGTTGTTACTGACACATCCTCTAT CTCAACTCTGACGAACATGTCCAGT AGTAAACAATGTCCTCTGCAAGCAT GG			disease-an expanding clinical spectrum. Nat. Rev. Nephrol. 11, 102-112 (2014). De Vas, M. G. et al. Hnf1b controls pancreas morphogenesis and the generation of Ngn3+ endocrine progenitors. Development 142,871-82 (2015). E1-Khairi, R. & Vallier, L. The role of hepatocyte nuclear factor 1β in disease and development. Diabetes, Obes. Metab. 18,23-32 (2016).
HNF4A	ATGCGACTCTCCAAAACCCTCGTCG ACATGGACATGGCCGACTACAGTG CTGCACTGGACCCAGCCTACACCAC CCTGGAATTTGAGAATGTGCAGGT GTTGACGATGGGCAATGACACGTC CCCATCAGAAGGCACCAACCTCAA CGCGCCCAACAGCCTGGGTGTCAG CGCCCTGTGTGCCATCTGCGGGGAC CGGGCCACGGGCAAACACTACGGT GCCTCGAGCTGTGACGGCTGCAAG GGCTTCTTCCGGAGGAGCGTGCGG AAGAACCACATGTACTCCTGCAGA TTTAGCCGGCAGTGCGTGGTGGAC AAAGACAAGAGGAACCAGTGCCGC TACTGCAGGCTCAAGAAATGCTTCC GGGCTGGCATGAAGAAGGAAGCCG TCCAGAATGAGCGGGACCGGATCA GCACTCGAAGGTCAAGCTATGAGG ACAGCAGCCTGCCCTCCATCAATGC GCTCCTGCAGGCGGAGGTCCTGTCC CGACAGATCACCTCCCCCGTCTCCG GGATCAACGGCGACATTCGGGCGA AGAAGATTGCCAGCATCGCAGATG TGTGTGAGTCCATGAAGGAGCAGC TGCTGGTTCTCGTTGAGTGGGCCAA GTACATCCCAGCTTTCTGCGAGCTC CCCCTGGACGACCAGGTGGCCCTG CTCAGAGCCCATGCTGGCGAGCAC CTGCTGCTCGGAGCCACCAAGAGA TCCATGGTGTTCAAGGACGTGCTGC TCCTAGGCAATGACTACATTGTCCC TCGGCACTGCCCGGAGCTGGCGGA GATGAGCCGGGTGTCCATACGCAT CCTTGACGAGCTGGTGCTGCCCTTC CAGGAGCTGCAGATCGATGACAAT GAGTATGCCTACCTCAAAGCCATCA TCTTCTTTGACCCAGATGCCAAGGG GCTGAGCGATCCAGGGAAGATCAA GCGGCTGCGTTCCCAGGTGCAGGT	57	Involved in liver, kidney, pancreatic and gut development	Si-Tayeb, K.; Lemaigre, F. P.; Duncan, S. A. Organogenesis and Development of the Liver. Dev. Cell 18, 175-189 (2010). Martovetsky, G., Tee, J. B. & Nigam, S. K. Hepatocyte nuclear factors 4α and 1α regulate kidney developmenta 1 expression of drug- metabolizing enzymes and drug transporters. Mol. Pharmacol. 84,808-23 (2013). Maestro, M. A. et al. Distinct roles of HNF1b eta, HNF1alpha, and HNF4alpha in regulating pancreas

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	GAGCTTGGAGGACTACATCAACGA CCGCCAGTATGACTCGCGTGGCCGC TTTGGAGAGCTGCTGCTGCTGCTGC CCACCTTGCAGAGCATCACCTGGCA GATGATCGAGCAGATCCAGTTCATC AAGCTCTTCGGCATGGCCAAGATTG ACAACCTGTTGCAGGAGATGCTGCT GGGAGGTCCGTGCCAAGCCCAGGA GGGGCGGGGTTGGAGTGGGGACTC CCCAGGAGACAGGCCTCACACAGT GAGCTCACCCCTCAGCTCCTTGGCT TCCCCACTGTGCCGCTTTGGGCAAG TTGCT			development, beta-cell function and growth. Endocr. Dev. 12,33-45 (2007). Garrison, W. D. et al. Hepatocyte nuclear factor 4alpha is essential for embryonic development of the mouse colon. Gastroenterology 130, 1207-20 (2006).
HOXA1	ATGGACAACGCGCGGATGAATTCC TTCCTCGAGTACCCAATTTTGTCTA GTGGAGACAGTGGCACTTGCAGTG CCCGAGCCTATCCATCAGACCACA GAATTACAACATTCCAAAGCTGTGC GGTGTCAGCCAACAGTTGCGGCGG AGACGACCGCTTCCTGGTCGGAAG AGGGGTTCAAATTGGATCACCTCAC CATCACCATCACCACCACCATCACC ACCCCCAACCGGCGACTTACCAAA CCAGCGGCAATTTGGGCGTGAGCT ATAGCCATTCCTCATGTGGACCTTC CTATGGGTCTCAGAATTTCTCCGCC CCTTATAGCCCATACGCCCTGAACC AAGAGGCCGATGTATCAGGAGGCT ATCCCCAGTGCGCGCCAGCGGTTTA CTCAGGTAATCTTTCTAGCCCGATG GTCCAGCACCACCATCACCATCAA GGTTATGCCGGCGGTGCAGTCGGA TCCCCACAATACATACACCATAGTT ACGGCCAAGAGCACCAATCCCTGG CCCTCGCTACATATAACAACTCACT GTCTCCGCTTCATGCTTCCCACCAA GAAGCTTGTCGGAGTCCCGCCTCAG AAACTTCCTCTCCAGCTCAGACTTT TGATTGGATGAAGGTCAAGCGGAA TCCGCCTAAAACGGGCAAAGTAGG TGAATATGGCTATTTGGGACAGCCT AATGCTGTCCGCACCAATTTCACAA CAAAACAGCTTACTGAACTCGAGA AGGAATTTCATTTTAATAAGTATTT GACTCGAGCGAGACGAGTCGAAAT CGCCGCTAGTCTTCAACTTAACGAG ACCCAGGTTAAGATATGGTTCCAG AACAGAAGAATGAAACAAAAAAA GCGGGAGAAGGAAGGACTCCTCCC TATATCACCAGCCACACCCCCAGGT AACGACGAGAAGGCGGAGGAATCT TCAGAGAAGAGTTCCAGCTCCCCTT GTGTTCCTTCTCCTGGTAGCTCAAC CAGCGATACCCTCACGACGAGTCA C	58	Involved in neural and cardiovascular development	Tischfield, M. A. et al. Homozygous HOXA1 mutations disrupt human brainstem, inner ear, cardiovascular and cognitive development. Nat. Genet. 37, 1035-1037 (2005).
HOXA10	ATGTGTCAAGGCAATTCCAAAGGT GAAAACGCAGCCAACTGGCTCACG GCAAAGAGTGGTCGGAAGAAGCGC TGCCCCTACACGAAGCACCAGACA CTGGAGCTGGAGAAGGAGTTTCTG TTCAATATGTACCTTACTCGAGAGC GGCGCCTAGAGATTAGCCGCAGCG TCCACCTCACGGACAGACAAGTGA AAATCTGGTTTCAGAACCGCAGGA	59	Involved function in fertility, embryo viability, and regulation of hematopoetic lineage commitment	Buske, C. et al. Overexpression of HOXA10 perturbs human lympho-myelopoiesis in vitro and in

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	TGAAACTGAAGAAAATGAATCGAG AAAACCGGATCCGGGAGCTCACAG CCAACTTTAATTTTTCC			vivo. Blood 97, 2286-2292 (2001). Satokata, I., Benson, G. & Maas, R. Sexually dimorphic sterility phenotypes in Hoxa10-deficient mice. Nature 374, 460-463 (1995).
HOXA11	ATGGATTTTGATGAGCGTGGTCCCT GCTCCTCTAACATGTATTTGCCAAG TTGTACTTACTACGTCTCGGGTCCA GATTTCTCCAGCCTCCCTTCTTTTCT GCCCCAGACCCCGTCTTCGCGCCCA ATGACATACTCCTACTCCTCCAACC TGCCCCAGGTCCAACCCGTGCGCG AAGTGACCTTCAGAGAGTACGCCA TTGAGCCCGCCACTAAATGGCACCC CCGCGGCAATCTGGCCCACTGCTAC TCCGCGGAGGAGCTCGTGCACAGA GACTGCCTGCAGGCGCCCAGCGCG GCCGGCGTGCCTGGCGACGTGCTG GCCAAGAGCTCGGCCAACGTCTAC CACCACCCCACCCCCGCAGTCTCGT CCAATTTCTATAGCACCGTGGGCAG GAACGGCGTCCTGCCACAGGCTTTC GACCAGTTTTTCGAGACAGCCTACG GCACCCCGGAAAACCTCGCCTCCTC CGACTACCCCGGGGACAAGAGCGC CGAGAAGGGGCCCCCGGCGGCCAC GGCGACCTCCGCGGCGGCGGCGGC GGCTGCAACGGGCGCGCCGGCAAC TTCAAGTTCGGACAGCGGCGGCGG CGGCGGCTGCCGGGAGATGGCGGC GGCAGCAGAGGAGAAAGAGCGGC GGCGGCGCCCCGAGAGCAGCAGCA GCCCCGAGTCGTCTTCCGGCCACAC TGAGGACAAGGCCGGCGGCTCCAG TGGCCAACGCACCCGCAAAAAGCG CTGCCCCTATACCAAGTACCAGATC CGAGAGCTGGAACGGGAGTTCTTC TTCAGCGTCTACATTAACAAAGAG AAGCGCCTGCAACTGTCCCGCATGC TCAACCTCACTGATCGTCAAGTCAA AATCTGGTTTCAGAACAGGAGAAT GAAGGAAAAAAAAAATTAACAGAGA CCGTTTACAGTACTACTCAGCAAAT CCACTCCTCTTG	60	Involved in kidney development	Patterson, L. T., Pembaur, M. & Potter, S. S. Hoxa11 and Hoxd11 regulate branching morphogenesis of the ureteric bud in the developing kidney. Development 2153-2161 (2001).
HOXB6	ATGAGTTCCTATTTCGTGAACTCCA CCTTCCCCGTCACTCTGGCCAGCGG GCAGGAGTCCTTCCTGGGCCAGCTA CCGCTCTATTCGTCGGGCTATGCGG ACCCGCTGAGACATTACCCCGCGCC CTACGGGCCAGGGCCGGGCCAGGA CAAGGGCTTTGCCACTTCCTCCTAT TACCCGCCGGCGGGCGGTGGCTAC GGCCGAGCGGCGCCCTGCGACTAC GGGCCGGCGCCGGCCTTCTACCGC GAGAAAGAGTCGGCCTGCGCACTC TCCGGCGCCGACGAGCAGCCCCCG TTCCACCCCGAGCCGCGGAAGTCG GACTGCGCGCAGGACAAGAGCGTG TTCGGCGAGACAGAAGAGCAGAAG TGCTCCACTCCGGTCTACCCGTGGA TGCAGCGGATGAATTCGTGCAACA GTTCCTCCTTTGGGCCCAGCGGCCG	61	Involved in lung and epidermal development	1. Patterson, L. T., Pembaur, M. & Potter, S. S. Hoxa11 and Hoxd11 regulate branching morphogenesis of the ureteric bud in the developing kidney. Development 2153-2161 (2001). Komuves, L.

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	GCGAGGCCGCCAGACATACACACG TTACCAGACGCTGGAGCTGGAGAA GGAGTTTCACTACAATCGCTACCTG ACGCGGCGGCGGCGCATCGAGATC GCGCACGCCCTGTGCCTGACGGAG AGGCAGATCAAGATATGGTTCCAG AACCGACGCATGAAGTGGAAAAAG GAGAGCAAACTGCTCAGCGCGTCT CAGCTCAGTGCCGAGGAGGAGGAA GAAAAACAGGCCGAG			G. et al. Changes in HOXB6 homeodomain protein structure and localization during human epidermal development and differentiation. Dev. Dyn. 218, 636-647 (2000). Cardoso, W. V., Mitsialis, S. A., Brody, J. S. & Williams, M. C. Retinoic acid alters the expression of pattern-related genes in the developing rat lung. Dev. Dyn. 207, 47-59 (1996).
KLF4	ATGGCTGTCAGCGACGCGCTGCTCC CATCTTTCTCCACGTTCGCGTCTGG CCCGGCGGGAAGGGAGAAGACACT GCGTCAAGCAGGTGCCCCGAATAA CCGCTGGCGGGAGGAGCTCTCCCA CATGAAGCGACTTCCCCCAGTGCTT CCCGGCCGCCCCTATGACCTGGCGG CGGCGACCGTGGCCACAGACCTGG AGAGCGGCGGAGCCGGTGCGGCTT GCGGCGGTAGCAACCTGGCGCCCC TACCTCGGAGAGAGACCGAGGAGT TCAACGATCTCCTGGACCTGGACTT TATTCTCTCCAATTCGCTGACCCAT CCTCCGGAGTCAGTGGCCGCCACC GTGTCCTCGTCAGCGTCAGCCTCCT CTTCGTCGTCGCCGTCGAGCAGCGG CCCTGCCAGCGCGCCCTCCACCTGC AGCTTCACCTATCCGATCCGGGCCG GGAACGACCCGGGCGTGGCGCCGG GCGGCACGGGCGGAGGCCTCCTCT ATGGCAGGGAGTCCGCTCCCCCTCC GACGGCTCCCTTCAACCTGGCGGAC ATCAACGACGTGAGCCCCTCGGGC GGCTTCGTGGCCGAGCTCCTGCGGC CAGAATTGGACCCGGTGTACATTCC GCCGCAGCAGCCGCAGCCGCCAGG TGGCGGGCTGATGGGCAAGTTCGT GCTGAAGGCGTCGCTGAGCGCCCC TGGCAGCGAGTACGGCAGCCCGTC GGTCATCAGCGTCAGCAAAGGCAG CCCTGACGGCAGCCACCCGGTGGT GGTGGCGCCCTACAACGGCGGGCC GCCGCGCACGTGCCCCAAGATCAA GCAGGAGGCGGTCTCTTCGTGCACC CACTTGGGCGCTGGACCCCCTCTCA GCAATGGCCACCGGCCGGCTGCAC ACGACTTCCCCCTGGGGCGGCAGCT CCCCAGCAGGACTACCCCGACCCT GGGTCTTGAGGAAGTGCTGAGCAG CAGGGACTGTCACCCTGCCCTGCCG CTTCCTCCCGGCTTCCATCCCCACC CGGGGCCCAATTACCCATCCTTCCT GCCCGATCAGATGCAGCCGCAAGT	62	Involved in regulation of pluripotency and development of skin. Reprogramming factor for induction of pluripotency.	Fuchs, E., Segre, J. A. & Bauer, C. Klf4 is a transcription factor required for establishing the barrier function of the skin. Nat. Genet. 22, 356-400 (1999). Jiang, J. et al. A core Klf circuitry regulates self-renewal of embryonic stem cells. Nat. Cell Biol. 10, 353-360 (2008). Takahashi, K. & Yamanaka, S. Induction of pluripotent stem cells from mouse embryonic and adult fibroblast cultures by defined factors. Cell 126, 663-76 (2006). Takahashi, K. et al. Induction of pluripotent stem cells

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	CCCGCCGCTCCATTACCAAGAGCTC ATGCCACCCGGTTCCTGCATGCCAG AGGAGCCCAAGCCAAAGAGGGGAA GACGATCGTGGCCCCGGAAAAGGA CCGCCACCCACACTTGTGATTACGC GGGCTGCGGCAAAACCTACACAAA GAGTTCCCATCTCAAGGCACACCTG CGAACCCACACAGGTGAGAAACCT TACCACTGTGACTGGGACGGCTGTG GATGGAAATTCGCCCGCTCAGATG AACTGACCAGGCACTACCGTAAAC ACACGGGGCACCGCCCGTTCCAGT GCCAAAAATGCGACCGAGCATTTT CCAGGTCGGACCACCTCGCCTTACA CATGAAGAGGCATTTT			from adult human fibroblasts by defined factors. Cell 131, 861-72 (2007). Yu, J. et al. Induced Pluripotent Stem Cell Lines Derived from Human Somatic Cells. Science (80-.). 318, 1917-1920 (2007).
LHX3	ATGGAGGCGCGCGGGGAGCTGGGC CCGGCCCGGGAGTCGGCGGGAGGC GACCTGCTGCTAGCACTGCTGGCGC GGAGGGCGGACCTGCGCCGAGAGA TCCCGCTGTGCGCTGGCTGTGACCA GCACATCCTGGACCGCTTCATCCTC AAGGCTCTGGACCGCCACTGGCAC AGCAAGTGTCTCAAGTGCAGCGAC TGCCACACGCCACTGGCCGAGCGC TGCTTCAGCCGAGGGGAGAGCGTT TACTGCAAGGACGACTTTTTCAAGC GCTTCGGGACCAAGTGCGCCGCGT GCCAGCTGGGCATCCCGCCCACGC AGGTGGTGCGCCGCGCCCAGGACT TCGTGTACCACCTGCACTGCTTTGC CTGCGTCGTGTGCAAGCGGCAGCT GGCCACGGGCGACGAGTTCTACCT CATGGAGGACAGCCGGCTCGTGTG CAAGGCGGACTACGAAACCGCCAA GCAGCGAGAGGCCGAGGCCACGGC CAAGCGGCCGCGCACGACCATCAC CGCCAAGCAGCTGGAGACGCTGAA GAGCGCTTACAACACCTCGCCCAA GCCGGCGCGCCACGTGCGCGAGCA GCTCTCGTCCGAGACGGGCCTGGA CATGCGCGTGGTGCAGGTTTGGTTC CAGAACCGCCGGGCCAAGGAGAAG AGGCTGAAGAAGGACGCCGGCCGG CAGCGCTGGGGGCAGTATTTCCGC AACATGAAGCGCTCCCGCGGCGGC TCCAAGTCGGACAAGGACAGCGTT CAGGAGGGGCAGGACAGCGACGCT GAGGTCTCCTTCCCCGATGAGCCTT CCTTGGCGGAAATGGGCCCGGCCA ATGGCCTCTACGGGAGCTTGGGGG AACCCACCCAGGCCTTGGGCCGGC CCTCGGGAGCCCTGGGCAACTTCTC CCTGGAGCATGGAGGCCTGGCAGG CCCAGAGCAGTACCGAGAGCTGCG TCCCGGCAGCCCCTACGGTGTCCCC CCATCCCCCGCCGCCCCGCAGAGC CTCCCTGGCCCCCAGCCCCTCCTCT CCAGCCTGGTGTACCCAGACACCA GCTTGGGCCTTGTGCCCTCGGGAGC CCCCGGCGGGCCCCCACCCATGAG GGTGCTGGCAGGGAACGGACCCAG TTCTGACCTATCCACGGGGAGCAGC GGGGGTTACCCCGACTTCCCTGCCA GCCCCGCCTCCTGGCTGGATGAGGT AGACCACGCTCAGTTCTCAGGCCTC ATGGGCCCAGCTTTCTTGTAC	63	Involved in pituitary gland development	Sheng, H. Z. et al. Multistep Control of Pituitary Organogenesis. Science (80-.). 278, 1809-1812 (1997).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
LMX1A	ATGGAAGGAATCATGAACCCCTAC ACGGCTCTGCCCACCCCACAGCAG CTCCTGGCCATCGAGCAGAGTGTCT ACAGCTCAGATCCCTTCCGACAGG GTCTCACCCCACCCCAGATGCCTGG AGACCACATGCACCCTTATGGTGCC GAGCCCCTTTTCCATGACCTGGATA GCGACGACACCTCCCTCAGTAACCT GGGTGACTGTTTCCTAGCAACCTCA GAAGCTGGGCCTCTGCAGTCCAGA GTGGGAAACCCCATTGACCATCTGT ACTCCATGCAGAATTCTTACTTCAC ATCT	64	Involved in neuronal development	Lin, W. et al. Foxa1 and Foxa2 function both upstream of and cooperatively with Lmx1a and Lmx1b in a feedforward loop promoting meso-diencephalic dopaminergic neuron development. Dev. Biol. 333, 386-396 (2009). Qiaolin, D. et al. Specific and integrated roles of Lmx1a, Lmx1b and Phox2a in ventral midbrain development. Development 138, 3399-3408 (2011).
MEF2C	ATGGGGAGAAAAAAGATTCAGATT ACGAGGATTATGGATGAACGTAAC AGACAGGTGACATTTACAAAGAGG AAATTTGGGTTGATGAAGAAGGCT TATGAGCTGAGCGTGCTGTGTGACT GTGAGATTGCGCTGATCATCTTCAA CAGCACCAACAAGCTGTTCCAGTAT GCCAGCACCGACATGGACAAAGTG CTTCTCAAGTACACGGAGTACAAC GAGCCGCATGAGAGCCGGACAAAC TCAGACATCGTGGAGACGTTGAGA AAGAAGGGCCTTAATGGCTGTGAC AGCCCAGACCCCGATGCGGACGAT TCCGTAGGTCACAGCCCTGAGTCTG AGGACAAGTACAGGAAAATTAACG AAGATATTGATCTAATGATCAGCA GGCAAAGATTGTGTGCTGTTCCACC TCCCAACTTCGAGATGCCAGTCTCC ATCCCAGTGTCCAGCCACAACAGTT TGGTGTACAGCAACCCTGTCAGCTC ACTGGGAAACCCCAACCTATTGCC ACTGGCTCACCCTTCTCTGCAGAGG AATAGTATGTCTCCTGGTGTAACAC ATCGACCTCCAAGTGCAGGTAACA CAGGTGGTCTGATGGGTGGAGACC TCACGTCTGGTGCAGGCACCAGTGC AGGGAACGGGTATGGCAATCCCCG AAACTCACCAGGTCTGCTGGTCTCA CCTGGTAACTTGAACAAGAATATG CAAGCAAAATCTCCTCCCCCAATGA ATTTAGGAATGAATAACCGTAAAC CAGATCTCCGAGTTCTTATTCCACC AGGCAGCAAGAATACGATGCCATC AGTGTCTGAGGATGTCGACCTGCTT TTGAATCAAAGGATAAATAACTCC CAGTCGGCTCAGTCATTGGCTACCC CAGTGGTTTCCGTAGCAACTCCTAC TTTACCAGGACAAGGAATGGGAGG ATATCCATCAGCCATTTCAACAACA	65	Involved in cardiac development	Lin, Q. et al. Control of mouse cardiac morphogenesis and myogenesis by transcription factor MEF2C. Science 276, 1404-7 (1997).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	TATGGTACCGAGTACTCTCTGAGTA GTGCAGACCTGTCATCTCTGTCTGG GTTTAACACCGCCAGCGCTCTTCAC CTTGGTTCAGTAACTGGCTGGCAAC AGCAACACCTACATAACATGCCAC CATCTGCCCTCAGTCAGTTGGGAGC TTGCACTAGCACTCATTTATCTCAG AGTTCAAATCTCTCCCTGCCTTCTA CTCAAAGCCTCAACATCAAGTCAG AACCTGTTTCTCCTCCTAGAGACCG TACCACCACCCCTTCGAGATACCCA CAACACACGCGCCACGAGGCGGGG AGATCTCCTGTTGACAGCTTGAGCA GCTGTAGCAGTTCGTACGACGGGA GCGACCGAGAGGATCACCGGAACG AATTCCACTCCCCCATTGGACTCAC CAGACCTTCGCCGGACGAAAGGGA AAGTCCCTCAGTCAAGCGCATGCG ACTTTCTGAAGGATGGGCAACA			
MESP1	ATGGCCCAGCCCCTGTGCCCGCCGC TCTCCGAGTCCTGGATGCTCTCTGC GGCCTGGGGCCCAACTCGGCGGCC GCCGCCCTCCGACAAGGACTGCGG CCGCTCCCTCGTCTCGTCCCCAGAC TCATGGGGCAGCACCCCAGCCGAC AGCCCCGTGGCGAGCCCCGCGCGG CCAGGCACCCTCCGGGACCCCCGC GCCCCCTCCGTAGGTAGGCGCGGC GCGCGCAGCAGCCGCCTGGGCAGC GGGCAGAGGCAGAGCGCCAGTGAG CGGGAGAAACTGCGCATGCGCACG CTGGCCCGCGCCCTGCACGAGCTGC GCCGCTTTCTACCGCCGTCCGTGGC GCCCGCGGGCCAGAGCCTGACCAA GATCGAGACGCTGCGCCTGGCTATC CGCTATATCGGCCACCTGTCGGCCG TGCTAGGCCTCAGCGAGGAGAGTC TCCAGCGCCGGTGCCGGCAGCGCG GTGACGCGGGGTCCCCTCGGGGCT GCCCGCTGTGCCCCGACGACTGCCC CGCGCAGATGCAGACACGGACGCA GGCTGAGGGGCAGGGGCAGGGGCG CGGGCTGGGCCTGGTATCCGCCGTC CGCGCCGGGGCGTCCTGGGGATCC CCGCCTGCCTGCCCCGGAGCCCGA GCTGCACCCGAGCCGCGCGACCCG CCTGCGCTGTTCGCCGAGGCGGCGT GCCCGGAAGGGCAGGCGATGGAGC CAAGCCCACCGTCCCCGCTCCTTCC GGGCGACGTGCTGGCTCTGTTGGA GACCTGGATGCCCCTCTCGCCTCTG GAGTGGCTGCCTGAGGAGCCCAAG TTG	66	Involved in cardiac development	Bondue, A. et al. Mesp1 Acts as a Master Regulator of Multipotent Cardiovascular Progenitor Specification. Cell Stem Cell 3,69-84 (2008).
MITF	ATGCTGGAAATGCTAGAATATAAT CACTATCAGGTGCAGACCCACCTCG AAAACCCCACCAAGTACCACATAC AGCAAGCCCAACGGCAGCAGGTAA AGCAGTACCTTTCTACCACTTTAGC AAATAAACATGCCAACCAAGTCCT GAGCTTGCCATGTCCAAACCAGCCT GGCGATCATGTCATGCCACCGGTGC CGGGGAGCAGCGCACCCAACAGCC CCATGGCTATGCTTACGCTTAACTC CAACTGTGAAAAAGAGGGATTTTA TAAGTTTGAAGAGCAAAACAGGGC AGAGAGCGAGTGCCCAGGCATGAA CACACATTCACGAGCGTCCTGTATG CAGATGGATGATGTAATCGATGAC ATCATTAGCCTAGAATCAAGTTATA ATGAGGAAATCTTGGGCTTGATGG ATCCTGCTTTGCAAATGGCAAATAC GTTGCCTGTCTCGGGAAACTTGATT	67	Involved in pigment cell and melanocyte differentiation	Widlund, H. R. & Fisher, D. E. Microphthalamia-associated transcription factor: a critical regulator of pigment cell development and survival. Oncogene 22, 3035-3041 (2003).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	GATCTTTATGGAAACCAAGGTCTGC			
	CCCCACCAGGCCTCACCATCAGCA			
	ACTCCTGTCCAGCCAACCTTCCCAA			
	CATAAAAAGGGAGCTCACAGAGTC			
	TGAAGCAAGAGCACTGGCCAAAGA			
	GAGGCAGAAAAAGGACAATCACAA			
	CCTGATTGAACGAAGAAGAAGATT			
	TAACATAAATGACCGCATTAAAGA			
	ACTAGGTACTTTGATTCCCAAGTCA			
	AATGATCCAGACATGCGCTGGAAC			
	AAGGGAACCATCTTAAAAGCATCC			
	GTGGACTATATCCGAAAGTTGCAA			
	CGAGAACAGCAACGCGCAAAAGAA			
	CTTGAAAACCGACAGAAGAAACTG			
	GAGCACGCCAACCGGCATTTGTTGC			
	TCAGAATACAGGAACTTGAAATGC			
	AGGCTCGAGCTCATGGACTTTCCCT			
	TATTCCATCCACGGGTCTCTGCTCT			
	CCAGATTTGGTGAATCGGATCATCA			
	AGCAAGAACCCGTTCTTGAGAACT			
	GCAGCCAAGACCTCCTTCAGCATCA			
	TGCAGACCTAACCTGTACAACAACT			
	CTCGATCTCACGGATGGCACCATCA			
	CCTTCAACAACAACCTCGGAACTG			
	GGACTGAGGCCAACCAAGCCTATA			
	GTGTCCCCACAAAAATGGGATCCA			
	AACTGGAAGACATCCTGATGGACG			
	ACACCCTTTCTCCCGTCGGTGTCAC			
	TGATCCACTCCTTTCCTCAGTGTCC			
	CCCGGAGCTTCCAAAACAAGCAGC			
	CGGAGGAGCAGTATGAGCATGGAA			
	GAGACGGAGCACACTTGT			
MYC	ATGCCCCTCAACGTTAGCTTCACCA	68	Involved in cell proliferation, differentiation and apoptosis. Reprogramming factor for induction of pluripotency.	Pelengaris, S., Khan, M. & Evan, G. c-MYC: more than just a matter of life and death. Nat. Rev. Cancer 2, 764-776 (2002). Takahashi, K. & Yamanaka, S. Induction of pluripotent stem cells from mouse embryonic and adult fibroblast cultures by defined factors. Cell 126,663-76 (2006). Takahashi, K. et al. Induction of pluripotent stem cells from adult human fibroblasts by defined factors. Cell 131,861-72 (2007). Yu, J. et al. Induced Pluripotent Stem Cell
	ACAGGAACTATGACCTCGACTACG			
	ACTCGGTGCAGCCGTATTTCTACTG			
	CGACGAGGAGGAGAACTTCTACCA			
	GCAGCAGCAGCAGAGCGAGCTGCA			
	GCCCCCGGCGCCCAGCGAGGATAT			
	CTGGAAGAAATTCGAGCTGCTGCC			
	CACCCCGCCCCTGTCCCCTAGCCGC			
	CGCTCCGGGCTCTGCTCGCCCTCCT			
	ACGTTGCGGTCACACCCTTCTCCCT			
	TCGGGGAGACAACGACGGCGGTGG			
	CGGGAGCTTCTCCACGGCCGACCA			
	GCTGGAGATGGTGACCGAGCTGCT			
	GGGAGGAGACATGGTGAACCAGAG			
	TTTCATCTGCGACCCGGACGACGAG			
	ACCTTCATCAAAAACATCATCATCC			
	AGGACTGTATGTGGAGCGGCTTCTC			
	GGCCGCCGCCAAGCTCGTCTCAGA			
	GAAGCTGGCCTCCTACCAGGCTGC			
	GCGCAAAGACAGCGGCAGCCCGAA			
	CCCCGCCCGCGGCCACAGCGTCTG			
	CTCCACCTCCAGCTTGTACCTGCAG			
	GATCTGAGCGCCGCCGCCTCAGAG			
	TGCATCGACCCCTCGGTGGTCTTCC			
	CCTACCCTCTCAACGACAGCAGCTC			
	GCCCAAGTCCTGCGCCTCGCAAGA			
	CTCCAGCGCCTTCTCTCCGTCCTCG			
	GATTCTCTGCTCTCCTCGACGGAGT			
	CCTCCCCGCAGGGCAGCCCCGAGC			
	CCCTGGTGCTCCATGAGGAGACAC			
	CGCCCACCACCAGCAGCGACTCTG			
	AGGAGGAACAAGAAGATGAGGAA			
	GAAATCGATGTTGTTTCTGTGGAAA			
	AGAGGCAGGCTCCTGGCAAAAGGT			
	CAGAGTCTGGATCACCTTCTGCTGG			
	AGGCCACAGCAAACCTCCTCACAG			
	CCCACTGGTCCTCAAGAGGTGCCAC			
	GTCTCCACACATCAGCACAACTACG			
	CAGCGCCTCCCTCCACTCGGAAGG			
	ACTATCCTGCTGCCAAGAGGGTCA			
	AGTTGGACAGTGTCAGAGTCCTGA			

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	GACAGATCAGCAACAACCGAAAAT GCACCAGCCCCAGGTCCTCGGACA CCGAGGAGAATGTCAAGAGGCGAA CACACAACGTCTTGGAGCGCCAGA GGAGGAACGAGCTAAAACGGAGCT TTTTTGCCCTGCGTGACCAGATCCC GGAGTTGGAAAACAATGAAAAGGC CCCCAAGGTAGTTATCCTTAAAAAA GCCACAGCATACATCCTGTCCGTCC AAGCAGAGGAGCAAAAGCTCATTT CTGAAGAGGACTTGTTGCGGAAAC GACGAGAACAGTTGAAACACAAAC TTGAACAGCTACGGAACTCTTGTGC G			Lines Derived from Human Somatic Cells. Science (80-.). 318, 1917-1920 (2007).
MYCL	ATGGACTACGACTCGTACCAGCACT ATTTCTACGACTATGACTGCGGGGA GGATTTCTACCGCTCCACGGCGCCC AGCGAGGACATCTGGAAGAAATTC GAGCTGGTGCCATCGCCCCCCACGT CGCCGCCCTGGGGCTTGGGTCCCGG CGCAGGGGACCCGGCCCCCGGGAT TGGTCCCCCGGAGCCGTGGCCCGG AGGGTGCACCGGAGACGAAGCGGA ATCCCGGGGCCACTCGAAAGGCTG GGGCAGGAACTACGCCTCCATCAT ACGCCGTGACTGCATGTGGAGCGG CTTCTCGGCCCGGGAACGGCTGGA GAGAGCTGTGAGCGACCGGCTCGC TCCTGGCGCGCCCCGGGGGAACCC GCCCAAGGCGTCCGCCGCCCCGGA CTGCACTCCCAGCCTCGAAGCCGGC AACCCGGCGCCCGCCGCCCCCTGTC CGCTGGGCGAACCCAAGACCCAGG CCTGCTCCGGGTCCGAGAGCCCAA GCGACTCGGGTAAGGACCTCCCCG AGCCATCCAAGAGGGGGCCACCCC ATGGGTGGCCAAAGCTCTGCCCCTG CCTGAGGTCAGGCATTGGCTCTTCT CAAGCTCTTGGGCCATCTCCGCCTC TCTTTGGC	69	Involved in cell proliferation, differentiation and apoptosis.	Hatton, K. S. et al. Expression and activity of L-Myc in normal mouse development. Mol. Cell. Biol. 16, 1794-804 (1996).
MYCN	ATGCCGAGTTGTTCCACGTCTACGA TGCCAGGAATGATATGCAAGAACC CCGACTTGGAGTTTGACTCTTTGCA ACCATGCTTTTATCCGGATGAAGAC GACTTTTATTTCGGCGGCCCGGACA GCACCCCTCCTGGAGAGGACATCT GGAAAAAATTCGAACTTTTGCCTAC ACCCCCACTCAGTCCCTCTCGAGGA TTTGCGGAACACAGCAGTGAACCG CCGTCTTGGGTGACAGAGATGCTCC TCGAGAACGAATTGTGGGGAAGCC CTGCGGAGGAAGACGCTTTCGGGC TCGGTGGACTCGGAGGTCTCACGCC GAACCCAGTCATACTGCAGGATTG CATGTGGTCTGGATTCTCAGCTCGG GAGAAGCTGGAACGGGCAGTTTCT GAGAAACTCCAACATGGCCGGGGC CCTCCAACAGCGGGTTCTACCGCAC AGTCCCCTGGTGCTGGAGCCGCTAG TCCCGCGGGGAGAGGCCATGGGGG CGCGGCAGGAGCGGGTAGGGCCGG CGCTGCGTTGCCTGCTGAGCTTGCG CACCCCGCCGCTGAATGTGTAGATC CCGCGGTAGTGTTTCCGTTCCCCGT TAATAAGCGAGAACCGGCACCGGT GCCAGCCGCTCCTGCGTCTGCACCC GCGGCAGGTCCTGCTGTCGCCTCAG GAGCAGGTATTGCCGCTCCTGCAG GGGCACCAGGAGTAGCCCCTCCAA GGCCCGGCGGTAGGCAAACCTCCG GCGGCGACCACAAAGCACTCTCAA CGAGCGGAGAGGATACACTGTCCG	70	Involved in cell proliferation and differentiation	Malynn, B. A. et al. N-myc can functionally replace c-myc in murine development, cellular growth, and differentiation. Genes Dev. 14, 1390-9 (2000). Sawai, S. et al. Defects of embryonic organogenesis resulting from targeted disruption of the N-myc gene in the mouse. Development 117, 1445-1455 (1993). Stanton, B. R., Perkins, A. S., Tessarollo, L., Sassoon, D. A. & Parada,

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	ATAGTGATGACGAGGACGACGAAG AGGAGGACGAGGAGGAGGAGATA GATGTTGTCACGGTCGAGAAGCGA AGGAGTTCTTCAAATACAAAAGCG GTAACGACATTCACGATAACAGTA AGACCTAAGAACGCAGCCCTCGGT CCAGGGCGGGCCCAGTCCAGTGAG CTTATACTTAAGCGCTGCCTGCCGA TTCACCAGCAGCATAACTACGCGG CCCCTAGTCCCTACGTTGAGAGCGA GGATGCCCCCCCACAAAAAAAAAT AAAGTCTGAAGCGTCCCCCCGCCCC CTGAAATCCGTAATCCCCCCAAAG GCGAAGTCACTCAGTCCCAGGAAT TCAGATTCCGAGGACTCCGAACGG CGGCGGAATCATAACATACTTGAG AGACAACGACGCAATGACCTGAGG TCTTCTTTTTTGACCCTCCGAGATC ACGTCCCCGAGCTGGTTAAGAATG AGAAAGCTGCGAAGGTAGTCATAC TGAAAAAGGCCACCGAGTATGTCC ATAGTTTGCAAGCTGAGGAGCACC AGCTTCTCCTTGAAAAGGAGAAAC TTCAGGCACGACAACAGCAATTGC TGAAAAAGATTGAGCATGCACGCA CTTGT			L. F. Loss of N-myc function results in embryonic lethality and failure of the epithelial component of the embryo to develop. Genes Dev. 6, 2235-47 (1992).
MYOD1	ATGGAGCTACTGTCGCCACCGCTCC GCGACGTAGACCTGACGGCCCCCG ACGGCTCTCTCTGCTCCTTTGCCAC AACGGACGACTTCTATGACGACCC GTGTTTCGACTCCCCGGACCTGCGC TTCTTCGAAGACCTGGACCCGCGCC TGATGCACGTGGGCGCGCTCCTGA AACCCGAAGAGCACTCGCACTTCC CCGCGGCGGTGCACCCGGCCCCGG GCGCACGTGAGGACGAGCATGTGC GCGCGCCCAGCGGGCACCACCAGG CGGGCCGCTGCCTACTGTGGGCCTG CAAGGCGTGCAAGCGCAAGACCAC CAACGCCGACCGCCGCAAGGCCGC CACCATGCGCGAGCGGCGCCGCCT GAGCAAAGTAAATGAGGCCTTTGA GACACTCAAGCGCTGCACGTCGAG CAATCCAAACCAGCGGTTGCCCAA GGTGGAGATCCTGCGCAACGCCAT CCGCTATATCGAGGGCCTGCAGGCT CTGCTGCGCGACCAGGACGCCGCG CCCCCTGGCGCCGCAGCCGCCTTCT ATGCGCCGGGCCCGCTGCCCCCGG GCCGCGGCGGCGAGCACTACAGCG GCGACTCCGACGCGTCCAGCCCGC GCTCCAACTGCTCCGACGGCATGAT GGACTACAGCGGCCCCCCGAGCGG CGCCCGGCGGCGGAACTGCTACGA AGGCGCCTACTACAACGAGGCGCC CAGCGAACCCAGGCCCGGGAAGAG TGCGGCGGTGTCGAGCCTAGACTG CCTGTCCAGCATCGTGGAGCGCATC TCCACCGAGAGCCCTGCGGCGCCC GCCCTCCTGCTGGCGGACGTGCCTT CTGAGTCGCCTCCGCGCAGGCAAG AGGCTGCCGCCCCCAGCGAGGGAG AGAGCAGCGGCGACCCCACCCAGT CACCGGACGCCGCCCCGCAGTGCC CTGCGGGTGCGAACCCCAACCCGA TATACCAGGTGCTC	71	Involved in skeletal muscle specification and differentiation Demonstrated to induce differentiation of hPSCs to skeletal muscle	Tapscott, S. J. The circuitry of a master switch: Myod and the regulation of skeletal muscle gene transcription. Development 132, 2685-2695 (2005). Abujarour, R. et al. Myogenic differentiation of muscular dystrophy-specific induced pluripotent stem cells for use in drug discovery. Stem Cells Transl. Med. 3,149-60 (2014).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
MYOG	ATGGAGCTGTATGAGACATCCCCCT ACTTCTACCAGGAACCCCGCTTCTA TGATGGGGAAAACTACCTGCCTGTC CACCTCCAGGGCTTCGAACCACCA GGCTACGAGCGGACGGAGCTCACC CTGAGCCCCGAGGCCCCAGGGCCC CTTGAGGACAAGGGGCTGGGGACC CCCGAGCACTGTCCAGGCCAGTGC CTGCCGTGGGCGTGTAAGGTGTGTA AGAGGAAGTCGGTGTCCGTGGACC GGCGGCGGGCGGCCACACTGAGGG AGAAGCGCAGGCTCAAGAAGGTGA ATGAGGCCTTCGAGGCCCTGAAGA GAAGCACCCTGCTCAACCCCAACC AGCGGCTGCCCAAGGTGGAGATCC TGCGCAGTGCCATCCAGTACATCGA GCGCCTCCAGGCCCTGCTCAGCTCC CTCAACCAGGAGGAGCGTGACCTC CGCTACCGGGGCGGGGGCGGGCCC CAGCCAGGGGTGCCCAGCGAATGC AGCTCTCACAGCGCCTCCTGCAGTC CAGAGTGGGGCAGTGCACTGGAGT TCAGCGCCAACCCAGGGGATCATC TGCTCACGGCTGACCCTACAGATGC CCACAACCTGCACTCCCTCACCTCC ATCGTGGACAGCATCACAGTGGAA GATGTGTCTGTGGCCTTCCCAGATG AAACCATGCCCAAC	72	Involved in skeletal muscle specification and differentiation	Pownall, M. E., Gustafsson, M. K. & Emerson, C. P. Myogenic Regulatory Factors and the Specification of Muscle Progenitors in Vertebrate Embryos. Annu. Rev. Cell Dev. Biol. 18,747-783 (2002). Shi, X. & Garry, D. J. Muscle stem cells in development, regeneration, and disease. Genes Dev. 20,1692-708 (2006).
NEURO D1	ATGACCAAATCGTACAGCGAGAGT GGGCTGATGGGCGAGCCTCAGCCC CAAGGTCCTCCAAGCTGGACAGAC GAGTGTCTCAGTTCTCAGGACGAG GAGCACGAGGCAGACAAGAAGGA GGACGACCTCGAAGCCATGAACGC AGAGGAGGACTCACTGAGGAACGG GGGAGAGGAGGAGGACGAAGATG AGGACCTGGAAGAGGAGGAAGAA GAGGAAGAGGAGGATGACGATCAA AAGCCCAAGAGACGCGGCCCCAAA AAGAAGAAGATGACTAAGGCTCGC CTGGAGCGTTTTAAATTGAGACGCA TGAAGGCTAACGCCCGGGAGCGGA ACCGCATGCACGGACTGAACGCGG CGCTAGACAACCTGCGCAAGGTGG TGCCTTGCTATTCTAAGACGCAGAA GCTGTCCAAAATCGAGACTCTGCGC TTGGCCAAGAACTACATCTGGGCTC TGTCGGAGATCCTGCGCTCAGGCA AAAGCCCAGACCTGGTCTCCTTCGT TCAGACGCTTTGCAAGGGCTTATCC CAACCCACCACCAACCTGGTTGCG GGCTGCCTGCAACTCAATCCTCGGA CTTTTCTGCCTGAGCAGAACCAGGA CATGCCCCCCCACCTGCCGACGGCC AGCGCTTCCTTCCCTGTACACCCCT ACTCCTACCAGTCGCCTGGGCTGCC CAGTCCGCCTTACGGTACCATGGAC AGCTCCCATGTCTTCCACGTTAAGC CTCCGCCGCACGCCTACAGCGCAG CGCTGGAGCCCTTCTTTGAAAGCCC TCTGACTGATTGCACCAGCCCTTCC TTTGATGGACCCCTCAGCCCGCCGC TCAGCATCAATGGCAACTTCTCTTT CAAACACGAACCGTCCGCCGAGTT TGAGAAAAATTATGCCTTTACCATG CACTATCCTGCAGCGACACTGGCA GGGGCCCAAAGCCACGGATCAATC TTCTCAGGCACCGCTGCCCCTCGCT GCGAGATCCCCATAGACAATATTAT GTCCTTCGATAGCCATTCACATCAT GAGCGAGTCATGAGTGCCCAGCTC AATGCCATATTTCATGAT	73	Involved in neuronal specification and differentiation Demonstrated to induce neuronal differentiation in hPSCs	Pataskar, A. et al. NeuroD1 reprograms chromatin and transcription factor landscapes to induce the neuronal program. EMBO J. 35, 24-45 (2016). Zhang, Y. et al. Rapid single-step induction of functional neurons from human pluripotent stem cells. Neuron 78, 785-98 (2013).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
NEUROG1	ATGCCAGCCCGCCTTGAGACCTGCA TCTCCGACCTCGACTGCGCCAGCAG CAGCGGCAGTGACCTATCCGGCTTC CTCACCGACGAGGAAGACTGTGCC AGACTCCAACAGGCAGCCTCCGCTT CGGGGCCGCCCGCGCCGGCCCGCA GGGGCGCGCCCAATATCTCCCGGG CGTCTGAGGTTCCAGGGGCACAGG ACGACGAGCAGGAGAGGCGGCGGC GCCGCGGCCGGACGCGGGTCCGCT CCGAGGCGCTGCTGCACTCGCTGCG CAGGAGCCGGCGCGTCAAGGCCAA CGATCGCGAGCGCAACCGCATGCA CAACTTGAACGCGGCCCTGGACGC ACTGCGCAGCGTGCTGCCCTCGTTC CCCGACGACACCAAGCTCACCAAA ATCGAGACGCTGCGCTTCGCCTACA ACTACATCTGGGCTCTGGCCGAGAC ACTGCGCCTGGCGGATCAAGGGCT GCCCGGAGGCGGTGCCCGGGAGCG CCTCCTGCCGCCGCAGTGCGTCCCC TGCCTGCCCGGTCCCCCAAGCCCCG CCAGCGACGCGGAGTCCTGGGGCT CAGGTGCCGCCGCCGCCTCCCCGCT CTCTGACCCCAGTAGCCCAGCCGCC TCCGAAGACTTCACCTACCGCCCCG GCGACCCTGTTTTCTCCTTCCCAAG CCTGCCCAAAGACTTGCTCCACACA ACGCCCTGTTTCATTCCTTACCAC	74	Involved in neuronal specification and differentiation	Bertrand, N., Castro, D. S. & Guillemot, F. Proneural genes and the specification of neural cell types. Nat. Rev. Neurosci. 3, 517-530 (2002).
NEUROG3	ATGACACCACAACCATCTGGTGCTC CCACAGTCCAGGTGACGCGAGAGA CTGAAAGATCATTCCCACGCGCGTC CGAGGATGAGGTGACATGTCCAAC TAGCGCACCCCCCTCTCCTACCCGG ACCCGCGGGAATTGTGCTGAGGCC GAAGAGGGAGGATGCAGAGGAGC ACCAAGGAAACTTCGAGCCCGACG GGGTGGAAGAAGCCGCCCCAAGTC TGAGCTCGCCCTTAGCAAGCAGCG CCGCAGTCGGAGGAAAAAGGCAAA CGACCGGGAAAGGAATAGGATGCA TAATCTTAATTCTGCTCTGGACGCT CTGCGAGGCGTACTTCCTACTTTCC CGGATGACGCGAAATTGACCAAGA TAGAGACTCTCCGGTTTGCACATAA TTACATCTGGGCTCTTACACAAACA CTGAGAATTGCCGATCACAGTCTTT ACGCTCTTGAGCCACCCGCCCCGCA CTGTGGCGAGCTGGGTAGCCCCGG CGGCTCTCCTGGAGACTGGGGGTCT TTGTATTCTCCTGTCAGCCAAGCGG GATCTTTGAGTCCGGCTGCCAGTCT CGAAGAAAGACCCGGACTCCTTGG AGCGACTTTTTCAGCATGTCTGTCC CCTGGCTCATTGGCTTTCTCAGACT TTTTG	75	Involved in pancreatic development, and neuronal specification and differentiation	Bertrand, N., Castro, D. S. & Guillemot, F. Proneural genes and the specification of neural cell types. Nat. Rev. Neurosci. 3, 517-530 (2002). Arda, H. E. et al. Gene Regulatory Networks Governing Pancreas Development. Dev. Cell 25, 5-13 (2013).
NRL	ATGGCCCTGCCTCCCAGCCCGCTGG CCATGGAATATGTCAATGACTTTGA CTTGATGAAGTTTGAGGTAAAGCG GGAACCCTCTGAGGGCCGACCTGG CCCACCTACAGCCTCACTGGGATCC ACACCTTACAGCTCAGTGCCTCCTT CACCCACCTTCAGTGAACCAGGCAT GGTAGGGGCAACCGAGGGTACACG ACCAGGTTTGGAGGAGCTGTACTG GCTTGCTACCCTGCAGCAGCAGCTT GGGGCTGGGGAGGCATTGGGACTG AGTCCTGAAGAGGCCATGGAGCTA CTGCAAGGTCAGGGCCCAGTCCCT GTTGATGGACCCCATGGTTACTACC CAGGGAGCCCAGAGGAGACAGGAG	76	Involved in photoreceptor development	Mears, A. J. et al. Nr1 is required for rod photoreceptor development. Nat. Genet. 29, 447-452 (2001).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	CCCAGCACGTTCAGTTGGCAGAGC GGTTTTCCGACGCGGCGCTTGTCTC GATGTCTGTGCGAGAACTAAACCG GCAGCTGCGGGGATGCGGGAGAGA CGAGGCTCTACGACTGAAGCAGAG GCGTCGAACGCTGAAGAACCGTGG CTATGCGCAAGCATGTCGTTCCAAG AGGCTGCAACAGAGGCGAGGTCTT GAGGCCGAGCGCGCCCGTCTTGCA GCCCAGCTAGATGCGCTACGAGCT GAAGTAGCACGTTTGGCAAGAGAG CGAGATCTCTACAAGGCTCGCTGTG ACCGGCTAACCTCGAGTGGCCCCG GGTCCGGGGATCCCTCCCACCTTTT CCTCTGCCCAACTTTCTTGTACAAA GTTGTCCCC			
ONECUT1	ATGAACGCGCAGCTGACCATGGAA GCGATCGGCGAGCTGCACGGGGTG AGCCATGAGCCGGTGCCCGCCCCT GCCGACCTGCTGGGCGGCAGCCCC CACGCGCGCAGCTCCGTGGCGCAC CGCGGCAGCCACCTGCCCCCCGCG CACCCGCGCTCCATGGGCATGGCGT CCCTGCTGGACGGCGGCAGCGGCG GCGGAGATTACCACCACCACCACC GGGCCCCTGAGCACAGCCTGGCCG GCCCCCTGCATCCCACCATGACCAT GGCCTGCGAGACTCCCCCAGGTAT GAGCATGCCCACCACCTACACCAC CTTGACCCCTCTGCAGCCGCTGCCT CCCATCTCCACAGTCTCGGACAAGT TCCCCCACCATCACCACCACCACCA TCACCACCACCACCCGCACCACCA CCAGCGCCTGGCGGGCAACGTGAG CGGTAGCTTCACGCTCATGCGGGAT GAGCGCGGGCTGGCCTCCATGAAT AACCTCTATACCCCCTACCACAAGG ACGTGGCCGGCATGGGCCAGAGCC TCTCGCCCCTCTCCAGCTCCGGTCT GGGCAGCATCCACAACTCCCAGCA AGGGCTCCCCCACTATGCCCACCCG GGGGCCGCCATGCCCACCGACAAG ATGCTCACCCCCAACGGCTTCGAAG CCCACCACCCGGCCATGCTCGGCC GCCACGGGGAGCAGCACCTCACGC CCACCTCGGCCGGCATGGTGCCCAT CAACGGCCTTCCTCCGCACCATCCC CACGCCCACCTGAACGCCCAGGGC CACGGGCAACTCCTGGGCACAGCC CGGGAGCCCAACCCTTCGGTGACC GGCGCGCAGGTCAGCAATGGAAGT AATTCAGGGCAGATGGAAGAGATC AATACCAAAGAGGTGGCGCAGCGT ATCACCACCGAGCTCAAGCGCTAC AGCATCCCACAGGCCATCTTCGCGC AGAGGGTGCTCTGCCGCTCCCAGG GGACCCTCTCGGACCTGCTGCGCAA CCCCAAACCCTGGAGCAAACTCAA ATCCGGCCGGGAGACCTTCCGGAG GATGTGGAAGTGGCTGCAGGAGCC GGAGTTCCAGCGCATGTCCGCGCTC CGCTTAGCAGCATGCAAAAGGAAA GAACAAGAACATGGGAAGGATAGA GGCAACACACCCAAAAAGCCCAGG TTGGTCTTCACAGATGTCCAGCGTC GAACTCTACATGCAATATTCAAGG AAAATAAGCGTCCATCCAAAGAAT TGCAAATCACCATTTCCCAGCAGCT GGGGTTGGAGCTGAGCACTGTCAG	77	Involved in retinal, liver, gallbladder and pancreatic development	Chakrabarti, S. K., et al. Transcription factors direct the development and function of pancreatic β cells. Trends Endocrinol. Metab. 14, 78-84 (2003). Clotman, F. et al. The onecut transcription factor HNF6 is required for normal development of the biliary tract. Development 129,1819-1828 (2002). Sapkota, D. et al. Onecut1 and Onecut2 redundantly regulate early retinal cell fates during development. Proc. Natl. Acad. Sci. U. S. A. 111, E4086-95 (2014).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	CAACTTCTTCATGAACGCAAGAAG GAGGAGTCTGGACAAGTGGCAGGA CGAGGGCAGCTCCAATTCAGGCAA CTCATCTTCTTCATCAAGCACTTGT ACCAAAGCA			
OTX2	ATGATGTCTTATCTTAAGCAACCGC CTTACGCAGTCAATGGGCTGAGTCT GACCACTTCGGGTATGGACTTGCTG CACCCCTCCGTGGGCTACCCGGGGC CCTGGGCTTCTTGTCCCGCAGCCAC CCCCCGGAAACAGCGCCGGGAGAG GACGACGTTCACTCGGGCGCAGCT AGATGTGCTGGAAGCACTGTTTGCC AAGACCCGGTACCCAGACATCTTC ATGCGAGAGGAGGTGGCACTGAAA ATCAACTTGCCCGAGTCGAGGGTG CAGGTATGGTTTAAGAATCGAAGA GCTAAGTGCCGCCAACAACAGCAA CAACAGCAGAATGGAGGTCAAAAC AAAGTGAGACCTGCCAAAAAGAAG ACATCTCCAGCTCGGGAAGTGAGTT CAGAGAGTGGAACAAGTGGCCAAT TCACTCCCCCCTCTAGCACCTCAGT CCCGACCATTGCCAGCAGCAGTGCT CCTGTGTCTATCTGGAGCCCAGCTT CCATCTCCCCACTGTCAGATCCCTT GTCCACCTCCTCTTCCTGCATGCAG AGGTCCTATCCCATGACCTATACTC AGGCTTCAGGTTATAGTCAAGGAT ATGCTGGCTCAACTTCCTACTTTGG GGGCATGGACTGTGGATCATATTTG ACCCCTATGCATCACCAGCTTCCCG GACCAGGGGCCACACTCAGTCCCA TGGGTACCAATGCAGTCACCAGCC ATCTCAATCAGTCCCCAGCTTCTCT TTCCACCCAGGGATATGGAGCTTCA AGCTTGGGTTTTAACTCAACCACTG ATTGCTTGGATTATAAGGACCAAAC TGCCTCCTGGAAGCTTAACTTCAAT GCTGACTGCTTGGATTATAAAGATC AGACATCCTCGTGGAAATTCCAGGT TTTG	78	Involved in photoreceptor differentiation, pineal gland development and induction and specification of forebrain and midbrain	Rhinn, M. et al. Sequential roles for Otx2 in visceral endoderm and neuroectoderm for forebrain and midbrain induction and specification. Development 125, 845-856 (1998). Nishida, A. et al. Otx2 homeobox gene controls retinal photoreceptor cell fate and pineal gland development. Nat. Neurosci. 6,1255-1263 (2003).
PAX7	ATGGCGGCCCTTCCCGGCACGGTAC CGAGAATGATGCGGCCGGCTCCGG GGCAGAACTACCCCCGCACGGGAT TCCCTTTGGAAGTGTCCACCCCGCT TGGCCAAGGCCGGGTCAATCAGCT GGGAGGGGTCTTCATCAATGGGCG ACCCCTGCCTAACCACATCCGCCAC AAGATAGTGGAGATGGCCCACCAT GGCATCCGGCCCTGTGTCATCTCCC GACAGCTGCGTGTCTCCCACGGCTG CGTCTCCAAGATTCTTTGCCGCTAC CAGGAGACCGGGTCCATCCGGCCT GGGGCCATCGGCGGCAGCAAGCCC AGACAGGTGGCGACTCCGGATGTA GAGAAAAAGATTGAGGAGTACAAG AGGGAAAACCCAGGCATGTTCAGC TGGGAGATCCGGGACAGGCTGCTG AAGGATGGGCACTGTGACCGAAGC ACTGTGCCCTCAGTGAGTTCGATTA GCCGCGTGCTCAGAATCAAGTTCG GGAAGAAAGAGGAGGAGGATGAA GCGGACAAGAAGGAGGACGACGGC GAAAAGAAGGCCAAACACAGCATC GACGGCATCCTGGGCGACAAAGGG AACCGGCTGGACGAGGGCTCGGAT GTGGAGTCGGAACCTGACCTCCCA CTGAAGCGCAAGCAGCGACGCAGT CGGACCACATTCACGGCCGAGCAG CTGGAGGAGCTGGAGAAGGCCTTT GAGAGGACCCACTACCCAGACATA	79	Involved in specification and differentiation of satellite cells Demonstrated to induce myogenic precursor differentiation in hPSCs	Darabi, R. et al. Human ES- and iPS-derived myogenic progenitors restore DYSTROPHIN and improve contractility upon transplantation in dystrophic mice. Cell Stem Cell 10, 610-9 (2012). Seale, P., et al. Pax7 Is Required for the Specification of Myogenic Satellite Cells. Cell 102, 777-786 (2000).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	TACACCCGCGAGGAGCTGGCGCAG AGGACCAAGCTGACAGAGGCGCGT GTGCAGGTCTGGTTCAGTAACCGCC GCGCCCGTTGGCGTAAGCAGGCAG GAGCCAACCAGCTGGCGGCGTTCA ACCACCTTCTGCCAGGAGGCTTCCC GCCCACCGGCATGCCCACGCTGCC CCCCTACCAGCTGCCGGACTCCACC TACCCCACCACCACCATCTCCCAAG ATGGGGGCAGCACTGTGCACCGGC CTCAGCCCCTGCCACCGTCCACCAT GCACCAGGGCGGGCTGGCTGCAGC GGCTGCAGCCGCCGACACCAGCTC TGCCTACGGAGCCCGCCACAGCTTC TCCAGCTACTCTGACAGCTTCATGA ATCCGGCGGCGCCCTCCAACCACAT GAACCCGGTCAGCAACGGCCTGTC TCCTCAGGTGATGAGCATCTTGGGC AACCCCAGTGCGGTGCCCCCGCAG CCACAGGCTGACTTCTCCATCTCCC CGCTGCATGGCGGCCTGGACTCGG CCACCTCCATCTCAGCCAGCTGCAG CCAGCGGGCCGACTCCATCAAGCC AGGAGACAGCCTGCCCACCTCCCA GGCCTACTGCCCACCCACCTACAGC ACCACCGGCTACAGCGTGGACCCC GTGGCCGGCTATCAGTACGGCCAG TACGGCCAGAGTGAGTGCCTGGTG CCCTGGGCGTCCCCCGTCCCCATTC CTTCTCCCACCCCCAGGGCCTCCTG CTTGTTTATGGAGAGCTACAAGGTG GTGTCAGGGTGGGGAATGTCCATTT CACAGATGGAAAAATTGAAGTCCA GCCAGATGGAACAGTTCACC			
POU1F1	ATGAGTTGCCAAGCTTTTACTTCGG CTGATACCTTTATACCTCTGAATTC TGACGCCTCTGCAACTCTGCCTCTG ATAATGCATCACAGTGCTGCCGAGT GTCTACCAGTCTCCAACCATGCCAC CAATGTGATGTCTACAGCAACAGG ACTTCATTATTCTGTTCCTTCCTGTC ATTATGGAAACCAGCCATCAACCT ATGGAGTGATGGCAGGTAGTTTAA CCCCTTGTCTTTATAAATTTCCTGA CCACACCTTGAGTCATGGATTTCCT CCTATACACCAGCCTCTTCTGGCAG AGGACCCCACAGCTGCTGATTTCAA GCAGGAACTCAGGCGGAAAAGTAA ATTGGTGGAAGAGCCAATAGACAT GGATTCTCCAGAAATCAGAGAACT TGAAAAGTTTGCCAATGAATTTAAA GTGAGACGAATTAAATTAGGATAC ACCCAGACAAATGTTGGGGAGGCC CTGGCAGCTGTGCATGGCTCTGAAT TCAGTCAAACAACAATCTGCCGATT TGAAAATCTGCAGCTCAGCTTTAAA AATGCATGCAAACTGAAAGCAATA TTATCCAAATGGCTGGAGGAAGCT GAGCAAGTAGGAGCTTTGTACAAT GAAAAAGTGGGAGCAAATGAAAGG AAAAGAAAACGAAGAACAACTATA AGCATTGCTGCTAAAGATGCTCTGG AGAGACACTTTGGAGAACAGAATA AACCTTCTTCTCAAGAGATCATGAG GATGGCTGAAGAACTGAATCTGGA GAAAGAAGTAGTAAGAGTTTGGTT TTGCAACCGGAGGCAGAGAGAAAA ACGGGTGAAAACAAGTCTGAATCA GAGTTTATTTTCTATTTCTAAGGAA CATCTTGAGTGCAGATCAGGCCTCA TGGGCCCAGCTTTCTTGTAC	80	Involved in pituitary gland development	Turton, J. P. G. et al. Novel Mutations within the POU1F1 Gene Associated with Variable Combined Pituitary Hormone Deficiency. J. Clin. Endocrinol. Metab. 90, 4762-4770 (2005).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
POU5F1	ATGGCGGGACACCTGGCTTCAGATT TTGCCTTCTCGCCCCCTCCAGGTGG TGGAGGTGATGGGCCAGGGGGGCC GGAGCCGGGCTGGGTTGATCCTCG GACCTGGCTAAGCTTCCAAGGCCCT CCTGGAGGGCCAGGAATCGGGCCG GGGGTTGGGCCAGGCTCTGAGGTG TGGGGGATTCCCCCATGCCCCCCGC CGTATGAGTTCTGTGGGGGGATGG CGTACTGTGGGCCCCAGGTTGGAGT GGGGCTAGTGCCCCAAGGCGGCTT GGAGACCTCTCAGCCTGAGGGCGA AGCAGGAGTCGGGGTGGAGAGCAA CTCCGATGGGGCCTCCCCGGAGCCC TGCACCGTCACCCCTGGTGCCGTGA AGCTGGAGAAGGAGAAGCTGGAGC AAAACCCGGAGGAGTCCCAGGACA TCAAAGCTCTGCAGAAAGAACTCG AGCAATTTGCCAAGCTCCTGAAGC AGAAGAGGATCACCCTGGGATATA CACAGGCCGATGTGGGGCTCACCC TGGGGGTTCTATTTGGGAAGGTATT CAGCCAAACGACCATCTGCCGCTTT GAGGCTCTGCAGCTTAGCTTCAAGA ACATGTGTAAGCTGCGGCCCTTGCT GCAGAAGTGGGTGGAGGAAGCTGA CAACAATGAAAATCTTCAGGAGAT ATGCAAAGCAGAAACCCTCGTGCA GGCCCGAAAGAGAAAGCGAACCAG TATCGAGAACCGAGTGAGAGGCAA CCTGGAGAATTTGTTCCTGCAGTGC CCGAAACCCACACTGCAGCAGATC AGCCACATCGCCCAGCAGCTTGGG CTCGAGAAGGATGTGGTCCGAGTG TGGTTCTGTAACCGGCGCCAGAAG GGCAAGCGATCAAGCAGCGACTAT GCACAACGAGAGGATTTTGAGGCT GCTGGGTCTCCTTTCTCAGGGGGAC CAGTGTCCTTTCCTCTGGCCCCAGG GCCCCATTTTGGTACCCCAGGCTAT GGGAGCCCTCACTTCACTGCACTGT ACTCCTCGGTCCCTTTCCCTGAGGG GGAAGCCTTTCCCCCTGTCTCTGTC ACCACTCTGGGCTCTCCCATGCATT CAAAC	81	Involved in regulation of pluripotency and embryogenesis. Reprogramming factor for induction of pluripotency	Boyer, L. A., et al. Core Transcriptional Regulatory Circuitry in Human Embryonic Stem Cells. Cell 122, 947-956 (2005). Takahashi, K. & Yamanaka, S. Induction of pluripotent stem cells from mouse embryonic and adult fibroblast cultures by defined factors. Cell 126,663-76 (2006). Takahashi, K. et al. Induction of pluripotent stem cells from adult human fibroblasts by defined factors. Cell 131,861-72 (2007). Yu, J. et al. Induced Pluripotent Stem Cell Lines Derived from Human Somatic Cells. Science (80-.). 318, 1917-1920 (2007).
RUNX1	ATGGCTTCAGACAGCATATTTGAGT CATTTCCTTCGTACCCACAGTGCTT CATGAGAGAATGCATACTTGGAAT GAATCCTTCTAGAGACGTCCACGAT GCCAGCACGAGCCGCCGCTTCACG CCGCCTTCCACCGCGCTGAGCCCAG GCAAGATGAGCGAGGCGTTGCCGC TGGGCGCCCCGGACGCCGGCGCTG CCCTGGCCGGCAAGCTGAGGAGCG GCGACCGCAGCATGGTGGAGGTGC TGGCCGACCACCCGGGCGAGCTGG TGCGCACCGACAGCCCCAACTTCCT CTGCTCCGTGCTGCCTACGCACTGG CGCTGCAACAAGACCCTGCCCATC GCTTTCAAGGTGGTGGCCCTAGGG GATGTTCCAGATGGCACTCTGGTCA	82	Involved in haematopoetic cell development	Woolf, E. et al. Runx3 and Runx1 are required for CD8 T cell development during thymopoiesis. Proc. Natl. Acad. Sci. U. S. A. 100, 7731-6 (2003). Lacaud, G. et al. Runx1 is essential for

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	CTGTGATGGCTGGCAATGATGAAA			hematopoietic
	ACTACTCGGCTGAGCTGAGAAATG			commitment
	CTACCGCAGCCATGAAGAACCAGG			at the
	TTGCAAGATTTAATGACCTCAGGTT			hemangioblast
	TGTCGGTCGAAGTGGAAGAGGGAA			stage of
	AAGCTTCACTCTGACCATCACTGTC			development
	TTCACAAACCCACCGCAAGTCGCC			in vitro.
	ACCTACCACAGAGCCATCAAAATC			Blood 100,
	ACAGTGGATGGGCCCCGAGAACCT			458-66
	CGAAGACATCGGCAGAAACTAGAT			(2002).
	GATCAGACCAAGCCCGGGAGCTTG			
	TCCTTTTCCGAGCGGCTCAGTGAAC			
	TGGAGCAGCTGCGGCGCACAGCCA			
	TGAGGGTCAGCCCACACCACCCAG			
	CCCCCACGCCCAACCCTCGTGCCTC			
	CCTGAACCACTCCACTGCCTTTAAC			
	CCTCAGCCTCAGAGTCAGATGCAG			
	GATACAAGGCAGATCCAACCATCC			
	CCACCGTGGTCCTACGATCAGTCCT			
	ACCAATACCTGGGATCCATTGCCTC			
	TCCTTCTGTGCACCCAGCAACGCCC			
	ATTTCACCTGGACGTGCCAGCGGCA			
	TGACAACCCTCTCTGCAGAACTTTC			
	CAGTCGACTCTCAACGGCACCCGA			
	CCTGACAGCGTTCAGCGACCCGCG			
	CCAGTTCCCCGCGCTGCCCTCCATC			
	TCCGACCCCCGCATGCACTATCCAG			
	GCGCCTTCACCTACTCCCCGACGCC			
	GGTCACCTCGGGCATCGGCATCGG			
	CATGTCGGCCATGGGCTCGGCCAC			
	GCGCTACCACACCTACCTGCCGCCG			
	CCCTACCCCGGCTCGTCGCAAGCGC			
	AGGGAGGCCCGTTCCAAGCCAGCT			
	CGCCCTCCTACCACCTGTACTACGG			
	CGCCTCGGCCGGCTCCTACCAGTTC			
	TCCATGGTGGGCGGCGAGCGCTCG			
	CCGCCGCGCATCCTGCCGCCCTGCA			
	CCAACGCCTCCACCGGCTCCGCGCT			
	GCTCAACCCCAGCCTCCCGAACCA			
	GAGCGACGTGGTGGAGGCCGAGGG			
	CAGCCACAGCAACTCCCCCACCAA			
	CATGGCGCCCTCCGCGCGCCTGGA			
	GGAGGCCGTGTGGAGGCCCTAC			
SIX1	ATGTCGATGCTGCCGTCGTTTGGCT	83	Involved in	Zheng, W. et
	TTACGCAGGAGCAAGTGGCGTGCG		kidney, ear and	al. The role of
	TGTGCGAGGTTCTGCAGCAAGGCG		olfactory	Six1 in
	GAAACCTGGAGCGCCTGGGCAGGT		epithelium	mammalian
	TCCTGTGGTCACTGCCCGCCTGCGA		development	auditory
	CCACCTGCACAAGAACGAGAGCGT			system
	ACTCAAGGCCAAGGCGGTGGTCGC			development.
	CTTCCACCGCGGCAACTTCCGTGAG			Development
	CTCTACAAGATCCTGGAGAGCCAC			130, 3989-
	CAGTTCTCGCCTCACAACCACCCCA			4000 (2003).
	AACTGCAGCAACTGTGGCTGAAGG			Xu, P. et al.
	CGCATTACGTGGAGGCCGAGAAGC			Six1 is
	TGTGCGGCCGACCCCTGGGCGCCGT			required for
	GGGCAAATATCGGGTGCGCCGAAA			the early
	ATTTCCACTGCCGCGCACCATCTGG			organogenesis
	GACGGCGAGGAGACCAGCTACTGC			of mammalian
	TTCAAGGAGAAGTCGAGGGGTGTC			kidney.
	CTGCGGGAGTGGTACGCGCACAAT			Development
	CCCTACCCATCGCCGCGTGAGAAG			130, 3085-
	CGGGAGCTGGCCGAGGCCACCGGC			3094 (2003).
	CTCACCACCACCCAGGTCAGCAACT			Ikeda, K. et
	GGTTTAAGAACCGGAGGCAAAGAG			al. Six1 is
	ACCGGGCCGCGGAGGCCAAGGAAA			essential for
	GGGAGAACACCGAAAACAATAACT			early
	CCTCCTCCAACAAGCAGAACCAAC			neurogenesis
	TCTCTCCTCTGGAAGGGGGCAAGCC			in the
	GCTCATGTCCAGCTCAGAAGAGGA			development
	ATTCTCACCTCCCCAAAGTCCAGAC			of olfactory
	CAGAACTCGGTCCTTCTGCTGCAGG			epithelium.
	GCAATATGGGCCACGCCAGGAGCT			Dev. Biol.

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	CAAACTATTCTCTCCCGGGCTTAAC AGCCTCGCAGCCCAGTCACGGCCT GCAGACCCACCAGCATCAGCTCCA AGACTCTCTGCTCGGCCCCCTCACC TCCAGTCTGGTGGACTTGGGGTCC			311, 53-68 (2007).
SIX2	ATGTCCATGCTGCCCACCTTCGGCT TCACGCAGGAGCAAGTGGCGTGCG TGTGCGAGGTGCTGCAGCAGGGCG GCAACATCGAGCGGCTGGGCCGCT TCCTGTGGTCGCTGCCCGCCTGCGA GCACCTTCACAAGAATGAAAGCGT GCTCAAGGCCAAGGCCGTGGTGGC CTTCCACCGCGGCAACTTCCGCGAG CTCTACAAGATCCTGGAGAGCCAC CAGTTCTCGCCGCACAACCACGCCA AGCTGCAGCAGCTGTGGCTCAAGG CACACTACATCGAGGCGGAGAAGC TGCGCGGCCGACCCCTGGGCGCCG TGGGCAAATACCGCGTGCGCCGCA AATTCCCGCTGCCGCGCTCCATCTG GGACGGCGAGGAGACCAGCTACTG CTTCAAGGAAAAGAGTCGCAGCGT GCTGCGCGAGTGGTACGCGCACAA CCCCTACCCTTCACCCCGCGAGAAG CGTGAGCTGACGGAGGCCACGGGC CTCACCACCACACAGGTCAGCAAC TGGTTCAAGAACCGGCGGCAGCGC GACCGGGCGGCCGAGGCCAAGGAA AGGGAGAACAACGAGAACTCCAAT TCTAACAGCCACAACCCGCTGAAT GGCAGCGGCAAGTCGGTGTTAGGC AGCTCGGAGGATGAGAAGACTCCA TCGGGGACGCCAGACCACTCATCA TCCAGCCCCGCACTGCTCCTCAGCC CGCCGCCCCCTGGGCTGCCGTCCCT GCACAGCCTGGGCCACCCTCCGGG CCCCAGCGCAGTGCCAGTGCCGGT GCCAGGCGGAGGTGGAGCGGACCC ACTGCAACACCACCATGGCCTGCA GGACTCCATCCTCAACCCCATGTCA GCCAACCTCGTGGACCTGGGCTCC	84	Involved in kidney development	Kobayashi, A. et al. Six2 Defines and Regulates a Multipotent Self-Renewing Nephron Progenitor Population throughout Mammalian Kidney Development. Cell Stem Cell 3, 169-181 (2008).
SNAI2	ATGCCGCGCTCCTTCCTGGTCAAGA AGCATTTCAACGCCTCCAAAAAGC CAAACTACAGCGAACTGGACACAC ATACAGTGATTATTTCCCCGTATCT CTATGAGAGTTACTCCATGCCTGTC ATACCACAACCAGAGATCCTCAGC TCAGGAGCATACAGCCCCATCACT GTGTGGACTACCGCTGCTCCATTCC ACGCCCAGCTACCCAATGGCCTCTC TCCTCTTTCCGGATACTCCTCATCTT TGGGGCGAGTGAGTCCCCCTCCTCC ATCTGACACCTCCTCCAAGGACCAC AGTGGCTCAGAAAGCCCCATTAGT GATGAAGAGGAAAGACTACAGTCC AAGCTTTCAGACCCCCATGCCATTG AAGCTGAAAAGTTTCAGTGCAATTT ATGCAATAAGACCTATTCAACTTTT TCTGGGCTGGCCAAACATAAGCAG CTGCACTGCGATGCCCAGTCTAGAA AATCTTTCAGCTGTAAATACTGTGA CAAGGAATATGTGAGCCTGGGCGC CCTGAAGATGCATATTCGGACCCAC ACATTACCTTGTGTTTGCAAGATCT GCGGCAAGGCGTTTTCCAGACCCTG GTTGCTTCAAGGACACATTAGAACT CACACGGGGGAGAAGCCTTTTTCTT GCCCTCACTGCAACAGAGCATTTGC AGACAGGTCAAATCTGAGGGCTCA	85	Involved in neural crest development, epithelial-mesenchymal transition, and melanocyte stem cell development	Cobaleda, C., Perez-Caro, M., Vicente-Duelias, C. & Sanchez-Garcia, I. Function of the Zinc-Finger Transcription Factor SNAI2 in Cancer and Development. Annu. Rev. Genet. 41, 41-61 (2007).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	TCTGCAGACCCATTCTGATGTAAAG AAATACCAGTGCAAAAACTGCTCC AAAACCTTCTCCAGAATGTCTCTCC TGCACAAACATGAGGAATCTGGCT GCTGTGTAGCACAC			
SOX10	ATGGCGGAGGAGCAGGACCTATCG GAGGTGGAGCTGAGCCCCGTGGGC TCGGAGGAGCCCCGCTGCCTGTCCC CGGGGAGCGCGCCCTCGCTAGGGC CCGACGGCGGCGGCGGCGGATCGG GCCTGCGAGCCAGCCCGGGGCCAG GCGAGCTGGGCAAGGTCAAGAAGG AGCAGCAGGACGGCGAGGCGGACG ATGACAAGTTCCCCGTGTGCATCCG CGAGGCCGTCAGCCAGGTGCTCAG CGGCTACGACTGGACGCTGGTGCC CATGCCCGTGCGCGTCAACGGCGC CAGCAAAAGCAAGCCGCACGTCAA GCGGCCCATGAACGCCTTCATGGTG TGGGCTCAGGCAGCGCGCAGGAAG CTCGCGGACCAGTACCCGCACCTGC ACAACGCTGAGCTCAGCAAGACGC TGGGCAAGCTCTGGAGGCTGCTGA ACGAAAGTGACAAGCGCCCCTTCA TCGAGGAGGCTGAGCGGCTCCGTA TGCAGCACAAGAAAGACCACCCGG ACTACAAGTACCAGCCCAGGCGGC GGAAGAACGGGAAGGCCGCCCAGG GCGAGGCGGAGTGCCCCGGTGGGG AGGCCGAGCAAGGTGGGACCGCCG CCATCCAGGCCCACTACAAGAGCG CCCACTTGGACCACCGGCACCCAG GAGAGGGCTCCCCCATGTCAGATG GGAACCCCGAGCACCCCTCAGGCC AGAGCCATGGCCCACCCACCCCTC CAACCACCCCGAAGACAGAGCTGC AGTCGGGCAAGGCAGACCCGAAGC GGGACGGGCGCTCCATGGGGGAGG GCGGGAAGCCTCACATCGACTTCG GCAACGTGGACATTGGTGAGATCA GCCACGAGGTAATGTCCAACATGG AGACCTTTGATGTGGCTGAGTTGGA CCAGTACCTGCCGCCCAATGGGCA CCCAGGCCATGTGAGCAGCTACTC AGCAGCCGGCTATGGGCTGGGCAG TGCCCTGGCCGTGGCCAGTGGACA CTCCGCCTGGATCTCCAAGCCACCA GGCGTGGCTCTGCCCACGGTCTCAC CACCTGGTGTGGATGCCAAAGCCC AGGTGAAGACAGAGACCGCGGGGC CCCAGGGGCCCCCACACTACACCG ACCAGCCATCCACCTCACAGATCGC CTACACCTCCCTCAGCCTGCCCCAC TATGGCTCAGCCTTCCCCTCCATCT CCCGCCCCCAGTTTGACTACTCTGA CCATCAGCCCTCAGGACCCTATTAT GGCCACTCGGGCCAGGCCTCTGGC CTCTACTCGGCCTTCTCCTATATGG GGCCCTCGCAGCGGCCCCTCTACAC GGCCATCTCTGACCCCAGCCCCTCA GGGCCCCAGTCCCACAGCCCCACA CACTGGGAGCAGCCAGTATATACG ACACTGTCCCGGCCC	86	Involved in neural crest and neuronal development	Southard-Smith, E. M., Kos, L. & Pavan, W. J. SOX10 mutation disrupts neural crest development in Dom Hirschsprung mouse model. Nat. Genet. 18, 60-64 (1998). Britsch, S. et al. The transcription factor Sox10 is a key regulator of peripheral glial development. Genes Dev. 15, 66-78 (2001).
SOX2	ATGTACAACATGATGGAGACGGAG CTGAAGCCGCCGGGCCCGCAGCAA ACTTCGGGGGGCGGCGGCGGCAAC TCCACCGCGGCGGCGGCCGGCGGC AACCAGAAAAACAGCCCGGACCGC GTCAAGCGGCCCATGAATGCCTTCA TGGTGTGGTCCCGCGGGCAGCGGC GCAAGATGGCCCAGGAGAACCCCA AGATGCACAACTCGGAGATCAGCA	87	Involved in regulation of pluripotency and embryogenesis, and in neuronal development. Reprogramming factor for	Boyer, L. A., et al. Core Transcriptional Regulatory Circuitry in Human Embryonic Stem Cells. Cell 122,

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	AGCGCCTGGGCGCCGAGTGGAAAC TTTTGTCGGAGACGGAGAAGCGGC CGTTCATCGACGAGGCTAAGCGGC TGCGAGCGCTGCACATGAAGGAGC ACCCGGATTATAAATACCGGCCCC GGCGGAAAACCAAGACGCTCATGA AGAAGGATAAGTACACGCTGCCCG GCGGGCTGCTGGCCCCCGGCGGCA ATAGCATGGCGAGCGGGGTCGGGG TGGGCGCCGGCCTGGGCGCGGGCG TGAACCAGCGCATGGACAGTTACG CGCACATGAACGGCTGGAGCAACG GCAGCTACAGCATGATGCAGGACC AGCTGGGCTACCCGCAGCACCCGG GCCTCAATGCGCACGGCGCAGCGC AGATGCAGCCCATGCACCGCTACG ACGTGAGCGCCCTGCAGTACAACT CCATGACCAGCTCGCAGACCTACAT GAACGGCTCGCCCACCTACAGCAT GTCCTACTCGCAGCAGGGCACCCCT GGCATGGCTCTTGGCTCCATGGGTT CGGTGGTCAAGTCCGAGGCCAGCT CCAGCCCCCCTGTGGTTACCTCTTC CTCCCACTCCAGGGCGCCCTGCCAG GCCGGGGACCTCCGGGACATGATC AGCATGTATCTCCCCGGCGCCGAG GTGCCGGAACCCGCCGCCCCCAGC AGACTTCACATGTCCCAGCACTACC AGAGCGGCCCGGTGCCCGGCACGG CCATTAACGGCACACTGCCCCTCTC ACACATG		induction of pluripotency.	947-956 (2005). Graham, V. et al. SOX2 Functions to Maintain Neural Progenitor Identity. Neuron 39, 749-765 (2003). Wang, Z., Oron, E., Nelson, B., Razis, S. & Ivanova, N. Distinct Lineage Specification Roles for NANOG, OCT4, and SOX2 in Human Embryonic Stem Cells. Cell Stem Cell 10, 440-454 (2012). Takahashi, K. & Yamanaka, S. Induction of pluripotent stem cells from mouse embryonic and adult fibroblast cultures by defined factors. Cell 126, 663-76 (2006). Takahashi, K. et al. Induction of pluripotent stem cells from adult human fibroblasts by defined factors. Cell 131, 861-72 (2007). Yu, J. et al. Induced Pluripotent Stem Cell Lines Derived from Human Somatic Cells. Science (80-.). 318, 1917-1920 (2007).
SOX3	ATGCGACCTGTTCGAGAGAACTCAT CAGGTGCGAGAAGCCCGCGGGTTC CTGCTGATTTGGCGCGGAGCATTTT GATAAGCCTACCCTTCCCGCCGGAC TCGCTGGCCCACAGGCCCCCAAGCT CCGCTCCGACGGAGTCCCAGGGCC	88	Involved in neuronal and pituitary development	Rizzoti, K. et al. SOX3 is required during the formation of the

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	TTTTCACCGTGGCCGCTCCAGCCCC GGGAGCGCCTTCTCCTCCCGCCACG CTGGCGCACCTTCTTCCCGCCCCGG CAATGTACAGCCTTCTGGAGACTGA ACTCAAGAACCCCGTAGGGACACC CACACAAGCGGCGGGCACCGGCGG CCCCGCAGCCCCGGGAGGCGCAGG CAAGAGTAGTGCGAACGCAGCCGG CGGCGCGAACTCGGGCGGCGGCAG CAGCGGTGGTGCGAGCGGAGGTGG CGGGGGTACAGACCAGGACCGTGT GAAACGGCCCATGAACGCCTTCAT GGTATGGTCCCGCGGGCAGCGGCG CAAAATGGCCCTGGAGAACCCCAA GATGCACAATTCTGAGATCAGCAA GCGCTTGGGCGCCGACTGGAAACT GCTGACCGACGCCGAGAAGCGACC ATTCATCGACGAGGCCAAGCGACT TCGCGCCGTGCACATGAAGGAGTA TCCGGACTACAAGTACCGACCGCG CCGCAAGACCAAGACGCTGCTCAA GAAAGATAAGTACTCCCTGCCCAG CGGCCTCCTGCCTCCCGGTGCCGCG GCCGCCGCCGCCGCTGCCGCGGCC GCAGCCGCTGCCGCCAGCAGTCCG GTGGGCGTGGGCCAGCGCCTGGAC ACGTACACGCACGTGAACGGCTGG GCCAACGGCGCGTACTCGCTGGTG CAGGAGCAGCTGGGCTACGCGCAG CCCCCGAGCATGAGCAGCCCGCCG CCGCCGCCCGCGCTGCCGCCGATG CACCGCTACGACATGGCCGGCCTG CAGTACAGCCCAATGATGCCGCCC GGCGCTCAGAGCTACATGAACGTC GCTGCCGCGGCCGCCGCCGCCTCG GGCTACGGGGGCATGGCGCCCTCA GCCACAGCAGCCGCGGCCGCCGCC TACGGGCAGCAGCCCGCCACCGCC GCGGCCGCAGCTGCGGCCGCAGCC GCCATGAGCCTGGGCCCCATGGGC TCGGTAGTGAAGTCTGAGCCCAGCT CGCCGCCGCCCGCCATCGCATCGC ACTCTCAGCGCGCGTGCCTCGGCGA CCTGCGCGACATGATCAGCATGTAC CTGCCACCCGGCGGGGACGCGGCC GACGCCGCCTCTCCGCTGCCCGGCG GTCGCCTGCACGGCGTGCACCAGC ACTACCAGGGCGCCGGGACTGCAG TCAACGGAACGGTGCCGCTGACCC ACATC			hypothalamo-pituitary axis. Nat. Genet. 36, 247-255 (2004).
SPI1	ATGTTACAGGCGTGCAAAATGGAA GGGTTTCCCCTCGTCCCCCCTCAGC CATCAGAAGACCTGGTGCCCTATG ACACGGATCTATACCAACGCCAAA CGCACGAGTATTACCCCTATCTCAG CAGTGATGGGGAGAGCCATAGCGA CCATTACTGGGACTTCCACCCCCAC CACGTGCACAGCGAGTTCGAGAGC TTCGCCGAGAACAACTTCACGGAG CTCCAGAGCGTGCAGCCCCCGCAG CTGCAGCAGCTCTACCGCCACATGG AGCTGGAGCAGATGCACGTCCTCG ATACCCCCATGGTGCCACCCCATCC CAGTCTTGGCCACCAGGTCTCCTAC CTGCCCCGGATGTGCCTCCAGTACC CATCCCTGTCCCCAGCCCAGCCCAG CTCAGATGAGGAGGAGGGCGAGCG GCAGAGCCCCCCACTGGAGGTGTC TGACGGCGAGGCGGATGGCCTGGA GCCCGGGCCTGGGCTCCTGCCTGGG GAGACAGGCAGCAAGAAGAAGATC CGCCTGTACCAGTTCCTGTTGGACC TGCTCCGCAGCGGCGACATGAAGG	89	Involved in haematopoetic cell development	Scott, E. W. et al. Requirement of transcription factor PU.1 in the development of multiple hematopoietic lineages. Science 265, 1573-1577 (1994). Rosenbauer, F. & Tenen, D. G. Transcription factors in myeloid development: balancing differentiation

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	ACAGCATCTGGTGGGTGGACAAGG ACAAGGGCACCTTCCAGTTCTCGTC CAAGCACAAGGAGGCGCTGGCGCA CCGCTGGGGCATCCAGAAGGGCAA CCGCAAGAAGATGACCTACCAGAA GATGGCGCGCGCGCTGCGCAACTA CGGCAAGACGGGCGAGGTCAAGAA GGTGAAGAAGAAGCTCACCTACCA GTTCAGCGGCGAAGTGCTGGGCCG CGGGGGCCTGGCCGAGCGGCGCCA CCCGCCCCAC			with transformation. Nat. Rev. Immunol. 7, 105-117 (2007).
SPIB	ATGCTCGCCCTGGAGGCTGCACAG CTCGACGGGCCACACTTCAGCTGTC TGTACCCAGATGGCGTCTTCTATGA CCTGGACAGCTGCAAGCATTCCAG CTACCCTGATTCAGAGGGGGCTCCT GACTCCCTGTGGGACTGGACTGTGG CCCCACCTGTCCCAGCCACCCCCTA TGAAGCCTTCGACCCGGCAGCAGC CGCTTTTAGCCACCCCCAGGCTGCC CAGCTCTGCTACGAACCCCCCACCT ACAGCCCTGCAGGGAACCTCGAAC TGGCCCCCAGCCTGGAGGCCCCGG GGCCTGGCCTCCCCGCATACCCCAC GGAGAACTTCGCTAGCCAGACCCT GGTTCCCCCGGCATATGCCCCGTAC CCCAGCCCTGTGCTATCAGAGGAG GAAGACTTACCGTTGGACAGCCCT GCCCTGGAGGTCTCGGACAGCGAG TCGGATGAGGCCCTCGTGGCTGGCC CCGAGGGGAAGGGATCCGAGGCAG GGACTCGCAAGAAGCTGCGCCTGT ACCAGTTCCTGCTGGGGCTACTGAC GCGCGGGGACATGCGTGAGTGCGT GTGGTGGGTGGAGCCAGGCGCCGG CGTCTTCCAGTTCTCCTCCAAGCAC AAGGAACTCCTGGCGCGCCGCTGG GGCCAGCAGAAGGGGAACCGCAAG CGCATGACCTACCAGAAGCTGGCG CGCGCCCTCCGAAACTACGCCAAG ACCGGCGAGATCCGCAAGGTCAAG CGCAAGCTCACCTACCAGTTCGACA GCGCGCTGCTGCCTGCAGTCCGCCG GGCCTTG	90	Involved in differentiation of lymphoid cells	Maroulakou, I. G. & Bowe, D. B. Expression and function of Ets transcription factors in mammalian development: a regulatory network. Oncogene 19, 6432-6442 (2000).
SPIC	ATGACGTGTGTTGAACAAGACAAG CTGGGTCAAGCATTTGAAGATGCTT TTGAGGTTCTGAGGCAACATTCAAC TGGAGATCTTCAGTACTCGCCAGAT TACAGAAATTACCTGGCTTTAATCA ACCATCGTCCTCATGTCAAAGGAA ATTCCAGCTGCTATGGAGTGTTGCC TACAGAGGAGCCTGTCTATAATTGG AGAACGGTAATTAACAGTGCTGCG GACTTCTATTTTGAAGGAAATATTC ATCAATCTCTGCAGAACATAACTGA AAACCAGCTGGTACAACCCACTCTT CTCCAGCAAAAGGGGGGAAAAGGC AGGAAGAAGCTCCGACTGTTTGAA TACCTTCACGAATCCCTGTATAATC CGGAGATGGCATCTTGTATTCAGTG GGTAGATAAAACCAAAGGCATCTT TCAGTTTGTATCAAAAAACAAAGA AAAACTTGCCGAGCTTTGGGGGAA AAGAAAAGGCAACAGGAAGACCAT GACTTACCAGAAAATGGCCAGGGC ACTCAGAAATTACGGAAGAAGTGG GGAAATTACCAAAATCCGGAGGAA GCTGACTTACCAGTTCAGTGAGGCC ATTCTCCAAAGACTCTCTCCATCCT ATTTCCTGGGGAAAGAGATCTTCTA TTCACAGTGTGTTCAACCTGATCAA GAATATCTCAGTTTAAATAACTGGA	91	Involved in macrophage development	Kohyama, M. et al. Role for Spi-C in the development of red pulp macrophages and splenic iron homeostasis. Nature 457, 318-321 (2009).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	ATGCAAATTATAATTATACATATGC CAATTACCATGAGCTAAATCACCAT GATTGC			
SRY	ATGCAATCATATGCTTCTGCTATGT TAAGCGTATTCAACAGCGATGATTA CAGTCCAGCTGTGCAAGAGAATAT TCCCGCTCTCCGGAGAAGCTCTTCC TTCCTTTGCACTGAAAGCTGTAACT CTAAGTATCAGTGTGAAACGGGAG AAAACAGTAAAGGCAACGTCCAGG ATAGAGTGAAGCGACCCATGAACG CATTCATCGTGTGGTCTCGCGATCA GAGGCGCAAGATGGCTCTAGAGAA TCCCAGAATGCGAAACTCAGAGAT CAGCAAGCAGCTGGGATACCAGTG GAAAATGCTTACTGAAGCCGAAAA ATGGCCATTCTTCCAGGAGGCACA GAAATTACAGGCCATGCACAGAGA GAAATACCCGAATTATAAGTATCG ACCTCGTCGGAAGGCGAAGATGCT GCCGAAGAATTGCAGTTTGCTTCCC GCAGATCCCGCTTCGGTACTCTGCA GCGAAGTGCAACTGGACAACAGGT TGTACAGGGATGACTGTACGAAAG CCACACACTCAAGAATGGAGCACC AGCTAGGCCACTTACCGCCCATCAA CGCAGCCAGCTCACCGCAGCAACG GGACCGCTACAGCCACTGGACAAA GCTG	92	Involved in sex determination and spermatogenesis	Polanco, J. C. & Koopman, P. Sry and the hesitant beginnings of male development. Dev. Biol. 302,13-24 (2007). Koopman, P. et al. Male development of chromosomally female mice transgenic for Sry. Nature 351,117-121 (1991).
TBX5	ATGGCCGACGCAGACGAGGGCTTT GGCCTGGCGCACACGCCTCTGGAG CCTGACGCAAAAGACCTGCCCTGC GATTCGAAACCCGAGAGCGCGCTC GGGGCCCCCAGCAAGTCCCCGTCG TCCCCGCAGGCCGCCTTCACCCAGC AGGGCATGGAGGGAATCAAAGTGT TTCTCCATGAAAGAGAACTGTGGCT AAAATTCCACGAAGTGGGCACGGA AATGATCATAACCAAGGCTGGAAG GCGGATGTTTCCCAGTTACAAAGTG AAGGTGACGGGCCTTAATCCCAAA ACGAAGTACATTCTTCTCATGGACA TTGTACCTGCCGACGATCACAGATA CAAATTCGCAGATAATAAATGGTCT GTGACGGGCAAAGCTGAGCCCGCC ATGCCTGGCCGCCTGTACGTGCACC CAGACTCCCCCGCCACCGGGGCGC ATTGGATGAGGCAGCTCGTCTCCTT CCAGAAACTCAAGCTCACCAACAA CCACCTGGACCCATTTGGGCATATT ATTCTAAATTCCATGCACAAATACC AGCCTAGATTACACATCGTGAAAG CGGATGAAAATAATGGATTTGGCT CAAAAAATACAGCGTTCTGCACTC ACGTCTTTCCTGAGACTGCGTTTAT AGCAGTGACTTCCTACCAGAACCA CAAGATCACGCAATTAAAGATTGA GAATAATCCCTTTGCCAAAGGATTT CGGGGCAGTGATGACATGGAGCTG CACAGAATGTCAAGAATGCAAAGT AAAGAATATCCCGTGGTCCCCAGG AGCACCGTGAGGCAAAAAGTGGCC TCCAACCACAGTCCTTTCAGCAGCG AGTCTCGAGCTCTCTCCACCTCATC CAATTTGGGGTCCCAATACCAGTGT GAGAATGGTGTTTCCGGCCCCTCCC AGGACCTCCTGCCTCCACCCAACCC ATACCCACTGCCCCAGGAGCATAG CCAAATTTACCATTGTACCAAGAGG AAAGAGGAAGAATGTTCCACCACA GACCATCCCTATAAGAAGCCCTAC ATGGAGACATCACCCAGTGAAGAA	93	Involved in cardiac development	Bruneau, B. G. et al. A Murine Model of Holt-Oram Syndrome Defines Roles of the T-Box Transcription Factor Tbx5 in Cardiogenesis and Disease. Cell 106, 709-721 (2001).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	GATTCCTTCTACCGCTCTAGCTATC CACAGCAGCAGGGCCTGGGTGCCT CCTACAGGACAGAGTCGGCACAGC GGCAAGCTTGCATGTATGCCAGCTC TGCGCCCCCCAGCGAGCCTGTGCCC AGCCTAGAGGACATCAGCTGCAAC ACGTGGCCAAGCATGCCTTCCTACA GCAGCTGCACCGTCACCACCGTGC AGCCCATGGACAGGCTACCCTACC AGCACTTCTCCGCTCACTTCACCTC GGGGCCCCTGGTCCCTCGGCTGGCT GGCATGGCCAACCATGGCTCCCCA CAGCTGGGAGAGGGAATGTTCCAG CACCAGACCTCCGTGGCCCACCAG CCTGTGGTCAGGCAGTGTGGGCCTC AGACTGGCCTGCAGTCCCCTGGCAC CCTTCAGCCCCCTGAGTTCCTCTAC TCTCATGGCGTGCCAAGGACTCTAT CCCCTCATCAGTACCACTCTGTGCA CGGAGTTGGCATGGTGCCAGAGTG GAGCGACAATAGCTTG			
TFAP2C	ATGTTGTGGAAAATAACCGATAAT GTCAAGTACGAAGAGGACTGCGAG GATCGCCACGACGGGAGCAGCAAT GGGAATCCGCGGGTCCCCCACCTCT CCTCCGCCGGGCAGCACCTCTACAG CCCCGCGCCACCCCTCTCCCACACT GGAGTCGCCGAATATCAGCCGCCA CCCTACTTTCCCCCTCCCTACCAGC AGCTGGCCTACTCCCAGTCGGCCGA CCCCTACTCGCATCTGGGGGAAGC GTACGCCGCCGCCATCAACCCCCTG CACCAGCCGGCGCCCACAGGCAGC CAGCAGCAGGCCTGGCCCGGCCGC CAGAGCCAGGAGGGAGCGGGGCTG CCCTCGCACCACGGGCGCCCGGCC GGCCTACTGCCCCACCTCTCCGGGC TGGAGGCGGGCGCGGTGAGCGCCC GCAGGGATGCCTACCGCCGCTCCG ACCTGCTGCTGCCCCACGCACACGC CCTGGATGCCGCGGGCCTGGCCGA GAACCTGGGGCTCCACGACATGCC TCACCAGATGGACGAGGTGCAGAA TGTCGACGACCAGCACCTGTTGCTG CACGATCAGACAGTCATTCGCAAA GGTCCCATTTCCATGACCAAGAACC CTCTGAACCTCCCCTGTCAGAAGGA GCTGGTGGGGGCCGTAATGAACCC CACTGAGGTCTTCTGCTCAGTCCCT GGAAGATTGTCGCTCCTCAGCTCTA CGTCTAAATACAAAGTGACAGTGG CTGAAGTACAGAGGCGACTGTCCC CACCTGAATGCTTAAATGCCTCGTT ACTGGGAGGTGTTCTCAGAAGAGC CAAATCGAAAAATGGAGGCCGGTC CTTGCGGGAGAAGTTGGACAAGAT TGGGTTGAATCTTCCGGCCGGGAG GCGGAAAGCCGCTCATGTGACTCTC CTGACATCCTTAGTAGAAGGTGAA GCTGTTCATTTGGCTAGGGACTTTG CCTATGTCTGTGAAGCCGAATTTCC TAGTAAACCAGTGGCAGAATATTT AACCAGACCTCATCTTGGAGGACG AAATGAGATGGCAGCTAGGAAGAA CATGCTATTGGCGGCCCAGCAACTG TGTAAAGAATTCACAGAACTTCTCA GCCAAGACCGGACACCCCATGGGA CCAGCAGGCTCGCCCCAGTCTTGGA GACGAACATACAGAACTGCTTGTCT CATTTCAGCCTGATTACCCACGGGT TTGGCAGCCAGGCCATCTGTGCCGC GGTGTCTGCCCTGCAGAACTACATC AAAGAAGCCCTGATTGTCATAGAC	94	Involved in trophectoderm development	Cao, Z. et al. Transcription factor AP-2γ induces early Cdx2 expression and represses HIPPO signaling to specify the trophectoderm lineage. Development 142, 1606-15 (2015).

TABLE 1-continued

GENE	SEQUENCE	SEQ ID NO:	ROLE	REFERENCES
	AAATCCTACATGAACCCTGGAGAC CAGAGTCCAGCTGATTCTAACAAA ACCCTGGAGAAAATGGAGAAACAC AGGAAA			

TABLE 2

Sample_ID	Description	Media Condition	Estimated Number of Cells	Mean Reads per Cell	Median Genes per Cell
UP_TF_1	HighMOI, (−) TRA-1-60 MACS sorted	Pluripotent stem cell medium	3,640	45,983	3,317
UP_TF_2	HighMOI, Unsorted	Pluripotent stem cell medium	3,505	49,750	3,843
UP_TF_3	HighMOI, Unsorted	Pluripotent stem cell medium	4,223	45,403	3,972
UP_TF_4	HighMOI, (−) TRA-1-60 MACS sorted	Pluripotent stem cell medium	3,461	56,290	4,475
UP_TF_5	LowMOI, (−) TRA-1-60 MACS sorted	Pluripotent stem cell medium	3,748	46,895	4,165
UP_TF_8	Library, Endothelial	Endothelial growth medium	3,563	41,056	3,698
UP_TF_10	Library, Multilineage	Multilineage differentiation medium	2,129	70,519	5,605
UP_TF_11	Library, Endothelial	Endothelial growth medium	6,574	23,250	3,105
UP_TF_12	Library, Multilineage	Multilineage differentiation medium	4,678	30,340	3,882
UP_TF_13	KLF Family, cMYC Mutants	Pluripotent stem cell medium	5,590	35,913	3,620

Sample_ID	Number of Reads	Valid Barcodes	Reads Mapped Confidently to Exonic Regions	Sequencing Saturation	Fraction Reads in Cells	Median UMI Counts per Cell
UP_TF_1	167,381,505	97.90%	65.60%	17.00%	55.40%	11,785
UP_TF_2	174,376,238	98.40%	70.30%	20.80%	63.90%	15,985
UP_TF_3	191,740,141	98.10%	63.10%	18.90%	77.20%	16,090
UP_TF_4	194,819,799	98.20%	66.80%	25.00%	78.60%	19,132
UP_TF_5	175,765,276	98.10%	65.70%	17.70%	76.90%	17,349
UP_TF_8	146,283,407	98.20%	65.20%	16.60%	80.90%	15,049
UP_TF_10	150,135,344	98.20%	68.60%	20.20%	83.00%	27,785
UP_TF_11	152,847,871	98.20%	69.40%	11.20%	86.80%	10,681
UP_TF_12	141,934,669	98.20%	70.00%	11.00%	88.10%	14,526
UP_TF_13	200,756,922	98.00%	66.20%	15.50%	78.70%	14,286

TABLE 3

Genotype	Number of Genotyped Cells: Stem cell media	Endothelial media	Multilineage media
ASCL1	186	78	21
ASCL3	471	150	89
ASCL4	286	90	75

TABLE 3-continued

Genotype	Number of Genotyped Cells: Stem cell media	Endothelial media	Multilineage media
ASCL5	140	64	51
ATF7	97	49	45
CDX2	267	192	103

TABLE 3-continued

Genotype	Number of Genotyped Cells: Stem cell media	Endothelial media	Multilineage media
CRX	292	107	54
ERG	62	30	7
ESRRG	169	98	64
ETV2	60	22	21
FLI1	55	27	18
FOXA1	53	27	14
FOXA2	89	46	37
FOXA3	255	90	61
FOXP1	413	112	94
GATA1	288	111	72
GATA2	62	81	60
GATA4	71	101	58
GATA6	44	44	35
GLI1	27	11	16
HAND2	310	113	81
HNF1A	88	45	39
HNF1B	53	30	41
HOXA1	166	67	57
HOXA10	344	111	66
HOXA11	237	82	47
HOXB6	166	95	44
KLF4	298	259	145
LHX3	175	76	45
LMX1A	458	155	82
mCherry	1689	689	495
MEF2C	87	49	51
MESP1	227	70	55
MITF	73	63	45

TABLE 3-continued

Genotype	Number of Genotyped Cells: Stem cell media	Endothelial media	Multilineage media
MYC	291	113	36
MYCL	356	112	75
MYCN	50	33	12
MYODI	197	68	40
MYOG	284	122	81
NEUROD1	83	46	10
NEUROG1	154	103	23
NEUROG3	158	138	41
NRL	249	75	49
ONECUT1	159	109	58
OTX2	293	95	47
PAX7	86	56	28
POU1F1	126	61	50
POU5F1	78	30	24
RUNX1	139	47	43
SIX1	260	119	66
SIX2	295	103	84
SNAI2	485	96	50
SOX10	83	54	30
SOX2	137	53	27
SOX3	137	56	31
SPI1	264	142	67
SPIB	199	70	47
SPIC	147	80	35
SRY	166	61	65
TBX5	149	112	35
TFAP2C	90	58	34

TABLE 4

	Enrichment p-value for each genotype in clusters using Fisher's exact test: C6	C2	C5	C3	C1	C7	C4
CDX2	0.999581	0.502321	1	1	1	3.42E−58	1
KLF4	0.688329	1.12E−27	1	1	1	1	3.82E−21
FOXA1	0.848222	1	1	8.00E−08	1	1	1
FOXA2	0.559116	1	1	2.56E−15	1	0.788874	1
GATA2	0.002284	1	1.57E−10	1	1	0.91906	0.832613
GATA4	0.009787	0.781098	1.13E−09	1	0.553072	1	0.822422
GATA6	0.03266	0.23167	0.000147	1	1	1	1
SOX10	0.017774	0.043271	1	1	1	0.12661	1
NEUROD1	0.280233	1	1	1	1	0.34423	1
ETV2	0.016254	1	1	1	1	0.054486	1
SPIB	9.93E−07	1	0.29024	0.190193	1	1	1
SOX3	1.53E−05	1	1	1	1	1	0.063768
NEUROG3	6.23E−06	1	1	0.502271	1	0.50894	1
TBX5	1.71E−07	1	1	0.449045	1	1	1
MYOD1	3.73E−07	1	1	1	1	1	0.115324
MYC	9.91E−05	0.611641	1	1	0.394338	0.779857	1
ESRRG	5.02E−12	0.233929	1	1	0.58849	1	1
TFAP2C	6.90E−05	1	0.541387	1	1	1	0.638171
GLI1	0.017877	1	1	1	1	1	0.380973
NEUROG1	0.00162	1	1	1	1	0.620425	1
ASCL5	9.82E−08	0.737393	1	1	1	0.353463	1
FOXA3	3.08E−15	1	1	0.644816	1	1	1
ATF7	2.03E−09	1	1	0.534822	1	1	1
HOXA10	2.36E−09	1	0.4436	0.673452	0.599648	1	0.85978
SOX2	4.01E−06	1	0.461875	1	1	1	1
ONECUT1	2.98E−11	1	1	0.626421	1	1	0.822422
RUNX1	3.65E−07	1	1	1	0.450277	1	0.364314
SIX2	8.69E−16	0.888323	1	1	1	0.677188	0.710842
HOXA11	4.51E−09	1	1	1	1	0.860947	0.406197
SPIC	1.28E−06	1	1	1	1	1	0.648778
MYCL	2.52E−22	1	1	1	1	1	1
FOXP1	9.41E−17	0.702249	1	0.795614	0.374912	0.980162	1
SNAI2	4.89E−09	1	0.681398	1	1	0.616212	1
HNF1A	7.52E−11	1	1	1	1	1	1
LMX1A	2.74E−19	1	0.845485	1	1	1	0.912434

TABLE 4-continued

	Enrichment p-value for each genotype in clusters using Fisher's exact test						
	C6	C2	C5	C3	C1	C7	C4
ERG	0.164469	1	1	1	1	1	1
HAND2	7.41E−17	1	1	1	1	0.653393	1
MITF	2.07E−10	1	0.643049	1	1	1	1
PAX7	1.57E−05	1	1	1	1	0.692249	1
SIX1	1.58E−14	0.822135	1	1	0.599648	1	1
OTX2	3.17E−08	0.708559	1	1	1	1	0.754072
SPI1	5.65E−12	0.826686	1	1	1	0.767724	1
GATA1	2.36E−13	0.847734	1	1	1	1	0.629688
MYOG	7.41E−17	1	1	0.746058	1	0.966092	1
HNF1B	1.21E−06	1	1	1	0.434855	1	1
POU1F1	2.52E−14	1	1	1	1	1	1
FLI1	0.000193	1	1	1	1	1	1
HOXA1	3.20E−15	1	1	1	1	1	1
SRY	1.01E−17	1	1	1	1	1	1
CRX	4.15E−13	1	1	1	1	0.896121	1
ASCL1	0.000199	1	1	1	1	1	1
NRL	9.14E−09	1	1	1	0.494018	0.872071	1
LHX3	1.65E−11	1	1	1	1	1	1
MESP1	2.47E−11	1	1	1	0.534212	1	0.805949
HOXB6	3.05E−08	1	1	1	1	1	1
ASCL4	3.41E−17	1	1	1	0.646165	0.956545	1
MYCN	0.00932	1	1	1	1	1	1
MEF2C	3.40E−10	1	1	1	1	1	0.78156
POU5F1	3.21E−06	1	1	1	1	1	1
ASCL3	3.49E−19	1	1	1	0.707836	1	1
mCherry	1.64E−91	0.99443	0.961129	0.996934	0.263601	0.994961	0.947099

TABLE 5

Module	Description	n_genes
GM1	Cytoskeleton and polarity	444
GM2	Ion transport	973
GM3	Chromatin accessibility	1568
GM4	Signaling pathways	873
GM5	Neuron differentiation	444
GM6	Notch pathway	859

TABLE 5-continued

Module	Description	n_genes
GM7	Embryonic development	509
GM8	Mitochondrial metabolism and translation	2242
GM9	Ribosome biogenesis	190
GM10	Growth factor response	492
GM11	Pluripotent state	234

TABLE 6

Gene	Forward Primer (5'→3')	SEQ ID NO:	Reverse Primer (5'→3')	SEQ ID NO:
CDH5	AGACCACGCCTCTGTCATGTACCAAATC	95	CACGATCTCATACCTGGCCTGCTTC	113
PECAM1	GGTCAGCAGCATCGTGGTCAACATAAC	96	TGGAGCAGGACAGGTTCAGTCTTTCA	114
VWF	TCTCCGTGGTCCTGAAGCAGACATA	97	AGGTTGCTGCTGGTGAGGTCATT	115
KDR	AGCCATGTGGTCTCTCTGGTTGTGTATG	98	GTTTGAGTGGTGCCGTACTGGTAGGA	116
NANOG	TTTGTGGGCCTGAAGAAAACT	99	AGGGCTGTCCTGAATAAGCAG	117
POU5F1	CTTGAATCCCGAATGGAAAGGG	100	GTGTATATCCCAGGGTGATCCTC	118
SOX2	TACAGCATGTCCTACTCGCAG	101	GAGGAAGAGGTAACCACAGGG	119
DNMT3B	GAGTCCATTGCTGTTGGAACCG	102	ATGTCCCTCTTGTCGCCAACCT	120
SALL2	CAGCGGAAACCCCAACAGTTA	103	GAGGGTCAGTAGAACATGCGT	121
DPPA4	GACCTCCACAGAGAAGTCGAG	104	TGCCTTTTTCTTAGGGCAGAG	122
VIM	AGTCCACTGAGTACCGGAGAC	105	CATTTCACGCATCTGGCGTTC	123
CDH1	CGAGAGCTACACGTTCACGG	106	GGGTGTCGAGGGAAAAATAGG	124
CDH2	AGCCAACCTTAACTGAGGAGT	107	GGCAAGTTGATTGGAGGGATG	125

TABLE 6-continued

Gene	Forward Primer (5'→3')	SEQ ID NO:	Reverse Primer (5'→3')	SEQ ID NO:
EPCAM	TGATCCTGACTGCGATGAGAG	108	CTTGTCTGTTCTTCTGACCCC	126
LAMC1	GGCAACGTGGCCTTTTCTAC	109	AGTGGCAGTTACCCATTCCTG	127
SPP1	GAAGTTTCGCAGACCTGACAT	110	GTATGCACCATTCAACTCCTCG	128
THY1	ATCGCTCTCCTGCTAACAGTC	111	CTCGTACTGGATGGGTGAACT	129
TPM2	CTGAGACCCGAGCAGAGTTTG	112	TGAATCTCGACGTTCTCCTCC	130

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cggaccgtgc cagtttggct cgatgcccca aaactaacca ccgaggtccc attcagctgt 1080

ggcagttcct cctggagctg ctccacgacg gggcgcgtag cagctgcatc cgttggactg 1140

gcaacagccg cgagttccag ctgtgcgacc ccaaagaggt ggctcggctg tggggcgagc 1200

gcaagagaaa gccgggcatg aattacgaga agctgagccg gggccttcgc tactactatc 1260

gccgcgacat cgtgcgcaag agcgggggggc gaaagtacac gtaccgcttc gggggccgcg 1320

tgcccagcct agcctatccg gactgtgcgg gaggcggacg gggagcagag acacaataaa 1380

aattcccggt caaacctcaa aaaaaaaaaa aaa 1413

<210> SEQ ID NO 2
<211> LENGTH: 1275
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 2

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cagcccccgg cgggatcagg tagcggtagc cgccgctccg ggctctgctc gccctcctac 180

gttgcggtca cacccttctc ccttcgggga gacaacgacg gcggtggcgg gagcttctcc 240

acggccgacc agctggagat ggtgaccgag ctgctgggag gagacatggt gaaccagagt 300

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tggagcggct tctcggccgc cgccaagctc gtctcagaga agctggcctc ctaccaggct 420

gcgcgcaaag acagcggcag cccgaacccc gcccgcggcc acagcgtctg ctccacctcc 480

agcttgtacc tgcaggatct gagcgccgcc gcctcagagt gcatcgaccc ctcggtggtc 540

ttcccctacc ctctcaacga cagcagctcg cccaagtcct gcgcctcgca agactccagc 600

gccttctctc cgtcctcgga ttctctgctc tcctcgacgg agtcctcccc gcagggcagc 660

cccgagcccc tggtgctcca tgaggagaca ccgcccacca ccagcagcga ctctgaggag 720

gaacaagaag atgaggaaga aatcgatgtt gtttctgtgg aaaagaggca ggctcctggc 780

aaaaggtcag agtctggatc accttctgct ggaggccaca gcaaacctcc tcacagccca 840

ctggtcctca agaggtgcca cgtctccaca catcagcaca actacgcagc gcctccctcc 900

actcggaagg actatcctgc tgccaagagg gtcaagttgg acagtgtcag agtcctgaga 960

cagatcagca acaaccgaaa atgcaccagc cccaggtcct cggacaccga ggagaatgtc 1020

aagaggcgaa cacacaacgt cttggagcgc cagaggagga acgagctaaa acggagcttt 1080

tttgccctgc gtgaccagat cccggagttg gaaaacaatg aaaaggcccc caaggtagtt 1140

atccttaaaa aagccacagc atacatcctg tccgtccaag cagaggagca aaagctcatt 1200

tctgaagagg acttgttgcg gaaacgacga gaacagttga aacacaaact tgaacagcta 1260

cggaactctt gtgcg 1275

<210> SEQ ID NO 3
<211> LENGTH: 1287

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 3

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ccgtatttct actgcgacga ggaggagaac ttctaccagc agcagcagca gagcgagctg 120

cagcccccgg cgcccagcga ggatatctgg aagaaattcg agctgctgcc caccccgccc 180

ctgtccccta gccgccgctc cgggctctgc tcgccctcct acgttgcggt cacacccttc 240

tcccttcggg gagacaacga cggcggtggc gggagcttct ccacggccga ccagctggag 300

atggtgaccg agctgctggg aggagacatg gtgaaccaga gtttcatctg cgacccggac 360

gacgagacct tcatcaaaaa catcggatca ggtagcggtc tcgtctcaga gaagctggcc 420

tcctaccagg ctgcgcgcaa agacagcggc agcccgaacc ccgcccgcgg ccacagcgtc 480

tgctccacct ccagcttgta cctgcaggat ctgagcgccg ccgcctcaga gtgcatcgac 540

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ccgcagggca gccccgagcc cctggtgctc catgaggaga caccgcccac caccagcagc 720

gactctgagg aggaacaaga agatgaggaa gaaatcgatg ttgtttctgt ggaaaagagg 780

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gcgcctccct ccactcggaa ggactatcct gctgccaaga gggtcaagtt ggacagtgtc 960

agagtcctga gacagatcag caacaaccga aaatgcacca gccccaggtc ctcggacacc 1020

gaggagaatg tcaagaggcg aacacacaac gtcttggagc gccagaggag gaacgagcta 1080

aaacggagct tttttgccct gcgtgaccag atcccggagt tggaaaacaa tgaaaaggcc 1140

cccaaggtag ttatccttaa aaaagccaca gcatacatcc tgtccgtcca agcagaggag 1200

caaaagctca tttctgaaga ggacttgttg cggaaacgac gagaacagtt gaaacacaaa 1260

cttgaacagc tacggaactc ttgtgcg 1287

<210> SEQ ID NO 4
<211> LENGTH: 1305
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 4

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ccgtatttct actgcgacga ggaggagaac ttctaccagc agcagcagca gagcgagctg 120

cagcccccgg cgcccagcga ggatatctgg aagaaattcg agctgctgcc caccccgccc 180

ctgtccccta gccgccgctc cgggctctgc tcgccctcct acgttgcggt cacacccttc 240

tcccttcggg gagacaacga cggcggtggc gggagcttct ccacggccga ccagctggag 300

atggtgaccg agctgctggg aggagacatg gtgaaccaga gtttcatctg cgacccggac 360

gacgagacct tcatcaaaaa catcatcatc caggactgta tgtggagcgg cttctcggcc 420

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agcccgaacc ccgcccgcgg ccacagcgtc tgctccacct ccagcttgta cctgcaggat 540

ctgagcgccg ccgcctcaga gtgcatcgac ccctcggtgg tcttccccta ccctctcaac 600

gacagcagct cgcccaagtc ctgcgcctcg caagactcca gcgccttctc tccgtcctcg 660

gattctctgc tctcctcgac ggagtcctcc ccgcagggca gccccgagcc cctggtgctc 720

catgaggaga caccgcccac caccagcagc gactctgagg aggaacaaga agatgaggaa 780

gaaatcgatg ttgtttctgt ggaaaagagg caggctcctg gcaaaaggtc agagtctgga 840

tcaccttctg ctggaggcca cagcaaacct cctcacagcc cactggtcct caagaggtgc 900

cacgtctcca cacatcagca caactacgca gcgcctccct ccactcggaa ggactatgga 960

tcaggtagcg gtagtgtcag agtcctgaga cagatcagca acaaccgaaa atgcaccagc 1020

cccaggtcct cggacaccga ggagaatgtc aagaggcgaa cacacaacgt cttggagcgc 1080

cagaggagga acgagctaaa acggagcttt tttgccctgc gtgaccagat cccggagttg 1140

gaaaacaatg aaaaggcccc caaggtagtt atccttaaaa aagccacagc atacatcctg 1200

tccgtccaag cagaggagca aaagctcatt tctgaagagg acttgttgcg gaaacgacga 1260

gaacagttga aacacaaact tgaacagcta cggaactctt gtgcg 1305

<210> SEQ ID NO 5
<211> LENGTH: 1290
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 5

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ccgtatttct actgcgacga ggaggagaac ttctaccagc agcagcagca gagcgagctg 120

cagcccccgg cgcccagcga ggatatctgg aagaaattcg agctgctgcc caccccgccc 180

ctgtccccta gccgccgctc cgggctctgc tcgccctcct acgttgcggt cacacccttc 240

tcccttcggg gagacaacga cggcggtggc gggagcttct ccacggccga ccagctggag 300

atggtgaccg agctgctggg aggagacatg gtgaaccaga gtttcatctg cgacccggac 360

gacgagacct tcatcaaaaa catcatcatc caggactgta tgtggagcgg cttctcggcc 420

gccgccaagc tcgtctcaga gaagctggcc tcctaccagg ctgcgcgcaa agacagcggc 480

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gattctctgc tctcctcgac ggagtcctcc ccgcagggca gccccgagcc cctggtgctc 720

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cacgtctcca cacatcagca caactacgca gcgcctccct ccactcggaa ggactatcct 960

gctgccaaga gggtcaagtt ggacagtgtc agagtcctga gacagatcag caacaaccga 1020

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ctaaaacgga gctttttttgc cctgcgtgac cagatcccgg agttggaaaa caatgaaaag 1140

gccccccaagg tagttatcct taaaaaagcc acagcataca tcctgtccgt ccaagcagag 1200

gagcaaaagc tcatttctga agaggacttg ttgcggaaac gacgagaaca gttgaaacac 1260

aaacttgaac agctacggaa ctcttgtgcg 1290

<210> SEQ ID NO 6
<211> LENGTH: 1206
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 6

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ccgtatttct actgcgacga ggaggagaac ttctaccagc agcagcagca gagcgagctg 120

cagcccccgg cgcccagcga ggatatctgg aagaaattcg agctgctgcc caccccgccc 180

ctgtccccta gccgccgctc cgggctctgc tcgccctcct acgttgcggt cacacccttc 240

tcccttcggg gagacaacga cggcggtggc gggagcttct ccacggccga ccagctggag 300

atggtgaccg agctgctggg aggagacatg gtgaaccaga gtttcatctg cgacccggac 360

gacgagacct tcatcaaaaa catcatcatc caggactgta tgtggagcgg cttctcggcc 420

gccgccaagc tcgtctcaga gaagctggcc tcctaccagg ctgcgcgcaa agacagcggc 480

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gaaatcgatg ttgtttctgt ggaaaagagg caggctcctg gcaaaaggtc agagtctgga 840

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cacgtctcca cacatcagca caactacgca gcgcctccct ccactcggaa ggactatcct 960

gctgccaaga gggtcaagtt ggacagtgtc agagtcctga gacagatcag caacaaccga 1020

aaatgcacca gccccaggtc ctcggacacc gaggagaatg tcaagaggcg aacacacaac 1080

gtcttggagc gccagaggag gaacggatca ggtagcggtc aaaagctcat ttctgaagag 1140

gacttgttgc ggaaacgacg agaacagttg aaacacaaac ttgaacagct acggaactct 1200

tgtgcg 1206

<210> SEQ ID NO 7
<211> LENGTH: 1230
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 7

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cagcccccgg cgcccagcga ggatatctgg aagaaattcg agctgctgcc caccccgccc 180

ctgtccccta gccgccgctc cgggctctgc tcgccctcct acgttgcggt cacacccttc 240

tcccttcggg gagacaacga cggcggtggc gggagcttct ccacggccga ccagctggag 300

atggtgaccg agctgctggg aggagacatg gtgaaccaga gtttcatctg cgacccggac 360

gacgagacct tcatcaaaaa catcatcatc caggactgta tgtggagcgg cttctcggcc 420

gccgccaagc tcgtctcaga gaagctggcc tcctaccagg ctgcgcgcaa agacagcggc 480

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gaaatcgatg ttgtttctgt ggaaaagagg caggctcctg gcaaaaggtc agagtctgga 840

tcaccttctg ctggaggcca cagcaaacct cctcacagcc cactggtcct caagaggtgc 900

cacgtctcca cacatcagca caactacgca gcgcctccct ccactcggaa ggactatcct 960

gctgccaaga gggtcaagtt ggacagtgtc agagtcctga gacagatcag caacaaccga 1020

aaatgcacca gccccaggtc ctcggacacc gaggagaatg tcaagaggcg aacacacaac 1080

gtcttggagc gccagaggag gaacgagcta aaacggagct tttttgccct gcgtgaccag 1140

atcccggagt tggaaaacaa tgaaaaggcc cccaaggtag ttatccttaa aaaagccaca 1200

gcatacatcc tgtccgtcca agcagaggag 1230

<210> SEQ ID NO 8
<211> LENGTH: 906
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 8

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ctgcaggatc tgagcgccgc cgcctcagag tgcatcgacc cctcggtggt cttcccctac 180

cctctcaacg acagcagctc gcccaagtcc tgcgcctcgc aagactccag cgccttctct 240

ccgtcctcgg attctctgct ctcctcgacg gagtcctccc cgcagggcag ccccgagccc 300

ctggtgctcc atgaggagac accgcccacc accagcagcg actctgagga ggaacaagaa 360

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gagtctggat caccttctgc tggaggccac agcaaacctc ctcacagccc actggtcctc 480

aagaggtgcc acgtctccac acatcagcac aactacgcag cgcctccctc cactcggaag 540

gactatcctg ctgccaagag ggtcaagttg gacagtgtca gagtcctgag acagatcagc 600

aacaaccgaa aatgcaccag ccccaggtcc tcggacaccg aggagaatgt caagaggcga 660

acacacaacg tcttggagcg ccagaggagg aacgagctaa aacggagctt ttttgccctg 720

cgtgaccaga tcccggagtt ggaaaacaat gaaaaggccc ccaaggtagt tatccttaaa 780

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aaagccacag catacatcct gtccgtccaa gcagaggagc aaaagctcat ttctgaagag 840

gacttgttgc ggaaacgacg agaacagttg aaacacaaac ttgaacagct acggaactct 900

tgtgcg 906

<210> SEQ ID NO 9
<211> LENGTH: 1062
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 9

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ccgtatttct actgcgacga ggaggagaac ttctaccagc agcagcagca gagcgagctg 120

cagcccccgg cgcccagcga ggatatctgg aagaaattcg agctgctgcc caccccgccc 180

ctgtccccta gccgccgctc cgggctctgc tcgccctcct acgttgcggt cacacccttc 240

tcccttcggg gagacaacga cggcggtggc gggagcttct ccacggccga ccagctggag 300

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aaatgcacca gccccaggtc ctcggacacc gaggagaatg tc 1062

<210> SEQ ID NO 10
<211> LENGTH: 1317
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 10

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ccgtatttct actgcgacga ggaggagaac ttctaccagc agcagcagca gagcgcgctg 120

cagcccccgg cgcccagcga ggatatctgg aagaaattcg agctgctgcc caccccgccc 180

ctgtccccta gccgccgctc cgggctctgc tcgccctcct acgttgcggt cacacccttc 240

tcccttcggg gagacaacga cggcggtggc gggagcttct ccacggccga ccagctggag 300

atggtgaccg agctgctggg aggagacatg gtgaaccaga gtttcatctg cgacccggac 360

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gccgccaagc tcgtctcaga gaagctggcc tcctaccagg ctgcgcgcaa agacagcggc 480

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gctgccaaga gggtcaagtt ggacagtgtc agagtcctga gacagatcag caacaaccga 1020

aaatgcacca gccccaggtc ctcggacacc gaggagaatg tcaagaggcg aacacacaac 1080

gtcttggagc gccagaggag gaacgagcta aaacggagct tttttgccct gcgtgaccag 1140

atcccggagt tggaaaacaa tgaaaaggcc cccaaggtag ttatccttaa aaaagccaca 1200

gcatacatcc tgtccgtcca agcagaggag caaaagctca tttctgaaga ggacttgttg 1260

cggaaacgac gagaacagtt gaaacacaaa cttgaacagc tacggaactc ttgtgcg 1317

<210> SEQ ID NO 11
<211> LENGTH: 1317
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 11

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ccgtatttct actgcgacga ggaggagaac ttctaccagc agcagcagca gagcgagctg 120

cagcccccgg cgcccagcga ggatatctgg aagaaattcg agctgctgcc cgccccgccc 180

ctgtccccta gccgccgctc cgggctctgc tcgccctcct acgttgcggt cacacccttc 240

tcccttcggg gagacaacga cggcggtggc gggagcttct ccacggccga ccagctggag 300

atggtgaccg agctgctggg aggagacatg gtgaaccaga gtttcatctg cgacccggac 360

gacgagacct tcatcaaaaa catcatcatc caggactgta tgtggagcgg cttctcggcc 420

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gctgccaaga gggtcaagtt ggacagtgtc agagtcctga gacagatcag caacaaccga 1020

aaatgcacca gccccaggtc ctcggacacc gaggagaatg tcaagaggcg aacacacaac 1080

gtcttggagc gccagaggag gaacgagcta aaacggagct tttttgccct gcgtgaccag 1140

atcccggagt tggaaaacaa tgaaaaggcc cccaaggtag ttatccttaa aaaagccaca 1200

gcatacatcc tgtccgtcca agcagaggag caaaagctca tttctgaaga ggacttgttg 1260

cggaaacgac gagaacagtt gaaacacaaa cttgaacagc tacggaactc ttgtgcg 1317

<210> SEQ ID NO 12
<211> LENGTH: 1317
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 12

atgcccctca acgttagctt caccaacagg aactatgacc tcgactacga ctcggtgcag 60

ccgtatttct actgcgacga ggaggagaac ttctaccagc agcagcagca gagcgagctg 120

cagcccccgg cgcccagcga ggatatctgg aagaaattcg agctgctgcc caccccgccc 180

ctggccccta gccgccgctc cgggctctgc tcgccctcct acgttgcggt cacacccttc 240

tcccttcggg gagacaacga cggcggtggc gggagcttct ccacggccga ccagctggag 300

atggtgaccg agctgctggg aggagacatg gtgaaccaga gtttcatctg cgacccggac 360

gacgagacct tcatcaaaaa catcatcatc caggactgta tgtggagcgg cttctcggcc 420

gccgccaagc tcgtctcaga gaagctggcc tcctaccagg ctgcgcgcaa agacagcggc 480

agcccgaacc ccgcccgcgg ccacagcgtc tgctccacct ccagcttgta cctgcaggat 540

ctgagcgccg ccgcctcaga gtgcatcgac ccctcggtgg tcttccccta ccctctcaac 600

gacagcagct cgcccaagtc ctgcgcctcg caagactcca gcgccttctc tccgtcctcg 660

gattctctgc tctcctcgac ggagtcctcc ccgcagggca gccccgagcc cctggtgctc 720

catgaggaga caccgcccac caccagcagc gactctgagg aggaacaaga agatgaggaa 780

gaaatcgatg ttgtttctgt ggaaaagagg caggctcctg gcaaaaggtc agagtctgga 840

tcaccttctg ctggaggcca cagcaaacct cctcacagcc cactggtcct caagaggtgc 900

cacgtctcca cacatcagca caactacgca gcgcctccct ccactcggaa ggactatcct 960

gctgccaaga gggtcaagtt ggacagtgtc agagtcctga gacagatcag caacaaccga 1020

aaatgcacca gccccaggtc ctcggacacc gaggagaatg tcaagaggcg aacacacaac 1080

gtcttggagc gccagaggag gaacgagcta aaacggagct tttttgccct gcgtgaccag 1140

atcccggagt tggaaaacaa tgaaaaggcc cccaaggtag ttatccttaa aaaagccaca 1200

gcatacatcc tgtccgtcca agcagaggag caaaagctca tttctgaaga ggacttgttg 1260

cggaaacgac gagaacagtt gaaacacaaa cttgaacagc tacggaactc ttgtgcg 1317

<210> SEQ ID NO 13
<211> LENGTH: 1086
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

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<400> SEQUENCE: 13

atggcgactg cggagacagc acttccatca atctcaacac tcactgcact ggggccattt 60

ccagataccc aggacgattt ccttaagtgg tggcggtccg aagaggctca agacatggga 120

cctggtccgc cggatcccac cgaacctcct ctgcatgtca aaagtgaaga tcagcctggc 180

gaggaagagg atgacgaaag gggtgccgac gccacttggg acttggatct tctccttacc 240

aatttctctg gtccggaacc tggcggggca ccacagacgt gcgctctcgc tccctcagaa 300

gcgagcgggg ctcagtaccc acccctccc gaaactctgg gagcctatgc tgggggtcct 360

ggactggtgg ctgggttgct tggtagtgag gaccattctg gctgggtacg ccccgctttg 420

agggcccgcg ctccggacgc ctttgtggga ccggcgctcg ctcctgcacc ggctccggaa 480

ccaaaagccc tcgcgctgca gcccgtgtac cccggacccg gagccggatc ctcaggggga 540

tacttcccac ggaccggact cagcgttcca gcggcttccg gggcgccata cggattgttg 600

agcggctacc cggctatgta tcccgctccc cagtaccaag gacacttcca attgttccgg 660

ggtcttcaag ggcctgcgcc cgggcctgct accagtccca gtttcctcag ttgtctggga 720

ccgggaactg ttggcactgg acttggcggg actgcagagg acccaggcgt tatagcagag 780

acagcgccaa gtaaaagggg ccgacgaagc tgggccagga aacgccaagc tgcgcacact 840

tgtgcccatc caggttgcgg taaatcctac acgaagagca gtcatcttaa agcacatctt 900

cgcacacaca cgggcgagaa gccctacgcc tgtacttggg aaggttgcgg ctggagattc 960

gctagatctg acgagctcac ccggcattat cgaaaacaca ctggccagcg accgttccgg 1020

tgccaactct gcccaagggc gttcagtcgc tcagatcatc tggctttgca tatgaagcga 1080

cacctt 1086

<210> SEQ ID NO 14
<211> LENGTH: 1065
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 14

atggccctta gtgaacccat tcttcccagc ttttccacgt tcgcgtctcc ttgccgagag 60

agaggccttc aggaaaggtg gccgagggct gaacccgagt ctggaggtac ggatgatgat 120

cttaacagtg tgctcgattt catactctca atgggactgg acgggctggg agcggaggca 180

gctcctgaac caccaccacc ccctccgccc ccagcgtttt actacccgga gccaggtgcg 240

ccgccgccat attcagcccc ggcgggtggc ttggtgtccg agctcctccg gcctgaattg 300

gatgccccgc tcggcccggc gctgcatggt agatttctgc tcgcgcctcc gggtcgactc 360

gttaaggctg aacctcctga ggctgatggt ggaggtggct acggatgtgc ccccgggctt 420

acccgaggac cgagaggtct taagcgggaa ggggcacctg gcccggctgc aagctgtatg 480

cgggggcccg gtgggaggcc tcccccgccc cctgatacac ccccccttag tccagatgga 540

ccagctcgac ttcccgcacc tggccccaga gcgagtttcc cccctccatt tggaggaccg 600

gggtttggcg ccccaggtcc tggacttcac tacgcccctc ctgcccccc agcttttggt 660

cttttcgacg atgctgctgc tgccgcagca gccttgggcc ttgcgccgcc cgcagccagg 720

ggactgctca cgccaccggc aagccccctg gagctccttg aagccaagcc gaagcgagga 780

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cgcagatcat ggccgcgcaa gcggacagct acgcatacct gctcatatgc gggctgcgga 840

aaaacctaca caaagagttc acaccttaaa gcgcaccttc gcacacacac aggcgagaaa 900

ccatatcatt gtaactggga cggatgtgga tggaaatttg ctcggtctga tgagcttacg 960

agacattatc gaaagcatac cggacatcgg ccctttcaat gccatctttg tgacagagct 1020

ttttcccggt ctgaccacct cgctctgcac atgaagaggc acatg 1065

<210> SEQ ID NO 15
<211> LENGTH: 1035
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 15

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tacccatcta attacatgga atccatgaag cctaacaagt atggggtcat ctactccaca 120

ccattgcctg agaagttctt tcagacccca gaaggtctgt cgcacggaat acagatggag 180

ccagtggacc tcacggtgaa caagcggagt tcacccccct cggctgggaa ttcgccctcc 240

tctctgaagt tcccgtcctc acaccggaga gcctcgcctg ggttgagcat gccttcttcc 300

agcccaccga taaaaaaata ctcaccccct tctccaggcg tgcagcccct cggcgtgccg 360

ctgtccatgc caccagtgat ggcagctgcc ctctcgcggc atggaatacg gagcccgggg 420

atcctgcccg tcatccagcc ggtggtggtg cagcccgtcc cctttatgta cacaagtcac 480

ctccagcagc ctctcatggt ctccttatcg gaggagatgg aaaattccag tagtagcatg 540

caagtacctg taattgaatc atatgagaag cctatatcac agaaaaaaat taaaatagaa 600

cctgggatcg aaccacagag gacagattat tatcctgaag aaatgtcacc ccccttaatg 660

aactcagtgt ccccccgca agcattgttg caagagaatc acccttcggt catcgtgcag 720

cctgggaaga gacctttacc tgtggaatcc ccggatactc aaaggaagcg gaggatacac 780

agatgtgatt atgatggatg caacaaagtg tacactaaaa gctcccactt gaaagcacac 840

agaagaacac acacaggaga aaaaccctac aaatgtacat gggaagggtg cacatggaag 900

tttgctcggt ctgatgaact aacaagacat ttccgaaaac atactggaat caaacctttc 960

cagtgcccgg actgtgaccg cagcttctcc cgttctgacc atcttgccct ccataggaaa 1020

cgccacatgc tagtc 1035

<210> SEQ ID NO 16
<211> LENGTH: 1371
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 16

atggctacaa gggtgctgag catgagcgcc cgcctgggac ccgtgcccca gccgccggcg 60

ccgcaggacg agccggtgtt cgcgcagctc aagccggtgc tgggcgccgc gaatccggcc 120

cgcgacgcgg cgctcttccc cggcgaggag ctgaagcacg cgcaccaccg cccgcaggcg 180

cagcccgcgc ccgcgcaggc cccgcagccg gcccagccgc ccgccaccgg cccgcggctg 240

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cctccagagg acctggtcca gacaagatgt gaaatggaga agtatctgac acctcagctt 300

cctccagttc ctataattcc agagcataaa aagtatagac gagacagtgc ctcagtcgta 360

gaccagttct tcactgacac tgaagggtta ccttacagta tcaacatgaa cgtcttcctc 420

cctgacatca ctcacctgag aactggcctc tacaaatccc agagaccgtg cgtaacacac 480

atcaagacag aacctgttgc cattttcagc caccagagtg aaacgactgc ccctcctccg 540

gccccgaccc aggccctccc tgagttcacc agtatattca gctcacacca gaccgcagct 600

ccagaggtga acaatatttt catcaaacaa gaacttccta caccagatct tcatctttct 660

gtccctaccc agcagggcca cctgtaccag ctactgaata caccggatct agatatgccc 720

agttctacaa atcagacagc agcaatggac actcttaatg tttctatgtc agctgccatg 780

gcaggcctta acacacacac ctctgctgtt ccgcagactg cagtgaaaca attccagggc 840

atgccccctt gcacatacac aatgccaagt cagtttcttc cacaacaggc cacttacttt 900

cccccgtcac caccaagctc agagcctgga agtccagata gacaagcaga gatgctccag 960

aatttaaccc cacctccatc ctatgctgct acaattgctt ctaaactggc aattcacaat 1020

ccaaatttac ccaccaccct gccagttaac tcacaaaaca tccaacctgt cagatacaat 1080

agaaggagta accccgattt ggagaaacga cgcatccact actgcgatta ccctggttgc 1140

acaaaagttt ataccaagtc ttctcattta aaagctcacc tgaggactca cactggtgaa 1200

aagccataca agtgtacctg ggaaggctgc gactggaggt tcgcgcgatc ggatgagctg 1260

acccgccact accggaagca cacaggcgcc aagcccttcc agtgcggggt gtgcaaccgc 1320

agcttctcgc gctctgacca cctggccctg catatgaaga ggcaccagaa c 1371

<210> SEQ ID NO 17
<211> LENGTH: 849
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 17

atggacgtgc tccccatgtg cagcatcttc caggagctcc agatcgtgca cgagaccggc 60

tacttctcgg cgctgccgtc tctggaggag tactggcaac agacctgcct agagctggaa 120

cgttacctcc agagcgagcc ctgctatgtt tcagcctcag aaatcaaatt tgacagccag 180

gaagatctgt ggaccaaaat cattctggct cgggagaaaa aggaggaatc cgaactgaag 240

atatcttcca gtcctccaga ggacactctc atcagcccga gcttttgtta caacttagag 300

accaacagcc tgaactcaga tgtcagcagc gaatcctctg acagctccga ggaactttct 360

cccacggcca agtttacctc cgaccccatt ggcgaagttt tggtcagctc gggaaaattg 420

agctcctctg tcacctccac gcctccatct tctccggaac tgagcaggga accttctcaa 480

ctgtggggtt gcgtgcccgg ggagctgccc tcgccaggga aggtgcgcag cgggacttcg 540

gggaagccag gtgacaaggg aaatggcgat gcctcccccg acggcaggag gagggtgcac 600

cggtgccact ttaacggctg caggaaagtt tacaccaaaa gctcccactt gaaagcacac 660

cagcggacgc acacaggaga aaagccttac agatgctcat gggaagggtg tgagtggcgt 720

tttgcaagaa gtgatgagtt aaccaggcac ttccgaaagc acaccggggc caagcctttt 780

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aaatgctccc actgtgacag gtgtttttcc aggtctgacc acctggccct gcacatgaag 840

aggcacctc 849

<210> SEQ ID NO 18
<211> LENGTH: 906
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 18

atggacgtgt tggctagtta tagtatattc caggagctac aacttgtcca cgacaccggc 60

tacttctcag ctttaccatc cctggaggag acctggcagc agacatgcct tgaattggaa 120

cgctacctac agacggagcc ccggaggatc tcagagacct ttggtgagga cttggactgt 180

ttcctccacg cttcccctcc cccgtgcatt gaggaaagct tccgtcgctt agacccccctg 240

ctgctccccg tggaagcggc catctgtgag aagagctcgg cagtggacat cttgctctct 300

cgggacaagt tgctatctga gacctgcctc agcctccagc cggccagctc ttctctagac 360

agctacacag ccgtcaacca ggcccagctc aacgcagtga cctcattaac gcccccatcg 420

tcccctgagc tcagccgcca tctggtcaaa acctcacaaa ctctctctgc cgtggatggc 480

acggtgacgt tgaaactggt ggccaagaag gctgctctca gctccgtaaa ggtgggaggg 540

gtcgcaacag ctgcagcagc cgtgacggct gcgggggccg ttaagagtgg acagagcgac 600

agtgaccaag gagggctagg ggctgaagca tgtcccgaaa acaagaagag ggttcaccgc 660

tgtcagttta acgggtgccg gaaagtttat acaaaaagct cccacttaaa ggcccaccag 720

aggactcaca caggtgagaa gccttataag tgctcatggg agggatgtga gtggcgtttt 780

gcacgaagcg atgagctcac gaggcactac aggaaacaca caggtgcaaa gcccttcaaa 840

tgcaaccact gcgacaggtg tttttccagg tctgaccatc ttgccctcca catgaagaga 900

catatc 906

<210> SEQ ID NO 19
<211> LENGTH: 1077
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 19

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tcaatgcagg tattcaagca ggtcactgct tctgttcgga acagagatcc ccctgagata 120

gaatacagaa gtaatatgac ttctccaaca ctcctggatg ccaaccccat ggagaaccca 180

gcactgttta atgacatcaa gattgagccc ccagaagaac ttttggctag tgatttcagc 240

ctgccccaag tggaaccagt tgacctctcc tttcacaagc ccaaggctcc tctccagcct 300

gctagcatgc tacaagctcc aatacgtccc cccaagccac agtcttctcc ccagaccctt 360

gtggtgtcca cgtcaacatc tgacatgagc acttcagcaa acattcctac tgttctgacc 420

ccaggctctg tcctgacctc ctctcagagc actggtagcc agcagatctt acatgtcatt 480

cacactatcc cctcagtcag tctgccaaat aagatgggtg gcctgaagac catcccagtg 540

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gtagtgcagt ctctgcccat ggtgtatact actttgcctg cagatggggg ccctgcagcc 600

attacagtcc cactcattgg aggagatggt aaaaatgctg gatcagtgaa agttgacccc 660

acctccatgt ctccactgga aattccaagt gacagtgagg agagtacaat tgagagtgga 720

tcctcagcct tgcagagtct gcagggacta cagcaagaac cagcagcaat ggcccaaatg 780

cagggagaag agtcgcttga cttgaagaga agacggattc accaatgtga ctttgcagga 840

tgcagcaaag tgtacaccaa aagctctcac ctgaaagctc accgcagaat ccatacagga 900

gagaagcctt ataaatgcac ctgggatggc tgctcctgga aatttgctcg ctcagatgag 960

ctcactcgcc atttccgcaa gcacacaggc atcaagcctt ttcggtgcac agactgcaac 1020

cgcagctttt ctcgttctga ccacctgtcc ctgcatcgcc gtcgccatga caccatg 1077

<210> SEQ ID NO 20
<211> LENGTH: 732
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 20

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cgcgaggtga ccaaggagca cggtgacccg ggggacacct ggaaggatta ctgcacactg 180

gtcaccatcg ccaagagctt gttggacctg aacaagtacc gacccatcca gacccccctcc 240

gtgtgcagcg acagtctgga aagtccagat gaggatatgg gatccgacag cgacgtgacc 300

accgaatctg ggtcgagtcc ttcccacagc ccggaggaga gacaggatcc tggcagcgcg 360

cccagcccgc tctccctcct ccatcctgga gtggctgcga aggggaaaca cgcctccgaa 420

aagaggcaca agtgccccta cagtggctgt gggaaagtct atggaaaatc ctcccatctc 480

aaagcccatt acagagtgca tacaggtgaa cggccctttc cctgcacgtg gccagactgc 540

cttaaaaagt tctcccgctc agacgagctg acccgccact accggaccca cactggggaa 600

aagcagttcc gctgtccgct gtgtgagaag cgcttcatga ggagtgacca cctcacaaag 660

cacgcccggc ggcacaccga gttccacccc agcatgatca agcgatcgaa aaaggcgctg 720

gccaacgctt tg 732

<210> SEQ ID NO 21
<211> LENGTH: 1440
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 21

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gaaaggccaa aagagagtat gtattcctgg aacaaaactg cagagaaaag tgattttgaa 120

gctgtagaag cacttatgtc aatgagctgc agttggaagt ctgattttaa gaaatacgtt 180

gaaaacagac ctgttacacc agtatctgat ttgtcagagg aagagaatct gcttccggga 240

acacctgatt ttcatacaat cccagcattt tgtttgactc caccttacag tccttctgac 300

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tttgaaccct ctcaagtgtc aaatctgatg gcaccagcgc catctactgt acacttcaag 360

tcactctcag atactgccaa acctcacatt gccgcacctt tcaaagagga agaaaagagc 420

ccagtatctg cccccaaact ccccaaagct caggcaacaa gtgtgattcg tcatacagct 480

gatgcccagc tatgtaacca ccagacctgc ccaatgaaag cagccagcat cctcaactat 540

cagaacaatt cttttagaag aagaacccac ctaaatgttg aggctgcaag aaagaacata 600

ccatgtgccg ctgtgtcacc aaacagatcc aaatgtgaga gaaacacagt ggcagatgtt 660

gatgagaaag caagtgctgc actttatgac ttttctgtgc cttcctcaga gacggtcatc 720

tgcaggtctc agccagcccc tgtgtcccca caacagaagt cagtgttggt ctctccacct 780

gcagtatctg caggggagt gccacctatg ccggtcatct gccagatggt tccccttcct 840

gccaacaacc ctgttgtgac aacagtcgtt cccagcactc ctcccagcca gccaccagcc 900

gtttgccccc ctgttgtgtt catgggcaca caagtcccca aaggcgctgt catgtttgtg 960

gtaccccagc ccgttgtgca gagttcaaag cctccggtgg tgagcccgaa tggcaccaga 1020

ctctctccca ttgcccctgc tcctgggttt tccccttcag cagcaaaagt cactcctcag 1080

attgattcat caaggataag gagtcacatc tgtagccacc caggatgtgg caagacatac 1140

tttaaaagtt cccatctgaa ggcccacacg aggacgcaca caggagaaaa gcctttcagc 1200

tgtagctgga aaggttgtga aaggaggttt gcccgttctg atgaactgtc cagacacagg 1260

cgaacccaca cgggtgagaa gaaatttgcg tgccccatgt gtgaccggcg gttcatgagg 1320

agtgaccatt tgaccaagca tgcccggcgc catctatcag ccaagaagct accaaactgg 1380

cagatggaag tgagcaagct aaatgacatt gctctacctc caacccctgc tcccacacag 1440

<210> SEQ ID NO 22
<211> LENGTH: 1536
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 22

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tgtgaatcta tactcgaaag aaagagacat gattcagagc gaagtacatg ctctatcctc 120

gagcaaacag acatggaggc ggtagaagct ctggtgtgca tgtccagttg gggtcagaga 180

tcccagaagg gggacttgct tagaatccga ccgcttactc cagtttccga tagcggcgac 240

gtaacaacta ctgttcatat ggacgcagcc acgcctgagc tgcccaaaga ctttcacagc 300

ctctcaactc tttgcatcac tccaccacag tcccccgatc ttgtcgaacc atcaacccgg 360

acccctgtta gcccgcaagt tacagattca aaggcgtgta ccgcgaccga tgttctgcag 420

agttcagcgg ttgtagcgcg ggcattgagc ggaggggctg aacgaggtct gttgggtctt 480

gaacccgtac cgagttctcc ttgtagagcc aagggtacta gtgttattcg gcataccggc 540

gagagtccgg cagcttgttt ccccaccata caaaccccag actgtcgcct tagtgattcc 600

cgggaagggg aggaacagct gttgggccac ttcgagacac ttcaagatac acacttgaca 660

gatagcttgc tgtccaccaa cctggtgtca tgtcaacctt gtttgcacaa gtccgggggt 720

ctccttctga ctgacaaagg tcaacaagcg ggatggcctg gcgctgtcca aacatgcagt 780

cctaaaaact acgaaaatga tttgcctagg aaaaccacgc cgcttatcag tgtgagtgtt 840

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cccgctccac ctgtcctgtg ccagatgatc cctgtaaccg ggcaatcatc tatgttgcct 900

gcgttcttga agccccccc acaactgtcc gttggtactg ttcgcccgat ccttgcgcaa 960

gcagcgcccg ccccgcaacc cgtgttcgtg gggcccgctg tcccgcaggg tgcagtcatg 1020

ttggttcttc cccaggggc cctcccgcca ccagctccgt gtgcagcgaa tgtcatggct 1080

gccggaaaca cgaaattgtt gccccttgca cccgctccag ttttcataac gagctcacag 1140

aattgtgtgc cacaagtcga cttctcacga agacggaact atgtgtgctc tttcccaggt 1200

tgcagaaaaa catatttcaa atcctctcat ctgaaagcac atcttcggac ccatacagga 1260

gagaagcctt ttaattgtag ctgggatggc tgtgataaaa aattcgcaag aagtgatgag 1320

ctcagtcgac atcgcaggac gcataccggg gaaaaaaaat tcgtttgtcc agtttgtgac 1380

agaagattta tgaggtccga ccatctcacc aagcacgcgc gacgccacat gactacaaag 1440

aaaattcctg gctggcaagc cgaggtggga aaactcaacc gaatcgcttc cgctgaatcc 1500

cccggcagcc cgctggtaag tatgcctgcc agtgcc 1536

<210> SEQ ID NO 23
<211> LENGTH: 1206
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 23

atgaacattc acatgaagcg caagacgata aagaacatca atacattcga gaaccgaatg 60

ttgatgttgg atggcatgcc cgctgtacgg gtaaaaaccg agctcctgga gtctgaacaa 120

ggatccccaa acgtccacaa ctacccggat atggaggcag tgccgctctt gctcaacaat 180

gtgaagggag agccgcctga ggactctctc tccgtagatc atttccagac acagactgag 240

cccgtagatc tttcaattaa caaagccaga acatctccta ctgcggtaag ttcttctccc 300

gtaagtatga cagcaagtgc atctagtcca agttctacga gcactagcag ttcttcatct 360

agtagacttg ctagttcacc aacggtgatc acaagtgttt ctagcgccag cagcagctca 420

acggtactga ctcccggtcc actcgtggca agcgctagtg gcgtgggtgg ccaacaattt 480

ctccatatta ttcaccccgt gcctccgtct agtccgatga atctccagag caacaagctt 540

agtcacgtac ataggatccc cgtcgtcgtc cagtcagttc ccgtcgtcta cacagctgtg 600

cgatcccctg ggaatgtcaa taatactata gttgttcctt tgcttgagga tggtaggggc 660

catgggaaag cacagatgga cccccgcggc ttgtcaccga gacagtctaa atccgatagt 720

gacgacgatg atttgcctaa cgtaacactg gactctgtga acgagaccgg gagtaccgct 780

ctgtcaatcg ctagggccgt acaggaggtc cacccaagcc ctgtgtcacg agtccgaggt 840

aacaggatga ataatcagaa atttccctgt agcatcagcc cattttctat agagtccact 900

cggagacagc gacgaagtga atcacccgac tccagaaaaa ggaggataca tcgctgtgac 960

tttgagggct gtaacaaggt ctacacaaaa agttcacacc tcaaggcgca tcgacggacg 1020

catactgggg aaaaaccgta caaatgcacc tgggagggat gcacgtggaa atttgcacgc 1080

tctgacgagt tgacacgcca ctatcgaaag catacgggcg taaagccgtt taaatgcgct 1140

gattgcgaca ggagttttag ccgctctgat caccttgctc ttcaccggag gcgacacatg 1200

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cttgtt 1206

<210> SEQ ID NO 24
<211> LENGTH: 864
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 24

atggctgcgg ctgcatatgt ggatcatttt gcggctgagt gcctggtgtc aatgtctagt 60

agagcggtgg tacacggtcc cagagaaggc ccagaatcac gcccagaggg cgccgccgtc 120

gctgcaacac cgacgctgcc tcgggtcgag gagcgccgcg acgggaagga cagtgcgtca 180

cttttcgtag tagcgagaat attggcagat ctgaatcaac aggctccagc acctgcgccc 240

gctgaacgcc gggagggcgc cgctgccaga aaggccagaa caccatgccg cttgccgcca 300

cctgcgccag aacccacaag tccaggtgcc gaaggtgcgg cggctgcccc tccttcaccg 360

gcctggtctg aaccagaacc agaggcaggt cttgaacctg agcgcgaacc cggccctgca 420

ggctctgggg aacctggcct gaggcagcgg gtgaggcgcg gccggagcag ggccgacctg 480

gaatcaccgc aaaggaaaca taaatgccat tatgctggtt gcgaaaaggt ttatggaaag 540

tcatcccacc tgaaagcaca cctccgcact cacacgggtg agcgaccttt tgcgtgttcc 600

tggcaagact gcaataaaaa gtttgctaga tctgatgaac ttgcacggca ttatcgaact 660

cataccggtg aaaagaagtt ctcatgccct atatgtgaga aacggttcat gcgctctgac 720

cacttgacga aacatgcaag acgacatgct aattttcatc cggggatgtt gcagagacgg 780

ggaggggaa gtaggactgg aagtctctcc gactattccc gatccgacgc ttcctcacca 840

acgattagcc ccgcaagcag tccc 864

<210> SEQ ID NO 25
<211> LENGTH: 969
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 25

atgtcagccg cagtcgcatg ccttgattac ttcgcggccg agtgtcttgt ttccatgtca 60

gcgggggctg tcgttcacag aagaccacca gacccggagg gagcgggagg ggcagctgga 120

tctgaagtcg gcgcggctcc acctgaatca gcgcttcccg gccctggtcc tccaggtccc 180

gctagcgtgc cccaactccc acaagtgcct gctccgagtc ctggagcggg cggagcagcc 240

ccgcatctcc ttgcagcatc agtgtgggcc gatcttcgcg gaagctccgg ggagggctcc 300

tgggaaaaca gcggagaggc cccgcgagct tcaagcggct tttccgatcc aatcccttgc 360

agtgttcaaa ccccatgctc cgagctcgcg cccgcgtccg gagctgcggc agtgtgcgca 420

cctgaaagct catccgatgc gccggccgtt ccatctgcgc cagctgctcc cggtgcaccc 480

gcagcatctg gcggctttag tggtggagct cttggggcgg gtcccgcccc tgcggcggat 540

caagctcctc gcaggcgcag tgttacgccc gcagcaaaac ggcatcaatg ccccttcct 600

ggttgtacaa aagcatacta taagtcatcc catctcaaga gtcaccagag gacgcataca 660

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ggtgagagac cttttagctg tgactggctc gattgcgaca agaaatttac gcggagcgac 720

gaacttgcgc ggcactaccg cactcacact ggagaaaaga ggttctcttg tcccctgtgt 780

cccaagcagt tctcacgcag tgatcacttg acaaaacatg ctaggagaca tccaacatac 840

catcccgaca tgatagagta tcgaggtagg cgacgcacac ctagaattga tcctccgctg 900

actagtgaag tcgagtcaag tgccagtgga agcggaccgg gtcccgcgcc ctcatttaca 960

acctgtctt 969

<210> SEQ ID NO 26
<211> LENGTH: 1248
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 26

atggtggacc acttacttcc agtggacgag aacttctcgt cgccaaaatg cccagttggg 60

tatctgggtg ataggctggt tggccggcgg gcatatcaca tgctgccctc acccgtctct 120

gaagatgaca gcgatgcctc cagcccctgc tcctgttcca gtcccgactc tcaagccctc 180

tgctcctgct atggtggagg cctgggcacc gagagccagg acagcatctt ggacttccta 240

ttgtcccagg ccacgctggg cagtggcggg ggcagcggca gtagcattgg ggccagcagt 300

ggccccgtgg cctgggggcc ctggcgaagg gcagcggccc ctgtgaaggg ggagcatttc 360

tgcttgcccg agtttccttt gggtgatcct gatgacgtcc cacggccctt ccagcctacc 420

ctggaggaga ttgaagagtt tctggaggag aacatggagc ctggagtcaa ggaggtccct 480

gagggcaaca gcaaggactt ggatgcctgc agccagctct cagctgggcc acacaagagc 540

cacctccatc ctgggtccag cgggagagag cgctgttccc ctccaccagg tggtgccagt 600

gcaggaggtg cccagggccc aggtgggggc cccacgcctg atggccccat cccagtgttg 660

ctgcagatcc agcccgtgcc tgtgaagcag gaatcgggca cagggcctgc ctcccctggg 720

caagccccag agaatgtcaa ggttgcccag ctcctggtca acatccaggg gcagaccttc 780

gcactcgtgc cccaggtggt accctcctcc aacttgaacc tgccctccaa gtttgtgcgc 840

attgcccctg tgcccattgc cgccaagcct gttggatcgg gacccctggg gcctggccct 900

gccggtctcc tcatgggcca gaagttcccc aagaacccag ccgcagaact catcaaaatg 960

cacaaatgta ctttccctgg ctgcagcaag atgtacacca aaagcagcca cctcaaggcc 1020

cacctgcgcc ggcacacggg tgagaagccc ttcgcctgca cctggccagg ctgcggctgg 1080

aggttctcgc gctctgacga gctgtcgcgg cacaggcgct cgcactcagg tgtgaagccg 1140

taccagtgtc ctgtgtgcga gaagaagttc gcgcggagcg accacctctc caagcacatc 1200

aaggtgcacc gcttcccgcg gagcagccgc tccgtgcgct ccgtgaac 1248

<210> SEQ ID NO 27
<211> LENGTH: 756
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 27

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atgtcagccg cggtcgcgtg cgtggattat tttgcagcag atgtgctgat ggcaatttca 60

tccggtgcag tagttcatcg cggaagacca ggtcctgagg gtgcggggcc tgcggccggg 120

ttggatgttc gcgccgcgcg cagggaagcc gcttctcccg gaacacctgg ccctcctcct 180

cctccgccgg cggcatcagg cccgggtcct ggtgcagctg cggctcctca cctgttggca 240

gcctccatac tggctgacct gcgaggggggg ccaggcgctg cacctggtgg cgcgagtcca 300

gcaagttcca gctccgcggc gtcctccccg agtagtgggc gagctccggg cgcggcacct 360

tctgctgccg ctaaatcaca ccgatgccct ttcccagact gcgcgaaggc gtattataag 420

tccagtcatt tgaaatcaca cttgaggaca cataccggcg agagaccttt tgcgtgcgac 480

tggcagggtt gtgataagaa atttgcgaga agcgacgaac tggcccgcca tcaccgcacc 540

cacacagggg aaaaaagatt ctcatgccca ctctgttcta agcgcttcac gcgaagcgac 600

catcttgcaa agcacgctag gagacaccct gggttccacc ccgacctctt gcgacgacct 660

ggcgcccggt ctactagccc gtctgactca ttgccgtgct ctctcgcagg gtcccctgct 720

ccgagccccg caccgtcccc agctcctgcc gggctt 756

<210> SEQ ID NO 28
<211> LENGTH: 1167
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 28

atgtacggcc gaccgcaggc tgagatggaa caggaggctg gggagctgag ccggtggcag 60

gcggcgcacc aggctgccca ggataacgag aactcagcgc ccatcttgaa catgtcttca 120

tcttctggaa gctctggagt gcacacctct tggaaccaag gcctaccaag cattcagcac 180

tttcctcaca gcgcagagat gctggggtcc cctttggtgt ctgttgaggc gccggggcag 240

aatgtgaatg aaggggggcc acagttcagt atgccactgc ctgagcgtgg tatgagctac 300

tgcccccaag cgactctcac tccttcccgg atgatttact gtcagagaat gtctcccccct 360

cagcaagaga tgacgatttt cagtgggccc caactaatgc ccgtaggaga gcccaatatt 420

ccaagggtag ccaggccctt cggtgggaat ctaaggatgc cccccaatgg gctgccagtc 480

tcggcttcca ctggaatccc aataatgtcc cacactggga accctccagt gccttaccct 540

ggcctctcga cagtaccttc tgacgaaaca ttgttgggcc cgactgtgcc ttccactgag 600

gcccaggcag tgctcccctc catggctcag atgttgcccc cgcaagatgc ccatgacctt 660

gggatgcccc cagctgagtc ccagtcattg ctggttttag gatctcagga ctctcttgtc 720

agtcagccag actctcaaga aggcccattt ctaccagagc agcccggacc tgctccacag 780

acagtagaga agaactccag gcctcaggaa gggactggta gaaggggctc ctcagaggca 840

aggccttact gctgcaacta cgagaactgc ggaaaagctt ataccaaacg ctcccacctc 900

gtgagccacc agcgcaagca cacaggtgag aggccatatt cttgcaactg ggaaagttgt 960

tcatggtctt tcttccgttc tgatgagctt agacgacata tgcgggtaca caccagatat 1020

cgaccatata aatgtgatca gtgcagccgg gagttcatga ggtctgacca tctcaagcaa 1080

caccagaaga ctcatcggcc gggaccctca gacccacagg ccaacaacaa caatggagag 1140

caggacagtc ctcctgctgc tggtcct 1167

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<210> SEQ ID NO 29
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic peptide

<400> SEQUENCE: 29

Gly Ser Gly Ser Gly Ser
1 5

<210> SEQ ID NO 30
<211> LENGTH: 59
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 30

gtctcgtggg ctcggagatg tgtataagag acagagaact atttcctggc tgttacgcg 59

<210> SEQ ID NO 31
<211> LENGTH: 58
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 31

acactctttc cctacacgac gctcttccga tctagaacta tttcctggct gttacgcg 58

<210> SEQ ID NO 32
<211> LENGTH: 56
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic primer

<400> SEQUENCE: 32

gactggagtt cagacgtgtg ctcttccgat cttgtcttcg ttgggagtga attagc 56

<210> SEQ ID NO 33
<211> LENGTH: 708
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 33

atggtgagca agggcgagga ggataacatg gccatcatca aggagttcat gcgcttcaag 60

gtgcacatgg agggctccgt gaacggccac gagttcgaga tcgagggcga gggcgagggc 120

cgcccctacg agggcaccca gaccgccaag ctgaaggtga ccaagggtgg cccctgccc 180

ttcgcctggg acatcctgtc ccctcagttc atgtacggct ccaaggccta cgtgaagcac 240

cccgccgaca tccccgacta cttgaagctg tccttccccg agggcttcaa gtgggagcgc 300

gtgatgaact tcgaggacgg cggcgtggtg accgtgaccc aggactcctc cctgcaggac 360

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ggcgagttca tctacaaggt gaagctgcgc ggcaccaact tcccctccga cggccccgta 420

atgcagaaga agaccatggg ctgggaggcc tcctccgagc ggatgtaccc cgaggacggc 480

gccctgaagg gcgagatcaa gcagaggctg aagctgaagg acggcggcca ctacgacgct 540

gaggtcaaga ccacctacaa ggccaagaag cccgtgcagc tgcccggcgc ctacaacgtc 600

aacatcaagt tggacatcac ctcccacaac gaggactaca ccatcgtgga acagtacgaa 660

cgcgccgagg gccgccactc caccggcggc atggacgagc tgtacaag 708

<210> SEQ ID NO 34
<211> LENGTH: 708
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 34

atggagtctt ctgctaaaat ggagtccgga ggcgcgggac aacaaccaca accgcaacca 60

caacaaccct tcctgccgcc ggccgcatgt tttttcgcga ccgctgctgc tgctgcagcg 120

gcggcggctg ctgccgccgc gcaatccgcc caacagcaac aacaacaaca gcagcagcag 180

caacaagcgc ctcaacttcg acccgctgca gacgggcagc cctcaggggg agggcacaag 240

agcgctccga agcaggttaa aaggcagagg agcagtagtc ccgaactgat gcgatgtaag 300

aggcgcctca attttagcgg ttttggttac tctttgcccc agcagcagcc ggctgccgta 360

gctcgccgaa atgagcggga aaggaaccgc gttaaacttg tgaatctcgg tttcgcgaca 420

cttcgagagc acgtaccaaa tggggcagct aacaagaaaa tgagtaaagt tgagacactg 480

cggtctgcag tggagtatat tagagctctt caacaattgc ttgacgagca cgatgccgta 540

tcagccgcat ttcaagccgg ggtgctgtcc ccaacaatat ctccgaacta cagcaatgat 600

cttaatagca tggcgggaag tcccgtttcc tcctactcct ctgatgaggg cagctacgac 660

cctctcagtc ccgaggagca agagcttctt gacttcacta actggttc 708

<210> SEQ ID NO 35
<211> LENGTH: 573
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 35

atgatggaca acagaggcaa ctctagtcta cctgacaaac ttcctatctt ccctgattct 60

gcccgcttgc cacttaccag gtccttctat ctggagccca tggtcacttt ccacgtgcac 120

ccagaggccc cggtgtcatc tccttactct gaggagctgc cacggctgcc ttttcccagc 180

gactctctta tcctgggaaa ttacagtgaa ccctgccccc tctctttccc gatgccttat 240

ccaaattaca gagggtgcga gtactcctac gggccagcct tcacccggaa aaggaatgag 300

cgggaaaggc agcgggtgaa atgtgtcaat gaaggctacg cccagctccg acatcatctg 360

ccagaggagt atttggagaa gcgactcagc aaagtggaaa ccctcagagc tgcgatcaag 420

tacattaact acctgcagtc tcttctgtac cctgataaag ctgagacaaa gaataaccct 480

ggaaaagttt cctccatgat agcaaccacc agccaccatg ctgaccctat gttcagaatt 540

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gtttgcccaa ctttcttgta caaagttgtc ccc 573

<210> SEQ ID NO 36
<211> LENGTH: 516
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 36

atggagacgc gtaaaccggc ggaacggctg gccttgccat actcgctgcg caccgcgccc 60

ctgggcgttc cggggaccct gcccggactc ccgcggaggg acccccctcag ggtcgccctg 120

cgtctggacg ccgcgtgctg ggagtgggcg cgcagcggct gcgcacgggg atggcagtac 180

ttgcccgtgc cgctggacag cgccttcgag cccgccttcc tccgcaagcg caacgagcgc 240

gagcggcagc gggtgcgctg cgtgaacgag ggctatgcgc gcctccgaga ccacctgccc 300

cgggagctgg cagacaagcg cctcagcaaa gtggagacgc tccgcgctgc catcgactac 360

atcaagcacc tgcaggagct gctggagcgc caggcctggg ggctcgaggg cgcggccggc 420

gccgtccccc agcgcagggc ggaatgcaac agcgacgggg agtccaaggc ctcttcggcg 480

ccttcgccca gcagcgagcc cgaggagggg ggcagc 516

<210> SEQ ID NO 37
<211> LENGTH: 833
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 37

atgccgatgg gggcagcaga aagaggtgct gggccccaat catctgcagc accatgggct 60

ggttcagaaa aggcggcaaa gagagggcca tcaaaaagct ggtacccaag agctgctgca 120

tctgatgtca cgtgcccgac tggtggtgat ggagctgacc caaaacctgg acctttttgga 180

ggtggtttag ctttagggcc tgcgcccaga ggaacaatga ataataattt ctgcagggcc 240

cttgttgaca gaaggccttt aggacccccct tcatgtatgc aattaggtgt aatgccaccg 300

ccaagacaag cgcccctccc gccggctgaa ccccttggaa atgtaccttt cctcctatac 360

cctggcccag ctgaaccacc atattatgat gcatatgctg gtgttttccc atatgtgcct 420

ttccctggtg cttttggtgt atatgaatac ccttttgagc cggcttttat ccaaaagagg 480

aatgaaagag agagacagag agtgaagtgt gtgaatgaag gatacgccag attgagaggc 540

catttgcctg gtgccctggc agaaaagaga ttatcaaaag ttgaaaccct gagggcggca 600

atcagatata taaaatacct ccaagaactc ctttcatcag cacctgatgg atcgacacca 660

ccggcttcaa gaggtttacc tggaactgga ccatgccctg caccgcctgc tacaccaagg 720

ccagacagac ctggagatgg agaagcaaga gcaccttctt cccttgtccc tgaatcttct 780

gaatcatcat gtttttcgcc ttccccctttt ttagaaagtg aagaatcctg gca 833

<210> SEQ ID NO 38
<211> LENGTH: 1482
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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

<400> SEQUENCE: 38

atgggagacg acagaccgtt tgtgtgcaat gccccgggct gtggacagag atttacaaac 60

gaggaccacc tggcagttca taaacacaag catgagatga cattgaaatt tggcccagcc 120

cgaactgact cagtcatcat tgcagatcaa acgcctactc caactagatt cctgaagaac 180

tgtgaggagg tgggactctt caatgaacta gctagctcct ttgaacatga attcaagaaa 240

gctgcagatg aggatgagaa aaaggcaaga agcaggactg ttgccaaaaa actggtggct 300

gctgctgggc cccttgacat gtctctgcct tccacaccag acatcaaaat caaagaagaa 360

gagccagtgg aggtagactc atccccacct gatagccctg cctctagtcc ctgttcccca 420

ccactgaagg agaaggaggt taccccaaag cctgttctga tctctacccc cacacccacc 480

attgtacgtc ctggctccct gcctctccac ttgggctatg atccacttca tccaaccctt 540

ccctccccaa cctctgtcat cacacaggct ccaccatcca acaggcaaat ggggtctccc 600

actggctccc tccctcttgt catgcatctt gctaatggac agaccatgcc tgtgttgcca 660

gggcctccag tacagatgcc gtctgttata tcgctggcca gacctgtgtc catggtgccc 720

aacattcctg gtatccctgg cccaccagtt aacagtagtg gctccatttc tccctctggc 780

caccctatac catcagaagc caagatgaga ctgaaagcca ccctaactca ccaagtctcc 840

tcaatcaatg gtggttgtgg aatggtggtg ggtactgcca gcaccatggt gacagcccgc 900

ccagagcaga gccagattct catccagcac cctgatgccc catcccctgc ccagccacag 960

gtctcaccag ctcagcccac ccctagtact ggggggcgac ggcggcgcac agtagatgaa 1020

gatccagatg agcgacggca gcgctttctg gagcgcaacc gggctgcagc ctcccgctgc 1080

cgccaaaagc gaaagctgtg ggtgtcctcc ctagagaaga aggccgaaga actcacttct 1140

cagaacattc agctgagtaa tgaagtcaca ttactacgca atgaggtggc ccagttgaaa 1200

cagctactgt tagctcataa agactgccca gtcactgcac tacagaaaaa gactcaaggc 1260

tatttagaaa gccccaagga aagctcagag ccaacgggtt ctccagcccc tgtgattcag 1320

cacagctcag caacagcccc tagcaatggc ctcagtgttc gctctgcagc tgaagctgtg 1380

gccacctcgg tcctcactca gatggccagc caaaggacag aactgagcat gccgatacaa 1440

tcgcatgtaa tcatgacccc acagtcccag tctgcgggca ga 1482

<210> SEQ ID NO 39
<211> LENGTH: 939
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 39

atgtacgtga gctacctcct ggacaaggac gtgagcatgt accctagctc cgtgcgccac 60

tctggcggcc tcaacctggc gccgcagaac ttcgtcagcc ccccgcagta cccggactac 120

ggcggttacc acgtggcggc cgcagctgca gcggcagcga acttggacag cgcgcagtcc 180

ccggggccat cctggccggc agcgtatggc gccccactcc gggaggactg gaatggctac 240

gcgcccggag gcgccgcggc cgccgccaac gccgtggctc acggcctcaa cggtggctcc 300

-continued

ccggccgcag ccatgggcta cagcagcccc gcagactacc atccgcacca ccacccgcat 360

caccacccgc accacccggc cgccgcgcct tcctgcgctt ctgggctgct gcaaacgctc 420

aaccccggcc ctcctgggcc cgccgccacc gctgccgccg agcagctgtc tcccggcggc 480

cagcggcgga acctgtgcga gtggatgcgg aagccggcgc agcagtccct cggcagccaa 540

gtgaaaacca ggacgaaaga caaatatcga gtggtgtaca cggaccacca gcggctggag 600

ctggagaagg agtttcacta cagtcgctac atcaccatcc ggaggaaagc cgagctagcc 660

gccacgctgg ggctctctga gaggcaggtt aaaatctggt ttcagaaccg cagagcaaag 720

gagaggaaaa tcaacaagaa gaagttgcag cagcaacagc agcagcagcc accacagccg 780

cctccgccgc caccacagcc tccccagcct cagccaggtc ctctgagaag tgtcccagag 840

cccttgagtc cggtgtcttc cctgcaagcc tcagtgtctg gctctgtccc tggggttctg 900

gggccaactg gggggggtgct aaaccccacc gtcacccag 939

<210> SEQ ID NO 40
<211> LENGTH: 897
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 40

atgatggcgt atatgaaccc ggggccccac tattctgtca acgccttggc cctaagtggc 60

cccagtgtgg atctgatgca ccaggctgtg ccctacccaa gcgcccccag gaagcagcgg 120

cgggagcgca ccaccttcac ccggagccaa ctggaggagc tggaggcact gtttgccaag 180

acccagtacc cagacgtcta tgcccgtgag gaggtggctc tgaagatcaa tctgcctgag 240

tccagggttc aggtttggtt caagaaccgg agggctaaat gcaggcagca gcgacagcag 300

cagaaacagc agcagcagcc cccagggggc caggccaagg cccggcctgc caagaggaag 360

gcgggcacgt ccccaagacc ctccacagat gtgtgtccag accctctggg catctcagat 420

tcctacagtc cccctctgcc cggcccctca ggctccccaa ccacggcagt ggccactgtg 480

tccatctgga gcccagcctc agagtccccc ttgcctgagg cgcagcgggc tgggctggtg 540

gcctcagggc cgtctctgac ctccgccccc tatgccatga cctacgcccc ggcctccgct 600

ttctgctctt ccccctccgc ctatgggtct ccgagctcct atttcagcgg cctagacccc 660

tacctttctc ccatggtgcc ccagctaggg ggcccggctc ttagcccccc ctctggcccc 720

tccgtgggac cttccctggc ccagtccccc acctccctat caggccagag ctatggcgcc 780

tacagccccg tggatagctt ggaattcaag gaccccacgg gcacctggaa attcacctac 840

aatcccatgg accctctgga ctacaaggat cagagtgcct ggaagtttca gatcttg 897

<210> SEQ ID NO 41
<211> LENGTH: 1437
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 41

atggccagca ctattaagga agccttatca gttgtgagtg aggaccagtc gttgtttgag 60

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tgtgcctacg gaacgccaca cctggctaag acagagatga ccgcgtcctc ctccagcgac 120

tatggacaga cttccaagat gagcccacgc gtccctcagc aggattggct gtctcaaccc 180

ccagccaggg tcaccatcaa aatggaatgt aaccctagcc aggtgaatgg ctcaaggaac 240

tctcctgatg aatgcagtgt ggccaaaggc gggaagatgg tgggcagccc agacaccgtt 300

gggatgaact acggcagcta catggaggag aagcacatgc cacccccaaa catgaccacg 360

aacgagcgca gagttatcgt gccagcagat cctacgctat ggagtacaga ccatgtgcgg 420

cagtggctgg agtgggcggt gaaagaatat ggccttccag acgtcaacat cttgttattc 480

cagaacatcg atgggaagga actgtgcaag atgaccaagg acgacttcca gaggctcacc 540

cccagctaca atgccgacat ccttctctca catctccact acctcagaga gactcctctt 600

ccacatttga cttcagatga tgttgataaa gccttacaaa actctccacg gttaatgcat 660

gctagaaaca caggggggtgc agcttttatt ttcccaaata cttcagtata tcctgaagct 720

acgcaaagaa ttacaactag gccagattta ccatatgagc cccccaggag atcagcctgg 780

accggtcacg gccaccccac gccccagtcg aaagctgctc aaccatctcc ttccacagtg 840

cccaaaactg aagaccagcg tcctcagtta gatccttatc agattcttgg accaacaagt 900

agccgccttg caaatccagg cagtggccag atccagcttt ggcagttcct cctggagctc 960

ctgtcggaca gctccaactc cagctgcatc acctgggaag gcaccaacgg ggagttcaag 1020

atgacggatc ccgacgaggt ggcccggcgc tggggagagc ggaagagcaa acccaacatg 1080

aactacgata agctcagccg cgccctccgt tactactatg acaagaacat catgaccaag 1140

gtccatggga agcgctacgc ctacaagttc gacttccacg ggatcgccca ggccctccag 1200

ccccaccccc cggagtcatc tctgtacaag tacccctcag acctcccgta catgggctcc 1260

tatcacgccc acccacagaa gatgaacttt gtggcgcccc accctccagc cctccccgtg 1320

acatcttcca gttttttttgc tgccccaaac ccatactgga attcaccaac tgggggtata 1380

taccccaaca ctaggctccc caccagccat atgccttctc atctgggcac ttactac 1437

<210> SEQ ID NO 42
<211> LENGTH: 1326
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 42

atgtcaaaca aagatcgaca cattgattcc agctgttcgt ccttcatcaa gacggaacct 60

tccagcccag cctccctgac ggacagcgtc aaccaccaca gccctggtgg ctcttcagac 120

gccagtggga gctacagttc aaccatgaat ggccatcaga acggacttga ctcgccacct 180

ctctaccctt ctgctcctat cctgggaggt agtgggcctg tcaggaaact gtatgatgac 240

tgctccagca ccattgttga agatccccag accaagtgtg aatacatgct caactcgatg 300

cccaagagac tgtgtttagt gtgtggtgac atcgcttctg ggtaccacta tggggtagca 360

tcatgtgaag cctgcaaggc attcttcaag aggacaattc aaggcaatat agaatacagc 420

tgccctgcca cgaatgaatg tgaaatcaca aagcgcagac gtaaatcctg ccaggcttgc 480

cgcttcatga agtgtttaaa agtgggcatg ctgaaagaag gggtgcgtct tgacagagta 540

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cgtggaggtc ggcagaagta caagcgcagg atagatgcgg agaacagccc atacctgaac 600

cctcagctgg ttcagccagc caaaaagcca ttgctctggt ctgatcctgc agataacaag 660

attgtctcac atttgttggt ggctgaaccg gagaagatct atgccatgcc tgaccctact 720

gtccccgaca gtgacatcaa agccctcact acactgtgtg acttggccga ccgagagttg 780

gtggttatca ttggatgggc gaagcatatt ccaggcttct ccacgctgtc cctggcggac 840

cagatgagcc ttctgcagag tgcttggatg gaaattttga tccttggtgt cgtataccgg 900

tctctttcgt ttgaggatga acttgtctat gcagacgatt atataatgga cgaagaccag 960

tccaaattag caggccttct tgatctaaat aatgctatcc tgcagctggt aaagaaatac 1020

aagagcatga agctggaaaa agaagaattt gtcaccctca aagctatagc tcttgctaat 1080

tcagactcca tgcacataga agatgttgaa gccgttcaga agcttcagga tgtcttacat 1140

gaagcgctgc aggattatga agctggccag cacatggaag accctcgtcg agctggcaag 1200

atgctgatga cactgccact cctgaggcag acctctacca aggccgtgca gcatttctac 1260

aacatcaaac tagaaggcaa agtcccaatg cacaaacttt ttttggaaat gttggaggcc 1320

aaggtc 1326

<210> SEQ ID NO 43
<211> LENGTH: 1110
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 43

atggatcttt ggaactggga tgaagcttcc cctcaagaag ttccccccgg aaataaactc 60

gcggggcttg gaagactccc tcgccttccg caacgcgtct ggggcggatg ccctggtgga 120

gcctcagcgg acccaaaccc tttgtctcca gcggaggggg caaagttggg tttctgcttc 180

ccggatcttg ctttgcaagg cgatactcca acggcgacgg cagagacctg ttggaaaggc 240

accagtagct ccctggccag ctttccgcag ctcgattggg ggtcagccct tctccatccc 300

gaagttccct ggggggcgga acccgactcc caagcccttc cctggagtgg tgattggaca 360

gatatggcat gcacagcctg ggacagttgg tccggggcgt cacagacatt gggaccagcc 420

ccacttggac cggggcctat ccccgcagca ggaagcgaag gagctgctgg tcagaactgt 480

gtgcccgtgg ctggtgaggc taccagttgg tccagggccc aggcagcagg cagtaacacc 540

agctgggatt gctcagtggg gcctgacggg gatacttatt ggggctctgg tcttggtgga 600

gaaccgagaa cggactgtac gataagttgg ggcggtccag ctgggcctga ttgtactacg 660

tcatggaatc ctggcttgca cgccggcggc acgacaagcc ttaagagata tcaaagttca 720

gcccttacag tttgctcaga accttccccg caaagtgacc gagcgtcact ggcgcgatgt 780

cctaaaacta atcatcgagg gccgatccag ttgtggcagt ttttgcttga actccttcac 840

gatggcgcga ggagcagttg catcagatgg accggtaaca gcagggagtt ccaattgtgt 900

gaccccaagg aagtggctcg actgtggggt gagcgcaaac ggaagcctgg tatgaattac 960

gaaaagttga gtaggggttt gcgatattac tataggcgcg acatcgttcg aaagtccggt 1020

ggtcgaaagt acacatacag attcggcggt cgcgtaccat ctcttgcata ccctgattgc 1080

gcaggcgggg gtaggggtgc ggaaacacaa 1110

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<210> SEQ ID NO 44
<211> LENGTH: 1356
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 44

atggacggga ctattaagga ggctctgtcg gtggtgagcg acgaccagtc cctctttgac 60

tcagcgtacg gagcggcagc ccatctcccc aaggccgaca tgactgcctc ggggagtcct 120

gactacgggc agccccacaa gatcaacccc ctcccaccac agcaggagtg gatcaatcag 180

ccagtgaggg tcaacgtcaa gcgggagtat gaccacatga atggatccag ggagtctccg 240

gtggactgca gcgttagcaa atgcagcaag ctggtgggcg gaggcgagtc caaccccatg 300

aactacaaca gctatatgga cgagaagaat ggcccccctc ctcccaacat gaccaccaac 360

gagaggagag tcatcgtccc cgcagacccc acactgtgga cacaggagca tgtgaggcaa 420

tggctggagt gggccataaa ggagtacagc ttgatggaga tcgacacatc ctttttccag 480

aacatggatg gcaaggaact gtgtaaaatg aacaaggagg acttcctccg cgccaccacc 540

ctctacaaca cggaagtgct gttgtcacac ctcagttacc tcagggaaag ttcactgctg 600

gcctataata caacctccca caccgaccaa tcctcacgat tgagtgtcaa agaagaccct 660

tcttatgact cagtcagaag aggagcttgg ggcaataaca tgaattctgg cctcaacaaa 720

agtcctcccc ttggaggggc acaaacgatc agtaagaata cagagcaacg gccccagcca 780

gatccgtatc agatcctggg cccgaccagc agtcgcctag ccaaccctgg aagcgggcag 840

atccagctgt ggcaattcct cctggagctg ctctccgaca gcgccaacgc cagctgtatc 900

acctgggagg ggaccaacgg ggagttcaaa atgacggacc ccgatgaggt ggccaggcgc 960

tggggcgagc ggaaaagcaa gcccaacatg aattacgaca agctgagccg ggccctccgt 1020

tattactatg ataaaaacat tatgaccaaa gtgcacggca aaagatatgc ttacaaattt 1080

gacttccacg gcattgccca ggctctgcag ccacatccga ccgagtcgtc catgtacaag 1140

tacccttctg acatctccta catgccttcc taccatgccc accagcagaa ggtgaacttt 1200

gtccctcccc atccatcctc catgcctgtc acttcctcca gcttctttgg agccgcatca 1260

caatactgga cctcccccac ggggggaatc taccccaacc ccaacgtccc ccgccatcct 1320

aacacccacg tgccttcaca cttaggcagc tactac 1356

<210> SEQ ID NO 45
<211> LENGTH: 1416
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 45

atgttgggca ccgtgaagat ggaggggcat gagacaagcg actggaattc ctactacgcg 60

gatacccaag aagcgtattc ttcagttccc gtaagcaata tgaactccgg attggggagc 120

atgaatagta tgaacacgta tatgacaatg aatacgatga ccaccagcgg caacatgaca 180

ccggcctcct ttaatatgtc atatgcgaac cctggtcttg gcgctggcct ctcaccaggt 240

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gcggtcgctg gaatgcccgg ggggagcgcc ggagcgatga actccatgac cgctgcgggc 300

gtgacggcca tgggtacggc cctgtcaccc agtggaatgg gagctatggg ggcccagcaa 360

gccgcctcaa tgaatggatt ggggccctat gccgcggcga tgaatccctg catgtcccct 420

atggcttatg cccccagcaa tttgggtcgc agtagagccg gcggtggtgg cgatgccaaa 480

accttcaagc gaagttatcc tcatgcgaag cctccttatt catatatatc cttgattacg 540

atggcgatac agcaggcccc gtctaagatg ctgactctga gtgagatata ccagtggatc 600

atggaccttt ttccttacta ccggcaaaac caacagagat ggcaaaactc aatacgccat 660

agcctttcct tcaatgattg ctttgtcaaa gtcgctcgga gccctgacaa gcccggtaaa 720

gggtcctatt ggacccttca tccagatagc ggcaatatgt tcgagaatgg ttgttatctt 780

agacggcaga aacgattcaa atgtgagaaa cagccaggtg ccggcggtgg tggcggcagc 840

ggttcaggcg gaagtggtgc caagggtggg cctgagtcta gaaaagaccc cagcggagca 900

agcaatccaa gcgcggactc tcccctgcac cgcggtgttc atggtaagac aggtcagctt 960

gagggggcgc ctgctccagg cccggctgcg tcaccgcaaa cactggacca tagtggagct 1020

acagcgaccg gaggtgcttc agaactcaag acgcctgcgt cctccactgc gcctccgatc 1080

tccagtggtc ccggtgcact tgcctctgtt cctgcatctc atccagcaca cggactcgcg 1140

ccgcacgagt cccagctcca tttgaaaggg gacccacact acagctttaa ccacccattc 1200

tctattaaca atttgatgtc atcctcagaa cagcagcata aactcgactt caaagcctat 1260

gaacaggccc tgcagtattc tccatatggc tctacacttc ctgcttctct tccattgggg 1320

tctgcaagtg tgacaacgcg ctccccaatc gagccaagtg ccctcgagcc tgcttattat 1380

caaggagtat attcccgacc agttttgaat acaagt 1416

<210> SEQ ID NO 46
<211> LENGTH: 1374
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 46

atgctgggag cggtgaagat ggaagggcac gagccgtccg actggagcag ctactatgca 60

gagcccgagg gctactcctc cgtgagcaac atgaacgccg gcctggggat gaacggcatg 120

aacacgtaca tgagcatgtc ggcggccgcc atgggcagcg gctcgggcaa catgagcgcg 180

ggctccatga acatgtcgtc gtacgtgggc gctggcatga gcccgtccct ggcggggatg 240

tcccccggcg cgggcgccat ggcgggcatg ggcggctcgg ccggggcggc tggcgtggcg 300

ggcatggggc cgcacttgag tcccagcctg agcccgctcg gggggcaggc ggccggggcc 360

atgggcggcc tggcccccta cgccaacatg aactccatga gccccatgta cgggcaggcg 420

ggcctgagcc gcgcccgcga ccccaagacc tacaggcgca gctacacgca cgcaaagccg 480

ccctactcgt acatctcgct catcaccatg gccatccagc agagccccaa caagatgctg 540

acgctgagcg agatctacca gtggatcatg gacctcttcc ccttctaccg gcagaaccag 600

cagcgctggc agaactccat ccgccactcg ctctccttca acgactgttt cctgaaggtg 660

ccccgctcgc ccgacaagcc cggcaagggc tccttctgga ccctgcaccc tgactcgggc 720

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aacatgttcg agaacggctg ctacctgcgc cgccagaagc gcttcaagtg cgagaagcag 780

ctggcgctga aggaggccgc aggcgccgcc ggcagcggca agaaggcggc cgccggggcc 840

caggcctcac aggctcaact cggggaggcc gccgggccgg cctccgagac tccggcgggc 900

accgagtcgc ctcactcgag cgcctccccg tgccaggagc acaagcgagg gggcctggga 960

gagctgaagg ggacgccggc tgcggcgctg agccccccag agccggcgcc ctctcccggg 1020

cagcagcagc aggccgcggc ccacctgctg ggcccgcccc accacccggg cctgccgcct 1080

gaggcccacc tgaagccgga acaccactac gccttcaacc acccgttctc catcaacaac 1140

ctcatgtcct cggagcagca gcaccaccac agccaccacc accaccagcc ccacaaaatg 1200

gacctcaagg cctacgaaca ggtgatgcac taccccggct acggttcccc catgcctggc 1260

agcttggcca tgggcccggt cacgaacaaa acgggcctgg acgcctcgcc cctggccgca 1320

gatacctcct actaccaggg ggtgtactcc cggcccatta tgaactcctc tttg 1374

<210> SEQ ID NO 47
<211> LENGTH: 1050
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 47

atgctgggct cagtgaagat ggaggcccat gacctggccg agtggagcta ctacccggag 60

gcgggcgagg tctactcgcc ggtgacccca gtgcccacca tggcccccct caactcctac 120

atgaccctga atcctctaag ctctccctat ccccctgggg ggctccctgc ctccccactg 180

ccctcaggac ccctggcacc cccagcacct gcagcccccc tggggcccac tttcccaggc 240

ctgggtgtca gcggtggcag cagcagctcc gggtacgggg ccccgggtcc tgggctggtg 300

cacgggaagg agatgccgaa ggggtatcgg cggcccctgg cacacgccaa gccaccgtat 360

tcctatatct cactcatcac catggccatc cagcaggcgc cgggcaagat gctgaccttg 420

agtgaaatct accagtggat catggacctc ttcccttact accgggagaa tcagcagcgc 480

tggcagaact ccattcgcca ctcgctgtct ttcaacgact gcttcgtcaa ggtggcgcgt 540

tccccagaca agcctggcaa gggctcctac tgggccctac accccagctc agggaacatg 600

tttgagaatg gctgctacct gcgccgccag aaacgcttca agctggagga gaaggtgaaa 660

aaaggggca gcggggctgc caccaccacc aggaacggga cagggtctgc tgcctcgacc 720

accacccccg cggccacagt cacctccccg ccccagcccc cgcctccagc ccctgagcct 780

gaggcccagg gcggggaaga tgtgggggct ctggactgtg gctcacccgc ttcctccaca 840

ccctatttca ctggcctgga gctcccaggg gagctgaagc tggacgcgcc ctacaacttc 900

aaccaccctt tctccatcaa caacctaatg tcagaacaga caccagcacc tcccaaactg 960

gacgtggggt ttgggggcta cggggctgaa ggtggggagc ctggagtcta ctaccagggc 1020

ctctattccc gctctttgct taatgcatcc 1050

<210> SEQ ID NO 48
<211> LENGTH: 342
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic

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polynucleotide

<400> SEQUENCE: 48

atgatgcaag aatctgggac tgagacaaaa agtaacggtt cagccatcca gaatgggtcg 60

ggcggcagca accacttact agagtgcggc ggtcttcggg aggggcggtc caacggagag 120

acgccggccg tggacatcgg ggcagctgac ctcgcccacg cccagcagca gcagcaacag 180

tggcatctca taaaccatca gccctctagg agtcccagca gttggcttaa gagactaatt 240

tcaagccctt gggagttgga agtcctgcag gtccccttgt ggggagcagt tgctgagacg 300

aagatgagtg gacctgtgtg tcagcctaac ccttccccat tt 342

<210> SEQ ID NO 49
<211> LENGTH: 1005
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 49

atggagttcc ctggcctggg gtccctgggg acctcagagc ccctccccca gtttgtggat 60

cctgctctgg tgtcctccac accagaatca ggggtttttct tcccctctgg gcctgagggc 120

ttggatgcag cagcttcctc cactgccccg agcacagcca ccgctgcagc tgcggcactg 180

gcctactaca gggacgctga ggcctacaga cactccccag tctttcaggt gtacccattg 240

ctcaactgta tggaggggat cccaggggcc tcaccatatg ccggctgggc ctacggcaag 300

acggggctct accctgcctc aactgtgtgt cccacccgcg aggactctcc tccccaggcc 360

gtggaagatc tggatggaaa aggcagcacc agcttcctgg agactttgaa gacagagcgg 420

ctgagcccag acctcctgac cctgggacct gcactgcctt catcactccc tgtccccaat 480

agtgcttatg ggggccctga cttttccagt accttctttt ctcccaccgg gagccccctc 540

aattcagcag cctattcctc tcccaagctt cgtggaactc tccccctgcc tccctgtgag 600

gccagggagt gtgtgaactg cggagcaaca gccactccac tgtggcggag ggacaggaca 660

ggccactacc tatgcaacgc ctgcggcctc tatcacaaga tgaatgggca gaacaggccc 720

ctcatccggc ccaagaagcg cctgattgtc agtaaacggg caggtactca gtgcaccaac 780

tgccagacga ccaccacgac actgtggcgg agaaatgcca gtggggatcc cgtgtgcaat 840

gcctgcggcc tctactacaa gctacaccac cagcactact gtggtggctc cgctcagctc 900

atgagggcac agagcatggc ctccagagga ggggtggtgt ccttctcctc ttgtagccag 960

aattctggac aacccaagtc tctgggcccc aggcaccccc tggct 1005

<210> SEQ ID NO 50
<211> LENGTH: 1440
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 50

atggaggtgg cgccggagca gccgcgctgg atggcgcacc cggccgtgct gaatgcgcag 60

caccccgact cacaccaccc gggcctggcg cacaactaca tggaacccgc gcagctgctg 120

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cctccagacg aggtggacgt cttcttcaat cacctcgact cgcagggcaa cccctactat 180

gccaaccccg ctcacgcgcg ggcgcgcgtc tcctacagcc ccgcgcacgc ccgcctgacc 240

ggaggccaga tgtgccgccc acacttgttg cacagcccgg gtttgccctg gctggacggg 300

ggcaaagcag ccctctctgc cgctgcggcc caccaccaca acccctggac cgtgagcccc 360

ttctccaaga cgccactgca cccctcagct gctggaggcc ctggaggccc actctctgtg 420

tacccagggg ctgggggtgg gagcgggggа ggcagcggga gctcagtggc ctccctcacc 480

cctacagcaa cccactctgg ctcccacctt ttcggcttcc cacccacgcc acccaaagaa 540

gtgtctcctg accctagcac cacgggggct gcgtctccag cctcatcttc cgcgggggggt 600

agtgcagccc gaggagagga caaggacggc gtcaagtacc aggtgtcact gacggagagc 660

atgaagatgg aaagtggcag tcccctgcgc ccaggcctag ctactatggg cacccagcct 720

gctacacacc accccatccc cacctacccc tcctatgtgc cggcggctgc ccacgactac 780

agcagcggac tcttccaccc cggaggcttc ctgggggggac cggcctccag cttcacccct 840

aagcagcgca gcaaggctcg ttcctgttca gaaggccggg agtgtgtcaa ctgtggggcc 900

acagccaccc ctctctggcg gcgggacggc accggccact acctgtgcaa tgcctgtggc 960

ctctaccaca agatgaatgg gcagaaccga ccactcatca agcccaagcg aagactgtcg 1020

gccgccagaa gagccggcac ctgttgtgca aattgtcaga cgacaaccac caccttatgg 1080

cgccgaaacg ccaacgggga ccctgtctgc aacgcctgtg gcctctacta caagctgcac 1140

aatgttaaca ggccactgac catgaagaag gaagggatcc agactcggaa ccggaagatg 1200

tccaacaagt ccaagaagag caagaaaggg gcggagtgct tcgaggagct gtcaaagtgc 1260

atgcaggaga agtcatcccc cttcagtgca gctgccctgg ctggacacat ggcacctgtg 1320

ggccacctcc cgcccttcag ccactccgga cacatcctgc ccactccgac gcccatccac 1380

ccctcctcca gcctctcctt cggccacccc cacccgtcca gcatggtgac cgccatgggc 1440

<210> SEQ ID NO 51
<211> LENGTH: 1326
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 51

atgtaccaga gcctggctat ggctgctaat catggacctc cccctggagc ctatgaagcc 60

ggaggacctg gcgcttttat gcatggagct ggcgccgctt cttctcccgt gtatgtgcct 120

acacctagag tgcccagcag cgtgctgggc ctttcttatc ttcagggagg aggagcagga 180

tctgcttctg gcggagcttc aggcggatct tctggaggcg ctgcttcagg tgctggacct 240

ggaactcaac agggatctcc tggatggtca caggcaggag ctgatggagc cgcttatacc 300

cctcctcctg tgagccccag gtttagcttt cctggcacaa caggctcttt agctgccgct 360

gctgctgcag ccgcagctag agaagcagct gcatattcta gtggcggagg agctgctgga 420

gccggcttag ctggaagaga gcagtacgga agagccggat ttgccggaag ctatagcagc 480

ccttaccctg cctatatggc cgatgttggc gcatcttggg cagccgccgc agcagcttct 540

gcaggacctt ttgactcacc tgtgcttcac tctctgcctg gcagagctaa tcctgccgcc 600

agacatccca acctggacat gttcgacgac ttcagcgagg gcagagaatg cgtgaactgc 660

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ggagccatga gcacccccct ttggagaaga gacggcaccg gccactacct ttgcaatgcc 720

tgtggcctgt accacaagat gaacggcatc aacagacccc tgatcaagcc ccagagaaga 780

ctgagcgcta gcagaagagt gggcctgtcc tgcgccaatt gccagaccac aaccaccaca 840

ctgtggagga gaaatgccga gggcgagcct gtgtgtaacg cctgtggact gtacatgaag 900

ctgcacggcg tgcccagacc tctggccatg agaaaggagg gcatccagac cagaaagaga 960

aagcccaaga acctgaacaa gagcaagacc cccgctgctc cttctggaag cgagagcctg 1020

cctccagcct ctggagccag cagcaatagc tctaacgcca ccacatcttc ttctgaggag 1080

atgaggccca tcaaaaccga gccaggcctg agcagccact acggccacag ctctagcgtg 1140

agccagactt ttagcgtgtc tgccatgtca ggccacggac ctagcattca ccctgtgctg 1200

agcgccctga agttgagccc acagggctat gcttctcctg tgtctcagag ccctcagacc 1260

tccagcaagc aggactcctg gaattctctg gtgctggccg acagccacgg cgatatcatc 1320

accgcc 1326

<210> SEQ ID NO 52
<211> LENGTH: 1785
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 52

atggccctga ccgacggcgg atggtgtctc cctaaaagat tcggcgccgc tggcgctgat 60

gcttctgaca gcagagcctt ccccgctagg gaacccagca caccacctag ccccatcagc 120

agctcaagct ctagctgtag cagaggcgga gagagaggac ctggaggcgc ttctaactgc 180

ggcacacctc agctggatac agaagccgcc gccggaccac cagccagatc tcttttactt 240

agcagctacg ccagccaccc ttttggcgct cctcatggac cctctgctcc tggtgtggcc 300

ggacctggcg gaaacctgag ctcttgggag gaccttctgc tgtttaccga cctggaccag 360

gctgccaccg ctagcaagct tctgtggagc agcaggggcg ctaagctgag ccctttgcc 420

cctgagcagc ccgaggagat gtaccagacc ctggctgctt taagctctca gggacctgcc 480

gcttatgacg gagcccctgg tggatttgtt cactcagcgg cagcagccgc agctgctgca 540

gccgctgcca gctcacctgt gtatgtgcct accacaagag tgggcagcat gttacctgga 600

cttccttacc atctgcaggg cagcggaagc ggccctgcta accatgccgg aggagctgga 660

gctcaccccg gatggcctca ggcttctgca gattctcctc cttatggatc tggaggagga 720

gcagctggag ggggagctgc aggaccaggt ggagccggaa gcgcagcagc acatgtgtct 780

gccagatttc cctatagccc tagccctcct atggccaatg gcgctgctag agaacccgga 840

ggatatgctg cggcaggctc tggcggcgct ggcggagttt ctggaggtgg atcttcactg 900

gccgctatgg gaggaagaga gcctcagtac tcttctctga gcgccgctag accactgaac 960

ggcacctatc atcaccacca ccatcaccat catcatcacc ccagccctta ctccccttat 1020

gtgggagccc cccttacacc cgcttggcct gccggccctt tcgagacacc tgtgctgcac 1080

agccttcagt ctagagctgg cgcaccttta ccagtgccta gaggcccctc tgccgacttg 1140

ctggaggatc tgagcgagag cagagagtgc gtgaactgtg gcagcatcca gacacccctg 1200

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tggagaagag acggcaccgg ccactacctg tgcaacgctt gcggcctgta cagcaagatg 1260

aatgggctga gcagacccct gatcaagccc cagaagaggg tgcccagcag cagacggctg 1320

ggactgagct gcgccaactg tcataccaca acaaccacac tgtggcggag aaacgccgag 1380

ggcgagcccg tgtgtaacgc ctgcggcctt tacatgaagc tgcacggcgt gcccagacct 1440

ctggccatga agaaggaggg aatccagacc agaaagagaa agcccaagaa catcaacaag 1500

agcaagacct gcagcggcaa cagcaacaac agcatcccca tgacccccac cagcacatct 1560

agcaacagcg acgactgtag caagaacaca tcacctacca cccagcccac agctagcgga 1620

gccggcgccc ccgtgatgac aggcgccgga gagtccacaa atcccgagaa tagcgaactg 1680

aagtactctg gacaggacgg actgtatatc ggcgtgagcc tggcttctcc cgccgaggtg 1740

accagctctg tcagacctga ctcttggtgt gccctcgccc tggcc 1785

<210> SEQ ID NO 53
<211> LENGTH: 3318
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 53

atgttcaact cgatgacccc accaccaatc agtagctatg gcgagccctg ctgtctccgg 60

cccctcccca gtcagggggc ccccagtgtg gggacagaag gactgtctgg cccgcccttc 120

tgccaccaag ctaacctcat gtccggcccc cacagttatg ggccagccag agagaccaac 180

agctgcaccg agggcccact cttttcttct ccccggagtg cagtcaagtt gaccaagaag 240

cgggcactgt ccatctcacc tctgtcggat gccagcctgg acctgcagac ggttatccgc 300

acctcaccca gctccctcgt agctttcatc aactcgcgat gcacatctcc aggaggctcc 360

tacggtcatc tctccattgg caccatgagc ccatctctgg gattcccagc ccagatgaat 420

caccaaaaag ggccctcgcc ttcctttggg gtccagcctt gtggtcccca tgactctgcc 480

cggggtggga tgatcccaca tcctcagtcc cggggaccct tcccaacttg ccagctgaag 540

tctgagctgg acatgctggt tggcaagtgc cgggaggaac ccttggaagg tgatatgtcc 600

agccccaact ccacaggcat acaggatccc ctgttgggga tgctggatgg gcgggaggac 660

ctcgagagag aggagaagcg tgagcctgaa tctgtgtatg aaactgactg ccgttgggat 720

ggctgcagcc aggaatttga ctcccaagag cagctggtgc accacatcaa cagcgagcac 780

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cacaagtgca cgtttgaagg gtgccggaag tcatactcac gcctcgaaaa cctgaagacg 960

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ggtcccatca gggaggaaag cagactgact gtgccagagg gtgccatgaa gccacagcca 1320

agccctgggg cccagtcatc ctgcagcagt gaccactccc cggcagggag tgcagccaat 1380

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acagacagtg gtgtggaaat gactggcaat gcaggggca gcactgaaga cctctccagc 1440

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acttcgccca ctgcagcatc cagcctggat cggataggtg gtcttcccat gcctccttgg 1860

agaagccgag ccgagtatcc aggatacaac cccaatgcag gggtcacccg gagggccagt 1920

gacccagccc aggctgctga ccgtcctgct ccagctagag tccagaggtt caagagcctg 1980

ggctgtgtcc ataccccacc cactgtggca gggggaggac agaactttga tccttacctc 2040

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gcttcacata gggcagcagc accacctcga cttctgcccc cattgcccac ttgctatggg 3000

cctctcaaag tgggaggcac aaaccccagc tgtggtcatc ctgaggtggg caggctagga 3060

gggggtcctg ccttgtaccc tcctcccgaa ggacaggtat gtaacccccc ggactctctt 3120

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cccaacatgg ctgtgggcaa catgagtgtc ttactgagat ccctacctgg ggaaacagaa 3300

ttcctcaact ctagtgcc 3318

<210> SEQ ID NO 54
<211> LENGTH: 540
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

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<400> SEQUENCE: 54

atgagtctgg taggtggttt tccccaccac ccggtggtgc accacgaggg ctacccgttt 60

gccgccgccg ccgccgccag ccgctgcagc catgaggaga acccctactt ccatggctgg 120

ctcatcggcc accccgagat gtcgcccccc gactacagca tggccctgtc ctacagcccc 180

gagtatgcca gcggcaccgc caaccgcaag gagcggcgca ggactcagag catcaacagc 240

gccttcgccg aactgcgcga gtgcatcccc aacgtacccg ccgacaccaa actctccaaa 300

atcaagaccc tgcgcctggc caccagctac atcgcctacc tcatggacct gctggccaag 360

gacgaccaga atggcgaggc ggaggccttc aaggcagaga tcaagaagac cgacgtgaaa 420

gaggagaaga ggaagaagga gctgaacgaa atcttgaaaa gcacagtgag cagcaacgac 480

aagaaaacca aaggccggac gggctggccg cagcacgtct gggccctgga gctcaagcag 540

<210> SEQ ID NO 55
<211> LENGTH: 1896
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 55

atggtttcta aactgagcca gctgcagacg gagctcctgg cggccctgct ggagtcaggg 60

ctgagcaaag aggcactgct ccaggcactg ggtgagccgg ggccctacct cctggctgga 120

gaaggccccc tggacaaggg ggagtcctgc ggcggcggtc gaggggagct ggctgagctg 180

cccaatgggc tgggggagac tcggggctcc gaggacgaga cggacgacga tggggaagac 240

ttcacgccac ccatcctcaa agagctggag aacctcagcc ctgaggaggc ggcccaccag 300

aaagccgtgg tggagaccct tctgcaggag gacccgtggc gtgtggcgaa gatggtcaag 360

tcctacctgc agcagcacaa catcccacag cgggaggtgg tcgataccac tggcctcaac 420

cagtcccacc tgtcccaaca cctcaacaag ggcactccca tgaagacgca gaagcgggcc 480

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cagaagaacc ctagcaagga ggagcgagag acgctagtgg aggagtgcaa tagggcggaa 720

tgcatccaga gaggggtgtc cccatcacag gcacaggggc tgggctccaa cctcgtcacg 780

gaggtgcgtg tctacaactg gtttgccaac cggcgcaaag aagaagcctt ccggcacaag 840

ctggccatgg acacgtacag cgggcccccc ccagggccag gcccgggacc tgcgctgccc 900

gctcacagct cccctggcct gcctccacct gccctctccc ccagtaaggt ccacggtgtg 960

cgctatggac agcctgcgac cagtgagact gcagaagtac cctcaagcag cggcggtccc 1020

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cagagccatg tgacccagag ccccttcatg gccaccatgg ctcagctgca gagcccccac 1500

gccctctaca gccacaagcc cgaggtggcc cagtacaccc acacaggcct gctcccgcag 1560

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tcagactcca gcaatggcca gagccacctg ctgccatcca accacagcgt catcgagacc 1860

ttcatctcca cccagatggc ctcttcctcc cagttg 1896

<210> SEQ ID NO 56
<211> LENGTH: 1671
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 56

atggttagca aactgacatc cctccagcag gaacttcttt ctgccctcct ctccagtggg 60

gtaaccaaag aggtactggt ccaggctttg gaggagttgc tcccctcacc gaattttggt 120

gtaaagttgg agactctccc cctctccccc ggttctggag cagagccgga tactaaaccg 180

gtatttcata cgcttacaaa cggacacgca aagggtcggc tttcaggtga cgaagggtct 240

gaggacggcg atgattatga caccccgccc atcctcaaag aactgcaggc ccttaataca 300

gaggaagcgg cggagcagcg agctgaagtt gacagaatgc tctcagaaga tccgtggaga 360

gctgcgaaaa tgattaaggg atatatgcag caacataaca ttccccagag agaggtagtt 420

gatgttaccg gccttaacca gagccacctg tctcagcatc tcaataaggg tactcctatg 480

aaaacacaga agcgagcggc cctttacaca tggtacgtgc ggaagcaacg agaaattctc 540

cgacagttca atcagacagt acaatcttca gggaacatga cggataaaag ctcacaggat 600

cagctcttgt ttctcttccc cgagttcagc caacagtccc acggtccagg tcaatctgat 660

gatgcttgca gtgaacctac aaacaaaaaa atgaggagga acaggtttaa atggggaccg 720

gcctctcagc agatactgta ccaagcgtac gatcggcaga aaaacccaag caaagaggag 780

cgcgaggcat tggtcgagga gtgtaatcgg gccgagtgct tgcaacgggg tgtaagtcct 840

agcaaagccc atggtctcgg ctcaaacttg gtcacggagg tgagggtata taattggttt 900

gccaacaggc ggaaggagga agcattccgg caaaagctgg cgatggatgc ctactcaagc 960

aaccagacac atagcctcaa ccctctgttg tcacacgggt cccctcatca ccaaccttct 1020

tcctctccac ccaacaaact ttctggtgtc cgatattccc agcaggggaa caacgagata 1080

acatcttcct ctactataag tcatcacgga aattctgcaa tggtaacgtc acagagtgtg 1140

ttgcaacagg tatcacccgc gtctcttgat ccaggccaca atctgttgag ccctgacgga 1200

aagatgatct ctgtttctgg tggcggactc ccgccggtct ccacacttac caacatacat 1260

agtctcagtc atcataatcc tcagcagagc caaaacctga ttatgactcc tcttagcgga 1320

gtgatggcta ttgcgcaatc tttgaacacc tcacaagcac aatctgtacc cgtcataaac 1380

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agcgtagcgg gctcattggc ggcgctccaa ccagtgcagt tctcccagca gctccattca 1440

ccccatcaac agcctctgat gcagcagagc cctggtagtc acatggctca acagccgttc 1500

atggcagctg tcactcagct ccagaactcc catatgtatg cccacaagca agaaccacca 1560

caatacagtc acacatcaag attccccagt gctatggttg ttactgacac atcctctatc 1620

tcaactctga cgaacatgtc cagtagtaaa caatgtcctc tgcaagcatg g 1671

<210> SEQ ID NO 57
<211> LENGTH: 1251
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 57

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ccagcctaca ccaccctgga atttgagaat gtgcaggtgt tgacgatggg caatgacacg 120

tccccatcag aaggcaccaa cctcaacgcg cccaacagcc tgggtgtcag cgccctgtgt 180

gccatctgcg gggaccgggc cacgggcaaa cactacggtg cctcgagctg tgacggctgc 240

aagggcttct tccggaggag cgtgcggaag aaccacatgt actcctgcag atttagccgg 300

cagtgcgtgg tggacaaaga caagaggaac cagtgccgct actgcaggct caagaaatgc 360

ttccgggctg gcatgaagaa ggaagccgtc cagaatgagc gggaccggat cagcactcga 420

aggtcaagct atgaggacag cagcctgccc tccatcaatg cgctcctgca ggcggaggtc 480

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tgggccaagt acatcccagc tttctgcgag ctccccctgg acgaccaggt ggccctgctc 660

agagcccatg ctggcgagca cctgctgctc ggagccacca agagatccat ggtgttcaag 720

gacgtgctgc tcctaggcaa tgactacatt gtccctcggc actgcccgga gctggcggag 780

atgagccggg tgtccatacg catccttgac gagctggtgc tgcccttcca ggagctgcag 840

atcgatgaca atgagtatgc ctacctcaaa gccatcatct tctttgaccc agatgccaag 900

gggctgagcg atccagggaa gatcaagcgg ctgcgttccc aggtgcaggt gagcttggag 960

gactacatca acgaccgcca gtatgactcg cgtggccgct ttggagagct gctgctgctg 1020

ctgcccacct tgcagagcat cacctggcag atgatcgagc agatccagtt catcaagctc 1080

ttcggcatgg ccaagattga caacctgttg caggagatgc tgctgggagg tccgtgccaa 1140

gcccaggagg ggcggggttg gagtggggac tccccaggag acaggcctca cacagtgagc 1200

tcacccctca gctccttggc ttccccactg tgccgctttg ggcaagttgc t 1251

<210> SEQ ID NO 58
<211> LENGTH: 1005
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 58

atggacaacg cgcggatgaa ttccttcctc gagtacccaa ttttgtctag tggagacagt 60

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ggcacttgca gtgcccgagc ctatccatca gaccacagaa ttacaacatt ccaaagctgt 120

gcggtgtcag ccaacagttg cggcggagac gaccgcttcc tggtcggaag aggggttcaa 180

attggatcac ctcaccatca ccatcaccac caccatcacc acccccaacc ggcgacttac 240

caaaccagcg gcaatttggg cgtgagctat agccattcct catgtggacc ttcctatggg 300

tctcagaatt tctccgcccc ttatagccca tacgccctga accaagaggc cgatgtatca 360

ggaggctatc cccagtgcgc gccagcggtt tactcaggta atctttctag cccgatggtc 420

cagcaccacc atcaccatca aggttatgcc ggcggtgcag tcggatcccc acaatacata 480

caccatagtt acggccaaga gcaccaatcc ctggccctcg ctacatataa caactcactg 540

tctccgcttc atgcttccca ccaagaagct tgtcggagtc ccgcctcaga aacttcctct 600

ccagctcaga cttttgattg gatgaaggtc aagcggaatc cgcctaaaac gggcaaagta 660

ggtgaatatg gctatttggg acagcctaat gctgtccgca ccaatttcac aacaaaacag 720

cttactgaac tcgagaagga atttcatttt aataagtatt tgactcgagc gagacgagtc 780

gaaatcgccg ctagtcttca acttaacgag acccaggtta agatatggtt ccagaacaga 840

agaatgaaac aaaaaaagcg ggagaaggaa ggactcctcc ctatatcacc agccacaccc 900

ccaggtaacg acgagaaggc ggaggaatct tcagagaaga gttccagctc cccttgtgtt 960

ccttctcctg gtagctcaac cagcgatacc ctcacgacga gtcac 1005

<210> SEQ ID NO 59
<211> LENGTH: 282
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 59

atgtgtcaag gcaattccaa aggtgaaaac gcagccaact ggctcacggc aaagagtggt 60

cggaagaagc gctgccccta cacgaagcac cagacactgg agctggagaa ggagtttctg 120

ttcaatatgt accttactcg agagcggcgc ctagagatta gccgcagcgt ccacctcacg 180

gacagacaag tgaaaatctg gtttcagaac cgcaggatga aactgaagaa aatgaatcga 240

gaaaaccgga tccgggagct cacagccaac tttaattttt cc 282

<210> SEQ ID NO 60
<211> LENGTH: 942
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 60

atggattttg atgagcgtgg tccctgctcc tctaacatgt atttgccaag ttgtacttac 60

tacgtctcgg gtccagattt ctccagcctc ccttcttttc tgccccagac cccgtcttcg 120

cgcccaatga catactccta ctcctccaac ctgccccagg tccaacccgt gcgcgaagtg 180

accttcagag agtacgccat tgagcccgcc actaaatggc acccccgcgg caatctggcc 240

cactgctact ccgcggagga gctcgtgcac agagactgcc tgcaggcgcc cagcgcggcc 300

ggcgtgcctg gcgacgtgct ggccaagagc tcggccaacg tctaccacca ccccaccccc 360

-continued

gcagtctcgt ccaatttcta tagcaccgtg ggcaggaacg gcgtcctgcc acaggctttc 420

gaccagtttt tcgagacagc ctacggcacc ccggaaaacc tcgcctcctc cgactacccc 480

ggggacaaga gcgccgagaa ggggcccccg gcggccacgg cgacctccgc ggcggcggcg 540

gcggctgcaa cgggcgcgcc ggcaacttca agttcggaca gcggcggcgg cggcggctgc 600

cgggagatgg cggcggcagc agaggagaaa gagcggcggc ggcgccccga gagcagcagc 660

agccccgagt cgtcttccgg ccacactgag gacaaggccg gcggctccag tggccaacgc 720

acccgcaaaa agcgctgccc ctataccaag taccagatcc gagagctgga acgggagttc 780

ttcttcagcg tctacattaa caaagagaag cgcctgcaac tgtcccgcat gctcaacctc 840

actgatcgtc aagtcaaaat ctggtttcag aacaggagaa tgaaggaaaa aaaaattaac 900

agagaccgtt tacagtacta ctcagcaaat ccactcctct tg 942

<210> SEQ ID NO 61
<211> LENGTH: 672
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 61

atgagttcct atttcgtgaa ctccaccttc cccgtcactc tggccagcgg gcaggagtcc 60

ttcctgggcc agctaccgct ctattcgtcg ggctatgcgg acccgctgag acattacccc 120

gcgccctacg ggccagggcc gggccaggac aagggctttg ccacttcctc ctattacccg 180

ccggcgggcg gtggctacgg ccgagcggcg ccctgcgact acgggccggc gccggccttc 240

taccgcgaga aagagtcggc ctgcgcactc tccggcgccg acgagcagcc cccgttccac 300

cccgagccgc ggaagtcgga ctgcgcgcag gacaagagcg tgttcggcga gacagaagag 360

cagaagtgct ccactccggt ctacccgtgg atgcagcgga tgaattcgtg caacagttcc 420

tcctttgggc ccagcggccg gcgaggccgc cagacataca cacgttacca gacgctggag 480

ctggagaagg agtttcacta caatcgctac ctgacgcggc ggcggcgcat cgagatcgcg 540

cacgccctgt gcctgacgga gaggcagatc aagatatggt tccagaaccg acgcatgaag 600

tggaaaaagg agagcaaact gctcagcgcg tctcagctca gtgccgagga ggaggaagaa 660

aaacaggccg ag 672

<210> SEQ ID NO 62
<211> LENGTH: 1410
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 62

atggctgtca gcgacgcgct gctcccatct ttctccacgt tcgcgtctgg cccggcggga 60

agggagaaga cactgcgtca agcaggtgcc ccgaataacc gctggcggga ggagctctcc 120

cacatgaagc gacttccccc agtgcttccc ggccgccccc atgacctggc ggcggcgacc 180

gtggccacag acctggagag cggcggagcc ggtgcggctt gcggcggtag caacctggcg 240

cccctacctc ggagagagac cgaggagttc aacgatctcc tggacctgga ctttattctc 300

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tccaattcgc tgacccatcc tccggagtca gtggccgcca ccgtgtcctc gtcagcgtca 360

gcctcctctt cgtcgtcgcc gtcgagcagc ggccctgcca gcgcgccctc cacctgcagc 420

ttcacctatc cgatccgggc cgggaacgac ccgggcgtgg cgccgggcgg cacgggcgga 480

ggcctcctct atggcaggga gtccgctccc cctccgacgg ctcccttcaa cctggcggac 540

atcaacgacg tgagcccctc gggcggcttc gtggccgagc tcctgcggcc agaattggac 600

ccggtgtaca ttccgccgca gcagccgcag ccgccaggtg gcgggctgat gggcaagttc 660

gtgctgaagg cgtcgctgag cgcccctggc agcgagtacg gcagcccgtc ggtcatcagc 720

gtcagcaaag gcagccctga cggcagccac ccggtggtgg tggcgcccta caacggcggg 780

ccgccgcgca cgtgccccaa gatcaagcag gaggcggtct cttcgtgcac ccacttgggc 840

gctggacccc ctctcagcaa tggccaccgg ccggctgcac acgacttccc cctggggcgg 900

cagctcccca gcaggactac cccgaccctg ggtcttgagg aagtgctgag cagcagggac 960

tgtcaccctg ccctgccgct tcctcccggc ttccatcccc acccggggcc caattaccca 1020

tccttcctgc ccgatcagat gcagccgcaa gtcccgccgc tccattacca agagctcatg 1080

ccacccggtt cctgcatgcc agaggagccc aagccaaaga ggggaagacg atcgtggccc 1140

cggaaaagga ccgccaccca cacttgtgat tacgcgggct gcggcaaaac ctacacaaag 1200

agttcccatc tcaaggcaca cctgcgaacc cacacaggtg agaaacctta ccactgtgac 1260

tgggacggct gtggatggaa attcgcccgc tcagatgaac tgaccaggca ctaccgtaaa 1320

cacacggggc accgcccgtt ccagtgccaa aaatgcgacc gagcattttc caggtcggac 1380

cacctcgcct tacacatgaa gaggcatttt 1410

<210> SEQ ID NO 63
<211> LENGTH: 1236
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 63

atggaggcgc gcggggagct gggcccggcc cgggagtcgg cgggaggcga cctgctgcta 60

gcactgctgg cgcggagggc ggacctgcgc cgagagatcc cgctgtgcgc tggctgtgac 120

cagcacatcc tggaccgctt catcctcaag gctctggacc gccactggca cagcaagtgt 180

ctcaagtgca gcgactgcca cacgccactg gccgagcgct gcttcagccg aggggagagc 240

gtttactgca aggacgactt tttcaagcgc ttcgggacca agtgcgccgc gtgccagctg 300

ggcatcccgc ccacgcaggt ggtgcgccgc gcccaggact tcgtgtacca cctgcactgc 360

tttgcctgcg tcgtgtgcaa gcggcagctg gccacgggcg acgagttcta cctcatggag 420

gacagccggc tcgtgtgcaa ggcggactac gaaaccgcca agcagcgaga ggccgaggcc 480

acggccaagc ggccgcgcac gaccatcacc gccaagcagc tggagacgct gaagagcgct 540

tacaacacct cgcccaagcc ggcgcgccac gtgcgcgagc agctctcgtc cgagacgggc 600

ctggacatgc gcgtggtgca ggtttggttc cagaaccgcc gggccaagga gaagaggctg 660

aagaaggacg ccggccggca gcgctggggg cagtatttcc gcaacatgaa gcgctcccgc 720

ggcggctcca agtcggacaa ggacagcgtt caggaggggc aggacagcga cgctgaggtc 780

tccttccccg atgagccttc cttggcggaa atgggcccgg ccaatggcct ctacgggagc 840

-continued

ttgggggaac ccacccaggc cttgggccgg ccctcgggag ccctgggcaa cttctccctg 900

gagcatggag gcctggcagg cccagagcag taccgagagc tgcgtcccgg cagcccctac 960

ggtgtccccc catcccccgc cgccccgcag agcctccctg gcccccagcc cctcctctcc 1020

agcctggtgt acccagacac cagcttgggc cttgtgccct cgggagcccc cggcgggccc 1080

ccacccatga gggtgctggc agggaacgga cccagttctg acctatccac ggggagcagc 1140

gggggttacc ccgacttccc tgccagcccc gcctcctggc tggatgaggt agaccacgct 1200

cagttctcag gcctcatggg cccagctttc ttgtac 1236

<210> SEQ ID NO 64
<211> LENGTH: 300
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 64

atggaaggaa tcatgaaccc ctacacggct ctgcccaccc cacagcagct cctggccatc 60

gagcagagtg tctacagctc agatcccttc cgacagggtc tcaccccacc ccagatgcct 120

ggagaccaca tgcaccctta tggtgccgag ccccttttcc atgacctgga tagcgacgac 180

acctccctca gtaacctggg tgactgtttc ctagcaacct cagaagctgg gcctctgcag 240

tccagagtgg gaaaccccat tgaccatctg tactccatgc agaattctta cttcacatct 300

<210> SEQ ID NO 65
<211> LENGTH: 1419
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 65

atggggagaa aaaagattca gattacgagg attatggatg aacgtaacag acaggtgaca 60

tttacaaaga ggaaatttgg gttgatgaag aaggcttatg agctgagcgt gctgtgtgac 120

tgtgagattg cgctgatcat cttcaacagc accaacaagc tgttccagta tgccagcacc 180

gacatggaca aagtgcttct caagtacacg gagtacaacg agccgcatga gagccggaca 240

aactcagaca tcgtggagac gttgagaaag aagggcctta atggctgtga cagcccagac 300

cccgatgcgg acgattccgt aggtcacagc cctgagtctg aggacaagta caggaaaatt 360

aacgaagata ttgatctaat gatcagcagg caaagattgt gtgctgttcc acctcccaac 420

ttcgagatgc cagtctccat cccagtgtcc agccacaaca gtttggtgta cagcaaccct 480

gtcagctcac tgggaaaccc caacctattg ccactggctc acccttctct gcagaggaat 540

agtatgtctc ctggtgtaac acatcgacct ccaagtgcag gtaacacagg tggtctgatg 600

ggtggagacc tcacgtctgg tgcaggcacc agtgcaggga acgggtatgg caatccccga 660

aactcaccag gtctgctggt ctcacctggt aacttgaaca agaatatgca agcaaaatct 720

cctcccccaa tgaatttagg aatgaataac cgtaaaccag atctccgagt tcttattcca 780

ccaggcagca agaatacgat gccatcagtg tctgaggatg tcgacctgct tttgaatcaa 840

aggataaata actcccagtc ggctcagtca ttggctaccc cagtggtttc cgtagcaact 900

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cctactttac caggacaagg aatgggagga tatccatcag ccatttcaac aacatatggt 960

accgagtact ctctgagtag tgcagacctg tcatctctgt ctgggtttaa caccgccagc 1020

gctcttcacc ttggttcagt aactggctgg caacagcaac acctacataa catgccacca 1080

tctgccctca gtcagttggg agcttgcact agcactcatt tatctcagag ttcaaatctc 1140

tccctgcctt ctactcaaag cctcaacatc aagtcagaac ctgtttctcc tcctagagac 1200

cgtaccacca ccccttcgag atacccacaa cacacgcgcc acgaggcggg gagatctcct 1260

gttgacagct tgagcagctg tagcagttcg tacgacggga gcgaccgaga ggatcaccgg 1320

aacgaattcc actcccccat tggactcacc agaccttcgc cggacgaaag ggaaagtccc 1380

tcagtcaagc gcatgcgact ttctgaagga tgggcaaca 1419

<210> SEQ ID NO 66
<211> LENGTH: 807
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 66

atggcccagc ccctgtgccc gccgctctcc gagtcctgga tgctctctgc ggcctggggc 60

ccaactcggc ggccgccgcc ctccgacaag gactgcggcc gctccctcgt ctcgtcccca 120

gactcatggg gcagcacccc agccgacagc cccgtggcga gccccgcgcg gccaggcacc 180

ctccgggacc cccgcgcccc ctccgtaggt aggcgcggcg cgcgcagcag ccgcctgggc 240

agcgggcaga ggcagagcgc cagtgagcgg gagaaactgc gcatgcgcac gctggcccgc 300

gccctgcacg agctgcgccg ctttctaccg ccgtccgtgg cgcccgcggg ccagagcctg 360

accaagatcg agacgctgcg cctggctatc cgctatatcg gccacctgtc ggccgtgcta 420

ggcctcagcg aggagagtct ccagcgccgg tgccggcagc gcggtgacgc ggggtcccct 480

cggggctgcc cgctgtgccc cgacgactgc cccgcgcaga tgcagacacg gacgcaggct 540

gaggggcagg ggcaggggcg cgggctgggc ctggtatccg ccgtccgcgc cggggcgtcc 600

tggggatccc cgcctgcctg ccccggagcc cgagctgcac ccgagccgcg cgacccgcct 660

gcgctgttcg ccgaggcggc gtgcccggaa gggcaggcga tggagccaag cccaccgtcc 720

ccgctccttc cgggcgacgt gctggctctg ttggagacct ggatgcccct ctcgcctctg 780

gagtggctgc ctgaggagcc caagttg 807

<210> SEQ ID NO 67
<211> LENGTH: 1239
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 67

atgctggaaa tgctagaata taatcactat caggtgcaga cccacctcga aaaccccacc 60

aagtaccaca tacagcaagc ccaacggcag caggtaaagc agtacctttc taccacttta 120

gcaaataaac atgccaacca agtcctgagc ttgccatgtc caaaccagcc tggcgatcat 180

gtcatgccac cggtgccggg gagcagcgca cccaacagcc ccatggctat gcttacgctt 240

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aactccaact gtgaaaaaga gggattttat aagtttgaag agcaaaacag ggcagagagc 300

gagtgcccag gcatgaacac acattcacga gcgtcctgta tgcagatgga tgatgtaatc 360

gatgacatca ttagcctaga atcaagttat aatgaggaaa tcttgggctt gatggatcct 420

gctttgcaaa tggcaaatac gttgcctgtc tcgggaaact tgattgatct ttatggaaac 480

caaggtctgc ccccaccagg cctcaccatc agcaactcct gtccagccaa ccttcccaac 540

ataaaaaggg agctcacaga gtctgaagca agagcactgg ccaaagagag gcagaaaaag 600

gacaatcaca acctgattga acgaagaaga agatttaaca taaatgaccg cattaaagaa 660

ctaggtactt tgattcccaa gtcaaatgat ccagacatgc gctggaacaa gggaaccatc 720

ttaaaagcat ccgtggacta tatccgaaag ttgcaacgag aacagcaacg cgcaaaagaa 780

cttgaaaacc gacagaagaa actggagcac gccaaccggc atttgttgct cagaatacag 840

gaacttgaaa tgcaggctcg agctcatgga ctttcccttа ttccatccac gggtctctgc 900

tctccagatt tggtgaatcg gatcatcaag caagaacccg ttcttgagaa ctgcagccaa 960

gacctccttc agcatcatgc agacctaacc tgtacaacaa ctctcgatct cacggatggc 1020

accatcacct tcaacaacaa cctcggaact gggactgagg ccaaccaagc ctatagtgtc 1080

cccacaaaaa tgggatccaa actggaagac atcctgatgg acgacaccct ttctcccgtc 1140

ggtgtcactg atccactcct ttcctcagtg tcccccggag cttccaaaac aagcagccgg 1200

aggagcagta tgagcatgga agagacggag cacacttgt 1239

<210> SEQ ID NO 68
<211> LENGTH: 1317
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 68

atgcccctca acgttagctt caccaacagg aactatgacc tcgactacga ctcggtgcag 60

ccgtatttct actgcgacga ggaggagaac ttctaccagc agcagcagca gagcgagctg 120

cagcccccgg cgcccagcga ggatatctgg aagaaattcg agctgctgcc caccccgccc 180

ctgtccccta gccgccgctc cgggctctgc tcgccctcct acgttgcggt cacacccttc 240

tcccttcggg gagacaacga cggcggtggc gggagcttct ccacggccga ccagctggag 300

atggtgaccg agctgctggg aggagacatg gtgaaccaga gtttcatctg cgacccggac 360

gacgagacct tcatcaaaaa catcatcatc caggactgta tgtggagcgg cttctcggcc 420

gccgccaagc tcgtctcaga gaagctggcc tcctaccagg ctgcgcgcaa agacagcggc 480

agcccgaacc ccgcccgcgg ccacagcgtc tgctccacct ccagcttgta cctgcaggat 540

ctgagcgccg ccgcctcaga gtgcatcgac ccctcggtgg tcttccccta ccctctcaac 600

gacagcagct cgcccaagtc ctgcgcctcg caagactcca gcgccttctc tccgtcctcg 660

gattctctgc tctcctcgac ggagtcctcc ccgcagggca gccccgagcc cctggtgctc 720

catgaggaga caccgcccac caccagcagc gactctgagg aggaacaaga agatgaggaa 780

gaaatcgatg ttgtttctgt ggaaaagagg caggctcctg gcaaaaggtc agagtctgga 840

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cacgtctcca cacatcagca caactacgca gcgcctccct ccactcggaa ggactatcct 960

gctgccaaga gggtcaagtt ggacagtgtc agagtcctga gacagatcag caacaaccga 1020

aaatgcacca gccccaggtc ctcggacacc gaggagaatg tcaagaggcg aacacacaac 1080

gtcttggagc gccagaggag gaacgagcta aaacggagct tttttgccct gcgtgaccag 1140

atcccggagt tggaaaacaa tgaaaaggcc cccaaggtag ttatccttaa aaaagccaca 1200

gcatacatcc tgtccgtcca agcagaggag caaaagctca tttctgaaga ggacttgttg 1260

cggaaacgac gagaacagtt gaaacacaaa cttgaacagc tacggaactc ttgtgcg 1317

<210> SEQ ID NO 69
<211> LENGTH: 618
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 69

atggactacg actcgtacca gcactatttc tacgactatg actgcgggga ggatttctac 60

cgctccacgg cgcccagcga ggacatctgg aagaaattcg agctggtgcc atcgcccccc 120

acgtcgccgc cctggggctt gggtcccggc gcaggggacc cggcccccgg gattggtccc 180

ccggagccgt ggcccggagg gtgcaccgga gacgaagcgg aatcccgggg ccactcgaaa 240

ggctggggca ggaactacgc ctccatcata cgccgtgact gcatgtggag cggcttctcg 300

gcccgggaac ggctggagag agctgtgagc gaccggctcg ctcctggcgc gccccggggg 360

aacccgccca aggcgtccgc cgccccggac tgcactccca gcctcgaagc cggcaacccg 420

gcgcccgccg ccccctgtcc gctgggcgaa cccaagaccc aggcctgctc cgggtccgag 480

agcccaagcg actcgggtaa ggacctcccc gagccatcca agaggggccc accccatggg 540

tggccaaagc tctgcccctg cctgaggtca ggcattggct cttctcaagc tcttgggcca 600

tctccgcctc tctttggc 618

<210> SEQ ID NO 70
<211> LENGTH: 1392
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 70

atgccgagtt gttccacgtc tacgatgcca ggaatgatat gcaagaaccc cgacttggag 60

tttgactctt tgcaaccatg cttttatccg gatgaagacg acttttattt cggcggcccg 120

gacagcaccc ctcctggaga ggacatctgg aaaaaattcg aacttttgcc tacaccccca 180

ctcagtccct ctcgaggatt tgcggaacac agcagtgaac cgccgtcttg ggtgacagag 240

atgctcctcg agaacgaatt gtggggaagc cctgcggagg aagacgcttt cgggctcggt 300

ggactcggag gtctcacgcc gaacccagtc atactgcagg attgcatgtg gtctggattc 360

tcagctcggg agaagctgga acgggcagtt tctgagaaac tccaacatgg ccggggccct 420

ccaacagcgg gttctaccgc acagtcccct ggtgctggag ccgctagtcc cgcggggaga 480

ggccatgggg gcgcggcagg agcgggtagg gccggcgctg cgttgcctgc tgagcttgcg 540

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cacccgccg ctgaatgtgt agatcccgcg gtagtgtttc cgttccccgt taataagcga 600

gaaccggcac cggtgccagc cgctcctgcg tctgcacccg cggcaggtcc tgctgtcgcc 660

tcaggagcag gtattgccgc tcctgcaggg gcaccaggag tagcccctcc aaggcccggc 720

ggtaggcaaa cctccggcgg cgaccacaaa gcactctcaa cgagcggaga ggatacactg 780

tccgatagtg atgacgagga cgacgaagag gaggacgagg aggaggagat agatgttgtc 840

acggtcgaga agcgaaggag ttcttcaaat acaaaagcgg taacgacatt cacgataaca 900

gtaagaccta agaacgcagc cctcggtcca gggcgggccc agtccagtga gcttatactt 960

aagcgctgcc tgccgattca ccagcagcat aactacgcgg cccctagtcc ctacgttgag 1020

agcgaggatg cccccccaca aaaaaaaata aagtctgaag cgtccccccg ccccctgaaa 1080

tccgtaatcc ccccaaaggc gaagtcactc agtcccagga attcagattc cgaggactcc 1140

gaacggcggc ggaatcataa catacttgag agacaacgac gcaatgacct gaggtcttct 1200

tttttgaccc tccgagatca cgtccccgag ctggttaaga atgagaaagc tgcgaaggta 1260

gtcatactga aaaaggccac cgagtatgtc catagtttgc aagctgagga gcaccagctt 1320

ctccttgaaa aggagaaact tcaggcacga caacagcaat tgctgaaaaa gattgagcat 1380

gcacgcactt gt 1392

<210> SEQ ID NO 71
<211> LENGTH: 960
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 71

atggagctac tgtcgccacc gctccgcgac gtagacctga cggcccccga cggctctctc 60

tgctcctttg ccacaacgga cgacttctat gacgacccgt gtttcgactc cccggacctg 120

cgcttcttcg aagacctgga cccgcgcctg atgcacgtgg gcgcgctcct gaaacccgaa 180

gagcactcgc acttccccgc ggcggtgcac ccggccccgg gcgcacgtga ggacgagcat 240

gtgcgcgcgc ccagcgggca ccaccaggcg ggccgctgcc tactgtgggc ctgcaaggcg 300

tgcaagcgca agaccaccaa cgccgaccgc cgcaaggccg ccaccatgcg cgagcggcgc 360

cgcctgagca aagtaaatga ggcctttgag acactcaagc gctgcacgtc gagcaatcca 420

aaccagcggt tgcccaaggt ggagatcctg cgcaacgcca tccgctatat cgagggcctg 480

caggctctgc tgcgcgacca ggacgccgcg ccccctggcg ccgcagccgc cttctatgcg 540

ccgggcccgc tgcccccggg ccgcggcggc gagcactaca gcggcgactc cgacgcgtcc 600

agcccgcgct ccaactgctc cgacggcatg atggactaca gcggcccccc gagcggcgcc 660

cggcggcgga actgctacga aggcgcctac tacaacgagg cgcccagcga acccaggccc 720

gggaagagtg cggcggtgtc gagcctagac tgcctgtcca gcatcgtgga gcgcatctcc 780

accgagagcc ctgcggcgcc cgccctcctg ctggcggacg tgccttctga gtcgcctccg 840

cgcaggcaag aggctgccgc ccccagcgag ggagagagca gcggcgaccc cacccagtca 900

ccggacgccg ccccgcagtg ccctgcgggt gcgaacccca acccgatata ccaggtgctc 960

<210> SEQ ID NO 72
<211> LENGTH: 672

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<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 72

atggagctgt atgagacatc cccctacttc taccaggaac cccgcttcta tgatggggaa 60

aactacctgc ctgtccacct ccagggcttc gaaccaccag gctacgagcg gacggagctc 120

accctgagcc ccgaggcccc agggcccctt gaggacaagg ggctggggac ccccgagcac 180

tgtccaggcc agtgcctgcc gtgggcgtgt aaggtgtgta agaggaagtc ggtgtccgtg 240

gaccggcggc gggcggccac actgagggag aagcgcaggc tcaagaaggt gaatgaggcc 300

ttcgaggccc tgaagagaag caccctgctc aaccccaacc agcggctgcc caaggtggag 360

atcctgcgca gtgccatcca gtacatcgag cgcctccagg ccctgctcag ctccctcaac 420

caggaggagc gtgacctccg ctaccggggc gggggcgggc cccagccagg ggtgcccagc 480

gaatgcagct ctcacagcgc ctcctgcagt ccagagtggg gcagtgcact ggagttcagc 540

gccaacccag gggatcatct gctcacggct gaccctacag atgcccacaa cctgcactcc 600

ctcacctcca tcgtggacag catcacagtg gaagatgtgt ctgtggcctt cccagatgaa 660

accatgccca ac 672

<210> SEQ ID NO 73
<211> LENGTH: 1068
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 73

atgaccaaat cgtacagcga gagtgggctg atgggcgagc ctcagcccca aggtcctcca 60

agctggacag acgagtgtct cagttctcag gacgaggagc acgaggcaga caagaaggag 120

gacgacctcg aagccatgaa cgcagaggag gactcactga ggaacggggg agaggaggag 180

gacgaagatg aggacctgga agaggaggaa gaagaggaag aggaggatga cgatcaaaag 240

cccaagagac gcggccccaa aaagaagaag atgactaagg ctcgcctgga gcgttttaaa 300

ttgagacgca tgaaggctaa cgcccgggag cggaaccgca tgcacggact gaacgcggcg 360

ctagacaacc tgcgcaaggt ggtgccttgc tattctaaga cgcagaagct gtccaaaatc 420

gagactctgc gcttggccaa gaactacatc tgggctctgt cggagatcct gcgctcaggc 480

aaaagcccag acctggtctc cttcgttcag acgctttgca agggcttatc ccaacccacc 540

accaacctgg ttgcgggctg cctgcaactc aatcctcgga cttttctgcc tgagcagaac 600

caggacatgc ccccccacct gccgacggcc agcgcttcct tccctgtaca cccctactcc 660

taccagtcgc ctgggctgcc cagtccgcct tacggtacca tggacagctc ccatgtcttc 720

cacgttaagc ctccgccgca cgcctacagc gcagcgctgg agcccttctt tgaaagccct 780

ctgactgatt gcaccagccc ttcctttgat ggacccctca gcccgccgct cagcatcaat 840

ggcaacttct ctttcaaaca cgaaccgtcc gccgagtttg agaaaaatta tgcctttacc 900

atgcactatc ctgcagcgac actggcaggg gcccaaagcc acggatcaat cttctcaggc 960

accgctgccc ctcgctgcga gatccccata gacaatatta tgtccttcga tagccattca 1020

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catcatgagc gagtcatgag tgcccagctc aatgccatat ttcatgat 1068

<210> SEQ ID NO 74
<211> LENGTH: 711
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 74

atgccagccc gccttgagac ctgcatctcc gacctcgact gcgccagcag cagcggcagt 60

gacctatccg gcttcctcac cgacgaggaa gactgtgcca gactccaaca ggcagcctcc 120

gcttcggggc cgcccgcgcc ggcccgcagg ggcgcgccca atatctcccg ggcgtctgag 180

gttccagggg cacaggacga cgagcaggag aggcggcggc gccgcggccg gacgcgggtc 240

cgctccgagg cgctgctgca ctcgctgcgc aggagccggc gcgtcaaggc caacgatcgc 300

gagcgcaacc gcatgcacaa cttgaacgcg gccctggacg cactgcgcag cgtgctgccc 360

tcgttccccg acgacaccaa gctcaccaaa atcgagacgc tgcgcttcgc ctacaactac 420

atctgggctc tggccgagac actgcgcctg gcggatcaag ggctgcccgg aggcggtgcc 480

cgggagcgcc tcctgccgcc gcagtgcgtc ccctgcctgc ccggtccccc aagccccgcc 540

agcgacgcgg agtcctgggg ctcaggtgcc gccgccgcct ccccgctctc tgaccccagt 600

agcccagccg cctccgaaga cttcacctac cgccccggcg accctgtttt ctccttccca 660

agcctgccca aagacttgct ccacacaacg ccctgtttca ttccttacca c 711

<210> SEQ ID NO 75
<211> LENGTH: 642
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 75

atgacaccac aaccatctgg tgctcccaca gtccaggtga cgcgagagac tgaaagatca 60

ttcccacgcg cgtccgagga tgaggtgaca tgtccaacta gcgcaccccc ctctcctacc 120

cggacccgcg ggaattgtgc tgaggccgaa gagggaggat gcagaggagc accaaggaaa 180

cttcgagccc gacggggtgg aagaagccgc cccaagtctg agctcgccct tagcaagcag 240

cgccgcagtc ggaggaaaaa ggcaaacgac cgggaaagga ataggatgca taatcttaat 300

tctgctctgg acgctctgcg aggcgtactt cctactttcc cggatgacgc gaaattgacc 360

aagatagaga ctctccggtt tgcacataat tacatctggg ctcttacaca aacactgaga 420

attgccgatc acagtcttta cgctcttgag ccacccgccc cgcactgtgg cgagctgggt 480

agccccggcg gctctcctgg agactggggg tctttgtatt ctcctgtcag ccaagcggga 540

tctttgagtc cggctgccag tctcgaagaa agacccggac tccttggagc gacttttca 600

gcatgtctgt cccctggctc attggctttc tcagactttt tg 642

<210> SEQ ID NO 76
<211> LENGTH: 741
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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

<400> SEQUENCE: 76

atggccctgc ctcccagccc gctggccatg gaatatgtca atgactttga cttgatgaag 60

tttgaggtaa agcgggaacc ctctgagggc cgacctggcc cacctacagc ctcactggga 120

tccacacctt acagctcagt gcctccttca cccaccttca gtgaaccagg catggtaggg 180

gcaaccgagg gtacacgacc aggtttggag gagctgtact ggcttgctac cctgcagcag 240

cagcttgggg ctggggaggc attgggactg agtcctgaag aggccatgga gctactgcaa 300

ggtcagggcc cagtccctgt tgatggaccc catggttact acccagggag cccagaggag 360

acaggagccc agcacgttca gttggcagag cggttttccg acgcggcgct tgtctcgatg 420

tctgtgcgag aactaaaccg gcagctgcgg ggatgcggga gagacgaggc tctacgactg 480

aagcagaggc gtcgaacgct gaagaaccgt ggctatgcgc aagcatgtcg ttccaagagg 540

ctgcaacaga ggcgaggtct tgaggccgag cgcgcccgtc ttgcagccca gctagatgcg 600

ctacgagctg aagtagcacg tttggcaaga gagcgagatc tctacaaggc tcgctgtgac 660

cggctaacct cgagtggccc cgggtccggg gatccctccc acctttcct ctgcccaact 720

ttcttgtaca aagttgtccc c 741

<210> SEQ ID NO 77
<211> LENGTH: 1395
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 77

atgaacgcgc agctgaccat ggaagcgatc ggcgagctgc acggggtgag ccatgagccg 60

gtgcccgccc ctgccgacct gctgggcggc agcccccacg cgcgcagctc cgtggcgcac 120

cgcggcagcc acctgccccc cgcgcacccg cgctccatgg gcatggcgtc cctgctggac 180

ggcggcagcg gcggcggaga ttaccaccac caccaccggg cccctgagca cagcctggcc 240

ggcccccctgc atcccaccat gaccatggcc tgcgagactc ccccaggtat gagcatgccc 300

accacctaca ccaccttgac ccctctgcag ccgctgcctc ccatctccac agtctcggac 360

aagttccccc accatcacca ccaccaccat caccaccacc acccgcacca ccaccagcgc 420

ctggcgggca acgtgagcgg tagcttcacg ctcatgcggg atgagcgcgg gctggcctcc 480

atgaataacc tctatacccc ctaccacaag gacgtggccg gcatgggcca gagcctctcg 540

cccctctcca gctccggtct gggcagcatc cacaactccc agcaagggct cccccactat 600

gcccacccgg gggccgccat gcccaccgac aagatgctca cccccaacgg cttcgaagcc 660

caccacccgg ccatgctcgg ccgccacggg gagcagcacc tcacgcccac ctcggccggc 720

atggtgccca tcaacggcct tcctccgcac catccccacg cccacctgaa cgcccagggc 780

cacgggcaac tcctgggcac agcccgggag cccaaccctt cggtgaccgg cgcgcaggtc 840

agcaatggaa gtaattcagg gcagatggaa gagatcaata ccaaagaggt ggcgcagcgt 900

atcaccaccg agctcaagcg ctacagcatc ccacaggcca tcttcgcgca gagggtgctc 960

tgccgctccc aggggaccct ctcggacctg ctgcgcaacc ccaaaccctg gagcaaactc 1020

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aaatccggcc gggagacctt ccggaggatg tggaagtggc tgcaggagcc ggagttccag 1080

cgcatgtccg cgctccgctt agcagcatgc aaaaggaaag aacaagaaca tgggaaggat 1140

agaggcaaca cacccaaaaa gcccaggttg gtcttcacag atgtccagcg tcgaactcta 1200

catgcaatat tcaaggaaaa taagcgtcca tccaaagaat tgcaaatcac catttcccag 1260

cagctggggt tggagctgag cactgtcagc aacttcttca tgaacgcaag aaggaggagt 1320

ctggacaagt ggcaggacga gggcagctcc aattcaggca actcatcttc ttcatcaagc 1380

acttgtacca aagca 1395

<210> SEQ ID NO 78
<211> LENGTH: 891
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 78

atgatgtctt atcttaagca accgccttac gcagtcaatg ggctgagtct gaccacttcg 60

ggtatggact tgctgcaccc ctccgtgggc tacccggggc cctgggcttc ttgtcccgca 120

gccacccccc ggaaacagcg ccgggagagg acgacgttca ctcgggcgca gctagatgtg 180

ctggaagcac tgtttgccaa gacccggtac ccagacatct tcatgcgaga ggaggtggca 240

ctgaaaatca acttgcccga gtcgagggtg caggtatggt ttaagaatcg aagagctaag 300

tgccgccaac aacagcaaca acagcagaat ggaggtcaaa acaaagtgag acctgccaaa 360

aagaagacat ctccagctcg ggaagtgagt tcagagagtg gaacaagtgg ccaattcact 420

ccccctcta gcacctcagt cccgaccatt gccagcagca gtgctcctgt gtctatctgg 480

agcccagctt ccatctcccc actgtcagat cccttgtcca cctcctcttc ctgcatgcag 540

aggtcctatc ccatgaccta tactcaggct tcaggttata gtcaaggata tgctggctca 600

acttcctact ttgggggcat ggactgtgga tcatatttga cccctatgca tcaccagctt 660

cccggaccag gggccacact cagtcccatg ggtaccaatg cagtcaccag ccatctcaat 720

cagtccccag cttctctttc cacccaggga tatggagctt caagcttggg ttttaactca 780

accactgatt gcttggatta taaggaccaa actgcctcct ggaagcttaa cttcaatgct 840

gactgcttgg attataaaga tcagacatcc tcgtggaaat tccaggtttt g 891

<210> SEQ ID NO 79
<211> LENGTH: 1554
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 79

atggcggccc ttcccggcac ggtaccgaga atgatgcggc cggctccggg gcagaactac 60

ccccgcacgg gattcccttt ggaagtgtcc accccgcttg gccaaggccg ggtcaatcag 120

ctgggagggg tcttcatcaa tgggcgaccc ctgcctaacc acatccgcca caagatagtg 180

gagatggccc accatggcat ccggccctgt gtcatctccc gacagctgcg tgtctcccac 240

ggctgcgtct ccaagattct ttgccgctac caggagaccg ggtccatccg gcctggggcc 300

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atcggcggca gcaagcccag acaggtggcg actccggatg tagagaaaaa gattgaggag 360

tacaagaggg aaaacccagg catgttcagc tgggagatcc gggacaggct gctgaaggat 420

gggcactgtg accgaagcac tgtgccctca gtgagttcga ttagccgcgt gctcagaatc 480

aagttcggga agaaagagga ggaggatgaa gcggacaaga aggaggacga cggcgaaaag 540

aaggccaaac acagcatcga cggcatcctg ggcgacaaag ggaaccggct ggacgagggc 600

tcggatgtgg agtcggaacc tgacctccca ctgaagcgca agcagcgacg cagtcggacc 660

acattcacgg ccgagcagct ggaggagctg gagaaggcct ttgagaggac ccactaccca 720

gacatataca cccgcgagga gctggcgcag aggaccaagc tgacagaggc gcgtgtgcag 780

gtctggttca gtaaccgccg cgcccgttgg cgtaagcagg caggagccaa ccagctggcg 840

gcgttcaacc accttctgcc aggaggcttc ccgcccaccg gcatgcccac gctgcccccc 900

taccagctgc cggactccac ctaccccacc accaccatct cccaagatgg gggcagcact 960

gtgcaccggc ctcagcccct gccaccgtcc accatgcacc agggcgggct ggctgcagcg 1020

gctgcagccg ccgacaccag ctctgcctac ggagcccgcc acagcttctc cagctactct 1080

gacagcttca tgaatccggc ggcgccctcc aaccacatga acccggtcag caacggcctg 1140

tctcctcagg tgatgagcat cttgggcaac cccagtgcgg tgcccccgca gccacaggct 1200

gacttctcca tctccccgct gcatggcggc ctggactcgg ccacctccat ctcagccagc 1260

tgcagccagc gggccgactc catcaagcca ggagacagcc tgcccacctc ccaggcctac 1320

tgcccaccca cctacagcac caccggctac agcgtggacc ccgtggccgg ctatcagtac 1380

ggccagtacg gccagagtga gtgcctggtg ccctgggcgt cccccgtccc cattccttct 1440

cccaccccca gggcctcctg cttgtttatg gagagctaca aggtggtgtc agggtgggga 1500

atgtccattt cacagatgga aaaattgaag tccagccaga tggaacagtt cacc 1554

<210> SEQ ID NO 80
<211> LENGTH: 903
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 80

atgagttgcc aagcttttac ttcggctgat acctttatac ctctgaattc tgacgcctct 60

gcaactctgc ctctgataat gcatcacagt gctgccgagt gtctaccagt ctccaaccat 120

gccaccaatg tgatgtctac agcaacagga cttcattatt ctgttccttc ctgtcattat 180

ggaaaccagc catcaaccta tggagtgatg gcaggtagtt taacccctg tctttataaa 240

tttcctgacc acaccttgag tcatggattt cctcctatac accagcctct tctggcagag 300

gaccccacag ctgctgattt caagcaggaa ctcaggcgga aaagtaaatt ggtggaagag 360

ccaatagaca tggattctcc agaaatcaga gaacttgaaa agtttgccaa tgaatttaaa 420

gtgagacgaa ttaaattagg atacacccag acaaatgttg gggaggccct ggcagctgtg 480

catggctctg aattcagtca aacaacaatc tgccgatttg aaaatctgca gctcagcttt 540

aaaaatgcat gcaaactgaa agcaatatta tccaaatggc tggaggaagc tgagcaagta 600

ggagctttgt acaatgaaaa agtgggagca aatgaaagga aaagaaaacg aagaacaact 660

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ataagcattg ctgctaaaga tgctctggag agacactttg gagaacagaa taaaccttct 720

tctcaagaga tcatgaggat ggctgaagaa ctgaatctgg agaaagaagt agtaagagtt 780

tggttttgca accggaggca gagagaaaaa cgggtgaaaa caagtctgaa tcagagttta 840

ttttctattt ctaaggaaca tcttgagtgc agatcaggcc tcatgggccc agctttcttg 900

tac 903

<210> SEQ ID NO 81
<211> LENGTH: 1080
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 81

atggcgggac acctggcttc agattttgcc ttctcgcccc ctccaggtgg tggaggtgat 60

gggccagggg ggccggagcc gggctgggtt gatcctcgga cctggctaag cttccaaggc 120

cctcctggag ggccaggaat cgggccgggg gttgggccag gctctgaggt gtgggggatt 180

cccccatgcc ccccgccgta tgagttctgt ggggggatgg cgtactgtgg gccccaggtt 240

ggagtggggc tagtgcccca aggcggcttg gagacctctc agcctgaggg cgaagcagga 300

gtcggggtgg agagcaactc cgatggggcc tccccggagc cctgcaccgt caccctggt 360

gccgtgaagc tggagaagga gaagctggag caaaacccgg aggagtccca ggacatcaaa 420

gctctgcaga aagaactcga gcaatttgcc aagctcctga agcagaagag gatcaccctg 480

ggatatacac aggccgatgt ggggctcacc ctgggggttc tatttgggaa ggtattcagc 540

caaacgacca tctgccgctt tgaggctctg cagcttagct tcaagaacat gtgtaagctg 600

cggcccttgc tgcagaagtg ggtggaggaa gctgacaaca atgaaaatct tcaggagata 660

tgcaaagcag aaaccctcgt gcaggcccga aagagaaagc gaaccagtat cgagaaccga 720

gtgagaggca acctggagaa tttgttcctg cagtgcccga aacccacact gcagcagatc 780

agccacatcg cccagcagct tgggctcgag aaggatgtgg tccgagtgtg gttctgtaac 840

cggcgccaga agggcaagcg atcaagcagc gactatgcac aacgagagga ttttgaggct 900

gctgggtctc ctttctcagg gggaccagtg tcctttcctc tggccccagg gccccatttt 960

ggtaccccag gctatgggag ccctcacttc actgcactgt actcctcggt ccctttccct 1020

gaggggggaag cctttccccc tgtctctgtc accactctgg gctctcccat gcattcaaac 1080

<210> SEQ ID NO 82
<211> LENGTH: 1440
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 82

atggcttcag acagcatatt tgagtcattt ccttcgtacc cacagtgctt catgagagaa 60

tgcatacttg gaatgaatcc ttctagagac gtccacgatg ccagcacgag ccgccgcttc 120

acgccgcctt ccaccgcgct gagcccaggc aagatgagcg aggcgttgcc gctgggcgcc 180

ccggacgccg gcgctgccct ggccggcaag ctgaggagcg gcgaccgcag catggtggag 240

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gtgctggccg accacccggg cgagctggtg cgcaccgaca gccccaactt cctctgctcc 300

gtgctgccta cgcactggcg ctgcaacaag accctgccca tcgctttcaa ggtggtggcc 360

ctaggggatg ttccagatgg cactctggtc actgtgatgg ctggcaatga tgaaaactac 420

tcggctgagc tgagaaatgc taccgcagcc atgaagaacc aggttgcaag atttaatgac 480

ctcaggtttg tcggtcgaag tggaagaggg aaaagcttca ctctgaccat cactgtcttc 540

acaaacccac cgcaagtcgc cacctaccac agagccatca aaatcacagt ggatgggccc 600

cgagaacctc gaagacatcg gcagaaacta gatgatcaga ccaagcccgg gagcttgtcc 660

ttttccgagc ggctcagtga actggagcag ctgcggcgca cagccatgag ggtcagccca 720

caccacccag cccccacgcc caaccctcgt gcctccctga accactccac tgcctttaac 780

cctcagcctc agagtcagat gcaggataca aggcagatcc aaccatcccc accgtggtcc 840

tacgatcagt cctaccaata cctgggatcc attgcctctc cttctgtgca cccagcaacg 900

cccatttcac ctggacgtgc cagcggcatg acaaccctct ctgcagaact ttccagtcga 960

ctctcaacgg cacccgacct gacagcgttc agcgacccgc gccagttccc cgcgctgccc 1020

tccatctccg acccccgcat gcactatcca ggcgccttca cctactcccc gacgccggtc 1080

acctcgggca tcggcatcgg catgtcggcc atgggctcgg ccacgcgcta ccacacctac 1140

ctgccgccgc cctaccccgg ctcgtcgcaa gcgcagggag gcccgttcca agccagctcg 1200

ccctcctacc acctgtacta cggcgcctcg gccggctcct accagttctc catggtgggc 1260

ggcgagcgct cgccgccgcg catcctgccg ccctgcacca acgcctccac cggctccgcg 1320

ctgctcaacc ccagcctccc gaaccagagc gacgtggtgg aggccgaggg cagccacagc 1380

aactccccca ccaacatggc gccctccgcg cgcctggagg aggccgtgtg gaggccctac 1440

<210> SEQ ID NO 83
<211> LENGTH: 852
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 83

atgtcgatgc tgccgtcgtt tggctttacg caggagcaag tggcgtgcgt gtgcgaggtt 60

ctgcagcaag gcggaaacct ggagcgcctg ggcaggttcc tgtggtcact gcccgcctgc 120

gaccacctgc acaagaacga gagcgtactc aaggccaagg cggtggtcgc cttccaccgc 180

ggcaacttcc gtgagctcta caagatcctg gagagccacc agttctcgcc tcacaaccac 240

cccaaactgc agcaactgtg gctgaaggcg cattacgtgg aggccgagaa gctgtgcggc 300

cgacccctgg gcgccgtggg caaatatcgg gtgcgccgaa aatttccact gccgcgcacc 360

atctgggacg gcgaggagac cagctactgc ttcaaggaga agtcgagggg tgtcctgcgg 420

gagtggtacg cgcacaatcc ctacccatcg ccgcgtgaga agcgggagct ggccgaggcc 480

accggcctca ccaccaccca ggtcagcaac tggtttaaga accggaggca aagagaccgg 540

gccgcggagg ccaaggaaag ggagaacacc gaaaacaata actcctcctc caacaagcag 600

aaccaactct ctcctctgga agggggcaag ccgctcatgt ccagctcaga agaggaattc 660

tcacctcccc aaagtccaga ccagaactcg gtccttctgc tgcagggcaa tatgggccac 720

gccaggagct caaactattc tctcccgggc ttaacagcct cgcagcccag tcacggcctg 780

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cagacccacc agcatcagct ccaagactct ctgctcggcc ccctcacctc cagtctggtg 840

gacttggggt cc 852

<210> SEQ ID NO 84
<211> LENGTH: 873
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 84

atgtccatgc tgcccacctt cggcttcacg caggagcaag tggcgtgcgt gtgcgaggtg 60

ctgcagcagg gcggcaacat cgagcggctg ggccgcttcc tgtggtcgct gcccgcctgc 120

gagcaccttc acaagaatga aagcgtgctc aaggccaagg ccgtggtggc cttccaccgc 180

ggcaacttcc gcgagctcta caagatcctg gagagccacc agttctcgcc gcacaaccac 240

gccaagctgc agcagctgtg gctcaaggca cactacatcg aggcggagaa gctgcgcggc 300

cgacccctgg gcgccgtggg caaataccgc gtgcgccgca aattcccgct gccgcgctcc 360

atctgggacg gcgaggagac cagctactgc ttcaaggaaa agagtcgcag cgtgctgcgc 420

gagtggtacg cgcacaaccc ctacccttca ccccgcgaga agcgtgagct gacggaggcc 480

acgggcctca ccaccacaca ggtcagcaac tggttcaaga accggcggca gcgcgaccgg 540

gcggccgagg ccaaggaaag ggagaacaac gagaactcca attctaacag ccacaacccg 600

ctgaatggca gcggcaagtc ggtgttaggc agctcggagg atgagaagac tccatcgggg 660

acgccagacc actcatcatc cagccccgca ctgctcctca gcccgccgcc ccctgggctg 720

ccgtccctgc acagcctggg ccaccctccg ggccccagcg cagtgccagt gccggtgcca 780

ggcggaggtg gagcggaccc actgcaacac caccatggcc tgcaggactc catcctcaac 840

cccatgtcag ccaacctcgt ggacctgggc tcc 873

<210> SEQ ID NO 85
<211> LENGTH: 804
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 85

atgccgcgct ccttcctggt caagaagcat ttcaacgcct ccaaaaagcc aaactacagc 60

gaactggaca cacatacagt gattatttcc ccgtatctct atgagagtta ctccatgcct 120

gtcataccac aaccagagat cctcagctca ggagcataca gccccatcac tgtgtggact 180

accgctgctc cattccacgc ccagctaccc aatggcctct ctcctctttc cggatactcc 240

tcatctttgg ggcgagtgag tccccctcct ccatctgaca cctcctccaa ggaccacagt 300

ggctcagaaa gccccattag tgatgaagag gaaagactac agtccaagct ttcagacccc 360

catgccattg aagctgaaaa gtttcagtgc aatttatgca ataagaccta ttcaactttt 420

tctgggctgg ccaaacataa gcagctgcac tgcgatgccc agtctagaaa atctttcagc 480

tgtaaatact gtgacaagga atatgtgagc ctgggcgccc tgaagatgca tattcggacc 540

cacacattac cttgtgtttg caagatctgc ggcaaggcgt tttccagacc ctggttgctt 600

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caaggacaca ttagaactca cacgggggag aagccttttt cttgccctca ctgcaacaga 660

gcatttgcag acaggtcaaa tctgagggct catctgcaga cccattctga tgtaaagaaa 720

taccagtgca aaaactgctc caaaaccttc tccagaatgt ctctcctgca caaacatgag 780

gaatctggct gctgtgtagc acac 804

<210> SEQ ID NO 86
<211> LENGTH: 1398
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 86

atggcggagg agcaggacct atcggaggtg gagctgagcc ccgtgggctc ggaggagccc 60

cgctgcctgt ccccggggag cgcgccctcg ctagggcccg acggcggcgg cggcggatcg 120

ggcctgcgag ccagcccggg gccaggcgag ctgggcaagg tcaagaagga gcagcaggac 180

ggcgaggcgg acgatgacaa gttccccgtg tgcatccgcg aggccgtcag ccaggtgctc 240

agcggctacg actggacgct ggtgcccatg cccgtgcgcg tcaacggcgc cagcaaaagc 300

aagccgcacg tcaagcggcc catgaacgcc ttcatggtgt gggctcaggc agcgcgcagg 360

aagctcgcgg accagtaccc gcacctgcac aacgctgagc tcagcaagac gctgggcaag 420

ctctggaggc tgctgaacga aagtgacaag cgccccttca tcgaggaggc tgagcggctc 480

cgtatgcagc acaagaaaga ccacccggac tacaagtacc agcccaggcg gcggaagaac 540

gggaaggccg cccagggcga ggcggagtgc cccggtgggg aggccgagca aggtgggacc 600

gccgccatcc aggcccacta caagagcgcc cacttggacc accggcaccc aggagagggc 660

tcccccatgt cagatgggaa ccccgagcac ccctcaggcc agagccatgg cccacccacc 720

cctccaacca ccccgaagac agagctgcag tcgggcaagg cagacccgaa gcgggacggg 780

cgctccatgg gggagggcgg gaagcctcac atcgacttcg gcaacgtgga cattggtgag 840

atcagccacg aggtaatgtc caacatggag acctttgatg tggctgagtt ggaccagtac 900

ctgccgccca atgggcaccc aggccatgtg agcagctact cagcagccgg ctatgggctg 960

ggcagtgccc tggccgtggc cagtggacac tccgcctgga tctccaagcc accaggcgtg 1020

gctctgccca cggtctcacc acctggtgtg gatgccaaag cccaggtgaa gacagagacc 1080

gcggggcccc aggggccccc acactacacc gaccagccat ccacctcaca gatcgcctac 1140

acctccctca gcctgcccca ctatggctca gccttcccct ccatctcccg cccccagttt 1200

gactactctg accatcagcc ctcaggaccc tattatggcc actcgggcca ggcctctggc 1260

ctctactcgg ccttctccta tatggggccc tcgcagcggc ccctctacac ggccatctct 1320

gaccccagcc cctcagggcc ccagtcccac agccccacac actgggagca gccagtatat 1380

acgacactgt cccggccc 1398

<210> SEQ ID NO 87
<211> LENGTH: 951
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

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<400> SEQUENCE: 87

atgtacaaca tgatggagac ggagctgaag ccgccgggcc cgcagcaaac ttcgggggggc 60

ggcggcggca actccaccgc ggcggcggcc ggcggcaacc agaaaaacag cccggaccgc 120

gtcaagcggc ccatgaatgc cttcatggtg tggtcccgcg ggcagcggcg caagatggcc 180

caggagaacc ccaagatgca caactcggag atcagcaagc gcctgggcgc cgagtggaaa 240

cttttgtcgg agacggagaa gcggccgttc atcgacgagg ctaagcggct gcgagcgctg 300

cacatgaagg agcacccgga ttataaatac cggccccggc ggaaaaccaa gacgctcatg 360

aagaaggata agtacacgct gcccggcggg ctgctggccc ccggcggcaa tagcatggcg 420

agcggggtcg gggtgggcgc cggcctgggc gcgggcgtga accagcgcat ggacagttac 480

gcgcacatga acggctggag caacggcagc tacagcatga tgcaggacca gctgggctac 540

ccgcagcacc cgggcctcaa tgcgcacggc gcagcgcaga tgcagcccat gcaccgctac 600

gacgtgagcg ccctgcagta caactccatg accagctcgc agacctacat gaacggctcg 660

cccacctaca gcatgtccta ctcgcagcag ggcacccctg gcatggctct tggctccatg 720

ggttcggtgg tcaagtccga ggccagctcc agccccccctg tggttacctc ttcctcccac 780

tccagggcgc cctgccaggc cggggacctc cgggacatga tcagcatgta tctccccggc 840

gccgaggtgc cggaacccgc cgcccccagc agacttcaca tgtcccagca ctaccagagc 900

ggcccggtgc ccggcacggc cattaacggc acactgcccc tctcacacat g 951

<210> SEQ ID NO 88
<211> LENGTH: 1338
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 88

atgcgacctg ttcgagagaa ctcatcaggt gcgagaagcc cgcgggttcc tgctgatttg 60

gcgcggagca ttttgataag cctacccttc ccgccggact cgctggccca caggccccca 120

agctccgctc cgacggagtc ccagggcctt ttcaccgtgg ccgctccagc cccgggagcg 180

ccttctcctc ccgccacgct ggcgcacctt cttcccgccc cggcaatgta cagccttctg 240

gagactgaac tcaagaaccc cgtagggaca cccacacaag cggcgggcac cggcggcccc 300

gcagccccgg gaggcgcagg caagagtagt gcgaacgcag ccggcggcgc gaactcgggc 360

ggcggcagca gcggtggtgc gagcggaggt ggcgggggta cagaccagga ccgtgtgaaa 420

cggcccatga acgccttcat ggtatggtcc cgcgggcagc ggcgcaaaat ggccctggag 480

aaccccaaga tgcacaattc tgagatcagc aagcgcttgg gcgccgactg gaaactgctg 540

accgacgccg agaagcgacc attcatcgac gaggccaagc gacttcgcgc cgtgcacatg 600

aaggagtatc cggactacaa gtaccgaccg cgccgcaaga ccaagacgct gctcaagaaa 660

gataagtact ccctgcccag cggcctcctg cctcccggtg ccgcggccgc cgccgccgct 720

gccgcggccg cagccgctgc cgccagcagt ccggtgggcg tgggccagcg cctggacacg 780

tacacgcacg tgaacggctg ggccaacggc gcgtactcgc tggtgcagga gcagctgggc 840

tacgcgcagc ccccgagcat gagcagcccg ccgccgccgc ccgcgctgcc gccgatgcac 900

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cgctacgaca tggccggcct gcagtacagc ccaatgatgc cgcccggcgc tcagagctac 960

atgaacgtcg ctgccgcggc cgccgccgcc tcgggctacg ggggcatggc gccctcagcc 1020

acagcagccg cggccgccgc ctacgggcag cagcccgcca ccgccgcggc cgcagctgcg 1080

gccgcagccg ccatgagcct gggccccatg ggctcggtag tgaagtctga gcccagctcg 1140

ccgccgcccg ccatcgcatc gcactctcag cgcgcgtgcc tcggcgacct gcgcgacatg 1200

atcagcatgt acctgccacc cggcggggac gcggccgacg ccgcctctcc gctgcccggc 1260

ggtcgcctgc acggcgtgca ccagcactac cagggcgccg ggactgcagt caacggaacg 1320

gtgccgctga cccacatc 1338

<210> SEQ ID NO 89
<211> LENGTH: 813
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 89

atgttacagg cgtgcaaaat ggaagggttt cccctcgtcc cccctcagcc atcagaagac 60

ctggtgccct atgacacgga tctataccaa cgccaaacgc acgagtatta cccctatctc 120

agcagtgatg gggagagcca tagcgaccat tactgggact tccaccccca ccacgtgcac 180

agcgagttcg agagcttcgc cgagaacaac ttcacggagc tccagagcgt gcagcccccg 240

cagctgcagc agctctaccg ccacatggag ctggagcaga tgcacgtcct cgataccccc 300

atggtgccac cccatcccag tcttggccac caggtctcct acctgccccg gatgtgcctc 360

cagtacccat ccctgtcccc agcccagccc agctcagatg aggaggaggg cgagcggcag 420

agccccccac tggaggtgtc tgacggcgag gcggatggcc tggagcccgg gcctgggctc 480

ctgcctgggg agacaggcag caagaagaag atccgcctgt accagttcct gttggacctg 540

ctccgcagcg gcgacatgaa ggacagcatc tggtgggtgg acaaggacaa gggcaccttc 600

cagttctcgt ccaagcacaa ggaggcgctg gcgcaccgct ggggcatcca gaagggcaac 660

cgcaagaaga tgacctacca gaagatggcg cgcgcgctgc gcaactacgg caagacgggc 720

gaggtcaaga aggtgaagaa gaagctcacc taccagttca gcggcgaagt gctgggccgc 780

gggggcctgg ccgagcggcg ccacccgccc cac 813

<210> SEQ ID NO 90
<211> LENGTH: 789
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 90

atgctcgccc tggaggctgc acagctcgac gggccacact tcagctgtct gtacccagat 60

ggcgtcttct atgacctgga cagctgcaag cattccagct accctgattc agaggggggt 120

cctgactccc tgtgggactg gactgtggcc ccacctgtcc cagccacccc ctatgaagcc 180

ttcgacccgg cagcagccgc ttttagccac ccccaggctg cccagctctg ctacgaaccc 240

cccacctaca gccctgcagg gaacctcgaa ctggccccca gcctggaggc cccggggcct 300

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ggcctccccg cataccccac ggagaacttc gctagccaga ccctggttcc cccggcatat 360

gccccgtacc ccagccctgt gctatcagag gaggaagact taccgttgga cagccctgcc 420

ctggaggtct cggacagcga gtcggatgag gccctcgtgg ctggccccga ggggaaggga 480

tccgaggcag ggactcgcaa gaagctgcgc ctgtaccagt tcctgctggg gctactgacg 540

cgcggggaca tgcgtgagtg cgtgtggtgg gtggagccag gcgccggcgt cttccagttc 600

tcctccaagc acaaggaact cctggcgcgc cgctggggcc agcagaaggg gaaccgcaag 660

cgcatgacct accagaagct ggcgcgcgcc ctccgaaact acgccaagac cggcgagatc 720

cgcaaggtca agcgcaagct cacctaccag ttcgacagcg cgctgctgcc tgcagtccgc 780

cgggccttg 789

<210> SEQ ID NO 91
<211> LENGTH: 744
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 91

atgacgtgtg ttgaacaaga caagctgggt caagcatttg aagatgcttt tgaggttctg 60

aggcaacatt caactggaga tcttcagtac tcgccagatt acagaaatta cctggcttta 120

atcaaccatc gtcctcatgt caaaggaaat tccagctgct atggagtgtt gcctacagag 180

gagcctgtct ataattggag aacggtaatt aacagtgctg cggacttcta ttttgaagga 240

aatattcatc aatctctgca gaacataact gaaaaccagc tggtacaacc cactcttctc 300

cagcaaaagg ggggaaaagg caggaagaag ctccgactgt ttgaatacct tcacgaatcc 360

ctgtataatc cggagatggc atcttgtatt cagtgggtag ataaaaccaa aggcatcttt 420

cagtttgtat caaaaaacaa agaaaaactt gccgagcttt gggggaaaag aaaaggcaac 480

aggaagacca tgacttacca gaaaatggcc agggcactca gaaattacgg aagaagtggg 540

gaaattacca aaatccggag gaagctgact taccagttca gtgaggccat tctccaaaga 600

ctctctccat cctatttcct ggggaaagag atcttctatt cacagtgtgt tcaacctgat 660

caagaatatc tcagtttaaa taactggaat gcaaattata attatacata tgccaattac 720

catgagctaa atcaccatga ttgc 744

<210> SEQ ID NO 92
<211> LENGTH: 612
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 92

atgcaatcat atgcttctgc tatgttaagc gtattcaaca gcgatgatta cagtccagct 60

gtgcaagaga atattcccgc tctccggaga agctcttcct tcctttgcac tgaaagctgt 120

aactctaagt atcagtgtga aacgggagaa aacagtaaag gcaacgtcca ggatagagtg 180

aagcgaccca tgaacgcatt catcgtgtgg tctcgcgatc agaggcgcaa gatggctcta 240

gagaatccca gaatgcgaaa ctcagagatc agcaagcagc tgggatacca gtggaaaatg 300

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cttactgaag ccgaaaaatg gccattcttc caggaggcac agaaattaca ggccatgcac 360

agagagaaat acccgaatta taagtatcga cctcgtcgga aggcgaagat gctgccgaag 420

aattgcagtt tgcttcccgc agatcccgct tcggtactct gcagcgaagt gcaactggac 480

aacaggttgt acagggatga ctgtacgaaa gccacacact caagaatgga gcaccagcta 540

ggccacttac cgcccatcaa cgcagccagc tcaccgcagc aacgggaccg ctacagccac 600

tggacaaagc tg 612

<210> SEQ ID NO 93
<211> LENGTH: 1557
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 93

atggccgacg cagacgaggg ctttggcctg gcgcacacgc ctctggagcc tgacgcaaaa 60

gacctgccct gcgattcgaa acccgagagc gcgctcgggg cccccagcaa gtccccgtcg 120

tccccgcagg ccgccttcac ccagcagggc atggagggaa tcaaagtgtt tctccatgaa 180

agagaactgt ggctaaaatt ccacgaagtg ggcacggaaa tgatcataac caaggctgga 240

aggcggatgt ttcccagtta caaagtgaag gtgacgggcc ttaatcccaa aacgaagtac 300

attcttctca tggacattgt acctgccgac gatcacagat acaaattcgc agataataaa 360

tggtctgtga cgggcaaagc tgagcccgcc atgcctggcc gcctgtacgt gcacccagac 420

tcccccgcca ccggggcgca ttggatgagg cagctcgtct ccttccagaa actcaagctc 480

accaacaacc acctggaccc atttgggcat attattctaa attccatgca caaataccag 540

cctagattac acatcgtgaa agcggatgaa aataatggat ttggctcaaa aaatacagcg 600

ttctgcactc acgtctttcc tgagactgcg tttatagcag tgacttccta ccagaaccac 660

aagatcacgc aattaaagat tgagaataat ccctttgcca aaggatttcg gggcagtgat 720

gacatggagc tgcacagaat gtcaagaatg caaagtaaag aatatcccgt ggtccccagg 780

agcaccgtga ggcaaaaagt ggcctccaac cacagtcctt tcagcagcga gtctcgagct 840

ctctccacct catccaattt ggggtcccaa taccagtgtg agaatggtgt ttccggcccc 900

tcccaggacc tcctgcctcc acccaaccca tacccactgc cccaggagca tagccaaatt 960

taccattgta ccaagaggaa agaggaagaa tgttccacca cagaccatcc ctataagaag 1020

ccctacatgg agacatcacc cagtgaagaa gattccttct accgctctag ctatccacag 1080

cagcagggcc tgggtgcctc ctacaggaca gagtcggcac agcggcaagc ttgcatgtat 1140

gccagctctg cgccccccag cgagcctgtg cccagcctag aggacatcag ctgcaacacg 1200

tggccaagca tgccttccta cagcagctgc accgtcacca ccgtgcagcc catggacagg 1260

ctaccctacc agcacttctc cgctcacttc acctcggggc ccctggtccc tcggctggct 1320

ggcatggcca accatggctc cccacagctg ggagagggaa tgttccagca ccagacctcc 1380

gtggcccacc agcctgtggt caggcagtgt gggcctcaga ctggcctgca gtcccctggc 1440

acccttcagc cccctgagtt cctctactct catggcgtgc caaggactct atcccctcat 1500

cagtaccact ctgtgcacgg agttggcatg gtgccagagt ggagcgacaa tagcttg 1557

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<210> SEQ ID NO 94
<211> LENGTH: 1350
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic polynucleotide

<400> SEQUENCE: 94

atgttgtgga aaataaccga taatgtcaag tacgaagagg actgcgagga tcgccacgac 60

gggagcagca atgggaatcc gcgggtcccc cacctctcct ccgccgggca gcacctctac 120

agccccgcgc cacccctctc ccacactgga gtcgccgaat atcagccgcc accctacttt 180

ccccctccct accagcagct ggcctactcc cagtcggccg acccctactc gcatctgggg 240

gaagcgtacg ccgccgccat caacccccctg caccagccgg cgcccacagg cagccagcag 300

caggcctggc ccggccgcca gagccaggag ggagcggggc tgccctcgca ccacgggcgc 360

ccggccggcc tactgcccca cctctccggg ctggaggcgg gcgcggtgag cgcccgcagg 420

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actgaggtct tctgctcagt ccctggaaga ttgtcgctcc tcagctctac gtctaaatac 720

aaagtgacag tggctgaagt acagaggcga ctgtccccac ctgaatgctt aaatgcctcg 780

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ctcctgacat ccttagtaga aggtgaagct gttcatttgg ctagggactt tgcctatgtc 960

tgtgaagccg aatttcctag taaaccagtg gcagaatatt taaccagacc tcatcttgga 1020

ggacgaaatg agatggcagc taggaagaac atgctattgg cggcccagca actgtgtaaa 1080

gaattcacag aacttctcag ccaagaccgg acaccccatg ggaccagcag gctcgcccca 1140

gtcttggaga cgaacataca gaactgcttg tctcatttca gcctgattac ccacgggttt 1200

ggcagccagg ccatctgtgc cgcggtgtct gccctgcaga actacatcaa agaagccctg 1260

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agaccacgcc tctgtcatgt accaaatc 28

<210> SEQ ID NO 96
<211> LENGTH: 27
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primer

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ggtcagcagc atcgtggtca acataac 27

<210> SEQ ID NO 97
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agggctgtcc tgaataagca g 21

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<400> SEQUENCE: 118

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gaggaagagg taaccacagg g 21

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<210> SEQ ID NO 120
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<400> SEQUENCE: 120

atgtccctct tgtcgccaac ct 22

<210> SEQ ID NO 121
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<400> SEQUENCE: 121

gagggtcagt agaacatgcg t 21

<210> SEQ ID NO 122
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ggcaagttga ttggagggat g 21

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gtatgcacca ttcaactcct cg 22

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<400> SEQUENCE: 130

tgaatctcga cgttctcctc c 21

1. An isolated polynucleotide or vector comprising:
(a) a polynucleotide encoding a transcription factor (TF) open reading frame (ORF);
(b) a nucleic acid barcode, and
(c) an optional vector comprising (a) and (b);
wherein the nucleic acid barcode is located 3' to the TF ORF.

2. The polynucleotide or vector of claim **1**, wherein the TF ORF encodes a developmentally critical TF.

3. A TF screening library comprising a polynucleotide or vector of claim **1**.

4. A TF screening library comprising a polynucleotide or vector of claim **2**.

5. The TF screening library of claim **3**, wherein the developmentally critical TF is a TF selected from the TFs listed in Table 1.

6. The polynucleotide or vector of claim **1** wherein at least one nucleic acid or vector further comprises a nucleic acid encoding an expression control element.

7. A viral packaging system comprising the polynucleotide or vector of claim **1** and a packaging plasmid.

8. A method for producing a viral particle, the method comprising transfecting a packaging cell line with the system of claim **7** under conditions suitable to package the vector or the TF screening library into a viral particle.

9. A viral particle produced by the method of claim **8**, and optionally a carrier.

10. An isolated cell comprising the polynucleotide or vector of claim **1**, and optionally a carrier.

11. A kit comprising the polynucleotide or vector of claim **1** and optionally instructions for use.

12. A method of performing a high throughput gene activation screen, the method comprising:
(a) transducing a target cell with the viral particle of claim **9**; and
(b) performing scRNA-seq on the transduced target cell to identify the nucleic acid barcode.

13. The method of claim **12**, further comprising determining a fitness effect in the transduced target cell.

14. The method of claim **12**, further comprising identifying a co-perturbation network.

15. The method of claim **12**, further comprising identifying a functional gene module.

16. The method of claim **12**, wherein the target cell is a stem cell, optionally an embryonic stem cell (ESC) or an induced pluripotent stem cell (iPSC).

17. A method of driving differentiation of a stem cell into an endothelial cell, the method comprising inducing ectopic expression of ETV2 in a stem cell under conditions suitable to support differentiation of the stem cell into an endothelial cell.

18. The method of claim **17**, wherein ectopic expression of ETV2 is induced by transducing the stem cell with a vector comprising a nucleic acid encoding ETV2 and a nucleic acid encoding an expression control element, and optionally wherein the stem cell has been genetically modified.

19. The method of claim **17**, further comprising genetically modifying the stem cell or the endothelial cell.

20. An endothelial cell produced by the method of claim **19**, and optionally a carrier.

21. A method of treating a subject thereof, the method comprising administering the endothelial cell of claim **20** to the subject.

* * * * *