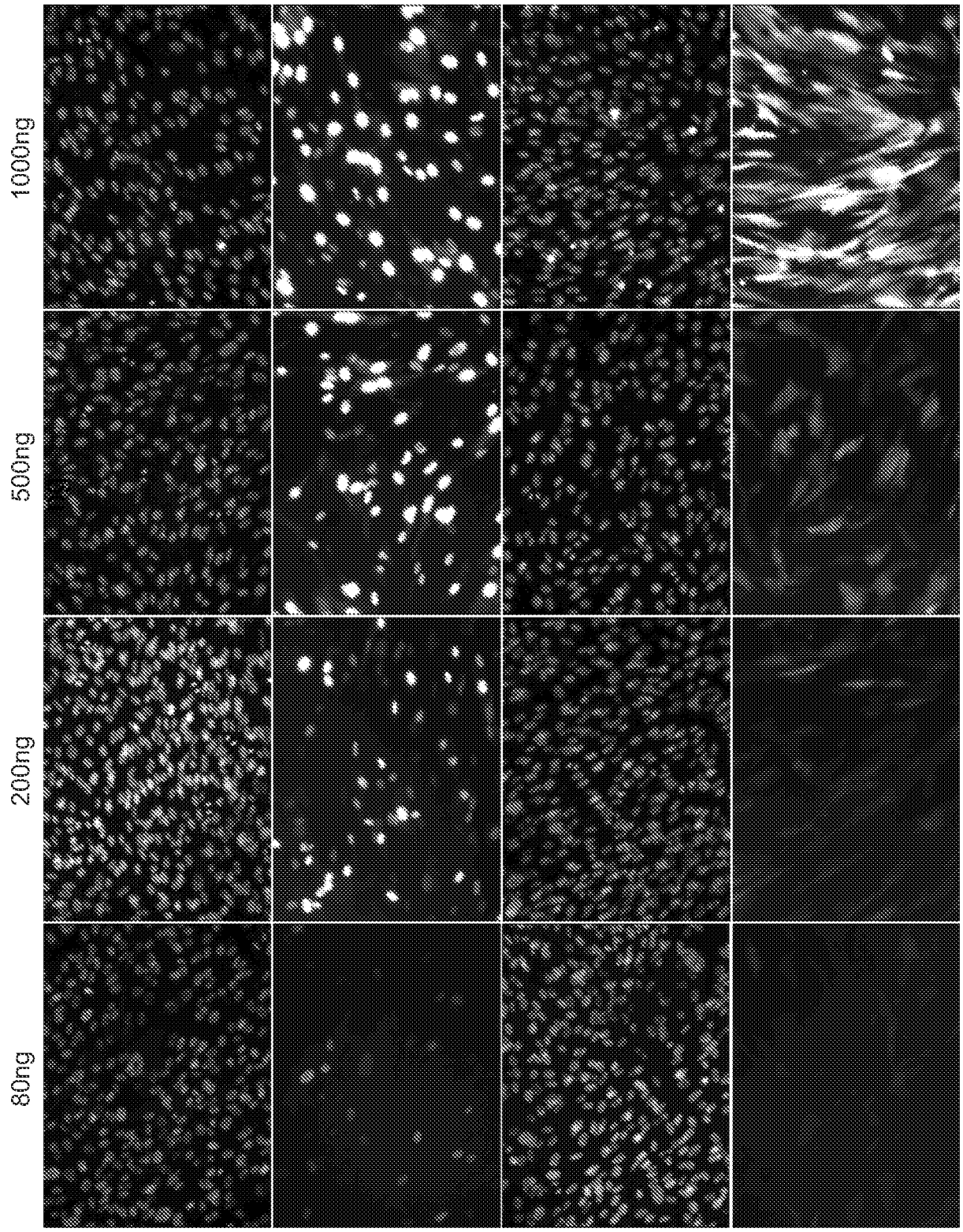

80ng
200ng
500ng
1000ng
Nuclear Hoechst
Nuclear GFP
Cytoplasmic Hoechst
Cytoplasmic GFP

FIG. 1

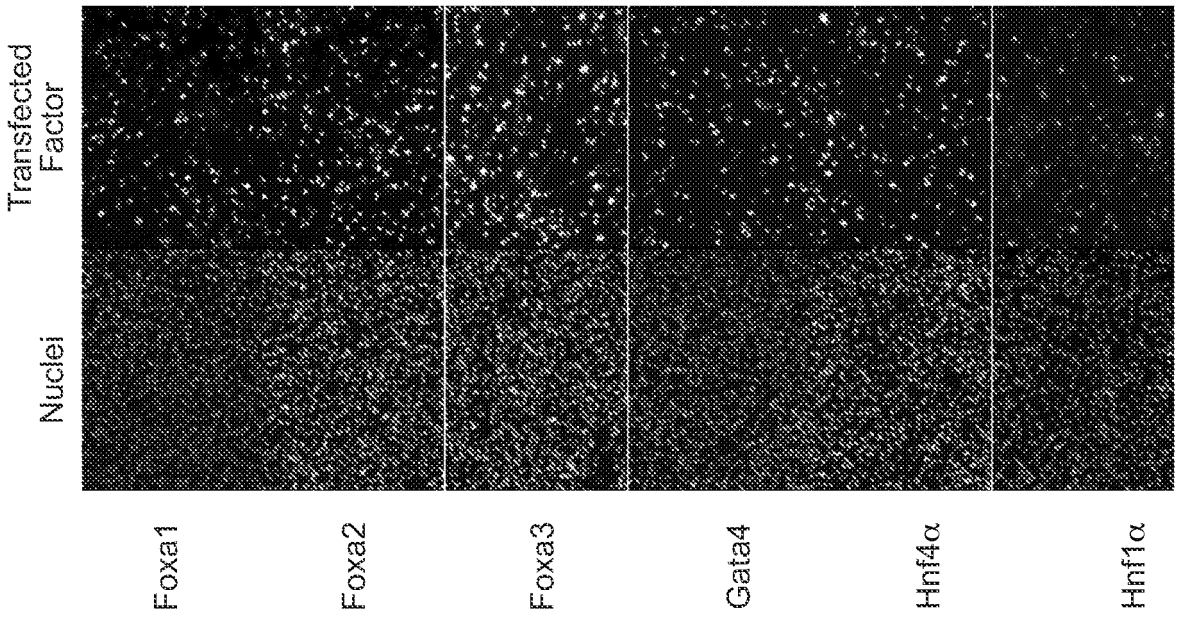

Transfected Factor
Nuclei
Foxa1
Foxa2
Foxa3
Gata4
Hnf4α
Hnf1α

FIG. 3

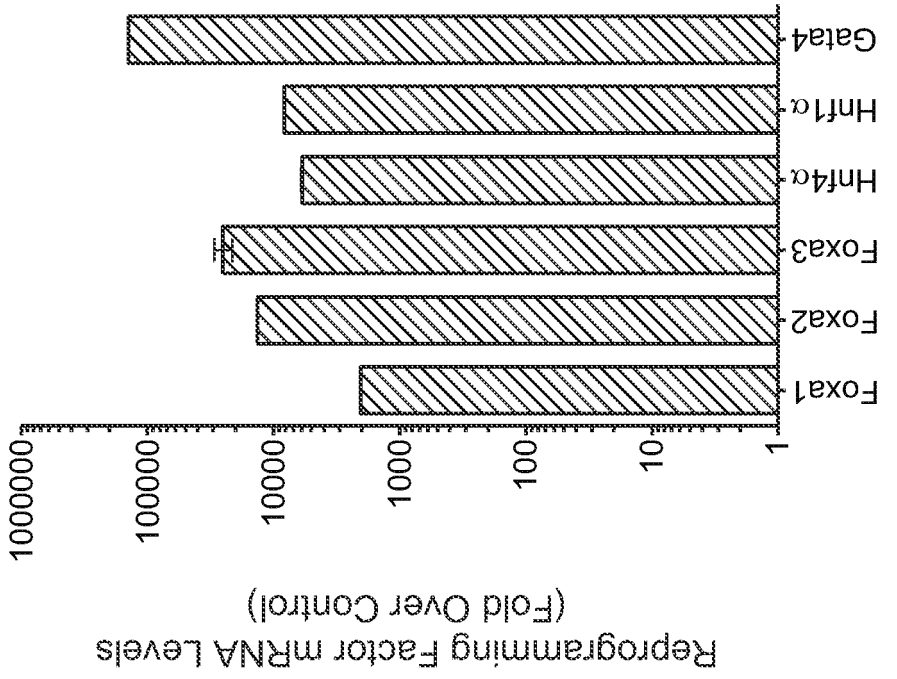

Reprogramming Factor mRNA Levels
(Fold Over Control)
1000000
100000
10000
1000
100
10
1
Foxa1
Foxa2
Foxa3
Hnf4α
Hnf1α
Gata4
Transfected Factor

FIG. 2

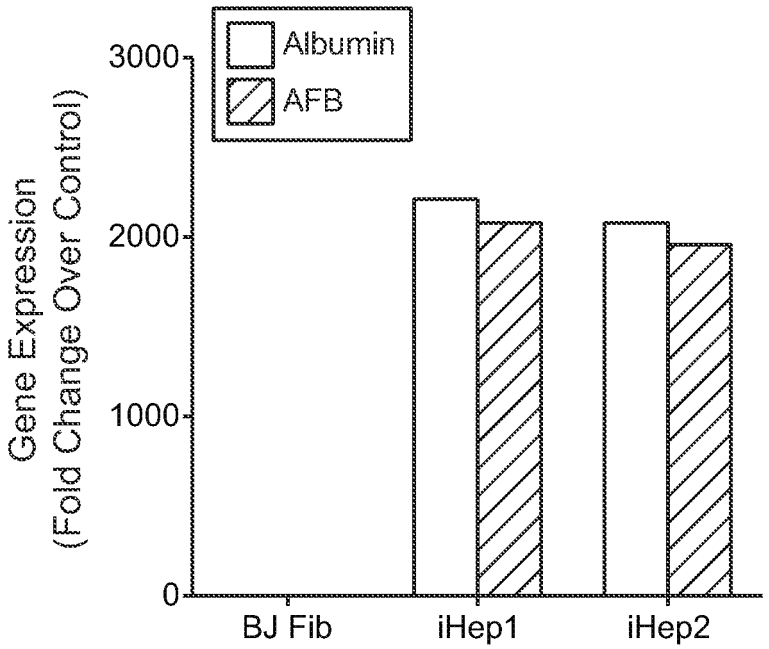

Albumin
AFB
3000
2000
1000
0
Gene Expression
(Fold Change Over Control)
BJ Fib
iHep1
iHep2

FIG. 4

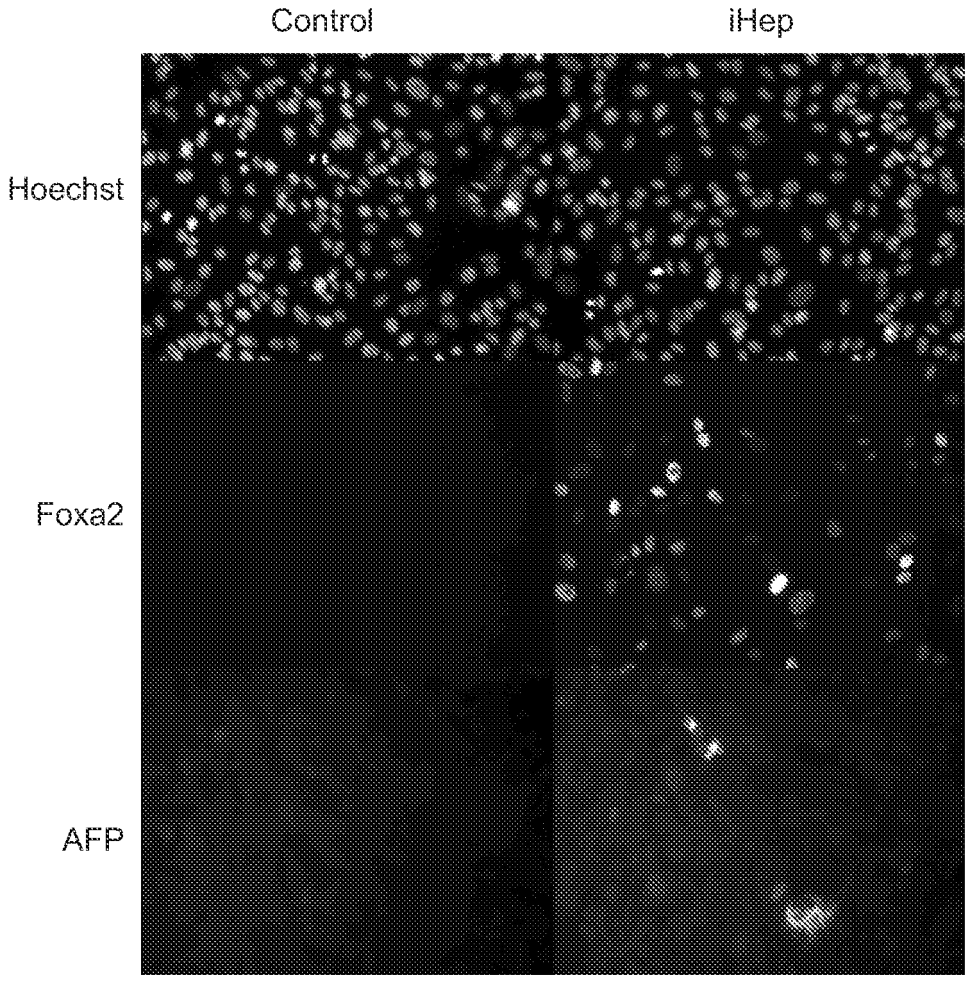

Control
iHep
Hoechst
Foxa2
AFP

FIG. 5

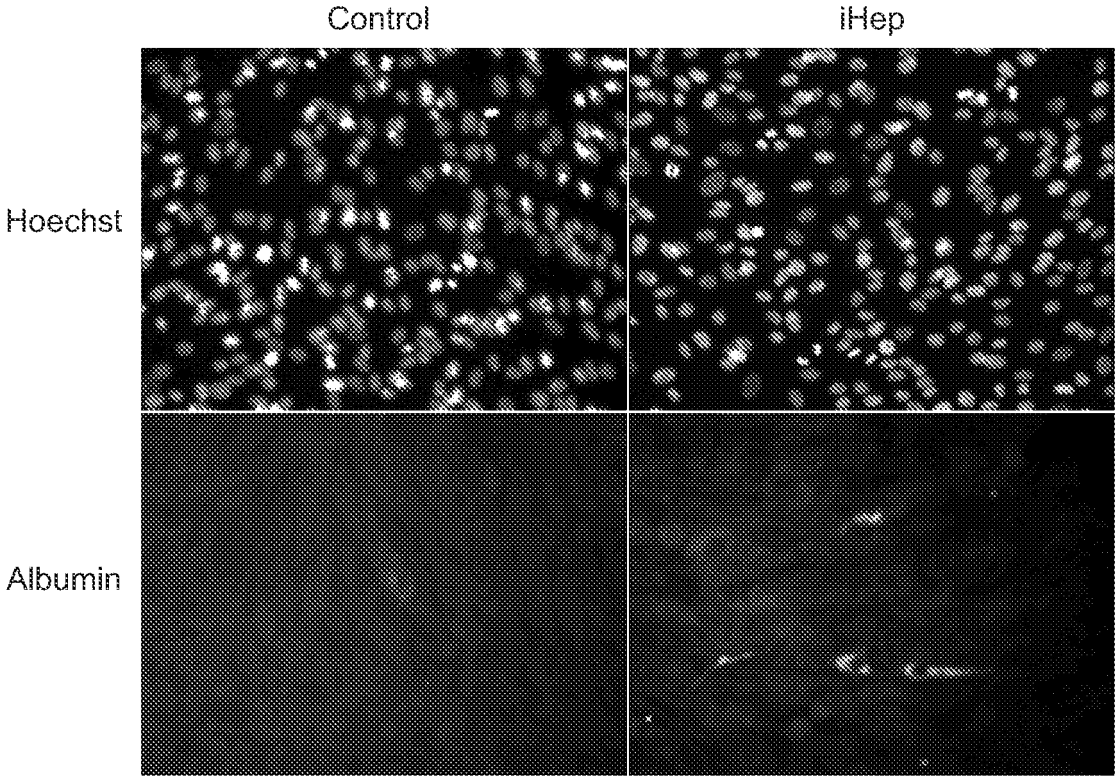

Control
iHep
Hoechst
Albumin

FIG. 6

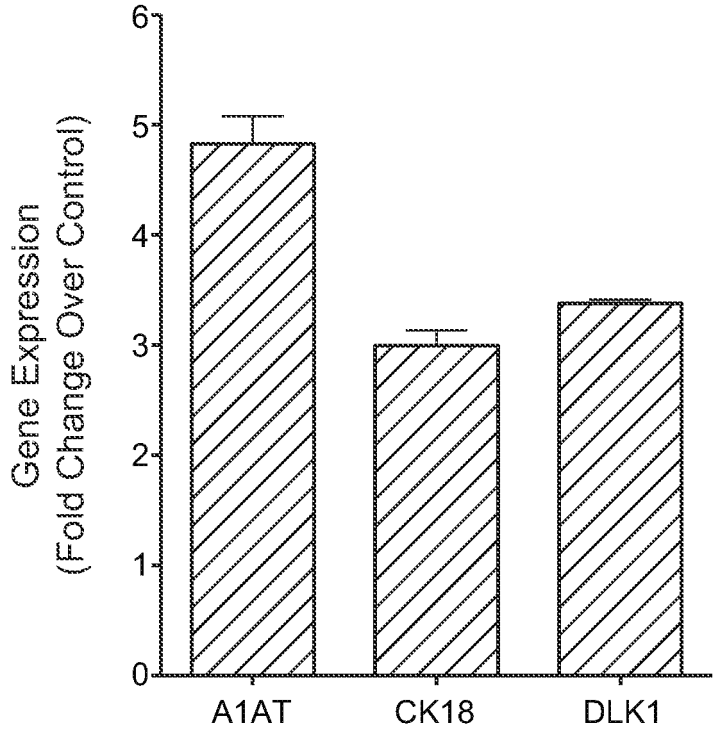

Gene Expression
(Fold Change Over Control)
0
1
2
3
4
5
6
A1AT
CK18
DLK1

FIG. 7

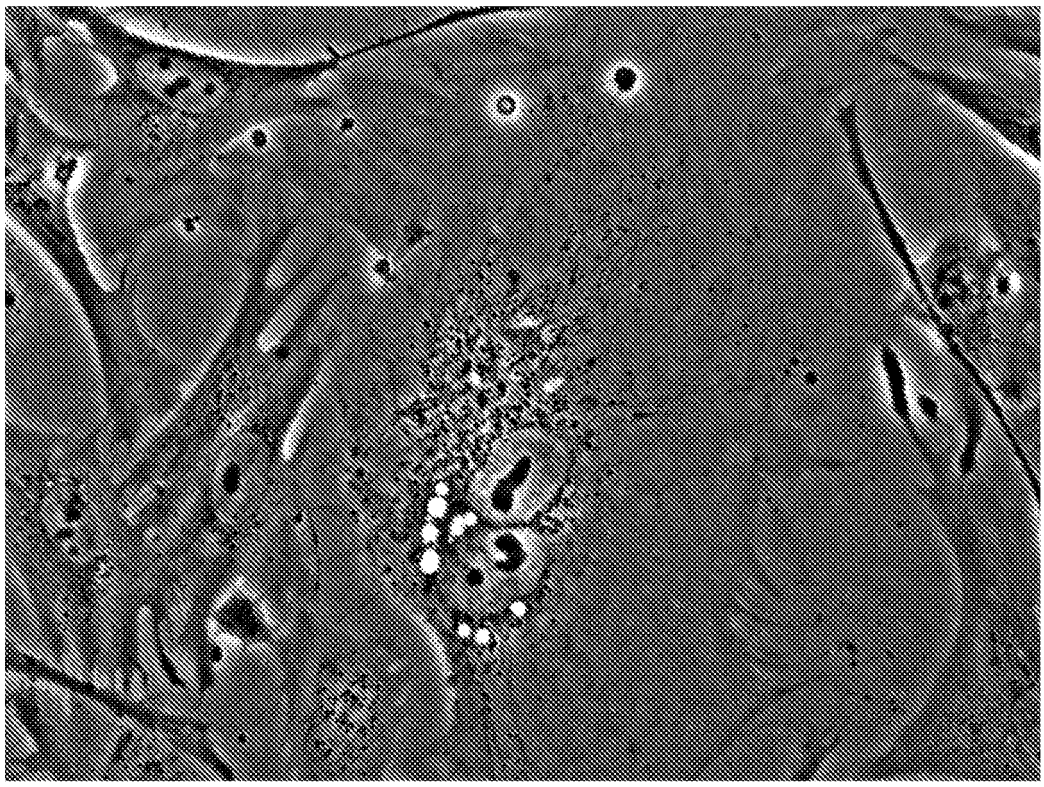


FIG. 8

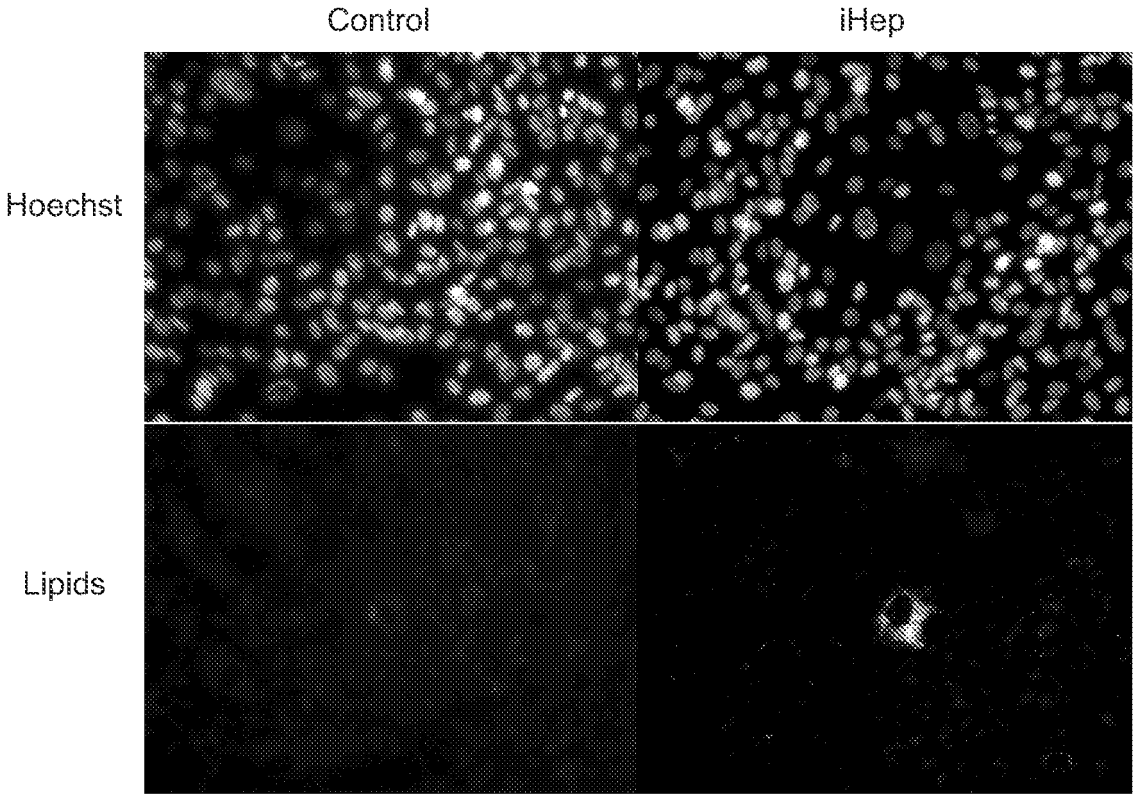


FIG. 9

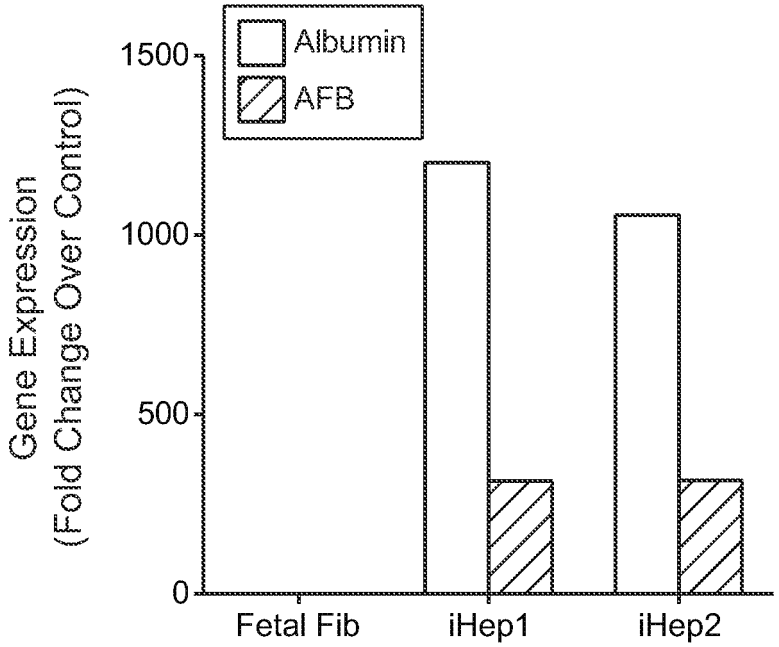


FIG. 10

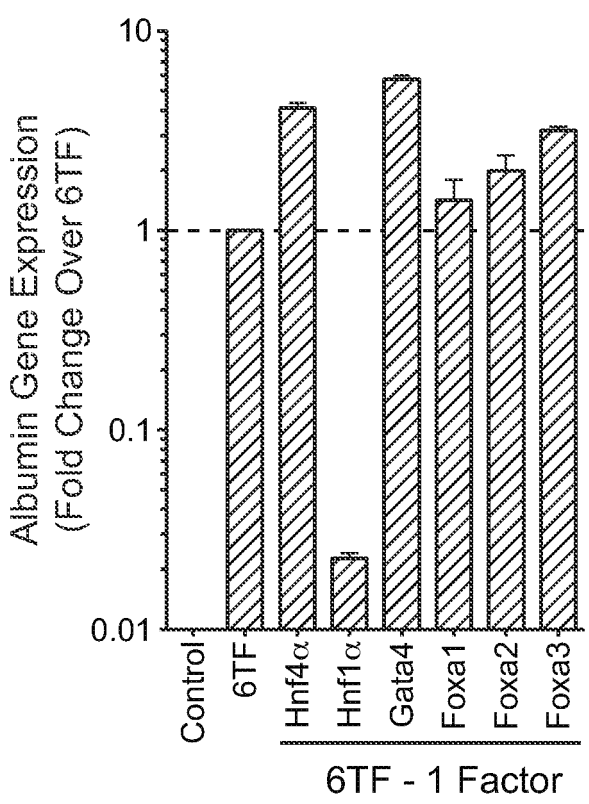


FIG. 11A

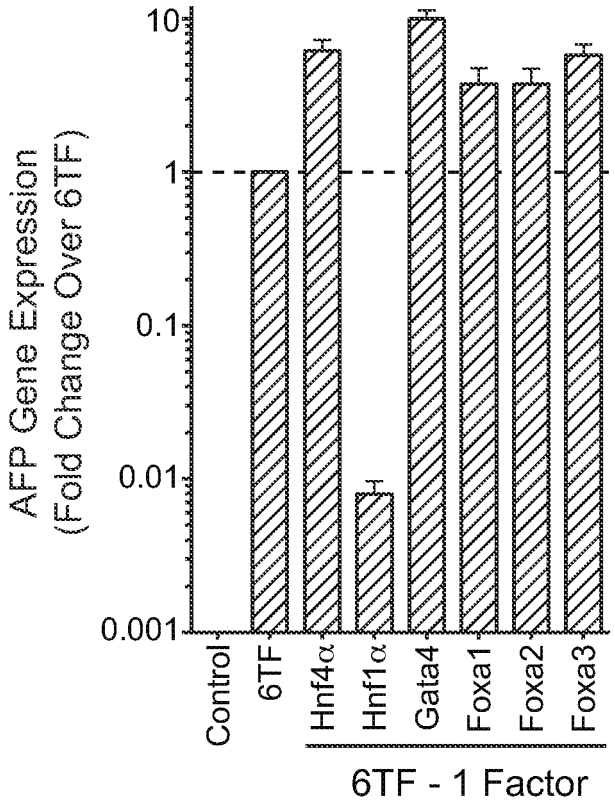


FIG. 11B

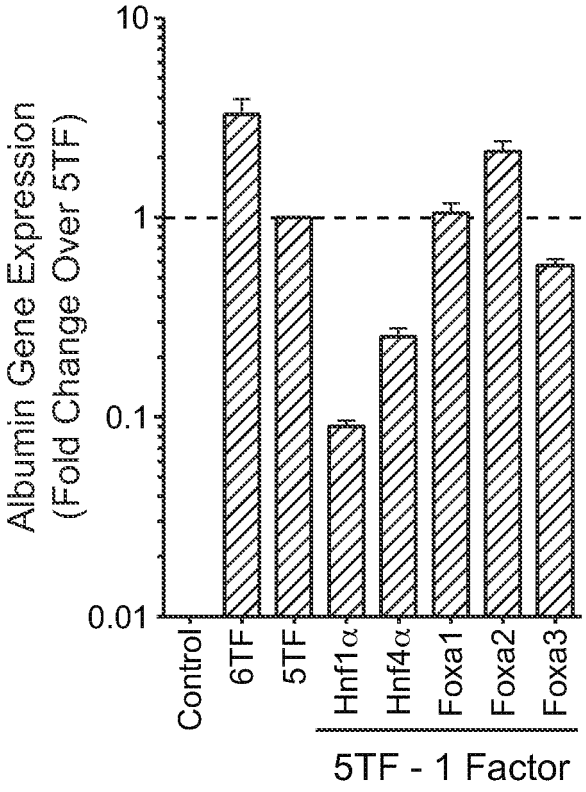


FIG. 12A

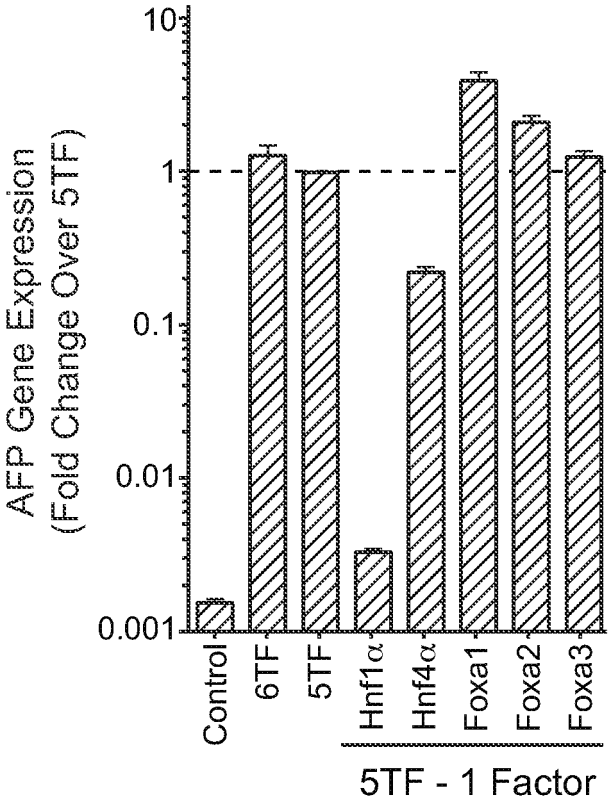


FIG. 12B

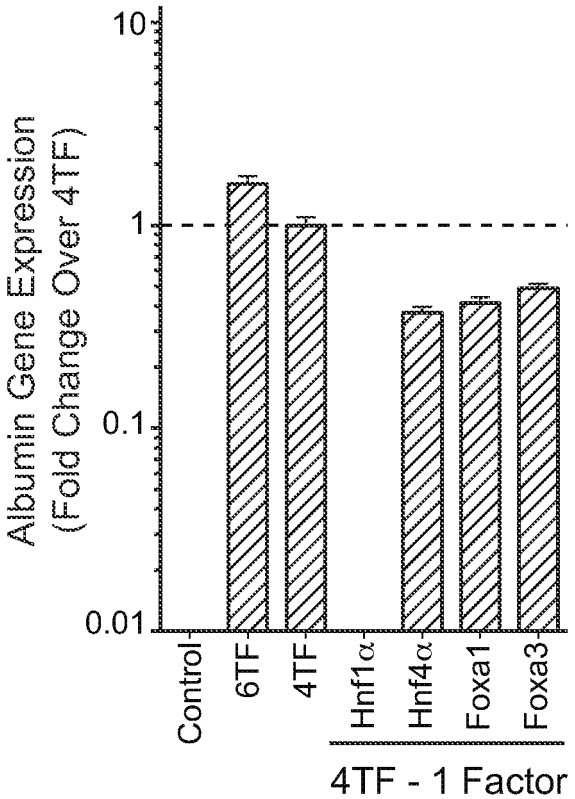


FIG. 13A

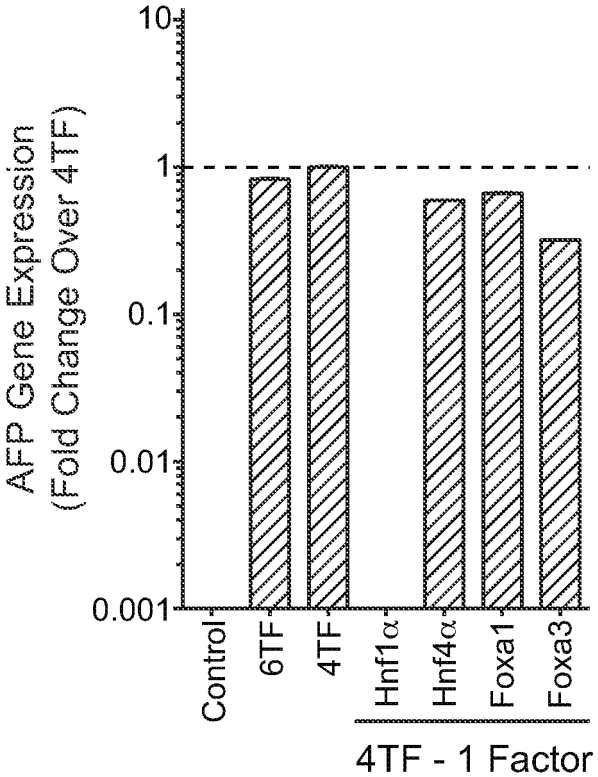


FIG. 13B

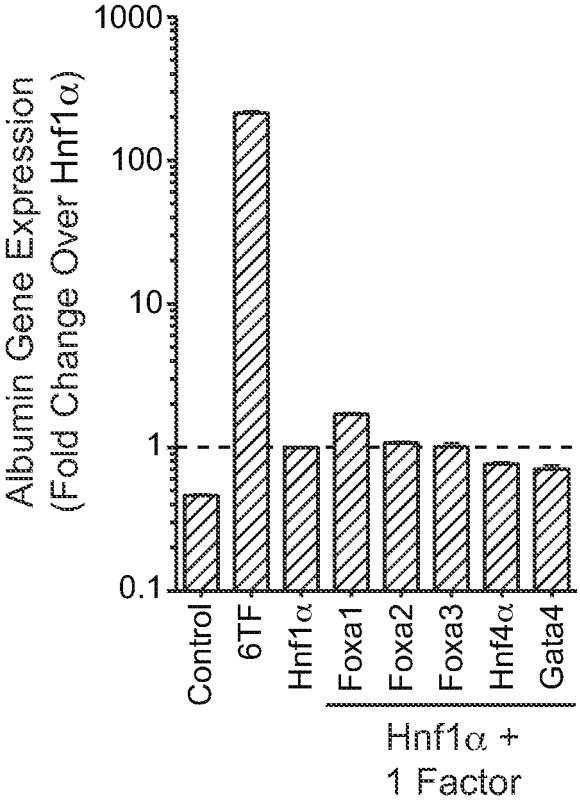


FIG. 14A

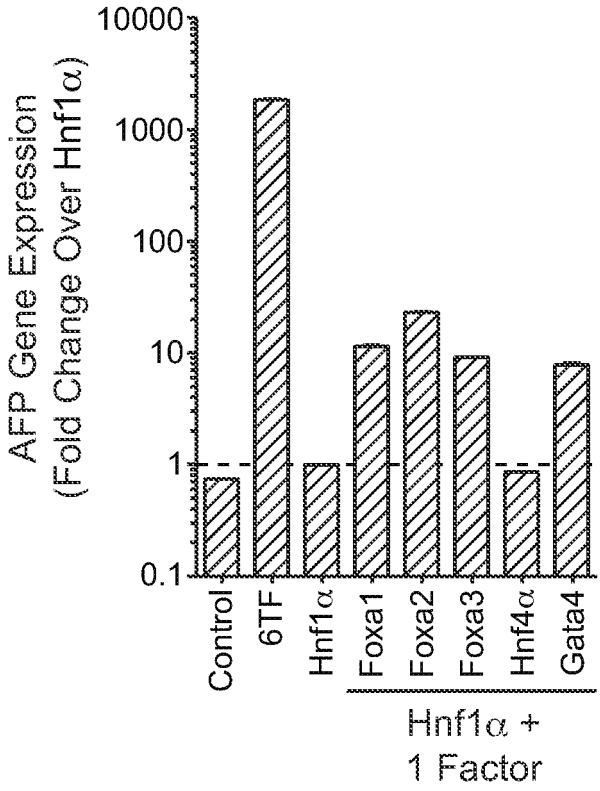


FIG. 14B

ATGTTAGGAACTGTGAAGATGGAAGGGCATGAAACCAGCGACTGGAACAGCTACTACGGCAGACACGGCAGGAGGC
CTACTCCTCCGTCCCGGTCAGCAACATGAACTCAGGGCCTGGGCTCCATGAACTCCATGAACACCTACATGACCAT
GAACACCATGACTACGAGCGGCGCAACATGACCCCGGCGTCCTTCAACATGTCCTATGCCAACCCGGGGCCTAGGGG
CCGGCCTGAGTCCCGGCGCAGTAACCGGCATGCCGGGGGGCTCGGCGGGCGCCATGAACAGCATGACTGCGG
CCGGCGTGACGGCCATGGGTACGGGCGCTGAGCCCCGAGCGGCATGGGCGCCATGGGTGCGCAGCAGGCGGCC
TCCATGAATGGCCTGGGCCCCTACGCGGCCGCCATGAACCCGTGCATGAGCCCCATGGCGTACGCGCCGTCCA
ACCTGGGCCGCAGCCGCGGGCGGCGACGCCAAGACGTTCAAGCGCAGCTACCCGCACGCCAAG
CCGCCCTACTCGTACATCTCGCTCATCACCATGGCCATCCAGCAGGCGCCCAGCAAGATGCTCACGCTGAGCGA
GATCTACCAGTGGATCATGGACCTCTTCCCCTATTACCGGCAGAACCAGCAGCGCTGGCAGAACTCCATCCGCCA
CTCGCTGTCCTTCAATGACTGCTTCGTCAAGGTGGCACGCTCCCCGGACAAGCCGGGGCAAGGGCTCCTACTGG
ACGCTGCACCCCGGACTCCGGCAACATGTTCGAGAACGGCTGCTACTTGCGCCGCCAGAAGCGCTTCAAGTGCG
AGAAGCAGCCGGGGGCCGGCGGGGAGCGGAAGCGGGGGCAGCCGGCGCCAAGGGCGGCCCTG
AGAGCCGCAAGGACCCCTCTGGCGCCTCTAACCCCAGCGCCGACTCGCCCCTCCATCGGGGTGTGCACGGGA
AGACCGGCCAGCTAGAGGGCGCGCCCCGGGCCCGCCGCCAGCCCCCAGACTCTGGACCACACAGTGGG
CTGAAAGGGGACCCCCCACTACTCCTTCAACCACCCGTTCTCCATCAACAACCTCATGTCCTCCTCGGAGCAGCA
GCATAAGCTGGACTTCAAGGCATACGAACAGGCACTGCAATACTCGCCTTACGGCTCTACGTTGCCCGCCAGCCT
GCCTCTAGGCAGCGCCTCGGTGACCACCAGGAGCCCCATCGAGCCCTCAGCCCTGGAGCCGGCGTACTACCAA
GGTGTGTATTCCAGACCCGTCCTAAACACTTCCTAG

FIG. 15

MLGTVKMEGHETSDWNSYYADTQEAYSSVPVSNMNSGLGSMNSMNTYMTMNTTSGNMTPASFNMSYANPGL
GAGLSPGAVTGMPGGSAGAMNSMTAAGVTAMGTALSPSGMGAMGAQQAASMNGLGPYAAAMNPCMSPMAYAPS
NLGRSRAGGGGDAKTFKRSYPHAKPPYSYISLITMAIQQAPSKMLTLSEIYQWIMDLFPYYRQNQQRWQNSIRHSLS
FNDCFVKVARSPDKPGKGSYWTLHPDSGNMFENGCYLRRQKRFKCEKQPGAGGGGSGGSGAKGGPESRKD
PSGASNPSADSPLHRGVHGKTGQLEGAPAPGPAASPQTLDHSGATATGGASELKTPASSTAPPISSGPGALASVPAS
HPAHGLAPHESQLHLKGDPHYSFNHPFSINNLMSSSEQQHKLDFKAYEQALQYSPYGSTLPASLPLGSASVTTRSPI
EPSALEPAYYQGVYSRPVLNTS

FIG. 16

ATGCACTCGGCTTCCAGTATGCTGGGAGCGGTGAAGATGGAAGGGCACGAGCCGTCCGACTGGAGCAGCTAC
TATGCAGAGCCCGAGGGCTACTCCTCCGTGAGCAACATGAACGCCGGCCTGGGGATGAACGGCATGAACACG
TACATGAGCATGTCGGCGGCCGCCATGGGCAGCGGCTCGGGCAACATGAGCGCGGGCTCCATGAACATGTCG
TCGTACGTGGGCGCTGGCATGAGCCCGTCCCTGGCGGGGATGTCCCCCGGCGCGGGCGCCATGGCGGGCAT
GGGCGGCTCGGCCGGGGCGGCTGGCGTGGCGGGCATGGGGCCGCACTTGAGTCCCAGCCTGAGCCCGCTC
GGGGGGCAGGCGGCCGGGGCCATGGGCGGCCTGGCCCCCTACGCCAACATGAACTCCATGAGCCCCATGTA
CGGGCAGGCGGGCCTGAGCCGCGCCCGCGACCCCAAGACCTACAGGCGCAGCTACACGCACGCAAAGCCGC
CCTACTCGTACATCTCGCTCATCACCATGGCCATCCAGCAGAGCCCCAACAAGATGCTGACGCTGAGCGAGATC
TACCAGTGGATCATGGACCTCTTCCCCTTCTACCGGCAGAACCAGCAGCGCTGGCAGAACTCCATCCGCCACT
CGCTCTCCTTCAACGACTGTTTCCTGAAGGTGCCCCGCTCGCCCGACAAGCCCGGCAAGGGCTCCTTCTGGA
CCCTGCACCCTGACTCGGGCAACATGTTCGAGAACGGCTGCTACCTGCGCCGCCAGAAGCGCTTCAAGTGCG
AGAAGCAGCTGGCGCTGAAGGAGGCCGCAGGCGCCGCCGGCAGCGGCAAGAAGGCGGCCGCCGGGGCCCA
GGCCTCACAGGCTCAACTCGGGGAGGCCGCCGGGCCGGCCTCCGAGACTCCGGCGGGCACCGAGTCGCCT
CACTCGAGCGCCTCCCCGTGCCAGGAGCACAAGCGAGGGGGCCTGGGAGAGCTGAAGGGGACGCCGGCTG
CGGCGCTGAGCCCCCCAGAGCCGGCGCCCTCTCCCGGGCAGCAGCAGCAGGCCGCGGCCCACCTGCTGGG
CCCGCCCCACCACCCGGGCCTGCCGCCTGAGGCCCACCTGAAGCCGGAACACCACTACGCCTTCAACCACCC
GTTCTCCATCAACAACCTCATGTCCTCGGAGCAGCAGCACCACCACAGCCACCACCACCACCAGCCCCACAAA
ATGGACCTCAAGGCCTACGAACAGGTGATGCACTACCCCGGCTACGGTTCCCCCATGCCTGGCAGCTTGGCCA
TGGGCCCGGTCACGAACAAAACGGGCCTGGACGCCTCGCCCCTGGCCGCAGATACCTCCTACTACCAGGGGG
TGTACTCCCGGCCCATTATGAACTCCTCTTAA

FIG. 17

MHSASSMLGAVKMEGHEPSDWSSYYAEPEGYSSVSNMNAGLGMNGMNTYMSMSAAAMGSGSGNMSAGSMNM
SSYVGAGMSPSLAGMSPGAGAMAGMGGSAGAAGVAGMGPHLSPSLSPLGGQAAGAMGGLAPYANMNSMSPM
YGQAGLSRARDPKTYRRSYTHAKPPYSYISLITMAIQQSPNKMLTLSEIYQWIMDLFPFYRQNQQRWQNSIRHSLSF
NDCFLKVPRSPDKPGKGSFWTLHPDSGNMFENGCYLRRQKRFKCEKQLALKEAAGAAGSGKKAAAGAQASQAQ
LGEAAGPASETPAGTESPHSSASPCQEHKRGGLGELKGTPAAALSPPEPAPSPGQQQQAAAHLLGPPHHPGLPPE
AHLKPEHHYAFNHPFSINNLMSSEQQHHHSHHHHQPHKMDLKAYEQVMHYPGYGSPMPGSLAMGPVTNKTGLD
ASPLAADTSYYQGVYSRPIMNSS

FIG. 18

ATGGCCCCCCTCAACTCCTACATGACCCTGAATCCTCTAAGCTCTCCCTATCCCCCTGGGGGGCTCCCTGCCTC
CCCACTGCCCTCAGGACCCCTGGCACCCCCAGCACCTGCAGCCCCCCTGGGGCCCACTTTCCCAGGCCTGG
GTGTCAGCGGTGGCAGCAGCAGCTCCGGGTACGGGGCCCCGGGTCCTGGGCTGGTGCACGGGAAGGAGAT
GCCGAAGGGGTATCGGCGGCCCCTGGCACACGCCAAGCCACCGTATTCCTATATCTCACTCATCACCATGGCC
ATCCAGCAGGCGCCGGGCAAGATGCTGACCTTGAGTGAAATCTACCAGTGGATCATGGACCTCTTCCCTTACTA
CCGGGAGAATCAGCAGCGCTGGCAGAACTCCATTCGCCACTCGCTGTCTTTCAACGACTGCTTCGTCAAGGTG
GCGCGTTCCCCAGACAAGCCTGGCAAGGGCTCCTACTGGGCCCTACACCCCAGCTCAGGGAACATGTTTGAG
AATGGCTGCTACCTGCGCCGCCAGAAACGCTTCAAGCTGGAGGAGAAGGTGAAAAAAGGGGGCAGCGGGGC
TGCCACCACCACCAGGAACGGGACAGGGTCTGCTGCCTCGACCACCACCCCCGCGGCCACAGTCACCTCCC
CGCCCCAGCCCCCGCCTCCAGCCCCTGAGCCTGAGGCCCAGGGCGGGGAAGATGTGGGGGCTCTGGACTGT
GGCTCACCCGCTTCCTCCACACCCTATTTCACTGGCCTGGAGCTCCCAGGGGAGCTGAAGCTGGACGCGCCC
TACAACTTCAACCACCCTTTCTCCATCAACAACCTAATGTCAGAACAGACACCAGCACCTCCCAAACTGGACGT
GGGGTTTGGGGGCTACGGGGCTGAAGGTGGGGAGCCTGGAGTCTACTACCAGGGCCTCTATTCCCGCTCTTT
GCTTAATGCATCCTAG

FIG. 19

MAPLNSYMTLNPLSSPYPPGGLPASPLPSGPLAPPAPAAPLGPTFPGLGVSGGSSSSGYGAPGPGLVHGKEMPK
GYRRPLAHAKPPYSYISLITMAIQQAPGKMLTLSEIYQWIMDLFPYYRENQQRWQNSIRHSLSFNDCFVKVARSPDK
PGKGSYWALHPSSGNMFENGCYLRRQKRFKLEEKVKKGGSGAATTTRNGTGSAASTTTPAATVTSPPQPPPPAP
EPEAQGGEDVGALDCGSPASSTPYFTGLELPGELKLDAPYNFNHPFSINNLMSEQTPAPPKLDVGFGGYGAEGGE
PGVYYQGLYSRSLLNAS

FIG. 20

ATGGTCAAGTCCTACCTGCAGCACAACATCCCACAGCGGGAGGTGGTCGATACCACTGGCCTCAACCAGT
CCCACCTGTCCCAACACCTCAACAAGGGCACTCCCATGAAGACGGCAGAAGCGGGCCGCCCTGTACACCTGGTA
CGTCCGCAAGCAGCGAGAGGTGGCGCAGCAGTTCACCCATGCAGGGCAGGGAGGCTGATTGAAGAGCCCA
CAGGTGATGAGCTACCAACCAAGAAGGGCGGAGGAACCGTTTCAAGTGGGGCCCAGCATCCCAGCAGATCCT
GTTCCAGGCCTATGAGAGGCAGAAGAACCCTAGCAAGGAGGAGCGAGAGACGCTAGTGGAGGAGTGCAATAG
GGCGGAATGCATCCAGAGAGGGGGTGTCCCCATCACAGGGCACAGGGGCTGGGCTCCAACCTCGTCACGGAGGT
GCGTGTCTACAACTGGTTTGCCAACCGGCGCAAAGAAGAAGCCTTCCGGCACAAGCTGGCCATGGACACGTAC
AGCGGGCCCCCCCCCAGGGCCAGGCCTGCGCTGCCCGCTCACAGCTCCCCTGGCCTGCCTCCACC
TGCCCTCTCCCCCAGTAAGGTCCACGGTGTGCGCTATGGACAGCCTGCGACCAGTGAGACTGCAGAAGTACCC
TCAAGCAGCGGCGGTCCCTTAGTGACAGTGTCTACACCCCTCCACCAAGTGTCCCCCACGGGGCCTGGAGCCCA
GCCACAGCCTGCTGAGTACAGAAGCCAAGCTGGTCTCAGCAGCTGGGGGCCCCCTCCCCCCTGTCAGCACCC
TGACAGCACTGCACACAGCTTGGAGCAGACATCCCCAGGCCTCAACCAGCAGCCCCCAGAACCTCATCATGGCCTC
ACTTCCTGGGGTCATGACCATCGGGCCTGCCTCCCTGGGTCCTACGTTCACCAACACAGGTGCC
TCCACCCTGGTCATCGGCCTGGCCTCCACGCAGGCACAGAGTGTGCCCGGTCATCAACAGCATGGGCAGCAGC
CTGACCACCCTGCAGCCCGTCCAGTTCTCCCAGCCGCTGCACCCCTCCTACCAGCAGCCGCTCATGCCACCTG
TGCAGAGCCATGTGACCCCAGAGCCCCTTCATGGCCACCATGGCTCAGCTGCAGAGCCCCCACGCCCTCTACAG
CCACAAGCCCCGAGGTGGCCCCAGTACACCCACACGGGCCTGCTCCCGCAGACTATGCTCATCACCGACACCACC
AACCTGAGCGCCCTGGCCAGCCCTCACGCCCACCAAGCAGGTCTTCACCTCAGACACTGAGGCCCTCCAGTGAG
TCCGGGCTTCACACGCCGGCATCTCAGGCCACCACCCTCCACGTCCCCAGCCAGGACCCTGCCCGGCATCCAG
CACCTGCAGCCGGCCCACCCGGCTCAGCGCCAGCCCCACAGTGTCCTCCAGCAGCCTGGTGCTGTACCAGAGC
TCAGACTCCAGCAATGGCCAGAGCCACCTGCTGCCATCCAACCACACAGCCGTCATCGAGACCTTCATCTCCACCCCA
GATGGCCTCTTCCTCCCAGTAA

FIG. 21

MVKSYLQQHNIPQREVVDTTGLNQSHLSQHLNKGTPMKTQKRAALYTWYVRKQREVAQQFTHAGQGGLIEEPTG
DELPTKKGRRNRFKWGPASQQILFQAYERQKNPSKEERETLVEECNRAECIQRGVSPSQAQGLGSNLVTEVRVYN
WFANRRKEEAFRHKLAMDTYSGPPPGPGPALPAHSSPGLPPPALSPSKVHGVRYGQPATSETAEVPSSSGGPL
VTVSTPLHQVSPTGLEPSHSLLSTEAKLVSAAGGPLPPVSTLTALHSLEQTSPGLNQQPQNLIMASLPGVMTIGPGE
PASLGPTFTNTGASTLVIGLASTQAQSVPVINSMGSSLTTLQPVQFSQPLHPSYQQPLMPPVQSHVTQSPFMATMA
QLQSPHALYSHKPEVAQYTHTGLLPQTMLITDTTNLSALASLTPTKQVFTSDTEASSESGLHTPASQATTLHVPSQD
PAGIQHLQPAHRLSASPTVSSSSLVLYQSSDSSNGQSHLLPSNHSVIETFISTQMASSSQ

FIG. 22

ATGCGACTCTCCAAAACCCTCGTCGACATGGACATGGCCGACTACAGTGCTGCACTGGACCCAGCCTACACCA
CCCTGGAATTTGAGAATGTGCAGGTGTTGACGATGGGCAATGACACGTCCCCATCAGAAGGCACCAACCTCAA
CGCGCCCAACAGCCTGGGTGTCAGCGCCCTGTGTGCCATCTGCGGGGACCGGGCCACGGGCAAACACTACG
GTGCCTCGAGCTGTGACGGCTGCAAGGGCTTCTTCCGGAGGAGCGTGCGGAAGAACCACATGTACTCCTGCA
GATTTAGCCGGCAGTGCGTGGTGGACAAAGACAAGAGGAACCAGTGCCGCTACTGCAGGCTCAAGAAATGCTT
CCGGGCTGGCATGAAGAAGGAAGCCGTCCAGAATGAGCGGGACCGGATCAGCACTCGAAGGTCAAGCTATGA
GGACAGCAGCCTGCCCTCCATCAATGCGCTCCTGCAGGCGGAGGTCCTGTCCCGACAGATCACCTCCCCCGT
CTCCGGGATCAACGGCGACATTCGGGCGAAGAAGATTGCCAGCATCGCAGATGTGTGTGAGTCCATGAAGGAG
CAGCTGCTGGTTCTCGTTGAGTGGGCCAAGTACATCCCAGCTTTCTGCGAGCTCCCCCTGGACGACCAGGTGG
CCCTGCTCAGAGCCCATGCTGGCGAGCACCTGCTGCTCGGAGCCACCAAGAGATCCATGGTGTTCAAGGACG
TGCTGCTCCTAGGCAATGACTACATTGTCCCTCGGCACTGCCCGGAGCTGGCGGAGATGAGCCGGGTGTCCAT
ACGCATCCTTGACGAGCTGGTGCTGCCCTTCCAGGAGCTGCAGATCGATGACAATGAGTATGCCTACCTCAAAG
CCATCATCTTCTTTGACCCAGATGCCAAGGGGCTGAGCGATCCAGGGAAGATCAAGCGGCTGCGTTCCCAGGT
GCAGGTGAGCTTGGAGGACTACATCAACGACCGCCAGTATGACTCGCGTGGCCGCTTTGGAGAGCTGCTGCT
GCTGCTGCCCACCTTGCAGAGCATCACCTGGCAGATGATCGAGCAGATCCAGTTCATCAAGCTCTTCGGCATG
GCCAAGATTGACAACCTGTTGCAGGAGATGCTGCTGGGAGGGTCCCCCAGCGATGCACCCCATGCCCACCAC
CCCCTGCACCCTCACCTGATGCAGGAACATATGGGAACCAACGTCATCGTTGCCAACACAATGCCCACTCACCT
CAGCAACGGACAGATGTGTGAGTGGCCCCGACCCAGGGGACAGGCAGCCACCCCTGAGACCCCACAGCCCT
CACCGCCAGGTGGCTCAGGGTCTGAGCCCTATAAGCTCCTGCCGGGAGCCGTCGCCACAATCGTCAAGCCCC
TCTCTGCCATCCCCCAGCCGACCATCACCAAGCAGGAAGTTATCTAG

FIG. 23

MRLSKTLVDMDMADYSAALDPAYTTLEFENVQVLTMGNDTSPSEGTNLNAPNSLGVSALCAICGDRATGKHYGAS
SCDGCKGFFRRSVRKNHMYSCRFSRQCVVDKDKRNQCRYCRLKKCFRAGMKKEAVQNERDRISTRRSSYEDS
SLPSINALLQAEVLSRQITSPVSGINGDIRAKKIASIADVCESMKEQLLVLVEWAKYIPAFCELPLDDQVALLRAHAGE
HLLLGATKRSMVFKDVLLLGNDYIVPRHCPELAEMSRVSIRILDELVLPFQELQIDDNEYAYLKAIIFFDPDAKGLSDP
GKIKRLRSQVQVSLEDYINDRQYDSRGRFGELLLLLPTLQSITWQMIEQIQFIKLFGMAKIDNLLQEMLLGGSPSDA
PHAHHPLHPHLMQEHMGTNVIVANTMPTHLSNGQMCEWPRPRGQAATPETPQPSPPGGSGSEPYKLLPGAVATI
VKPLSAIPQPTITKQEVI

FIG. 24

ATGTATCAGAGCTTGGCCATGGCCGCCAACCACGGGCCGCCCCCCGGTGCCTACGAGGCGGGCGGCCC
CGGCGCCTTCATGCACGGCGCGGGCGCCGCGTCCTCGCCAGTCTACGTGCCCACACCGCGGGTGCCCT
CCTCCGTGCTGGGCCTGTCCTACCTCCAGGGCGGAGGCGCGGGCTCTGCGTCCGGAGGCGCCTCGGG
CGGCAGCTCCGGTGGGGCCGCGTCTGGTGCGGGGCCCGGGACCCAGCAGGGCAGCCCGGGATGGAG
CCAGGCGGGAGCCGACGGAGCCGCTTACACCCCGCCGCCGGTGTCGCCGCGCTTCTCCTTCCCGGGG
ACCACCGGGTCCCTGGCGGCCGCCGCCGCCGCTGCCGCGGCCCGGGAAGCTGCGGCCTACAGCAGTG
GCGGCGGAGCGGCGGGTGCGGGCCTGGCGGGCCGCGAGCAGTACGGGCGCGCCGGCTTCGCGGGCT
CCTACTCCAGCCCCTACCCGGCTTACATGGCCGACGTGGGCGCGTCCTGGGCCGCAGCCGCCGCCGCC
TCCGCCGGCCCCTTCGACAGCCCGGTCCTGCACAGCCTGCCCGGCCGGGCCAACCCGGCCGCCCGAC
ACCCCAATCTCGATATGTTTGACGACTTCTCAGAAGGCAGAGAGTGTGTCAACTGTGGGGCTATGTCCACC
CCGCTCTGGAGGCGAGATGGGACGGGTCACTATCTGTGCAACGCCTGCGGCCTCTACCACAAGATGAAC
GGCATCAACCGGCCGCTCATCAAGCCTCAGCGCCGGCTGTCCGCCTCCCGCCGAGTGGGCCTCTCCTG
TGCCAACTGCCAGACCACCACCACCACGCTGTGGCGCCGCAATGCGGAGGGCGAGCCTGTGTGCAATG
CCTGCGGCCTCTACATGAAGCTCCACGGGGTCCCCAGGCCTCTTGCAATGCGGAAAGAGGGGATCCAAA
CCAGAAAACGGAAGCCCAAGAACCTGAATAAATCTAAGACACCAGCAGCTCCTTCAGGCAGTGAGAGCCT
TCCTCCCGCCAGCGGTGCTTCCAGCAACTCCAGCAACGCCACCACCAGCAGCAGCGAGGAGATGCGTC
CCATCAAGACGGAGCCTGGTCTGTCATCTCACTACGGGCACAGCAGCTCCGTGTCCCAGACGTTCTCAGT
CAGTGCGATGTCTGGCCATGGGCCCTCCATCCACCCTGTCCTCTCGGCCCTGAAGCTCTCCCCACAAGG
CTATGCGTCTCCCGTCAGCCAGTCTCCACAGACCAGCTCCAAGCAGGACTCTTGGAACAGCCTGGTCTTG
GCCGACAGTCACGGGGACATAATCACTGCGTAA

FIG. 25

MYQSLAMAANHGPPPGAYEAGGPGAFMHGAGAASSPVYVPTPRVPSSVLGLSYLQGGGAGSASGGASGGS
SGGAASGAGPGTQQGSPGWSQAGADGAAYTPPPVSPRFSFPGTTGSLAAAAAAAAAREAAAYSSGGGAAGA
GLAGREQYGRAGFAGSYSSPYPAYMADVGASWAAAAAASAGPFDSPVLHSLPGRANPAARHPNLDMFDDFS
EGRECVNCGAMSTPLWRRDGTGHYLCNACGLYHKMNGINRPLIKPQRRLSASRRVGLSCANCQTTTTTLWRR
NAEGEPVCNACGLYMKLHGVPRPLAMRKEGIQTRKRKPKNLNKSKTPAAPSGSESLPPASGASSNSSNATTSS
SEEMRPIKTEPGLSSHYGHSSSVSQTFSVSAMSGHGPSIHPVLSALKLSPQGYASPVSQSPQTSSKQDSWNSL
VLADSHGDIITA

FIG. 26

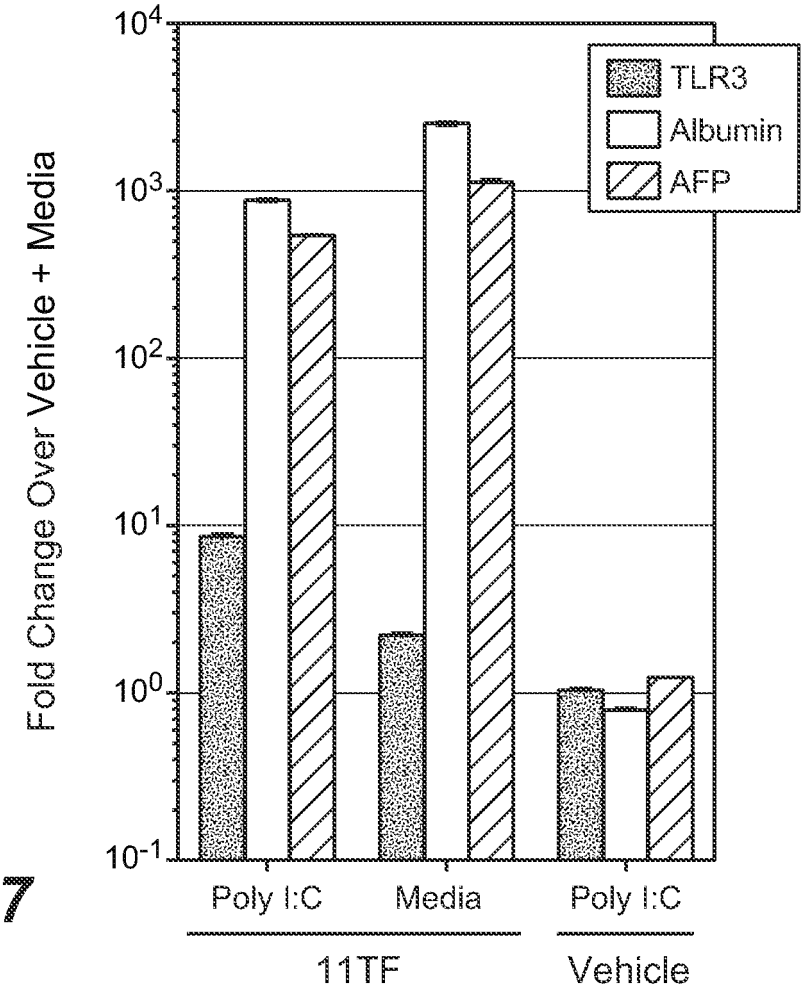

Fold Change Over Vehicle + Media
10^4
10^3
10^2
10^1
10^0
10^{-1}
TLR3
Albumin
AFP
Poly I:C
Media
Poly I:C
11TF
Vehicle

FIG. 27

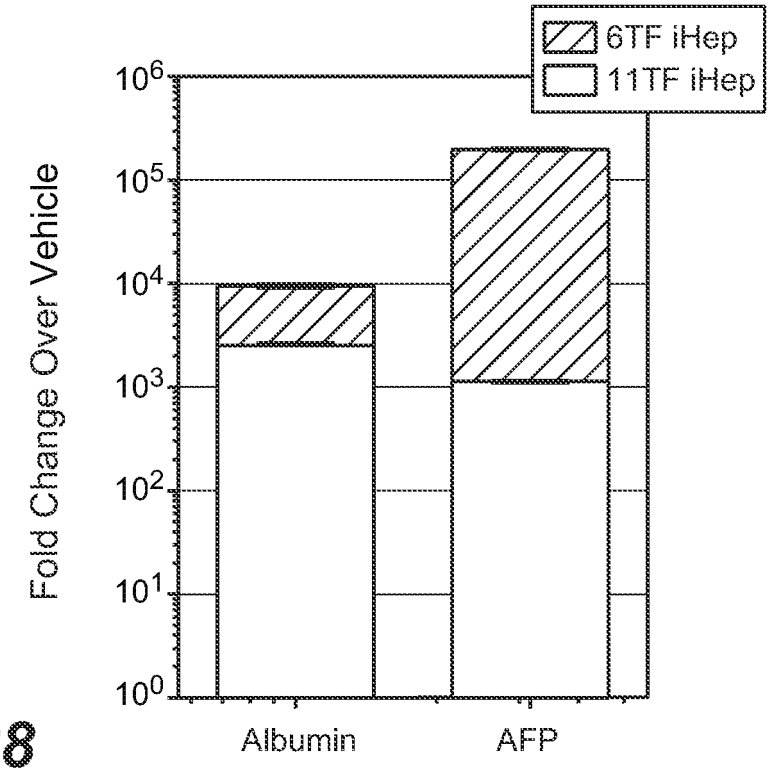

Fold Change Over Vehicle
10^6
10^5
10^4
10^3
10^2
10^1
10^0
6TF iHep
11TF iHep
Albumin
AFP

FIG. 28

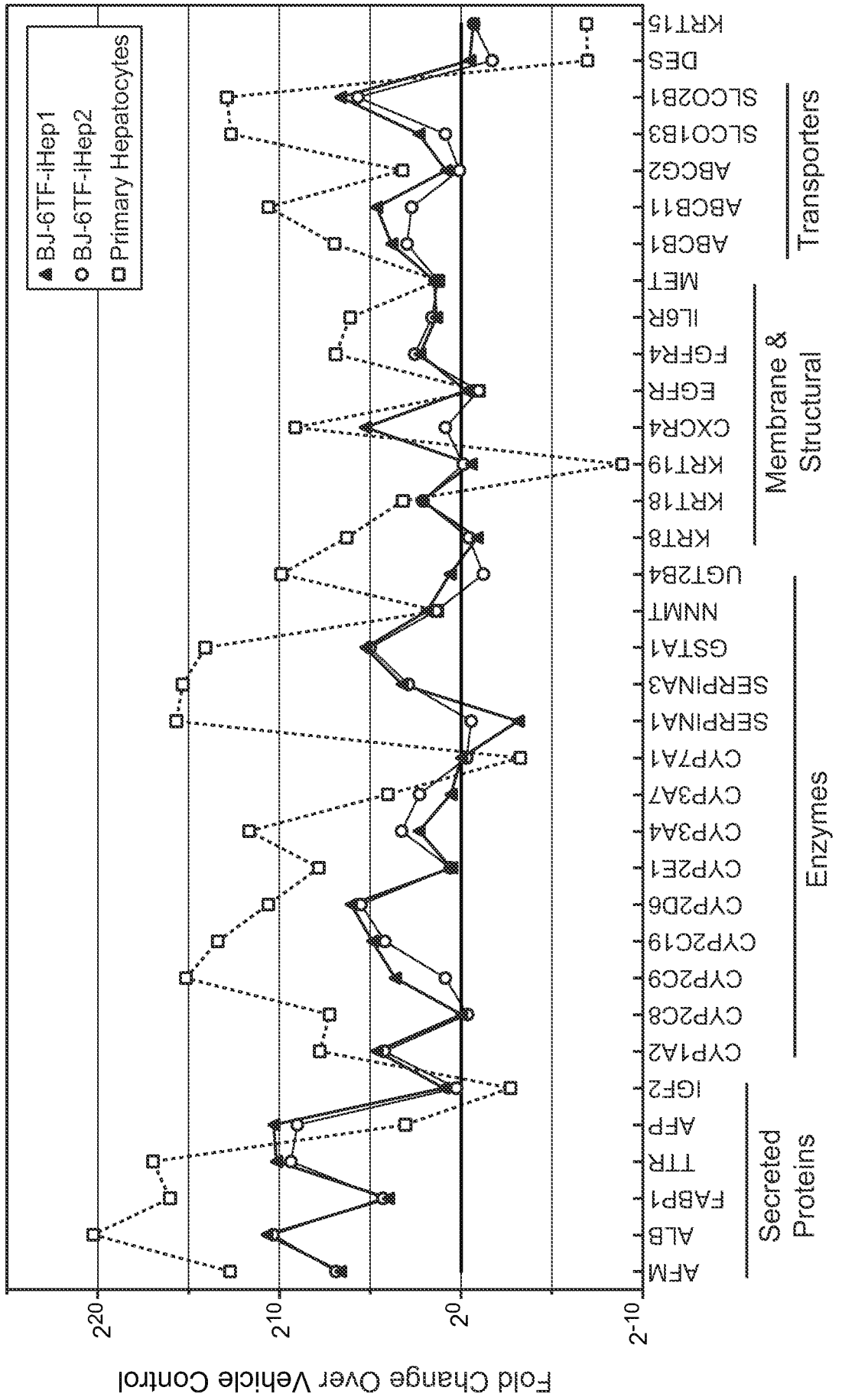

BJ-6TF-iHep1
BJ-6TF-iHep2
Primary Hepatocytes
Fold Change Over Vehicle Control
2^{20}
2^{10}
2^{0}
2^{-10}
AFM
ALB
FABP1
TTR
AFP
IGF2
CYP1A2
CYP2C8
CYP2C9
CYP2C19
CYP2D6
CYP2E1
CYP3A4
CYP3A7
CYP7A1
SERPINA1
SERPINA3
GSTA1
NNMT
UGT2B4
KRT8
KRT18
KRT19
CXCR4
EGFR
FGFR4
IL6R
MET
ABCB1
ABCB11
ABCG2
SLCO1B3
SLCO2B1
DES
KRT15
Secreted Proteins
Enzymes
Membrane & Structural
Transporters

FIG. 29A

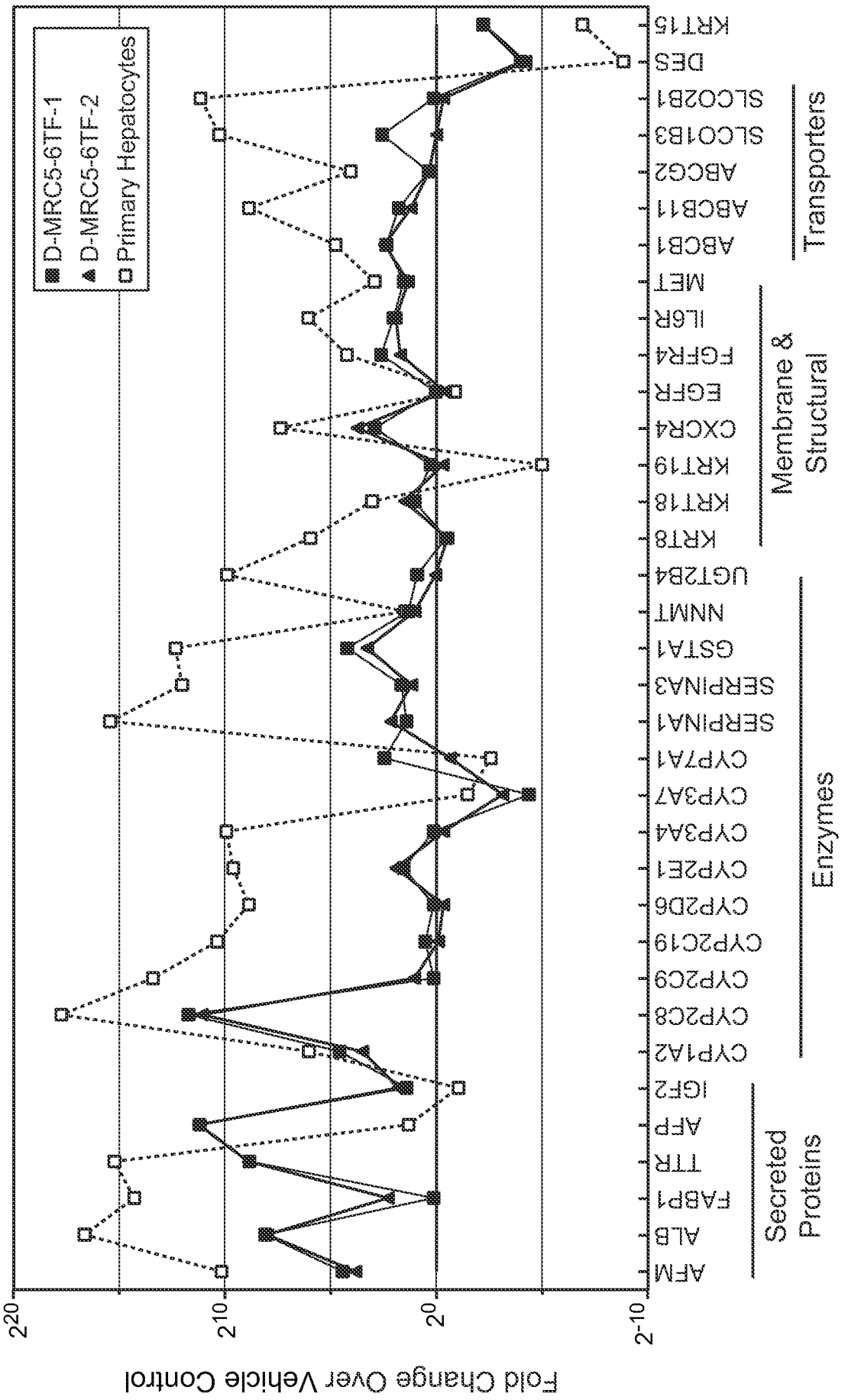

D-MRC5-6TF-1
D-MRC5-6TF-2
Primary Hepatocytes
Fold Change Over Vehicle Control
2^20
2^10
2^0
2^-10
AFM
ALB
FABP1
TTR
AFP
IGF2
CYP1A2
CYP2C8
CYP2C9
CYP2C19
CYP2D6
CYP2E1
CYP3A4
CYP3A7
CYP7A1
SERPINA1
SERPINA3
GSTA1
NNMT
UGT2B4
KRT8
KRT18
KRT19
CXCR4
EGFR
FGFR4
IL6R
MET
ABCB1
ABCB11
ABCG2
SLCO1B3
SLCO2B1
DES
KRT15
Secreted Proteins
Enzymes
Membrane & Structural
Transporters

FIG. 29B

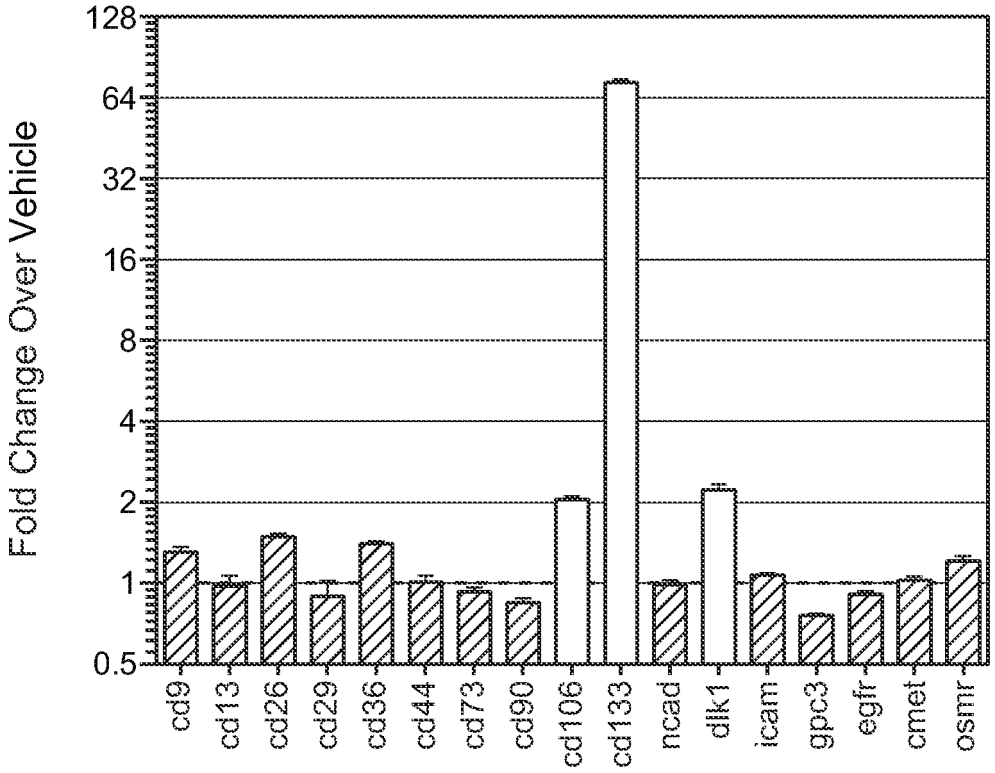

Fold Change Over Vehicle
128
64
32
16
8
4
2
1
0.5
cd9
cd13
cd26
cd29
cd36
cd44
cd73
cd90
cd106
cd133
ncad
dlk1
icam
gpc3
egfr
cmet
osmr

FIG. 30

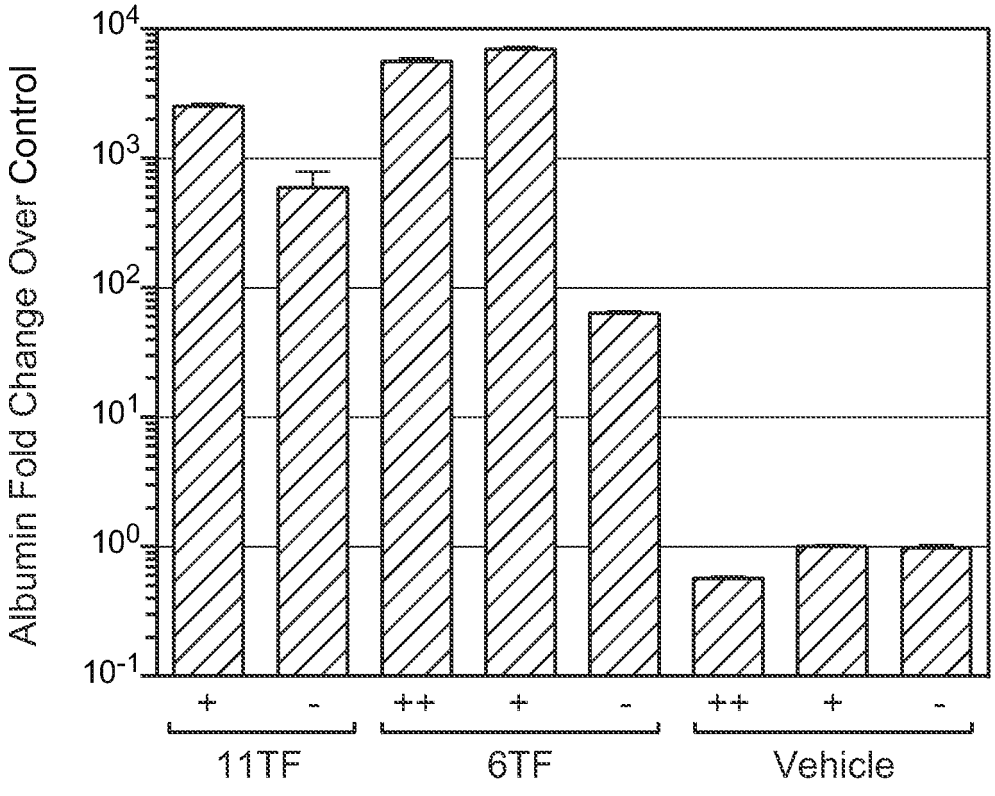

Albumin Fold Change Over Control
10^4
10^3
10^2
10^1
10^0
10^-1
+
-
++
+
-
++
+
-
11TF
6TF
Vehicle

FIG. 31

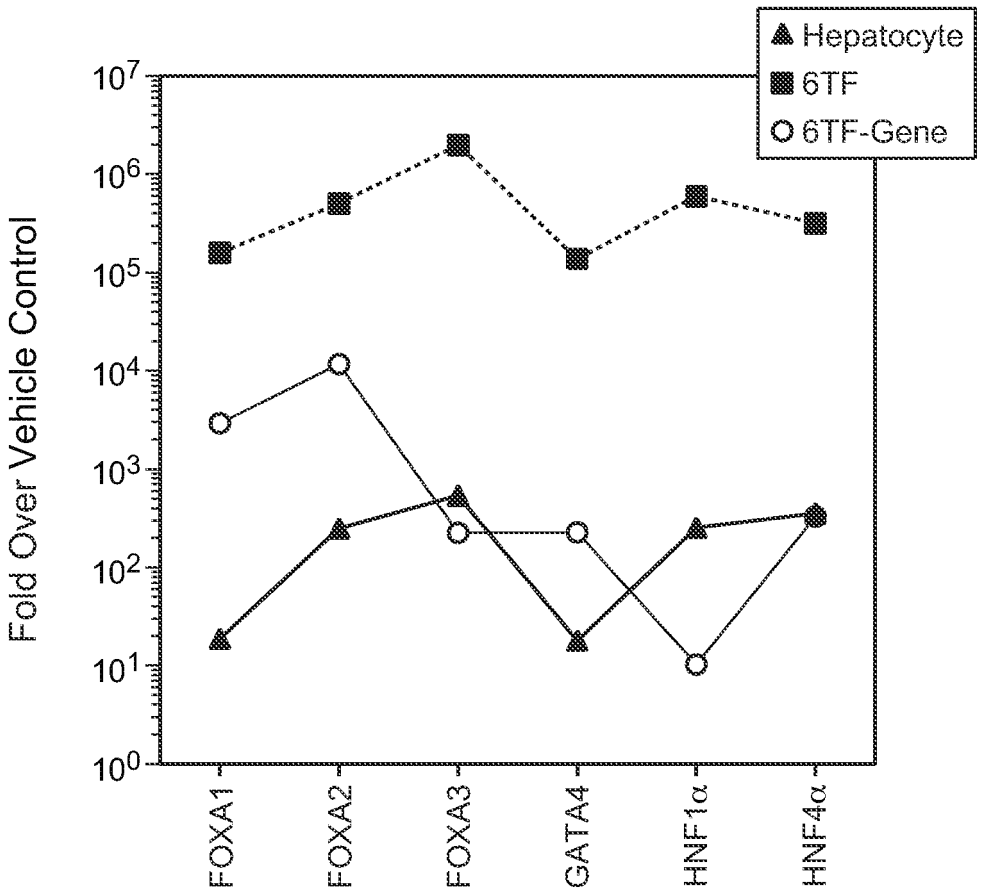

Hepatocyte
6TF
6TF-Gene
Fold Over Vehicle Control
10^7
10^6
10^5
10^4
10^3
10^2
10^1
10^0
FOXA1
FOXA2
FOXA3
GATA4
HNF1α
HNF4α

FIG. 32

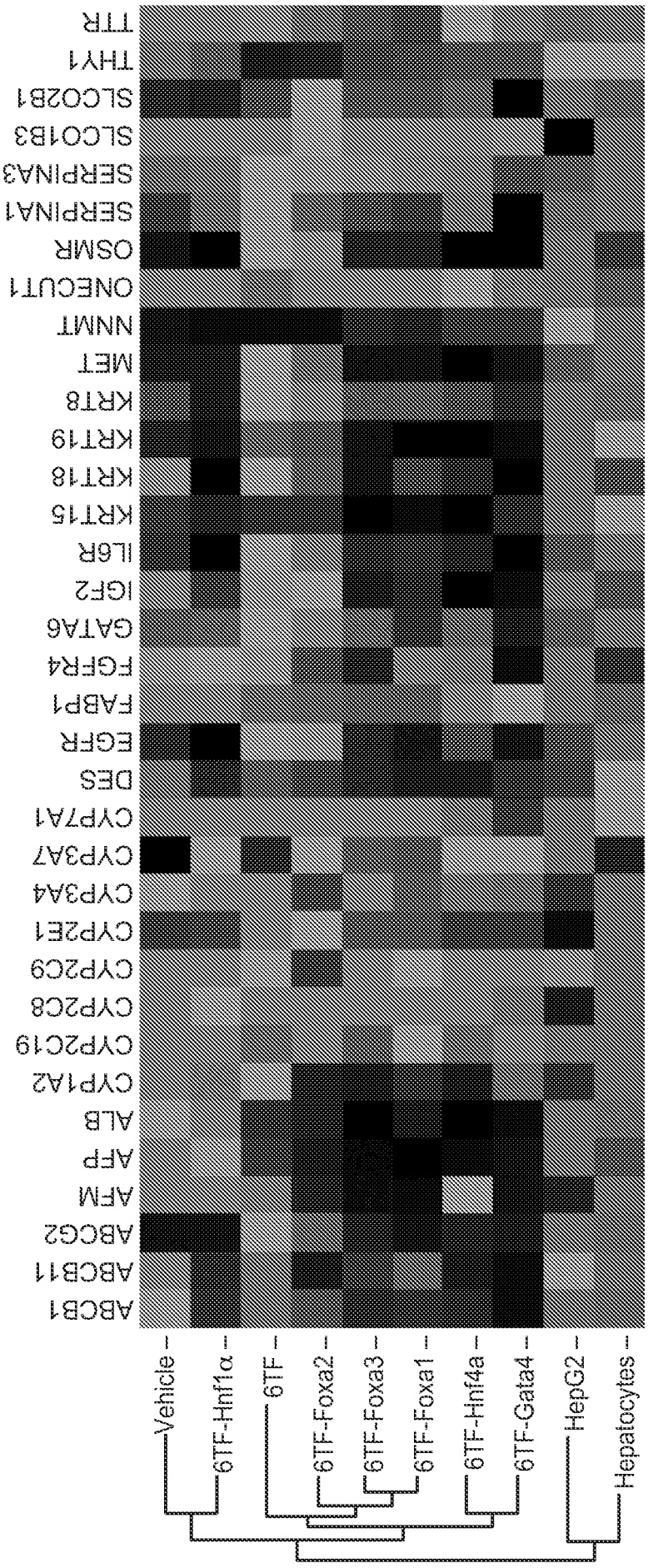

TTR
THY1
SLCO2B1
SLCO1B3
SERPINA3
SERPINA1
OSMR
ONECUT1
NNMT
MET
KRT8
KRT19
KRT18
KRT15
IL6R
IGF2
GATA6
FGFR4
FABP1
EGFR
DES
CYP7A1
CYP3A7
CYP3A4
CYP2E1
CYP2C9
CYP2C8
CYP2C19
CYP1A2
ALB
AFP
AFM
ABCG2
ABCB11
ABCB1
Vehicle
6TF-Hnf1α
6TF
6TF-Foxa2
6TF-Foxa3
6TF-Foxa1
6TF-Hnf4a
6TF-Gata4
HepG2
Hepatocytes

FIG. 33

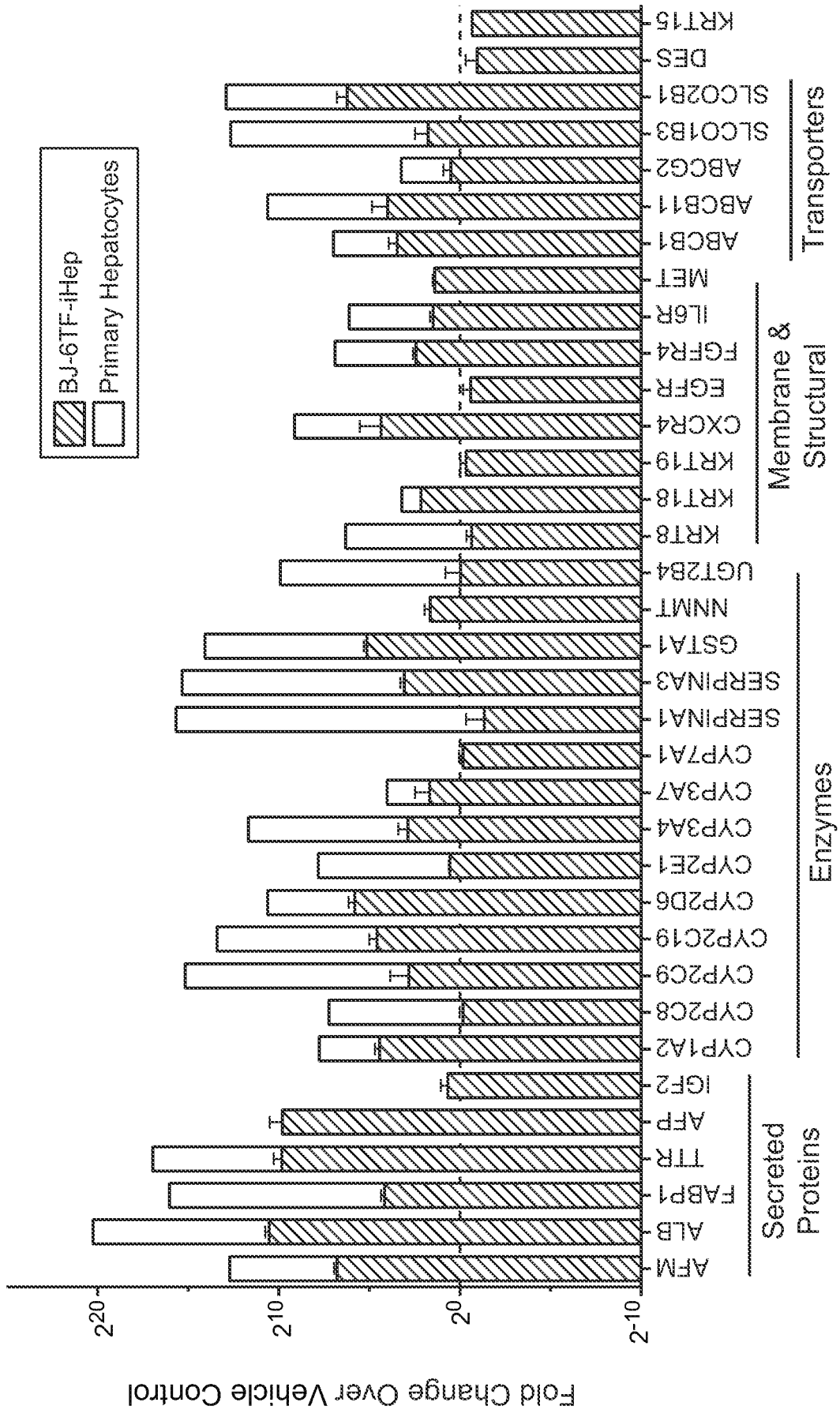

Fold Change Over Vehicle Control
2^{20}
2^{10}
2^{0}
2^{-10}
BJ-6TF-iHep
Primary Hepatocytes
AFM
ALB
FABP1
TTR
AFP
IGF2
CYP1A2
CYP2C8
CYP2C9
CYP2C19
CYP2D6
CYP2E1
CYP3A4
CYP3A7
CYP7A1
SERPINA1
SERPINA3
GSTA1
NNMT
UGT2B4
KRT8
KRT18
KRT19
CXCR4
EGFR
FGFR4
IL6R
MET
ABCB1
ABCB11
ABCG2
SLCO1B3
SLCO2B1
DES
KRT15
Secreted Proteins
Enzymes
Membrane & Structural
Transporters

FIG. 34A

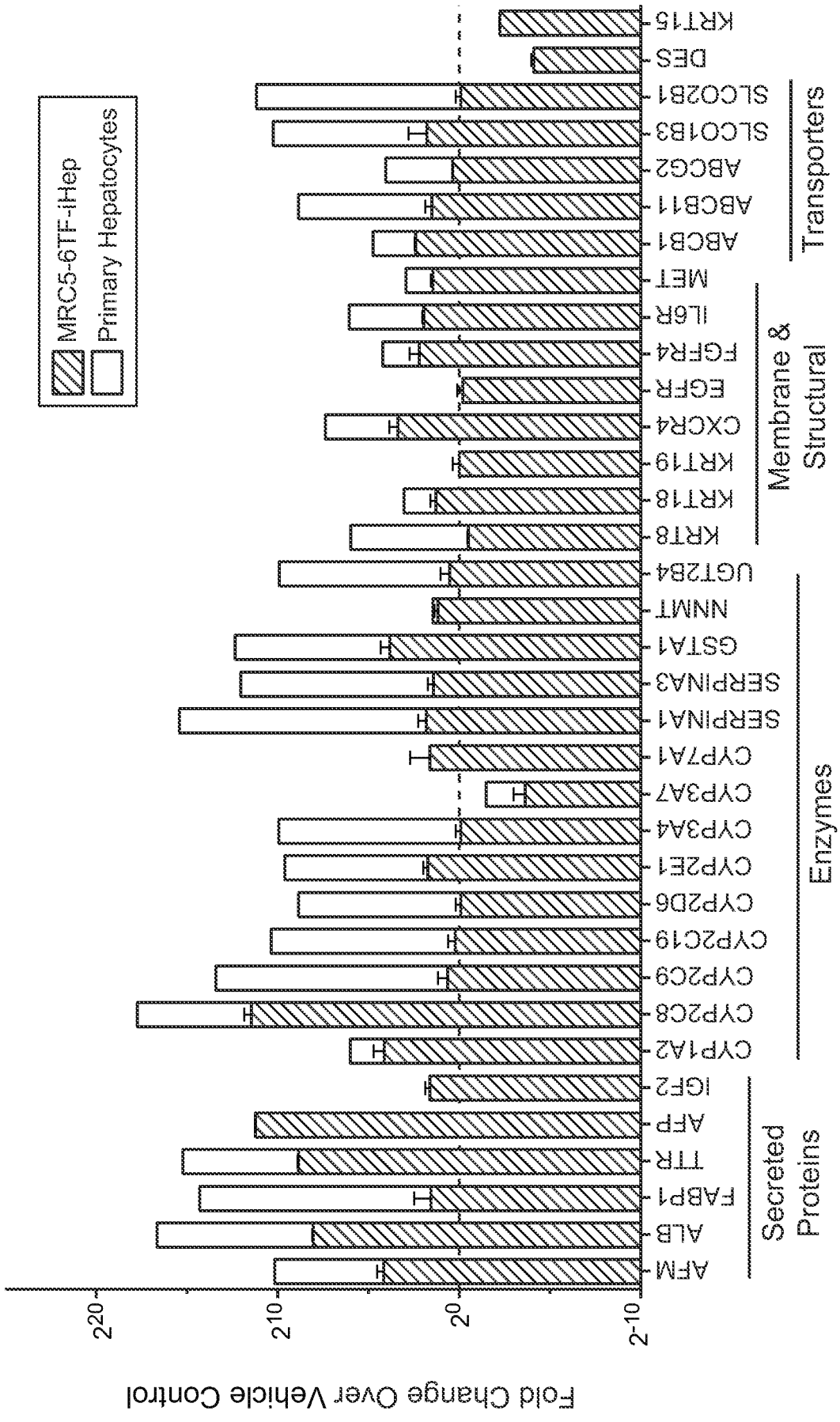

Fold Change Over Vehicle Control
2^{20}
2^{10}
2^{0}
2^{-10}
MRC5-6TF-iHep
Primary Hepatocytes
AFM
ALB
FABP1
TTR
AFP
IGF2
CYP1A2
CYP2C8
CYP2C9
CYP2C19
CYP2D6
CYP2E1
CYP3A4
CYP3A7
CYP7A1
SERPINA1
SERPINA3
GSTA1
NNMT
UGT2B4
KRT8
KRT18
KRT19
CXCR4
EGFR
FGFR4
IL6R
MET
ABCB1
ABCB11
ABCG2
SLCO1B3
SLCO2B1
DES
KRT15
Secreted Proteins
Enzymes
Membrane & Structural
Transporters

FIG. 34B

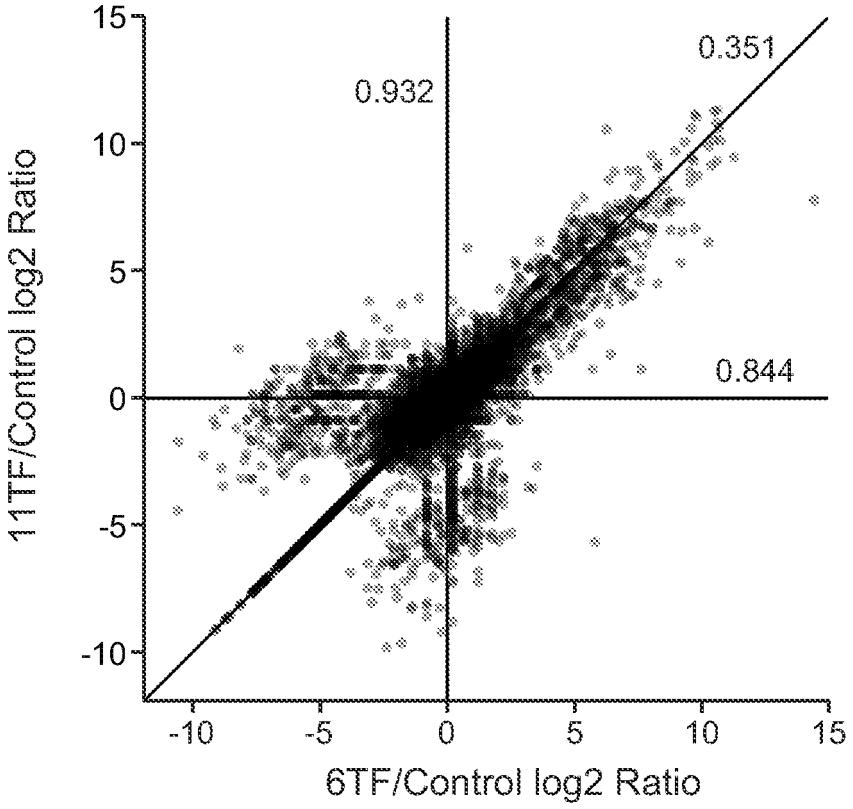


FIG. 35A

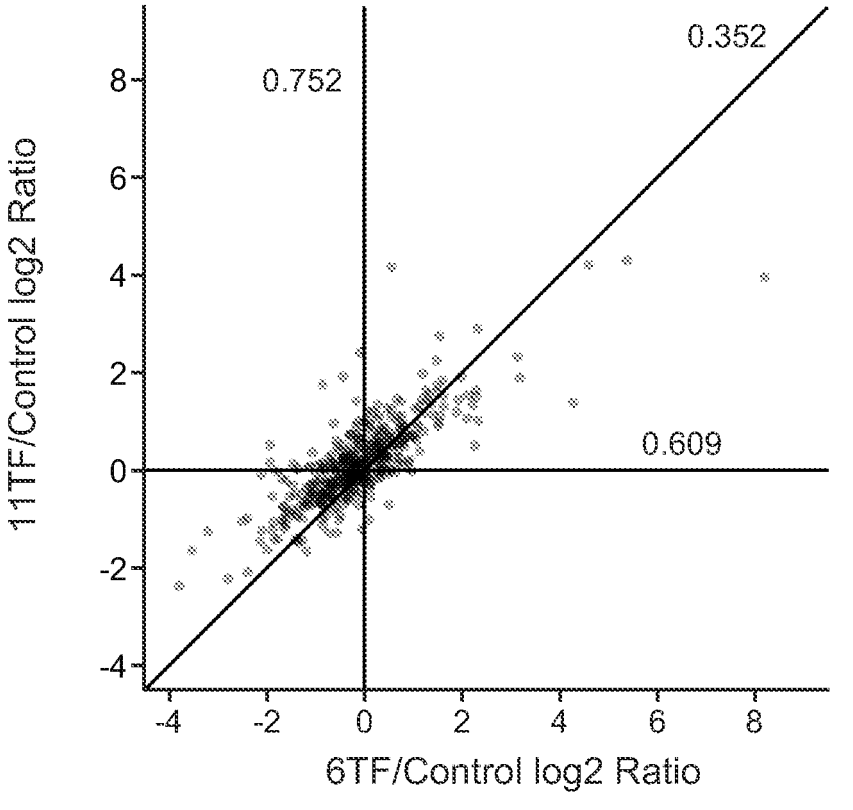


FIG. 35B

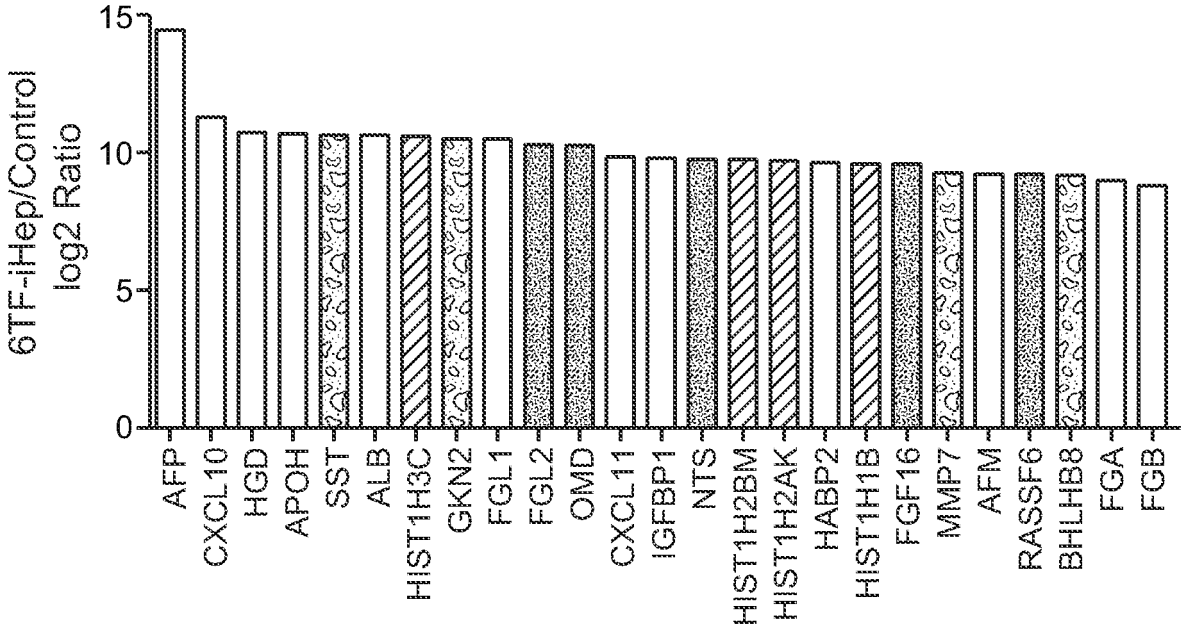

6TF-iHep/Control
log2 Ratio
15
10
5
0
AFP
CXCL10
HGD
APOH
SST
ALB
HIST1H3C
GKN2
FGL1
FGL2
OMD
CXCL11
IGFBP1
NTS
HIST1H2BM
HIST1H2AK
HABP2
HIST1H1B
FGF16
MMP7
AFM
RASSF6
BHLHB8
FGA
FGB

FIG. 36

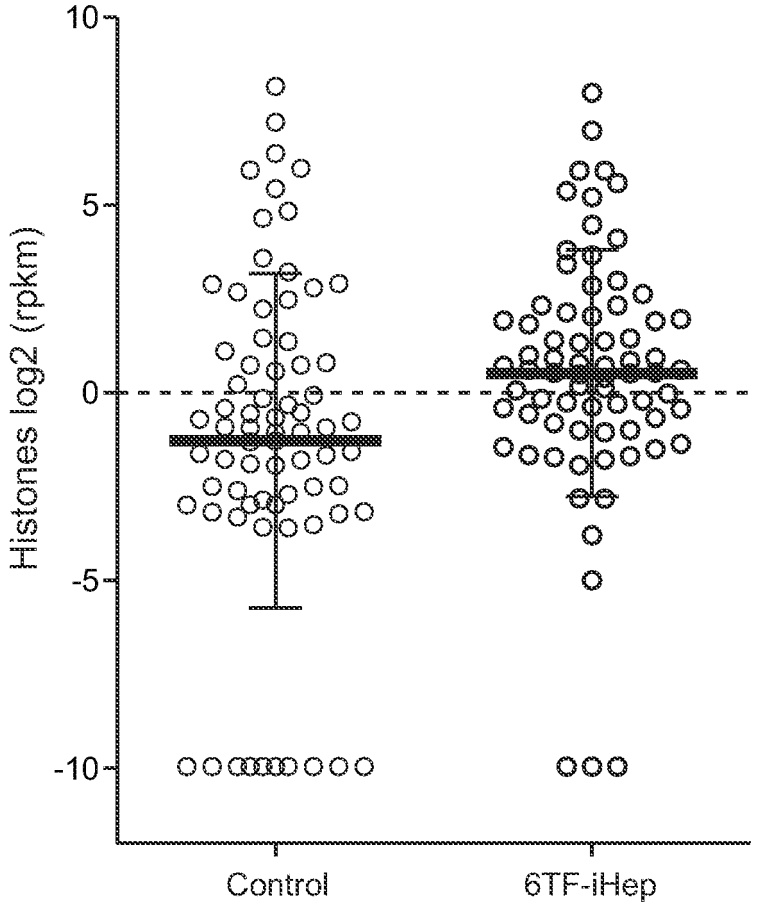

Histones log2 (rpkm)
10
5
0
-5
-10
Control
6TF-iHep

FIG. 37

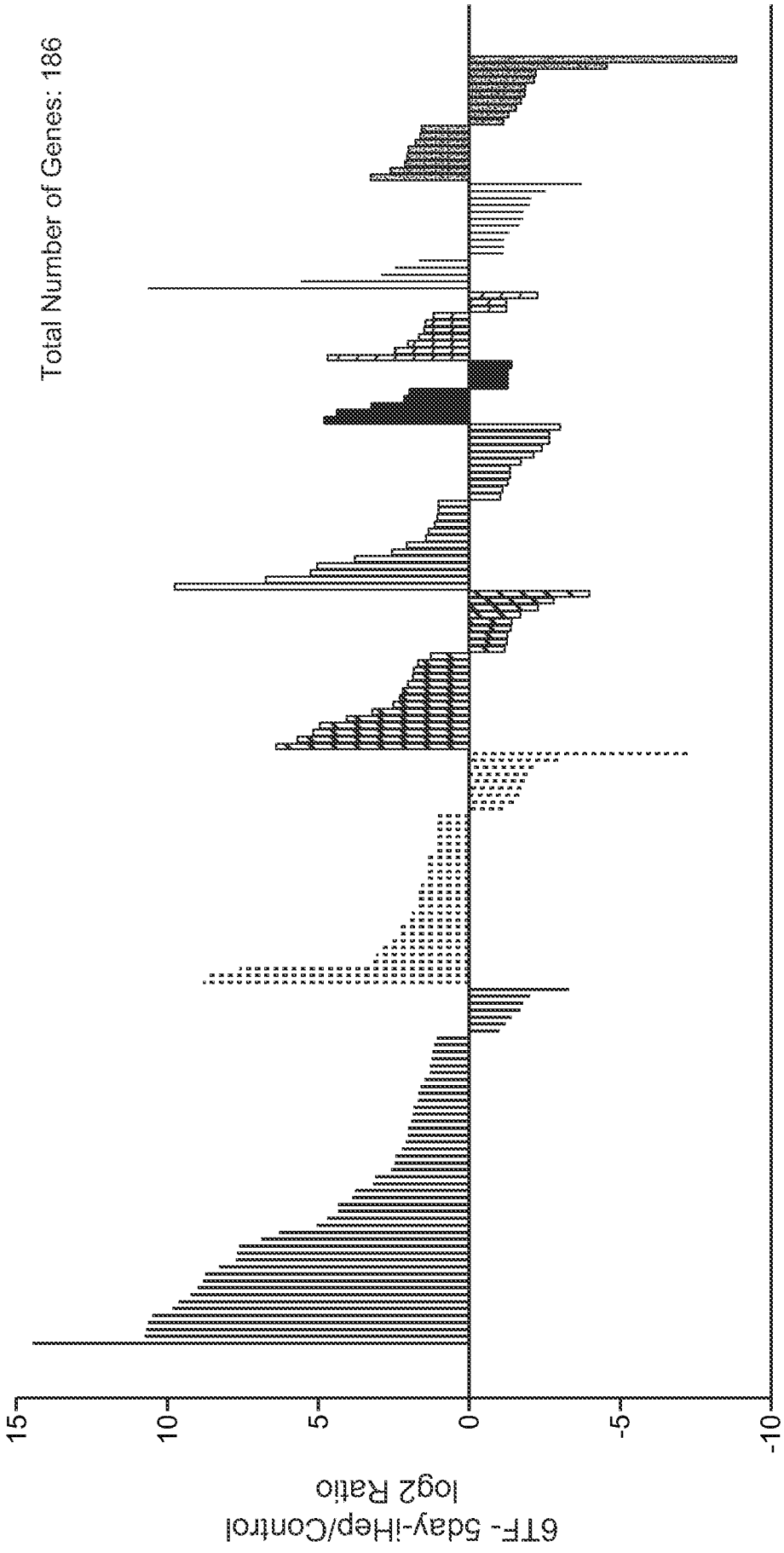

Total Number of Genes: 186
6TF- 5day-iHep/Control
log2 Ratio
15
10
5
0
-5
-10

FIG. 38