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(54) **HOST FACTORS THAT ENHANCE VIRAL PRODUCTION VIA VIRALLY DRIVEN FITNESS-BASED CRISPR SCREENING**

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C12N 7/00	(2006.01)
C12N 9/22	(2006.01)
C12N 15/11	(2006.01)

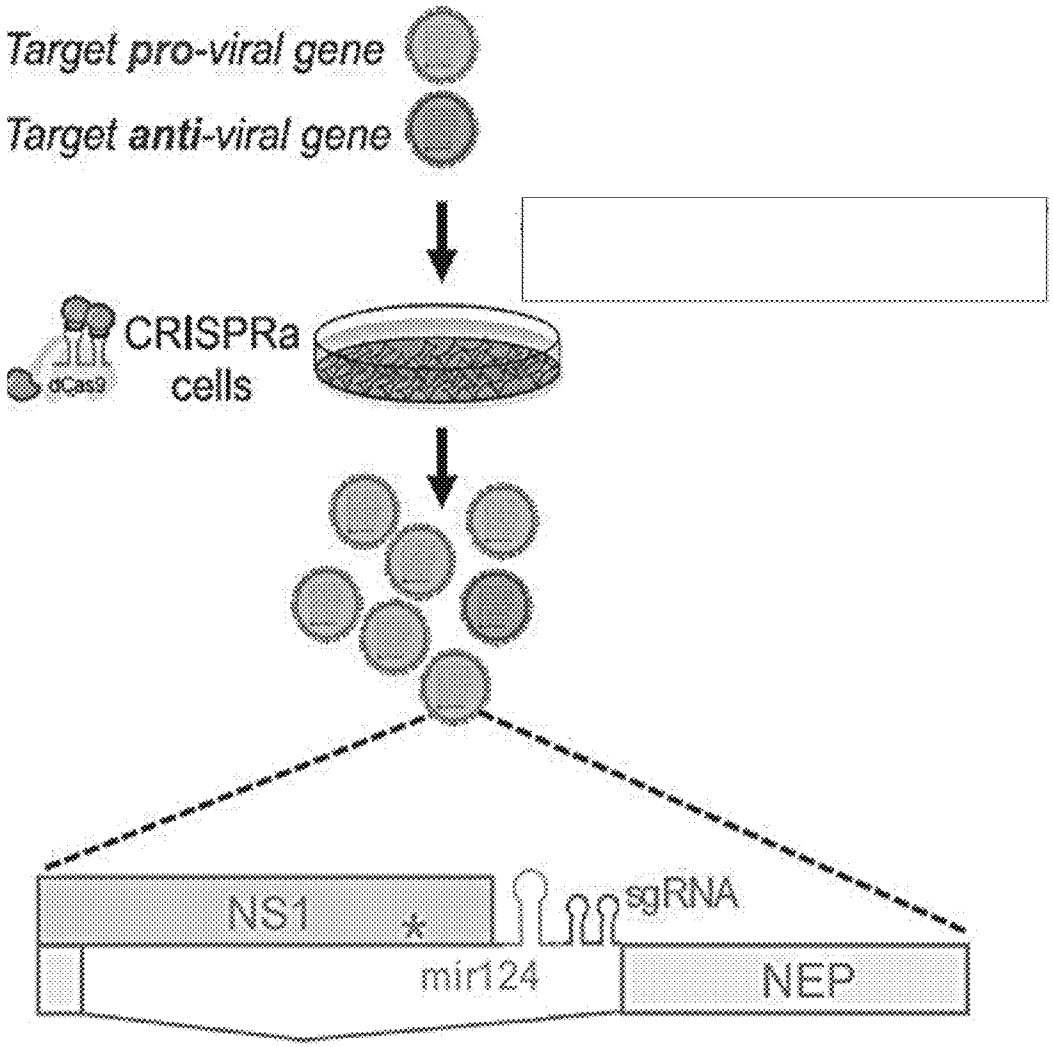
(52) **U.S. Cl.**

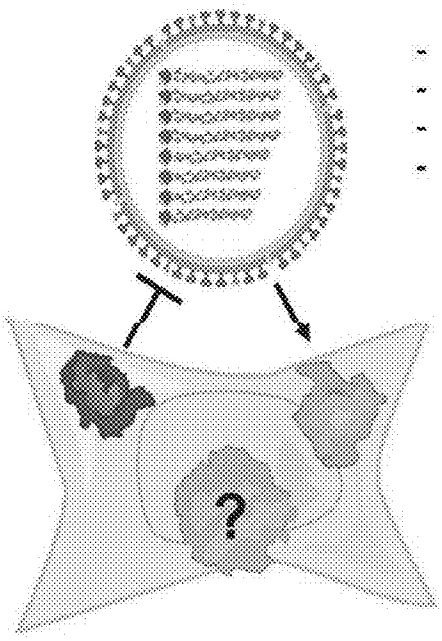
CPC ***C12N 15/1131*** (2013.01); ***C12N 7/00*** (2013.01); ***C12N 9/22*** (2013.01); ***C12N 15/11*** (2013.01); *C12N 2310/14* (2013.01); *C12N 2310/20* (2017.05); *C12N 2320/10* (2013.01); *C12N 2760/16151* (2013.01)

(57) **ABSTRACT**

Described herein are compositions and methods for a screening approach for identifying host factors that impact influenza viral production after the initial infection. Host factors that enhance influenza virus production were identified. Screening methods described herein include variations of the Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)/Cas9 system, termed CRISPR activation (CRISPRa) and CRISPR inhibition (CRISPRi).

Specification includes a Sequence Listing.





- Orthomyxovirus
- Types A, B, C, D
- Surface HA and NA define subtypes (18 HA, 11 NA)
- Segmented genome
  - ~14 proteins

Virus versus host
Avoid anti-viral factors (e.g. ISGs)
Utilize pro-viral factors (e.g. ANP32)

Fig. 1

Loss-of function

siRNA knockdowns

CRISPR-knockouts

CRISPR-inhibition (CRISPRi)

- Off-target activity
- Incomplete penetrance

- Difficulty with:
  - Cell viability genes
  - Low quantity gene products

Gain-of function

cDNA overexpression

CRISPR-activation (CRISPRa)

- Bias towards attachment & entry factors

Fig. 2

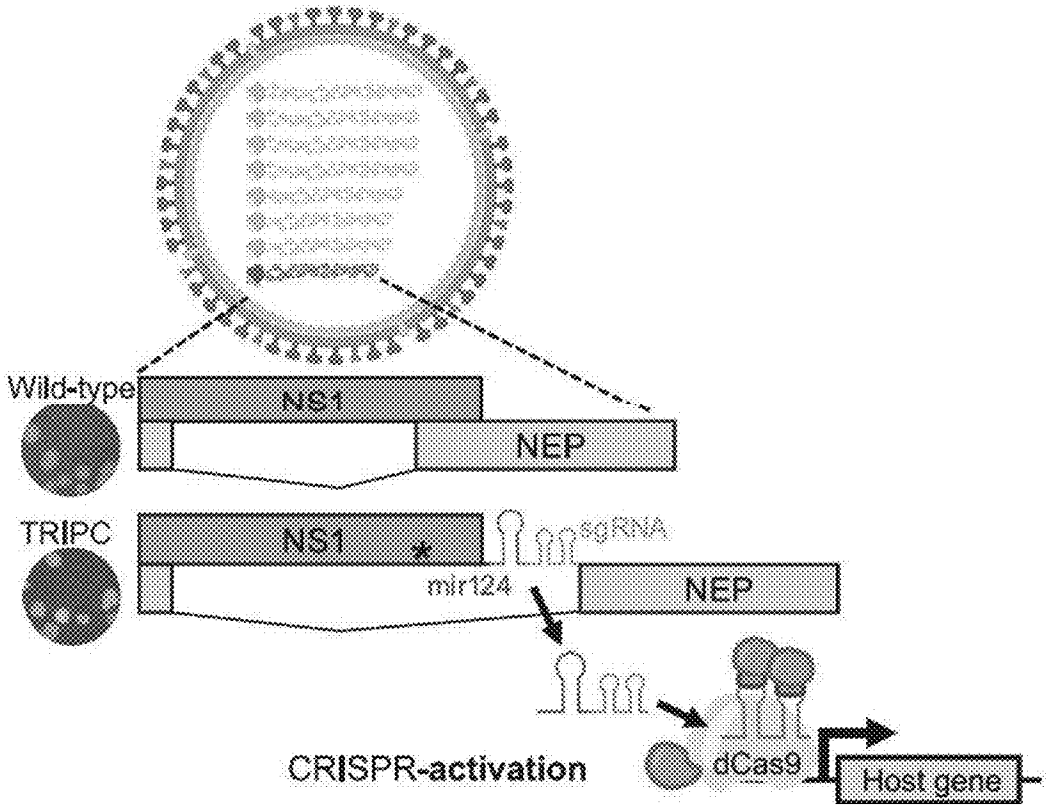

Wild-type
NS1
NEP
TRIPC
NS1
sgRNA
mir124
NEP
CRISPR-activation
dCas9
Host gene

Fig. 3

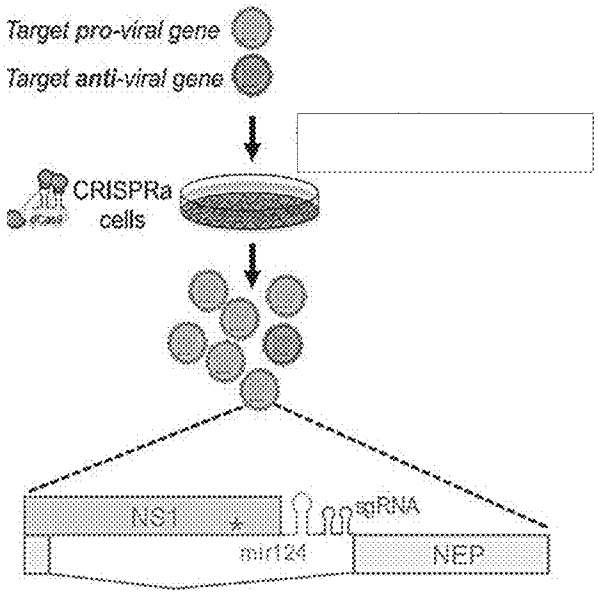

Target pro-viral gene
Target anti-viral gene
CRISPRa
cells
NS1
sgRNA
mir124
NEP

Fig. 4

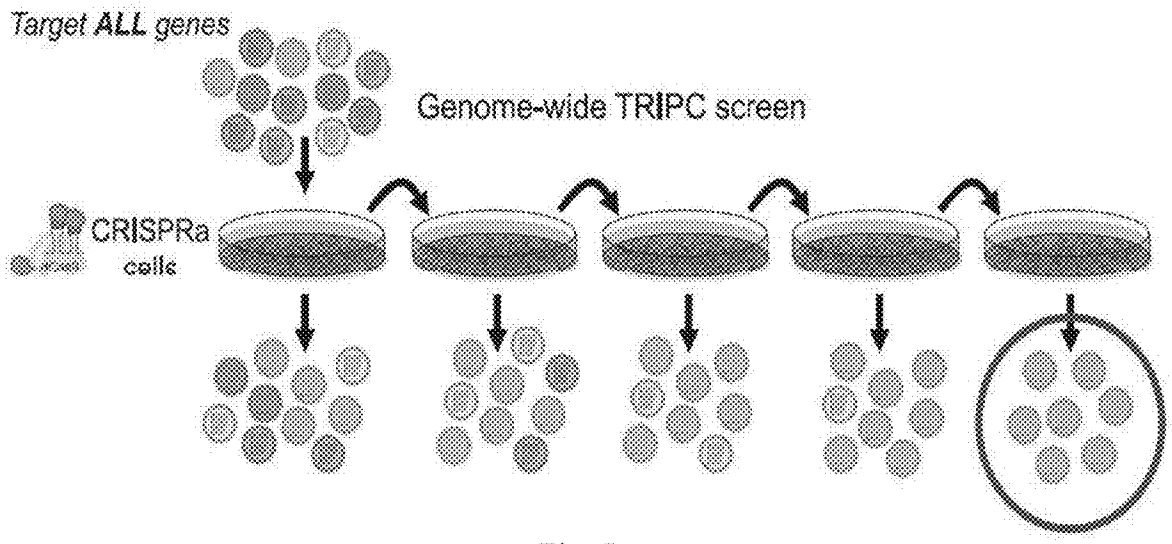

Target ALL genes
Genome-wide TRIPC screen
CRISPRa cells

Fig. 5

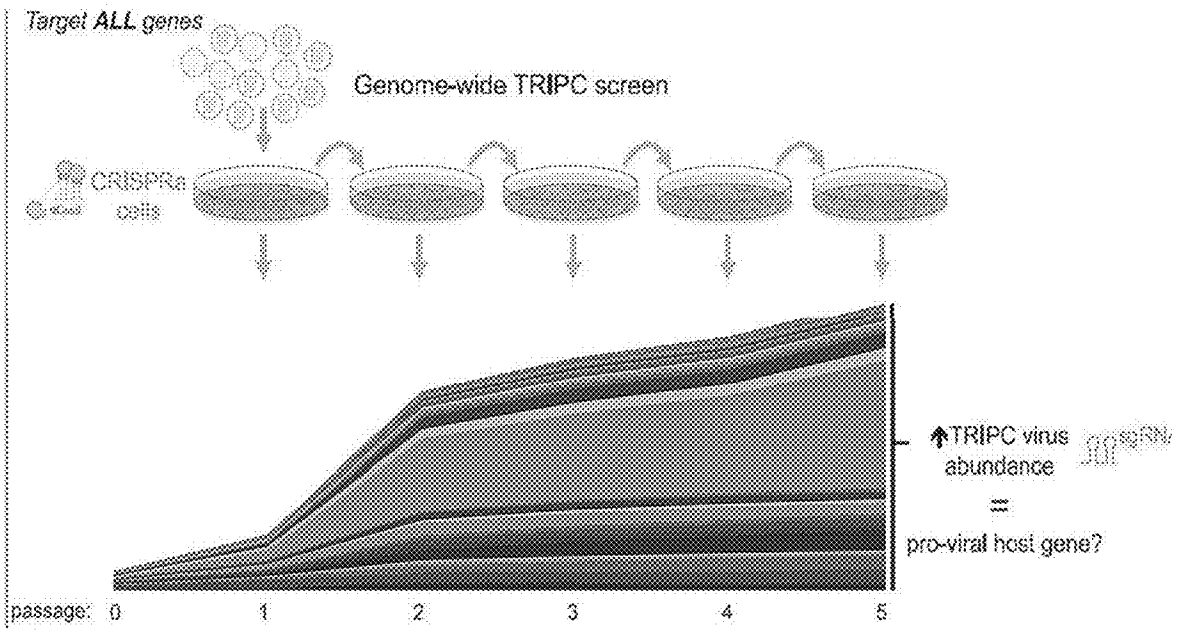

Target ALL genes
Genome-wide TRIPC screen
CRISPRa cells
TRIPC virus abundance
sgRNA
=
pro-viral host gene?
passage: 0 1 2 3 4 5

Fig. 6

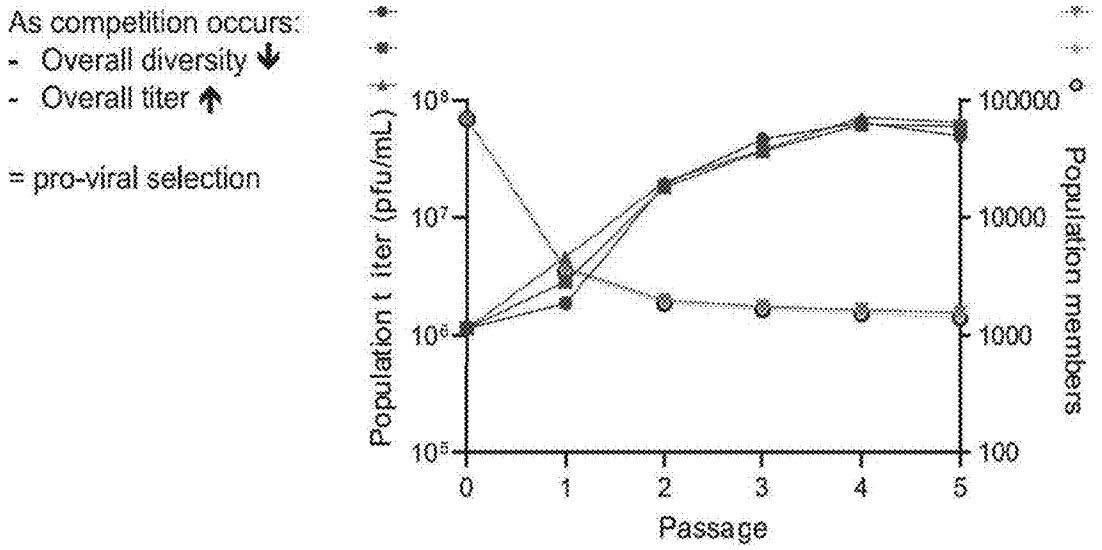

As competition occurs:
- Overall diversity
- Overall titer
= pro-viral selection
Population titer (pfu/mL)
Population members
Passage
0
1
2
3
4
5
100
1000
10000
100000

Fig. 7

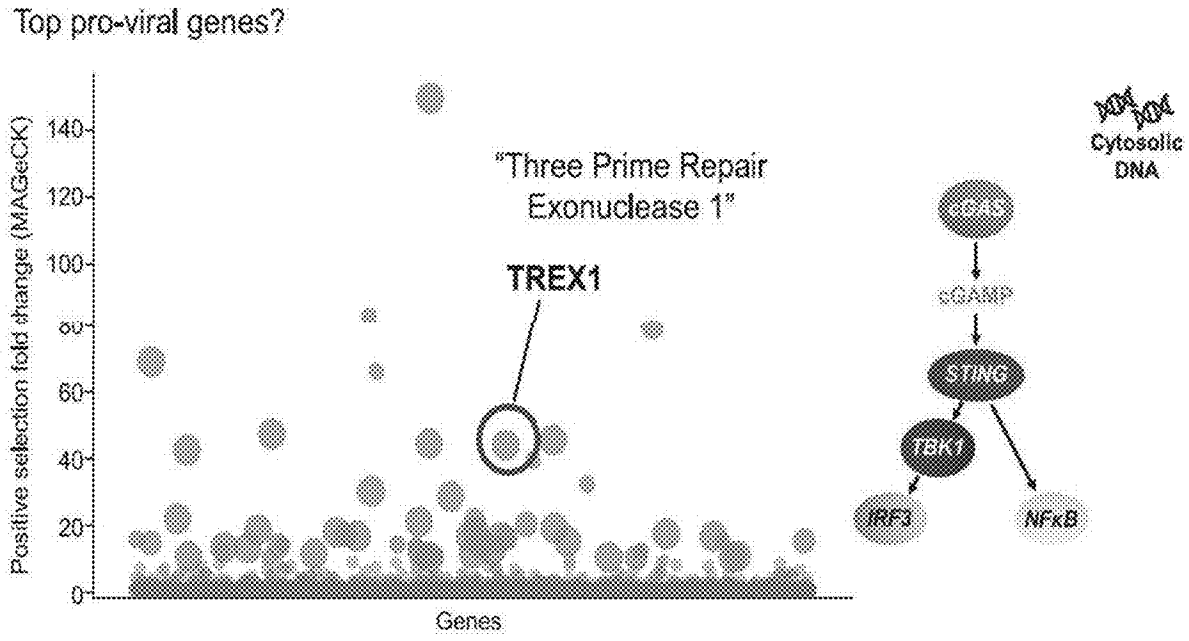
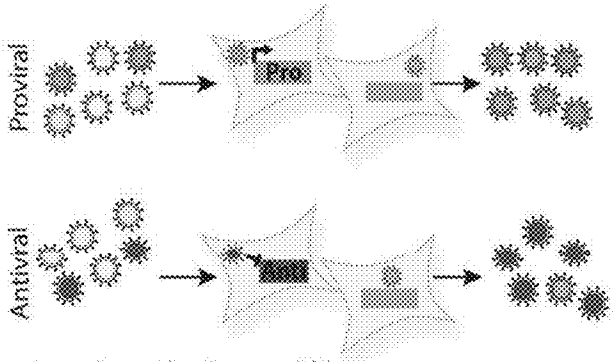

Top pro-viral genes?
Positive selection fold change (MAGeCK)
Genes
"Three Prime Repair Exonuclease 1"
TREX1
Cytosolic DNA
cGAS
cGAMP
STING
TBK1
IRF3
NFκB

Fig. 8

KO screens: powerful genetics, but....

- biased towards early events
- cannot screen essential genes
- often proxy phenotypes

Virus-driven selection of host modulators



- virus does the heavy lifting
- fitness rank-orders hits
- captures mid- to late stage of infection
- host cell manipulated only during infection, only in infected cell

Fig. 9

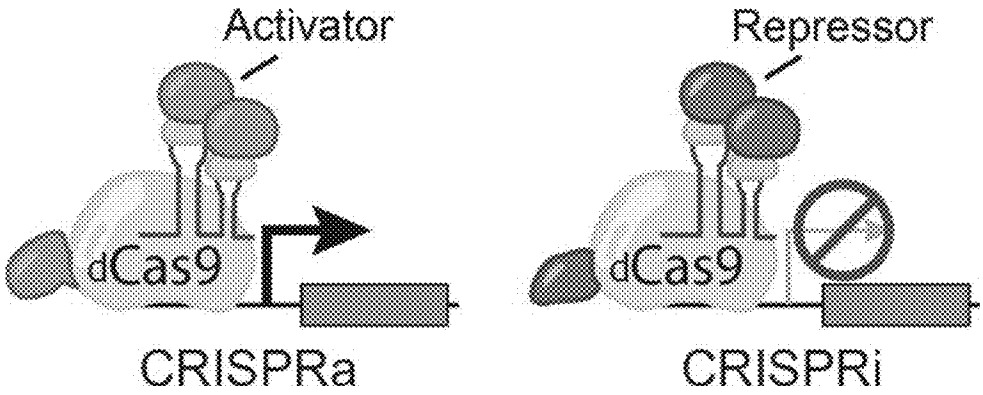


Fig. 10

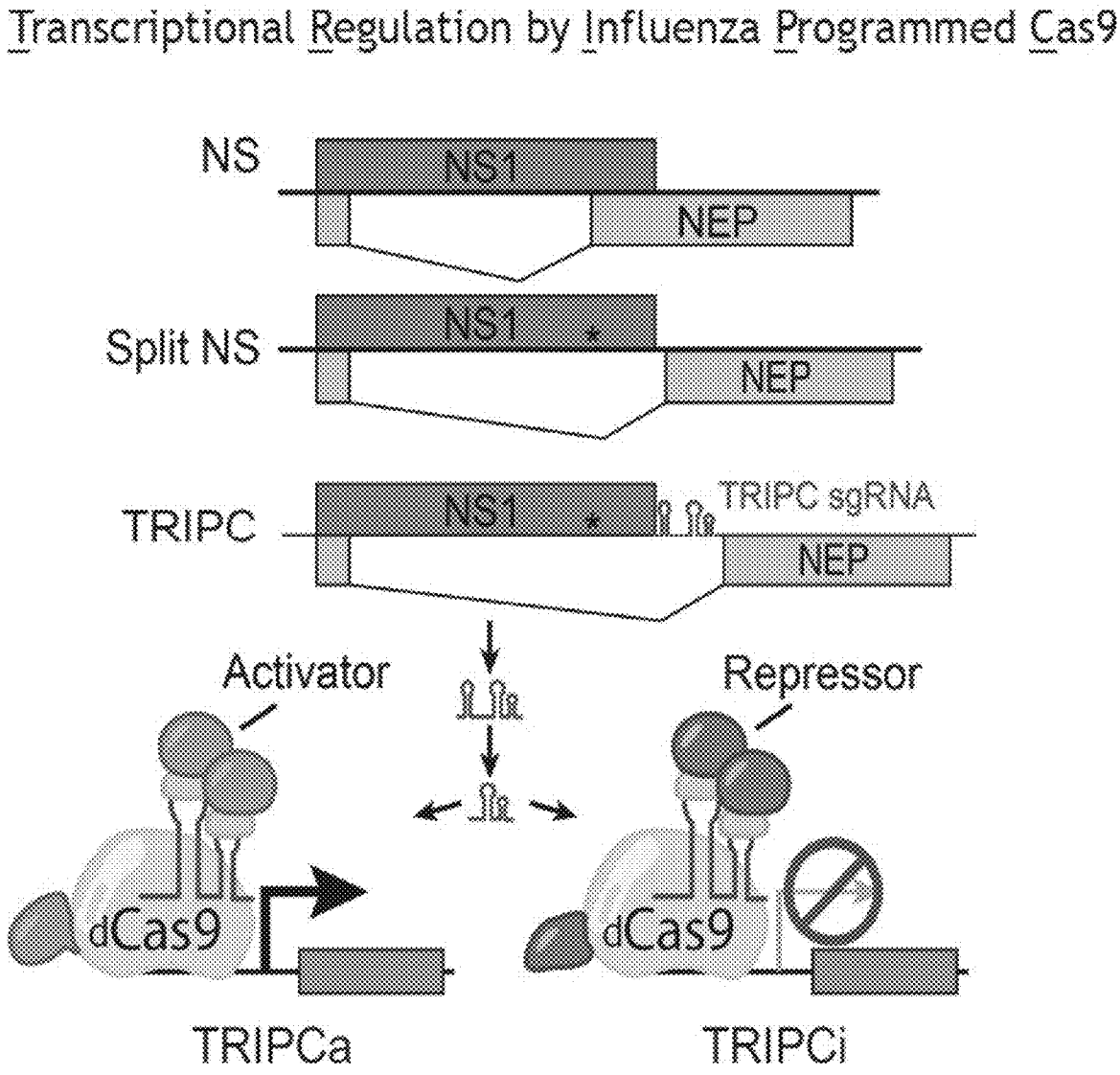

Transcriptional Regulation by Influenza Programmed Cas9
NS
NS1
NEP
Split NS
NS1
NEP
TRIPC
NS1
TRIPC sgRNA
NEP
Activator
Repressor
dCas9
dCas9
TRIPCa
TRIPCi

Fig. 11

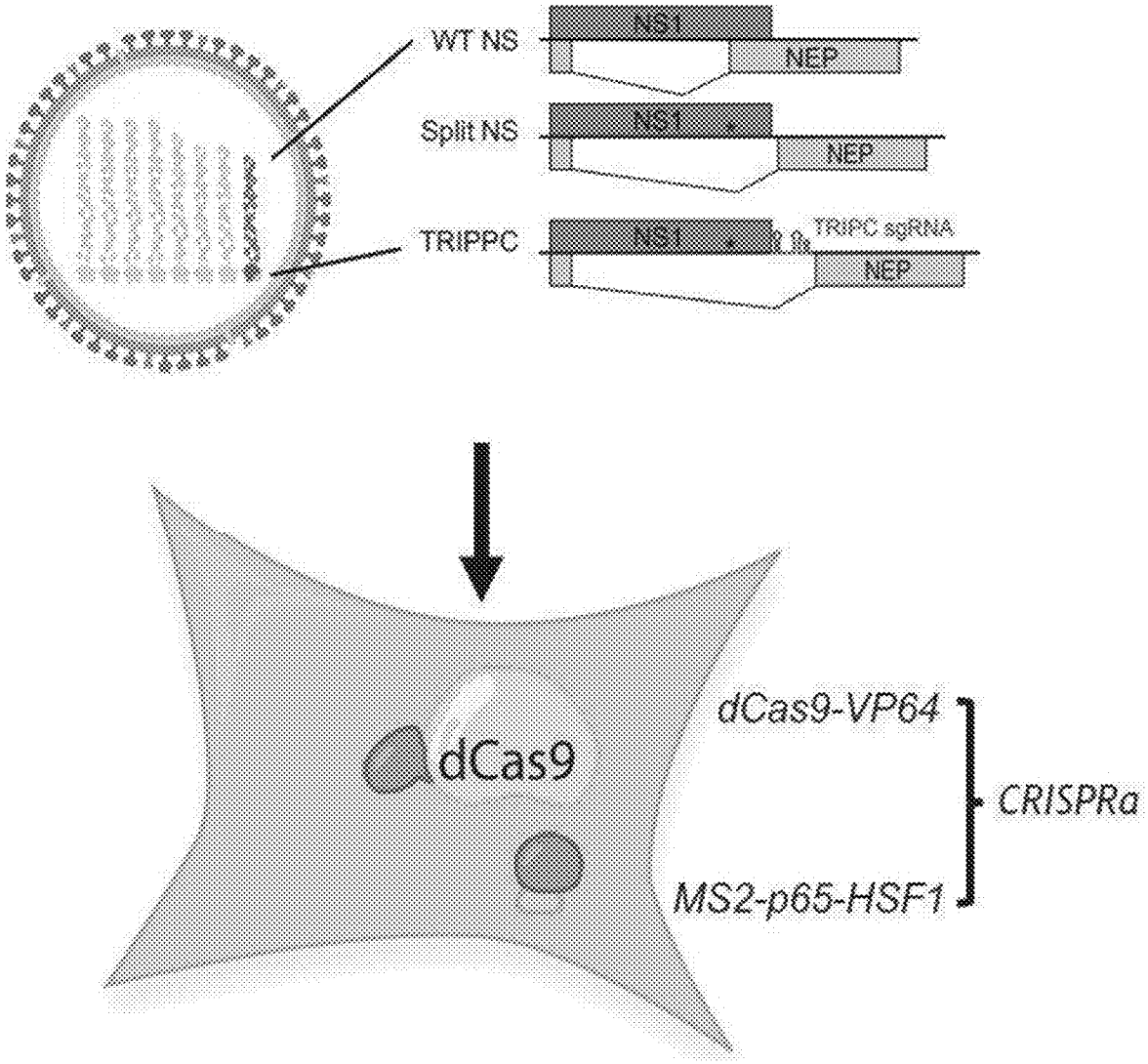

WT NS
NS1
NEP
Split NS
NS1
NEP
TRIPPC
NS1
TRIPC sgRNA
NEP
dCas9
dCas9-VP64
CRISPRa
MS2-p65-HSF1

Fig. 12

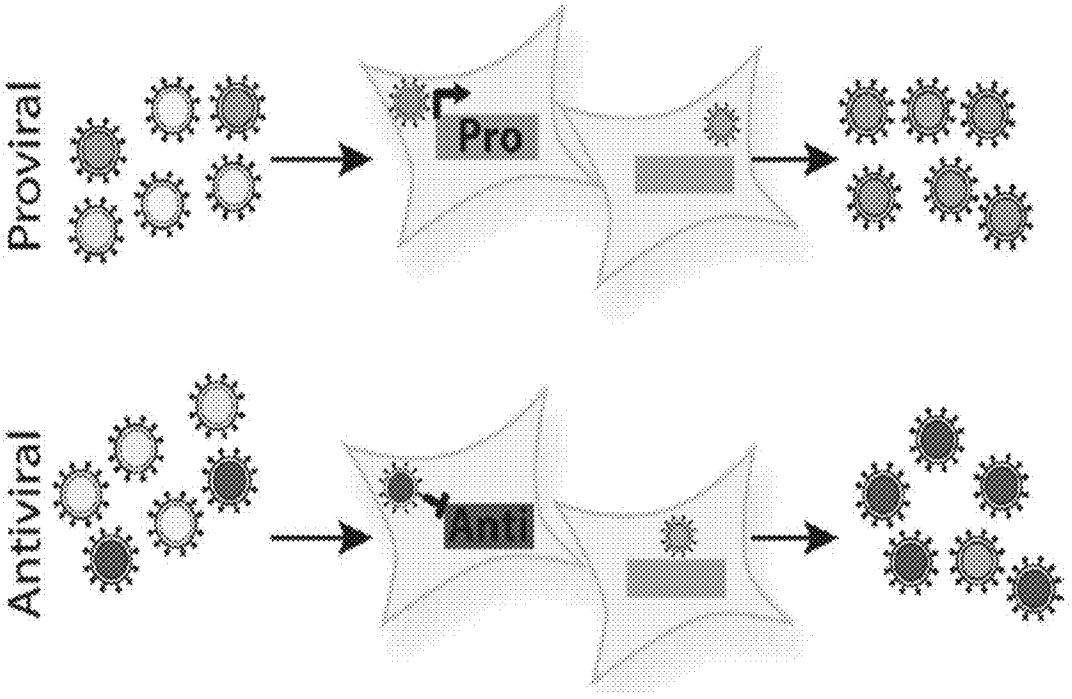


Fig. 13

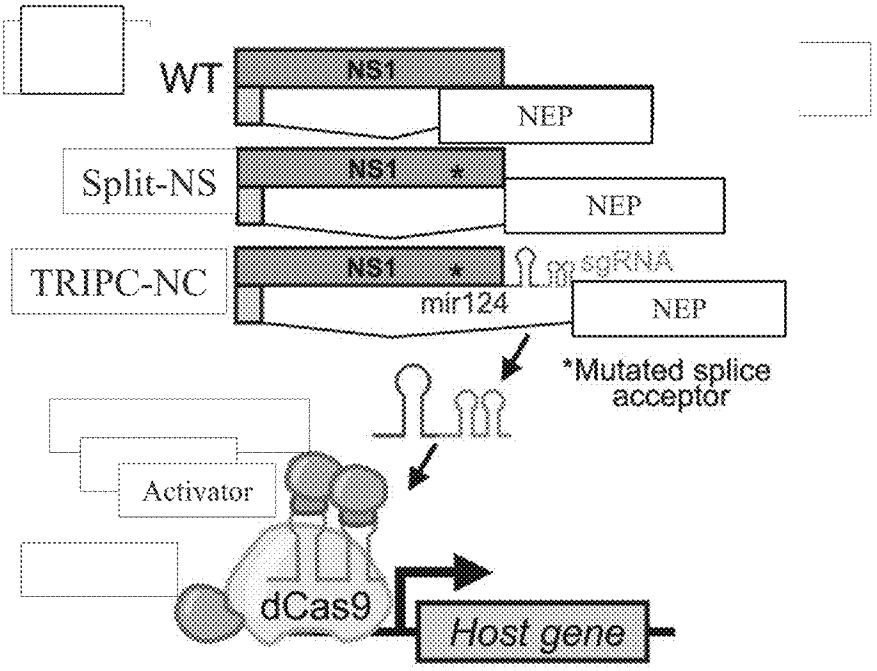


Fig. 14A

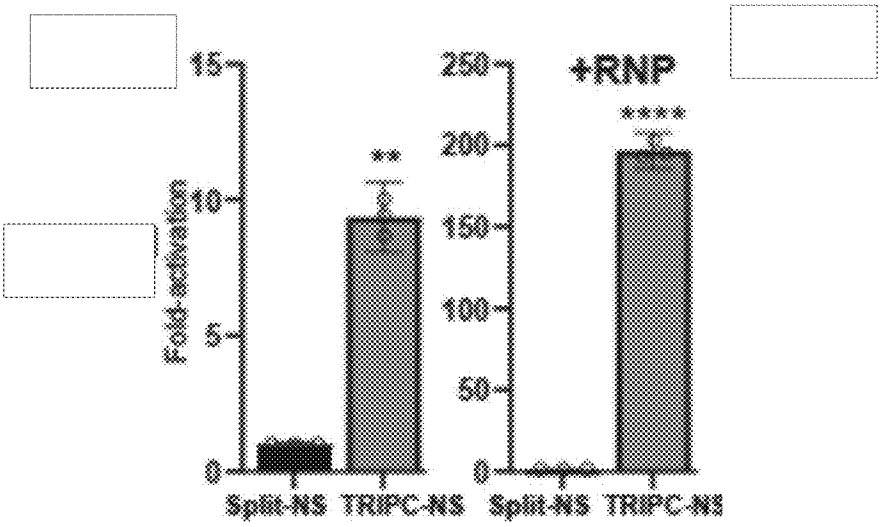


Fig. 14B

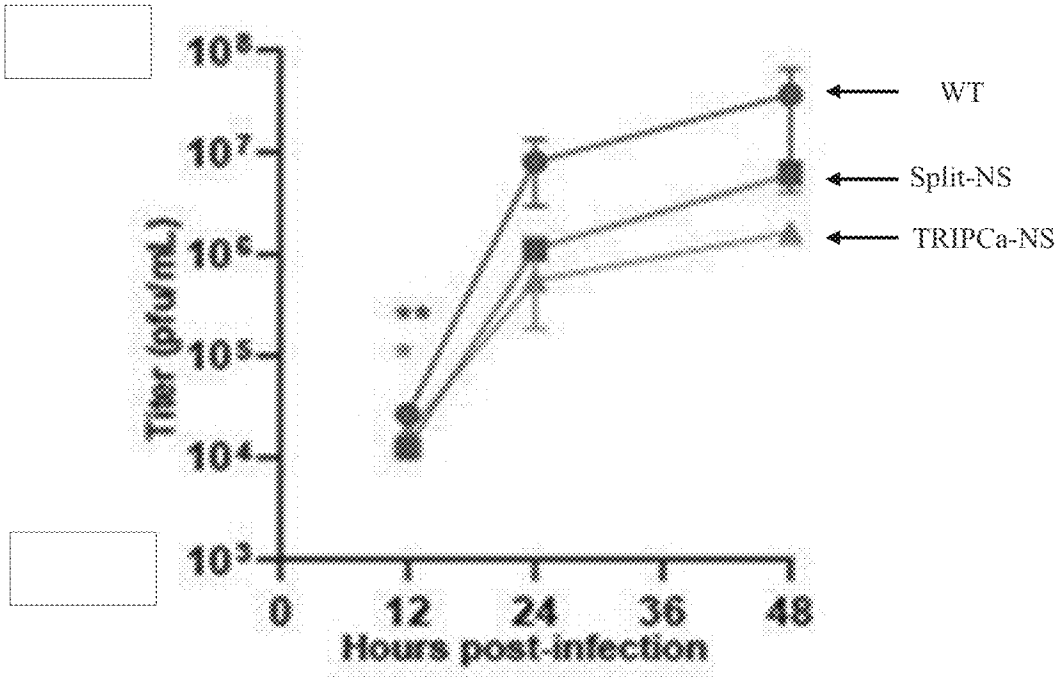


Fig. 14C

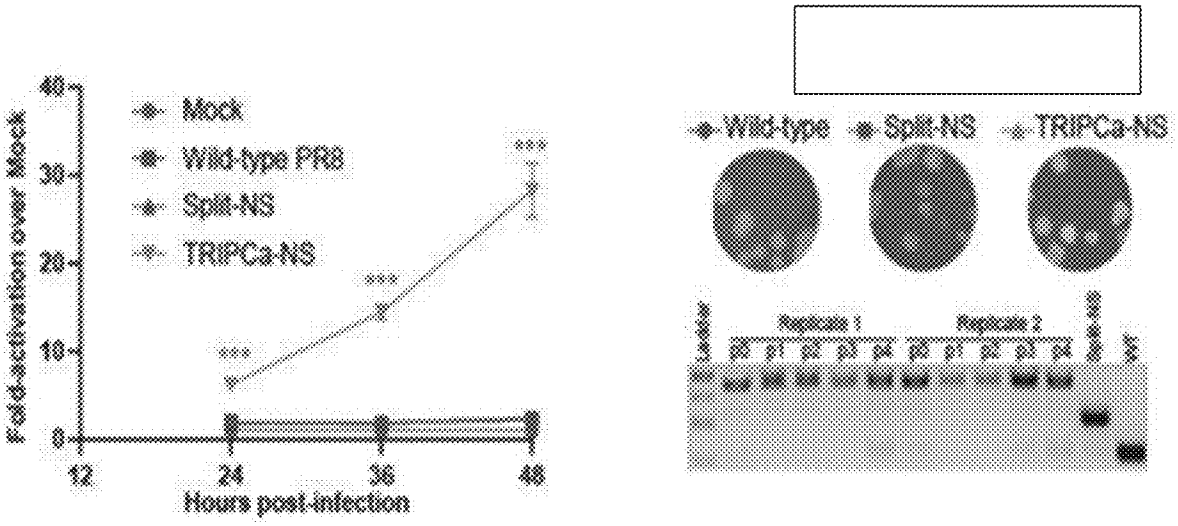


Fig. 14D

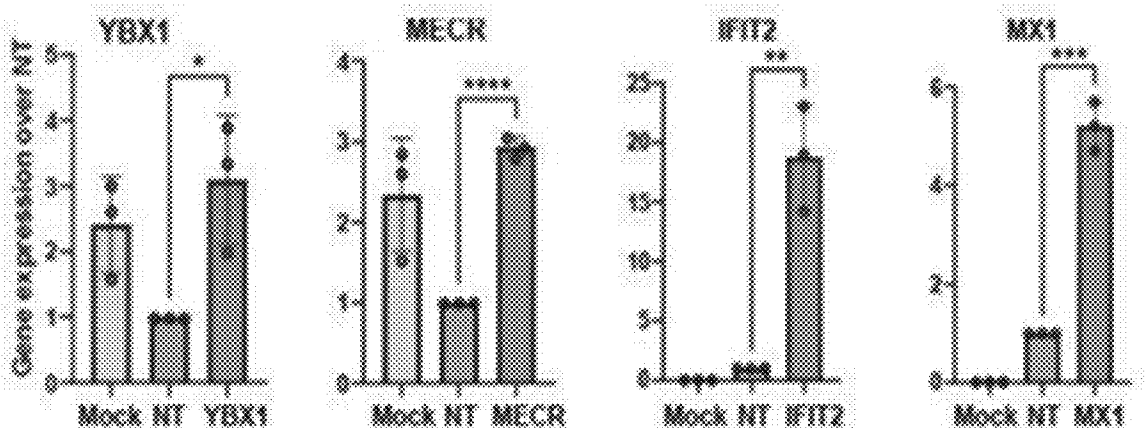


Fig. 14E

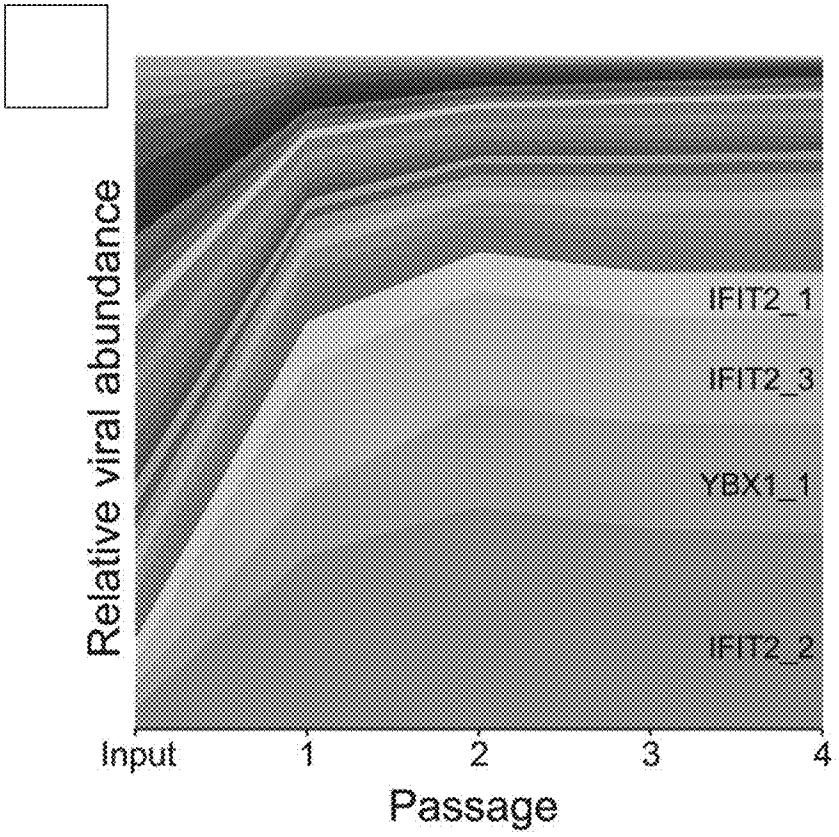


Fig. 14F

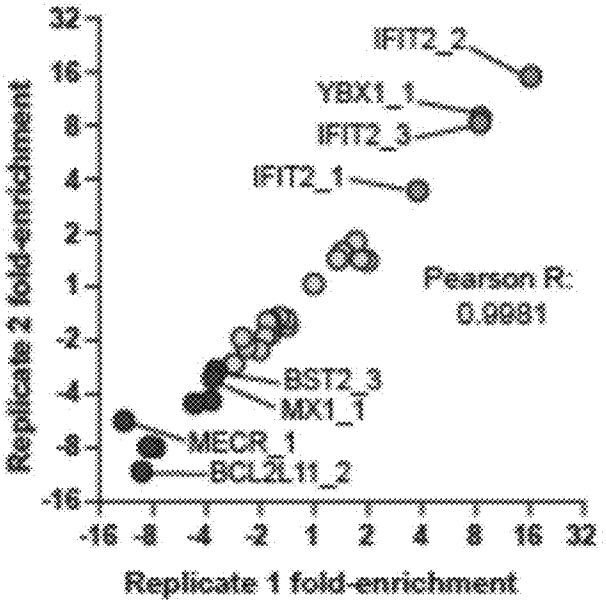


Fig. 14G

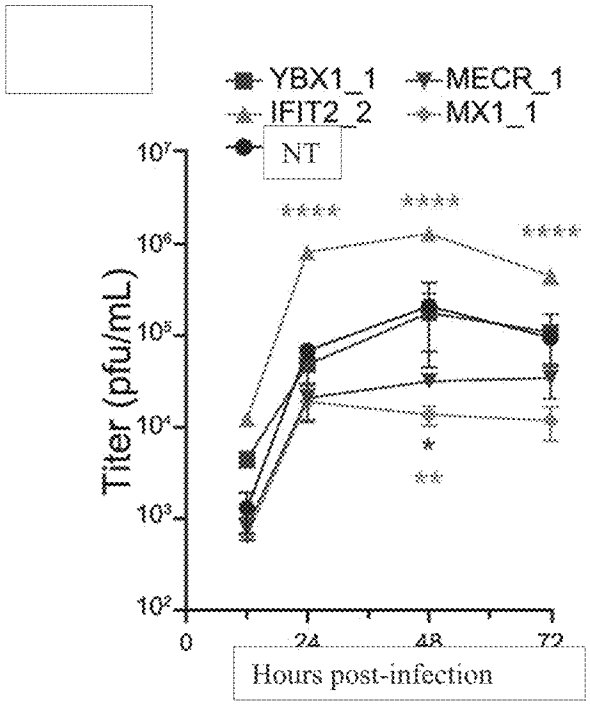


Fig. 14H

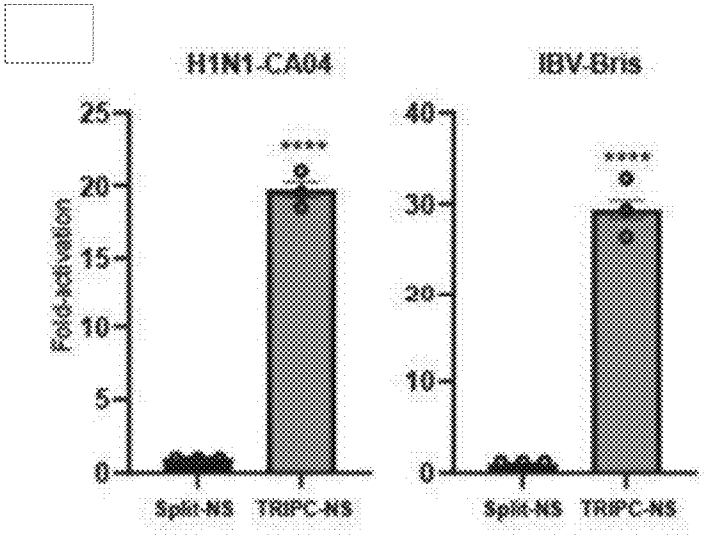


Fig. 15A

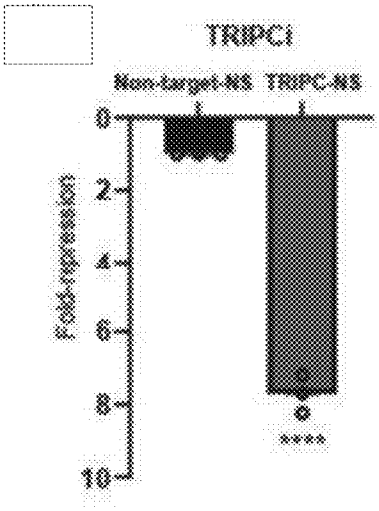


Fig. 15B

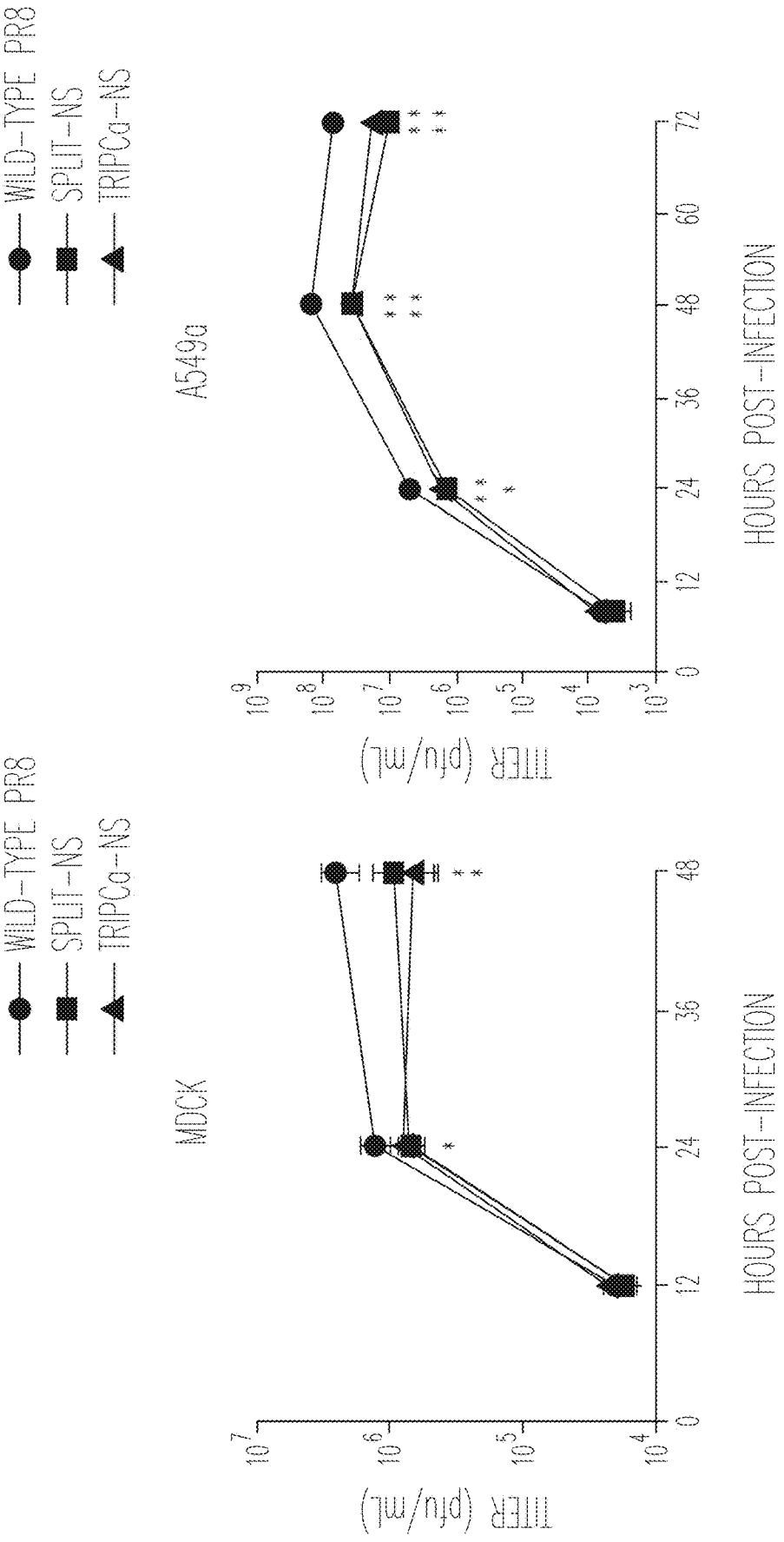

WILD-TYPE PR8
SPLIT-NS
TRIPCa-NS
A549a
TITER (pfu/mL)
HOURS POST-INFECTION
MDCK
TITER (pfu/mL)
HOURS POST-INFECTION

Fig.15C

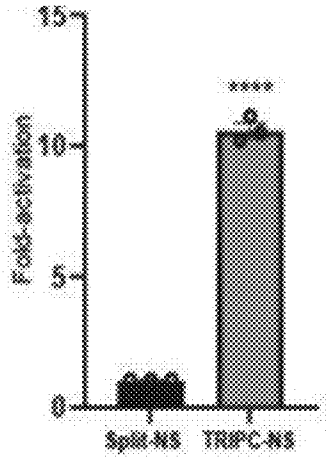


Fig. 15D

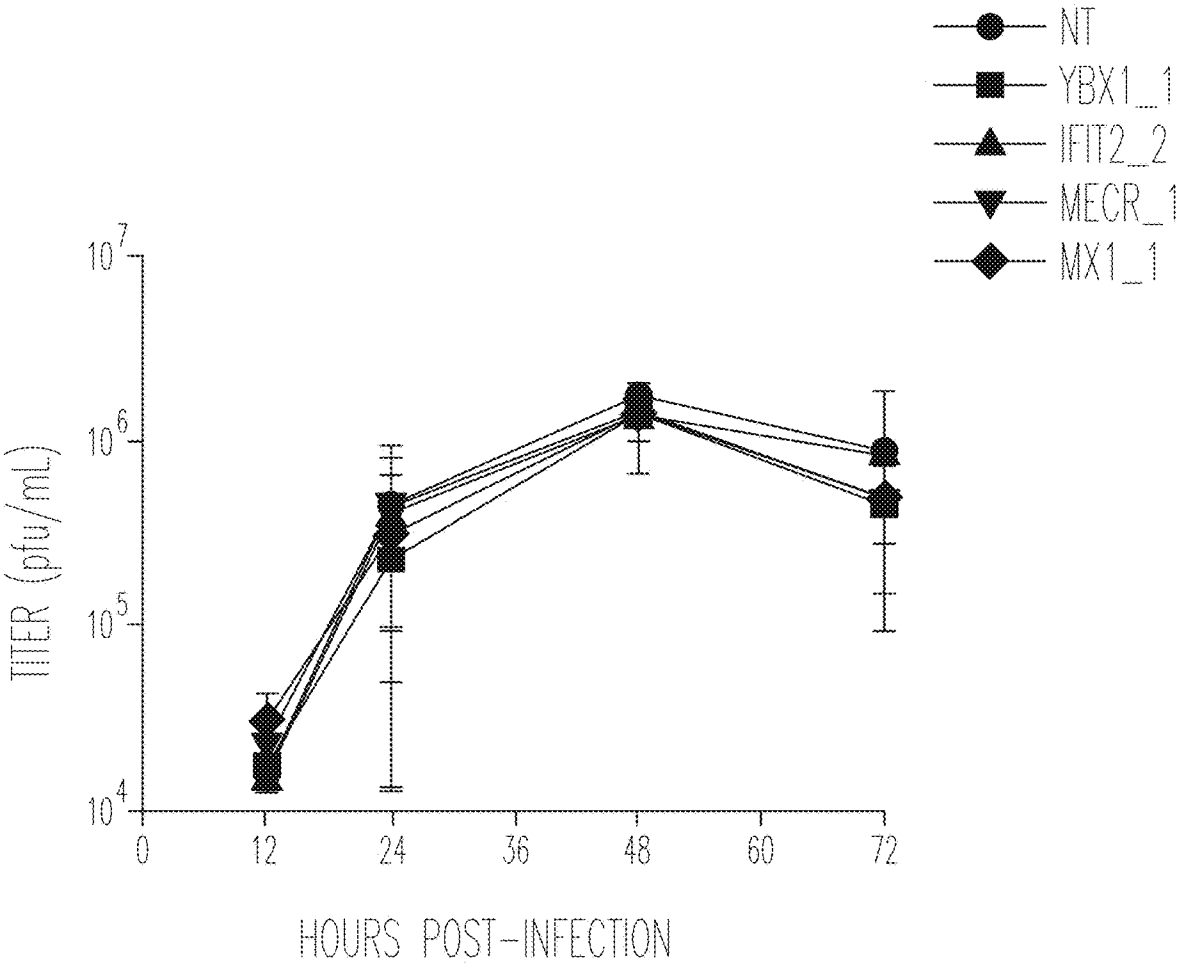

NT
YBX1_1
IFIT2_2
MECR_1
MX1_1
TITER (pfu/mL)
10^7
10^6
10^5
10^4
0
12
24
36
48
60
72
HOURS POST-INFECTION

Fig.15E

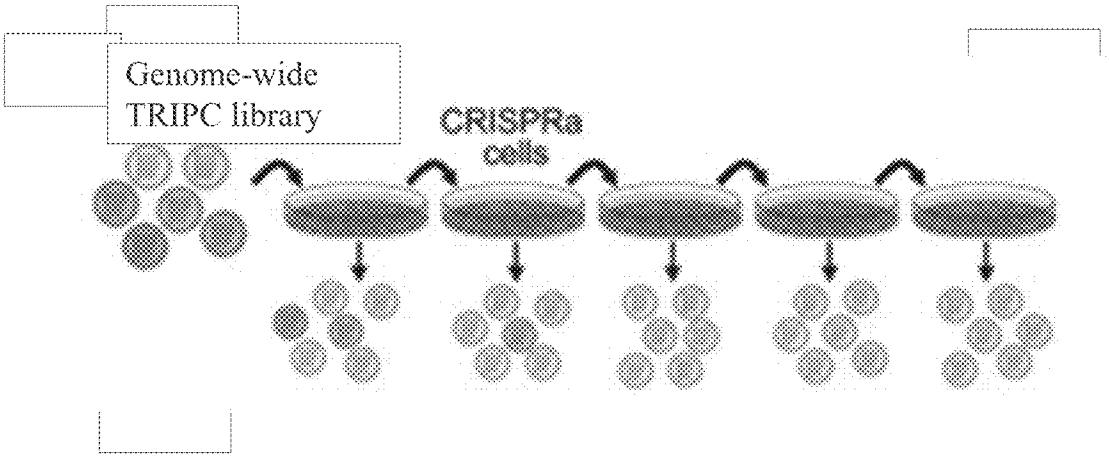


Fig. 16A

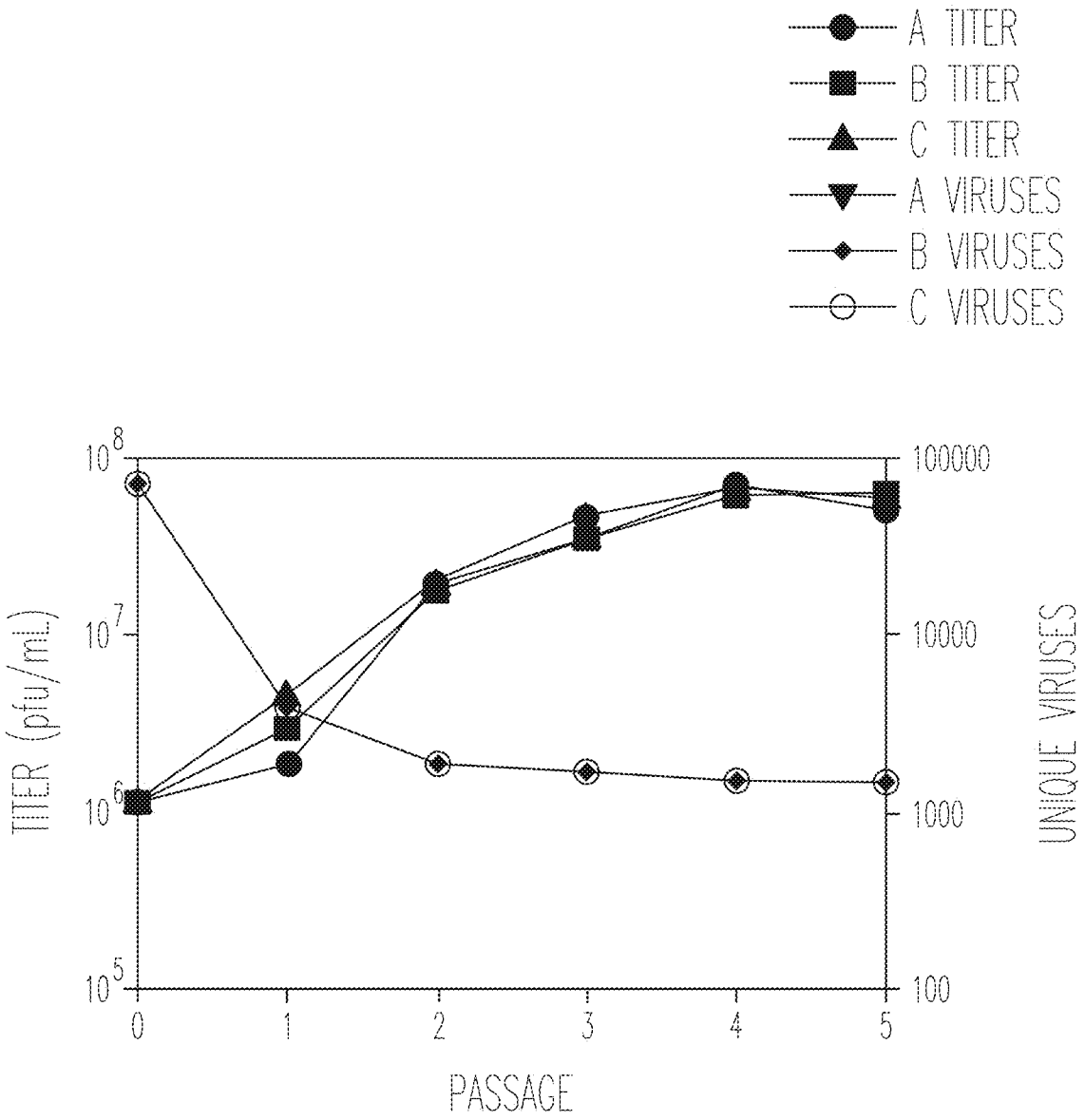

A TITER
B TITER
C TITER
A VIRUSES
B VIRUSES
C VIRUSES
TITER (pfu/mL)
10^8
10^7
10^6
10^5
UNIQUE VIRUSES
100000
10000
1000
100
0
1
2
3
4
5
PASSAGE

Fig.16B

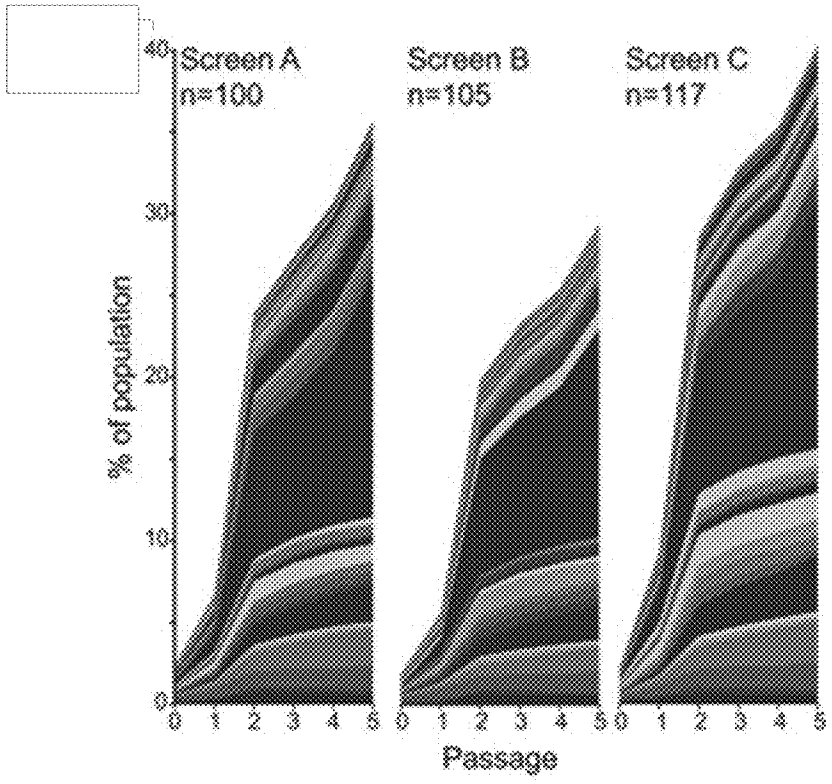

Screen A
n=100
Screen B
n=105
Screen C
n=117
% of population
0
10
20
30
40
0 1 2 3 4 5
Passage

Fig. 16C

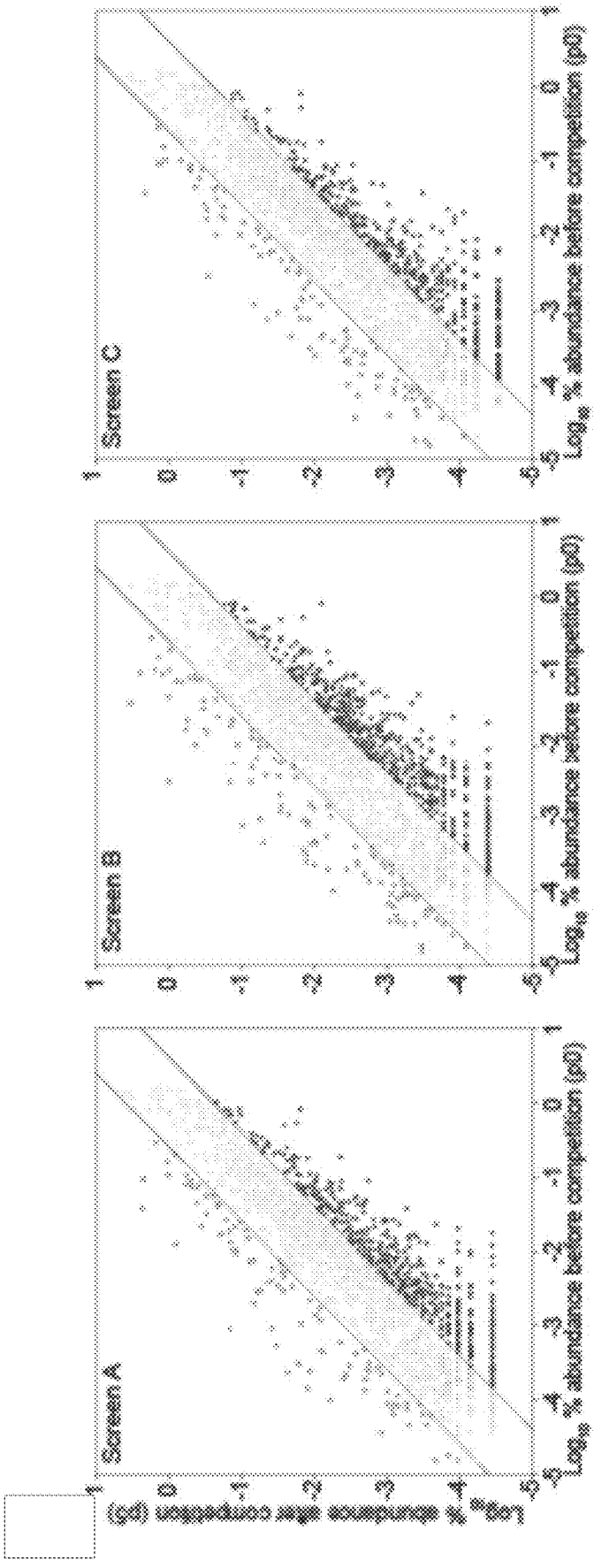

Screen C
Screen B
Screen A
Log10 % abundance before competition (pD)
Log10 % abundance after competition (pD)

Fig. 16D

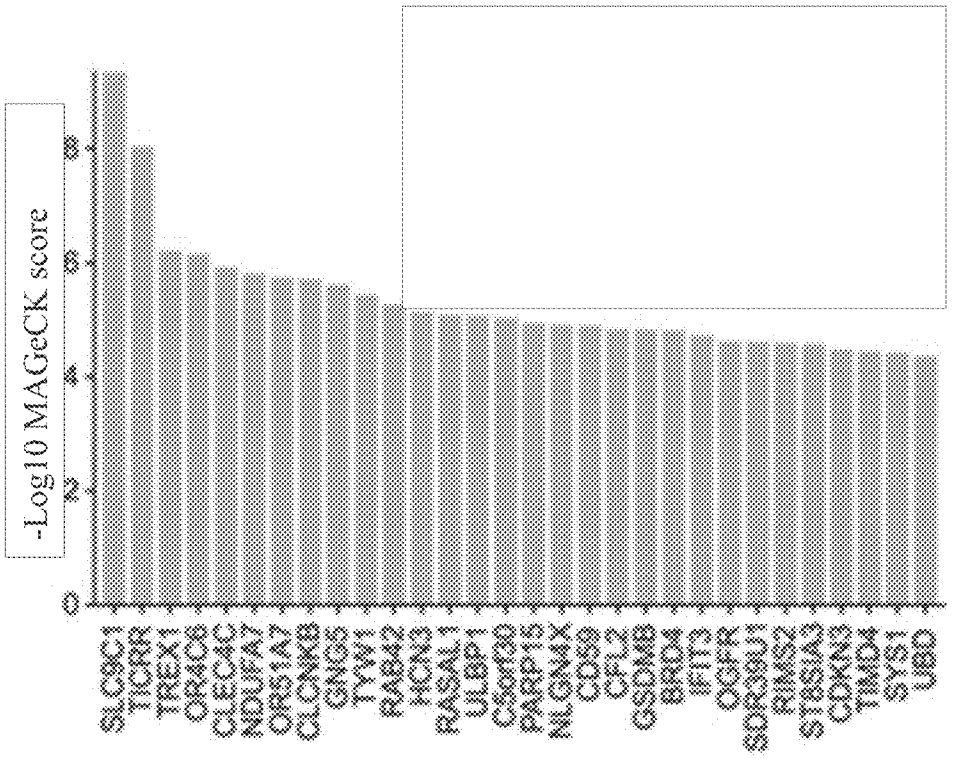


Fig. 16E

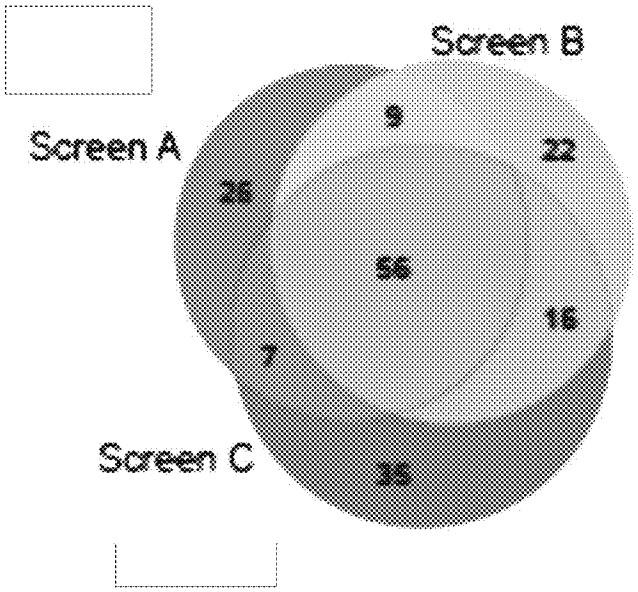


Fig. 16F

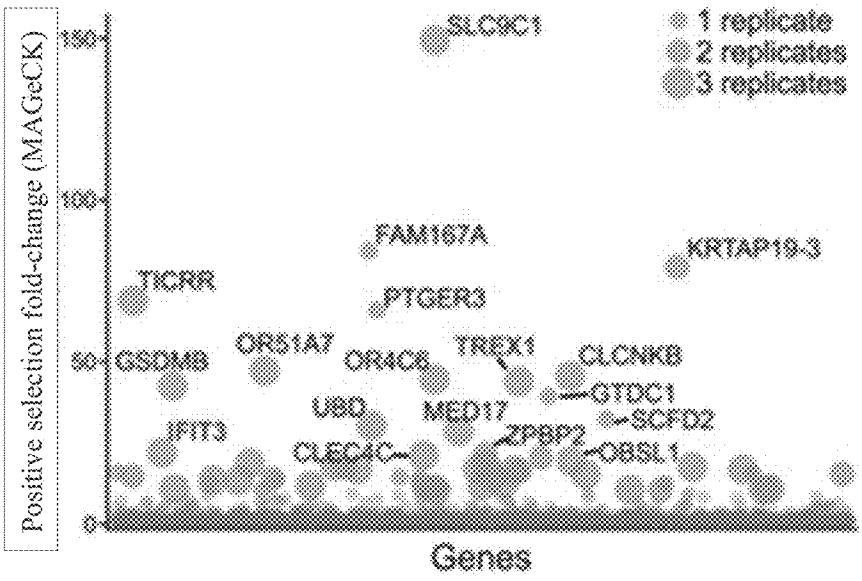

Positive selection fold-change (MAGeCK)
150
100
50
0
SLC9C1
1 replicate
2 replicates
3 replicates
FAM167A
KRTAP19-3
TICRR
PTGER3
OR51A7
OR4C6
TREX1
CLCNKB
GSDMB
GTDC1
SCFD2
UBQ
MED17
IFIT3
ZPBP2
CLEC4C
OBSL1
Genes

Fig. 16G

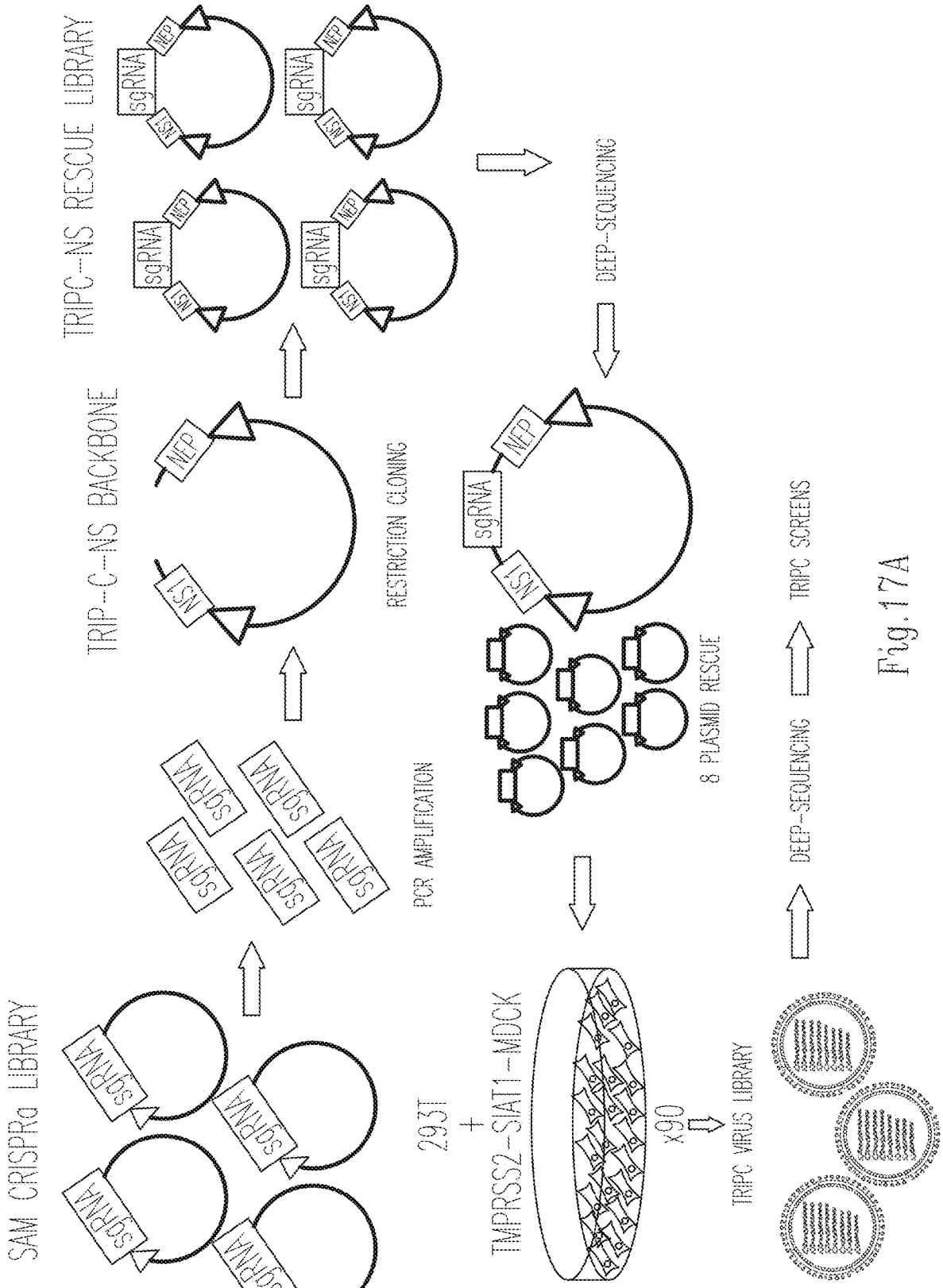

SAM CRISPRa LIBRARY
sgRNA
293T
+
TMPRSS2-SIAT1-MDCK
x90
TRIPC VIRUS LIBRARY
DEEP-SEQUENCING
TRIPC SCREENS
8 PLASMID RESCUE
sgRNA
NSI
NEP
DEEP-SEQUENCING
TRIP-C-NS BACKBONE
RESTRICTION CLONING
TRIPC-NS RESCUE LIBRARY
PCR AMPLIFICATION

Fig. 17A

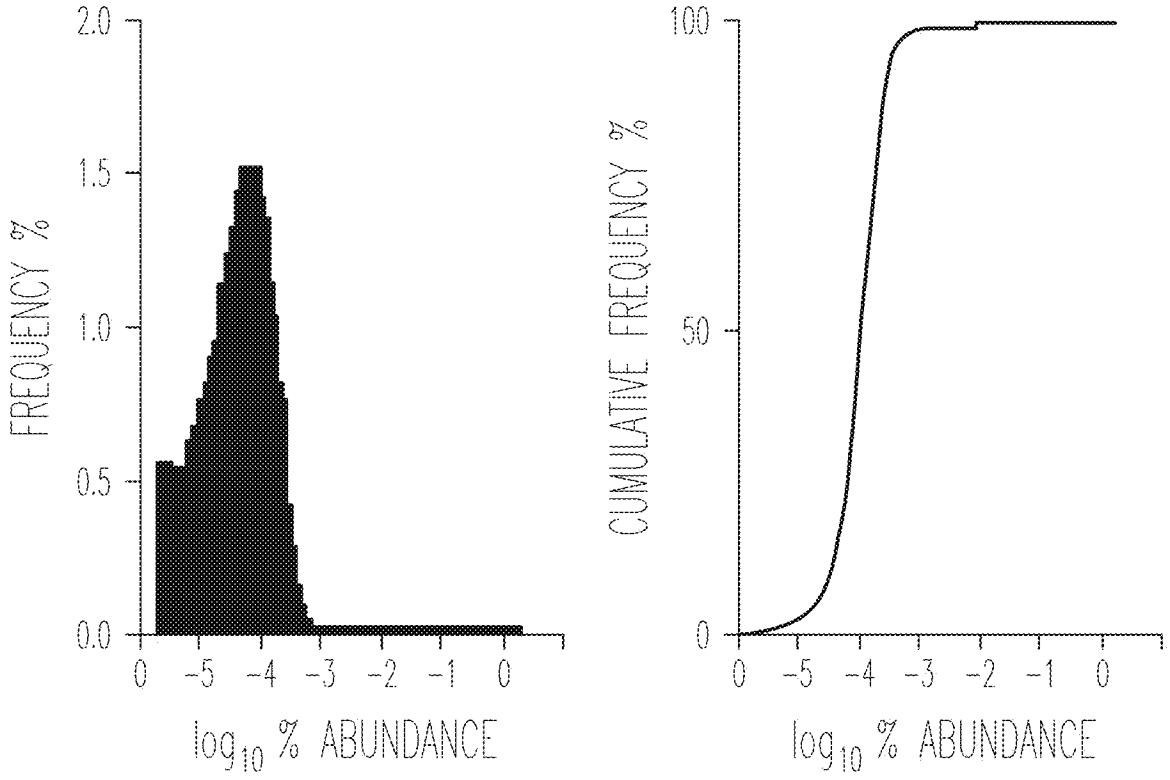

FREQUENCY %
2.0
1.5
1.0
0.5
0.0
0 -5 -4 -3 -2 -1 0
log10 % ABUNDANCE
CUMULATIVE FREQUENCY %
100
50
0
0 -5 -4 -3 -2 -1 0
log10 % ABUNDANCE

Fig.17B

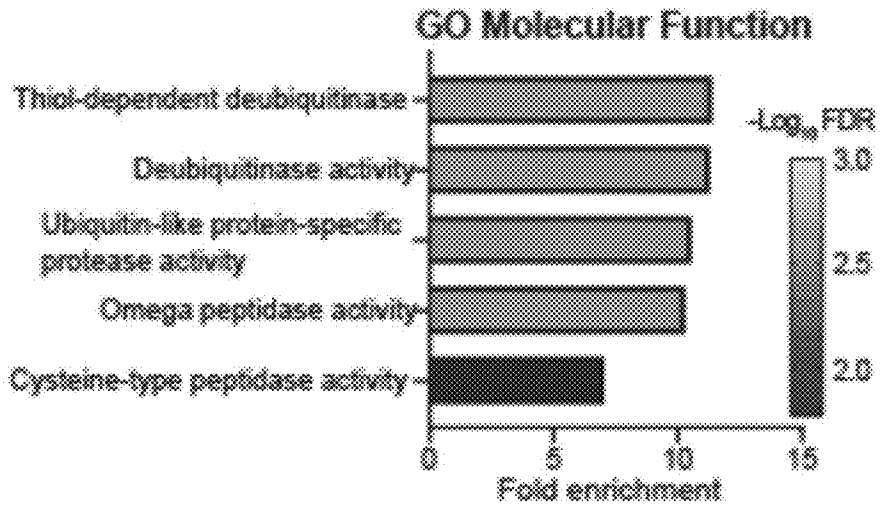

GO Molecular Function
Thiol-dependent deubiquitinase
Deubiquitinase activity
Ubiquitin-like protein-specific protease activity
Omega peptidase activity
Cysteine-type peptidase activity
-Log10 FDR
3.0
2.5
2.0
0
5
10
15
Fold enrichment

Fig. 17C

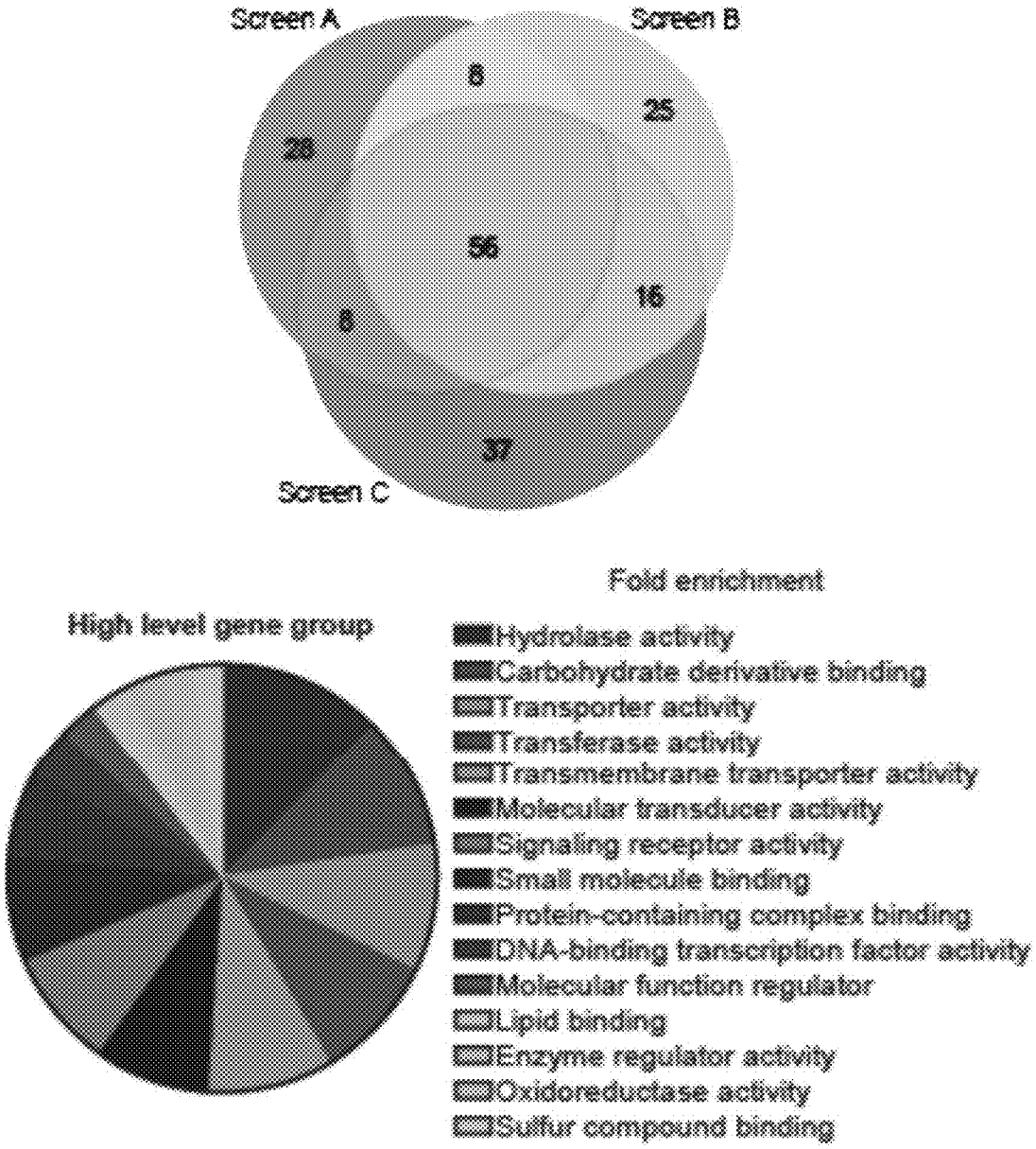

Screen A
Screen B
Screen C
8
25
28
56
16
8
37
High level gene group
Fold enrichment
Hydrolase activity
Carbohydrate derivative binding
Transporter activity
Transferase activity
Transmembrane transporter activity
Molecular transducer activity
Signaling receptor activity
Small molecule binding
Protein-containing complex binding
DNA-binding transcription factor activity
Molecular function regulator
Lipid binding
Enzyme regulator activity
Oxidoreductase activity
Sulfur compound binding

Fig. 17D

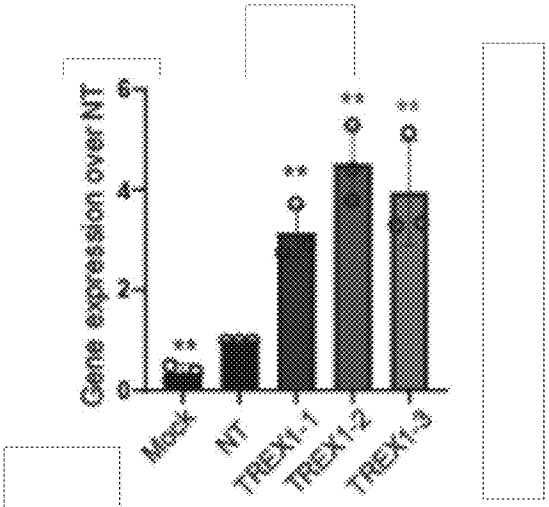


Fig. 18A

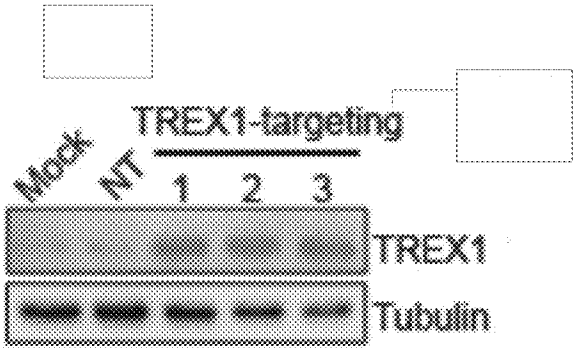


Fig. 18B

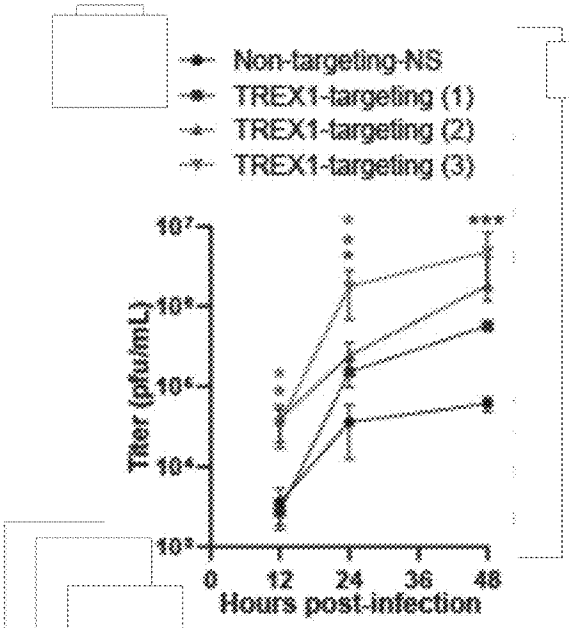


Fig. 18C

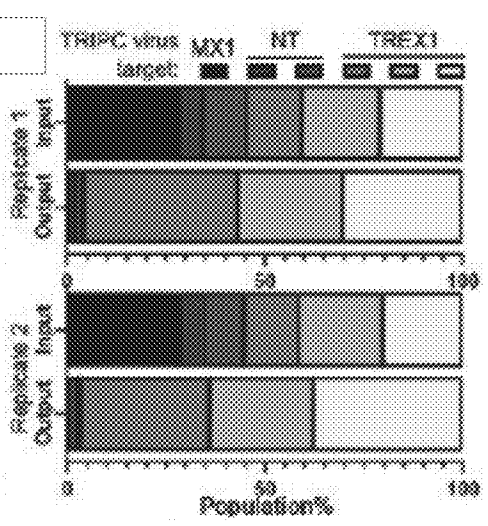


Fig. 18D

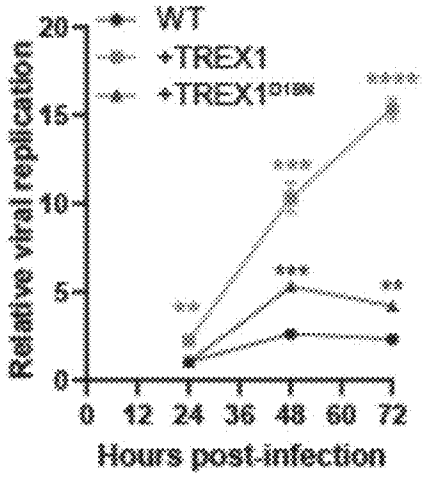


Fig. 18E

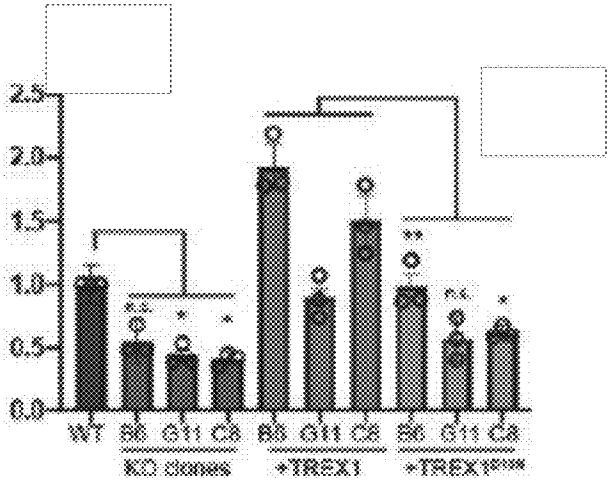


Fig. 18F

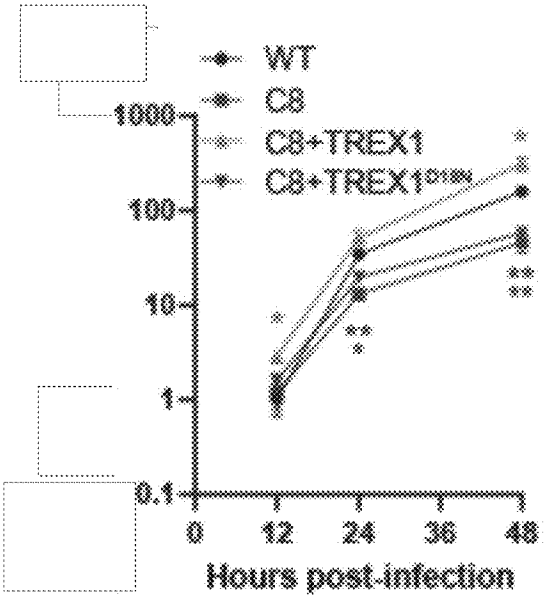


Fig. 18G

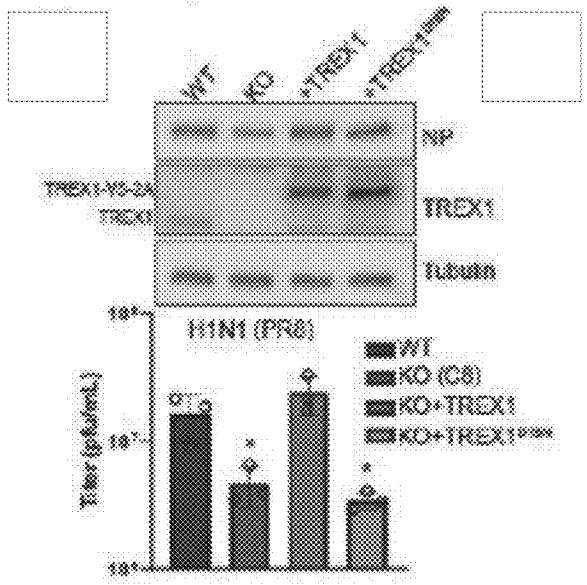


Fig. 18H

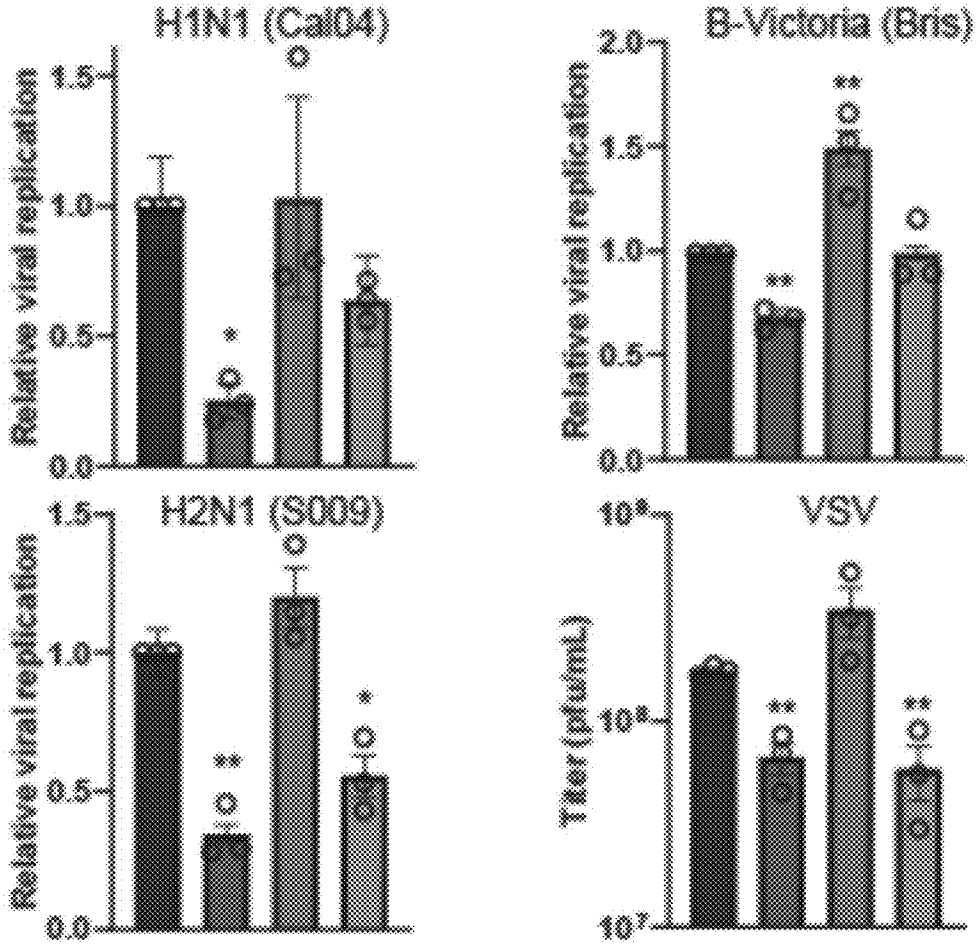


Fig. 18I

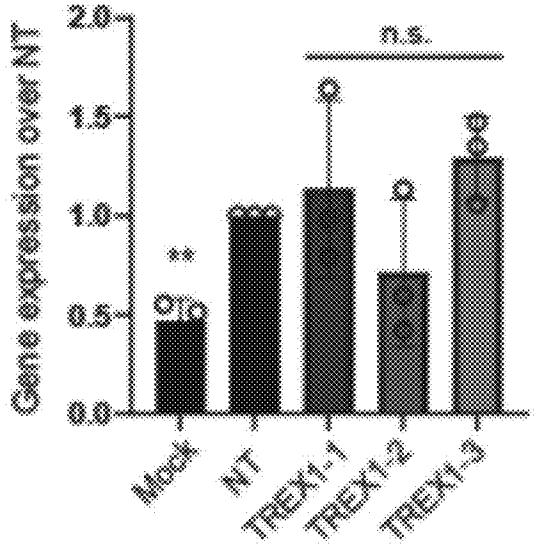


Fig. 19A

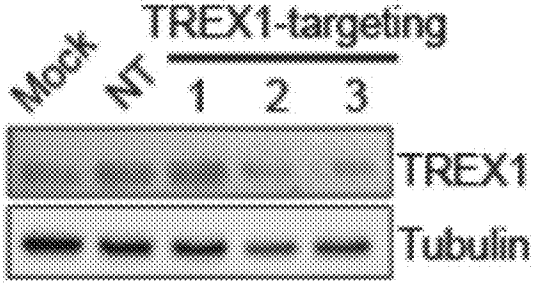


Fig. 19B

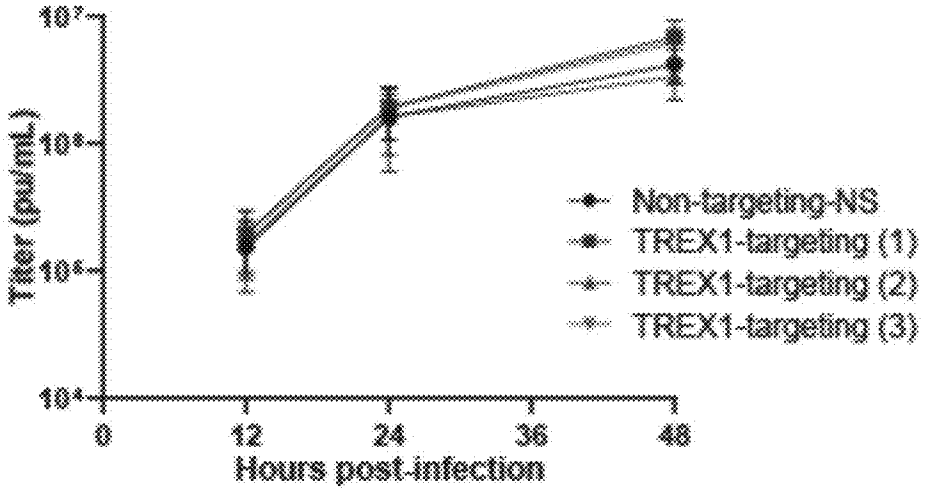


Fig. 19C

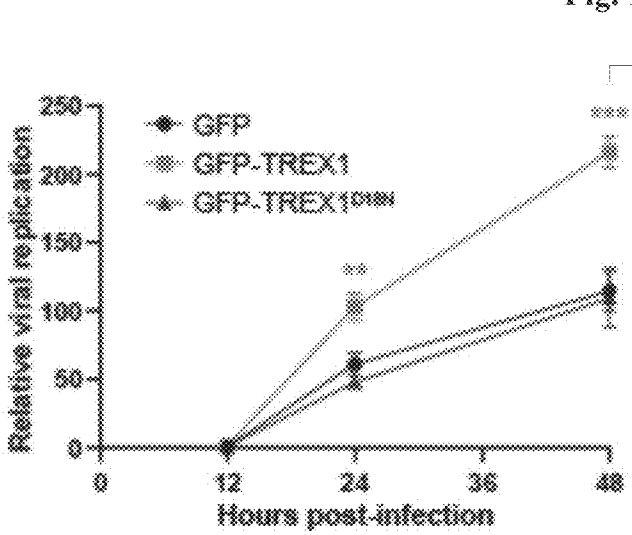


Fig. 19D

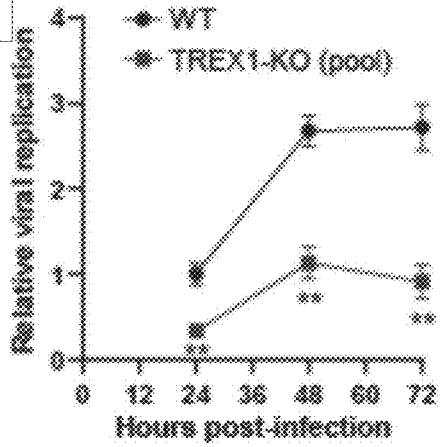


Fig. 19E

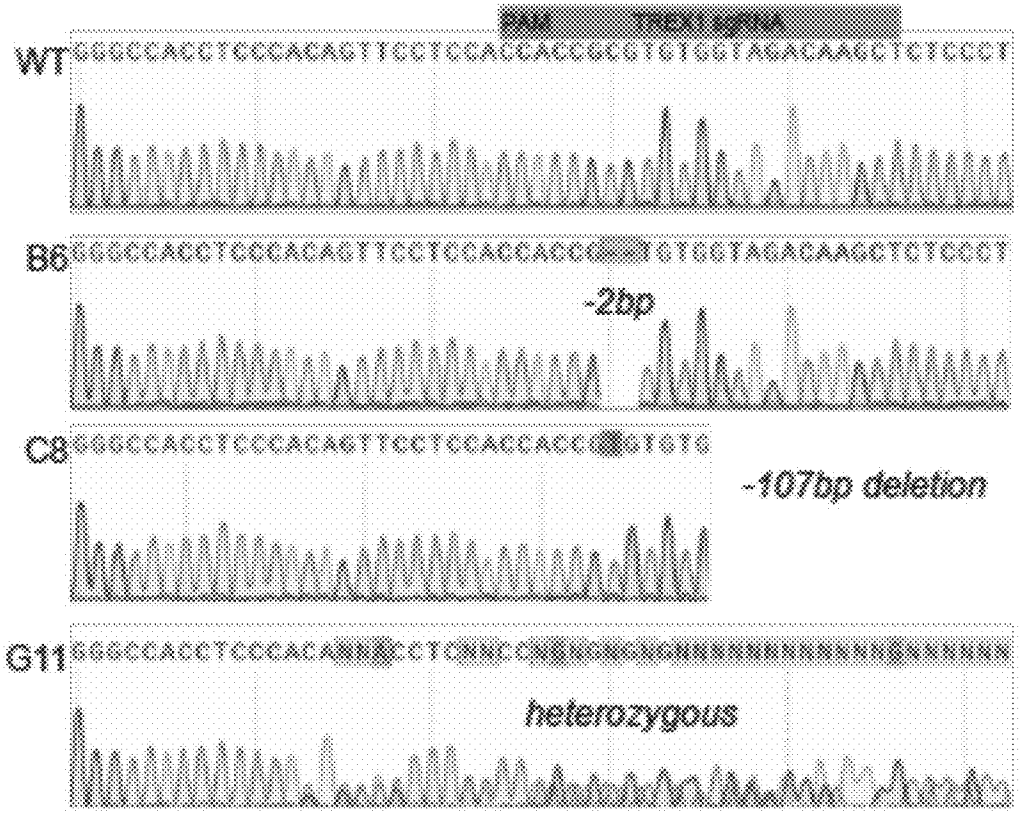


Fig. 19F

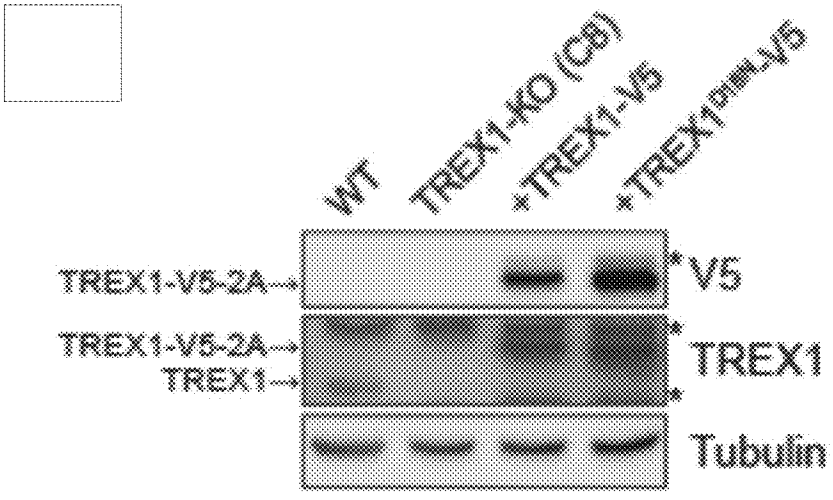


Fig. 19G

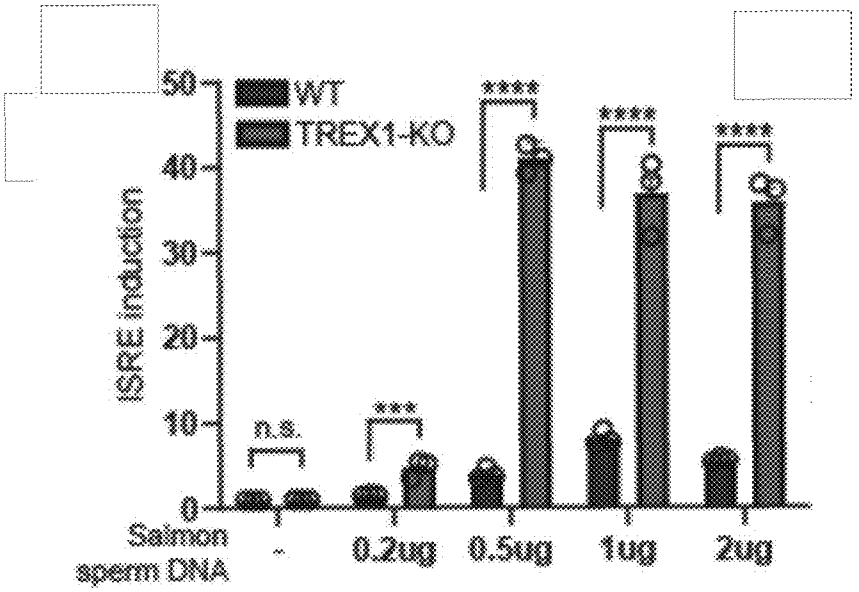


Fig. 20A

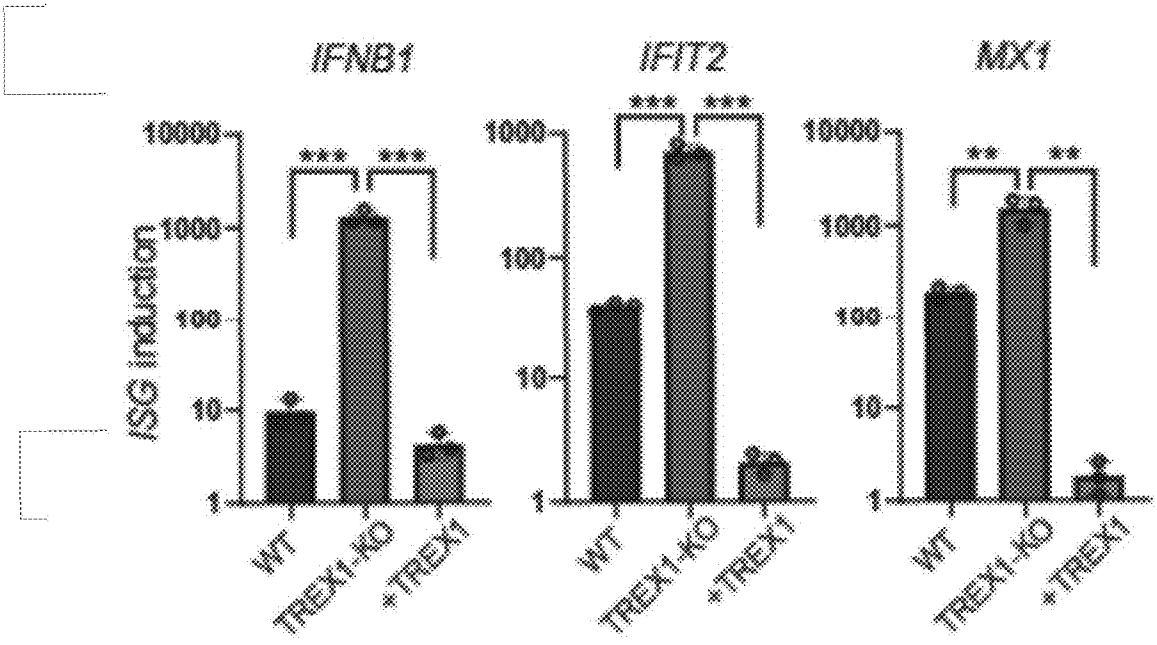


Fig. 20B

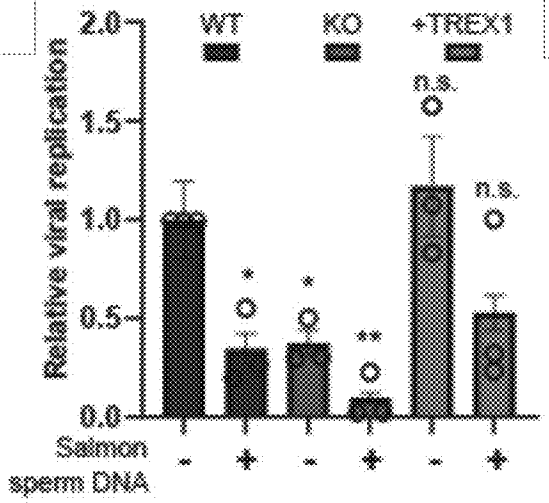


Fig. 20C

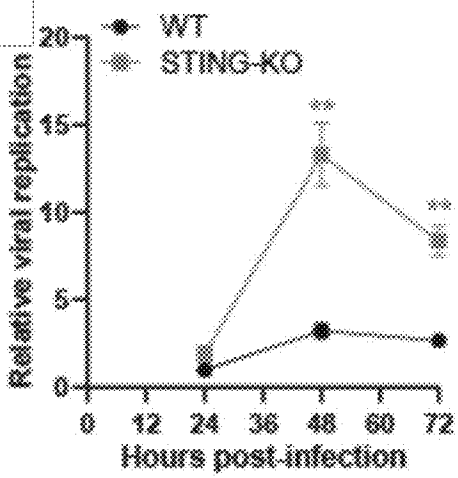


Fig. 20D

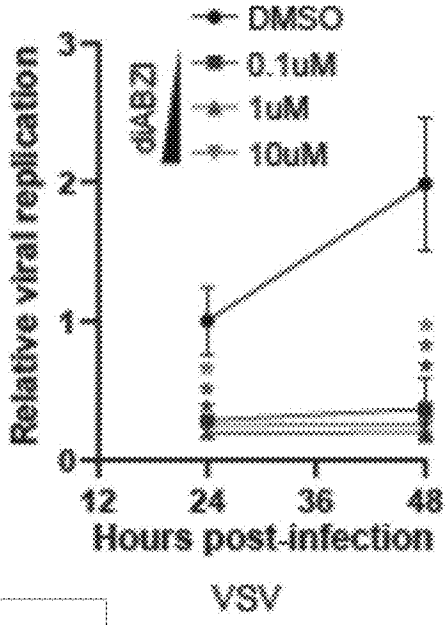


Fig. 20E

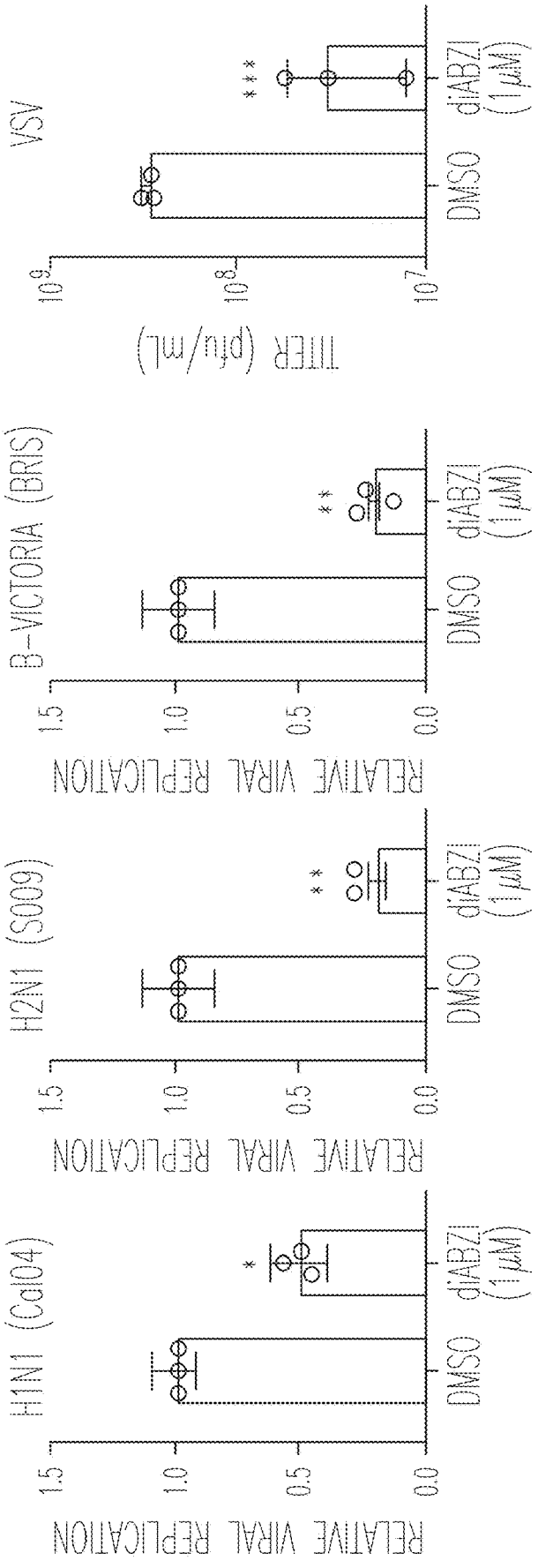

H1N1 (Ca104)
H2N1 (S009)
B-VICTORIA (BRIS)
VSV
RELATIVE VIRAL REPLICATION
TITER (pfu/mL)
1.5
1.0
0.5
0.0
10^9
10^8
10^7
DMSO
dIABZI (1μM)
*
**
***

Fig. 20F

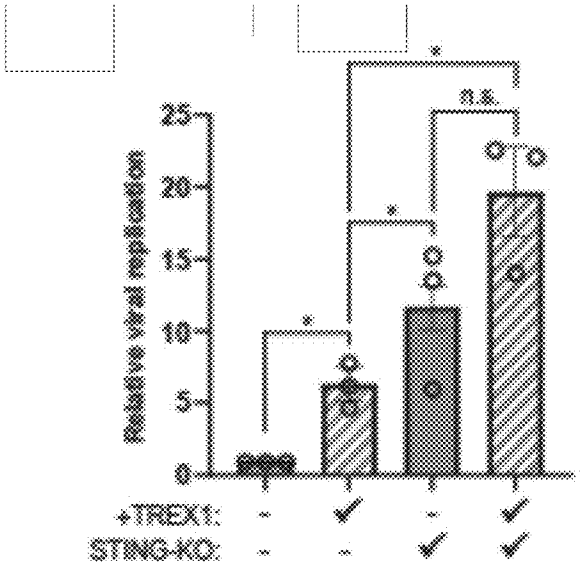


Fig. 20G

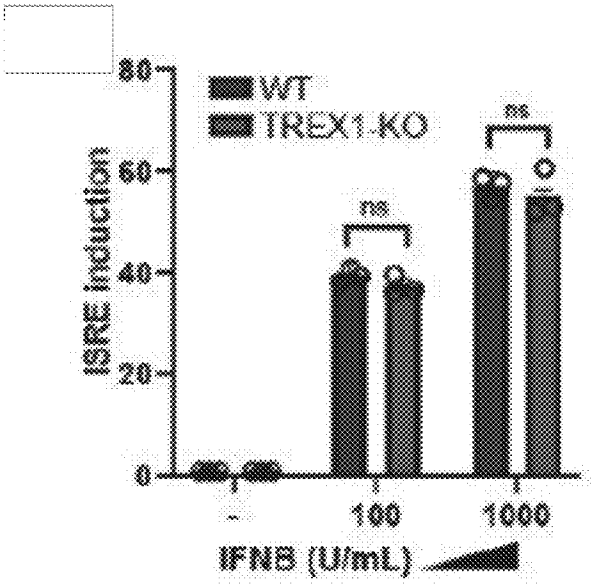


Fig. 21A

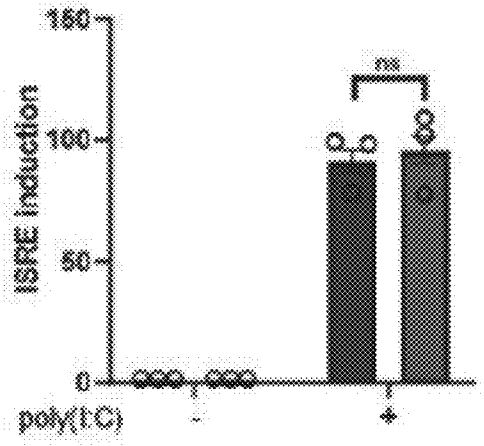


Fig. 21B

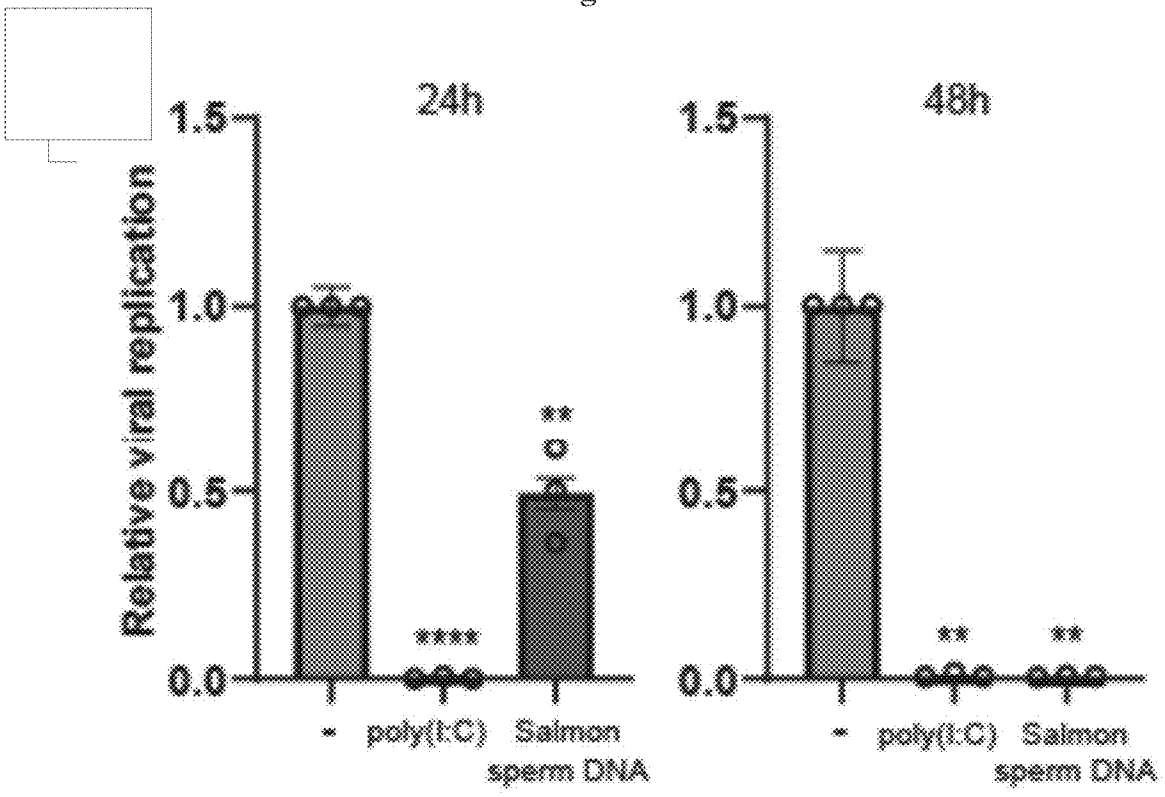


Fig. 21C

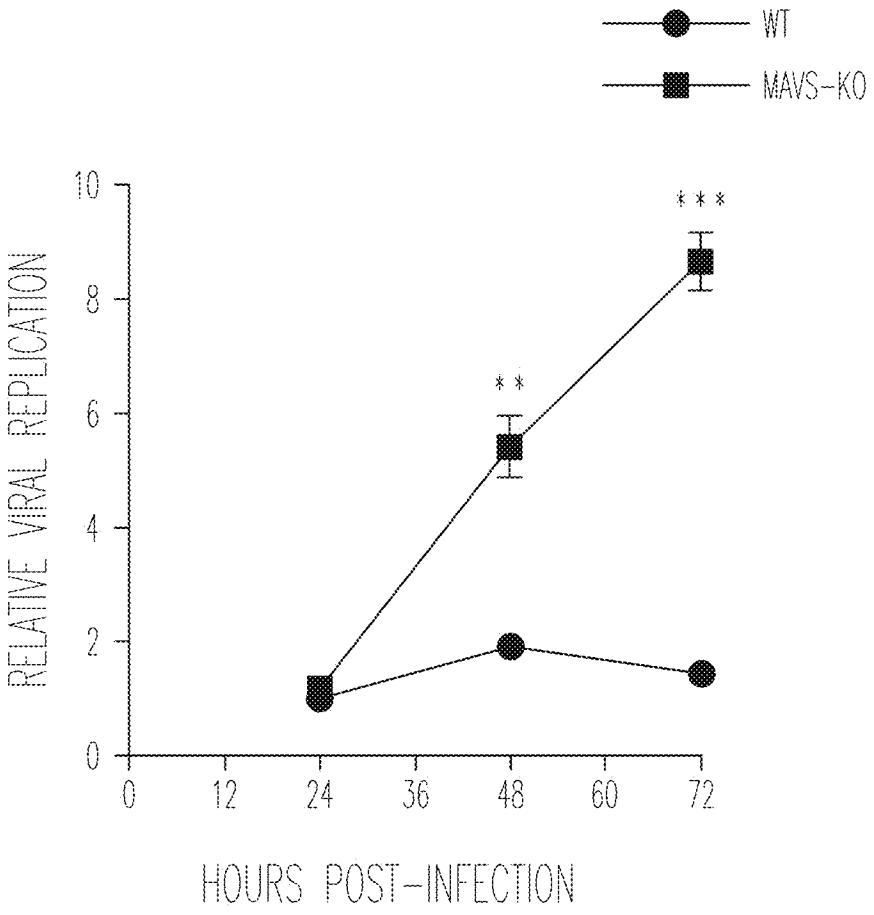

WT
MAVS-KO
RELATIVE VIRAL REPLICATION
0
2
4
6
8
10
0
12
24
36
48
60
72
HOURS POST-INFECTION
**
***

Fig.21D

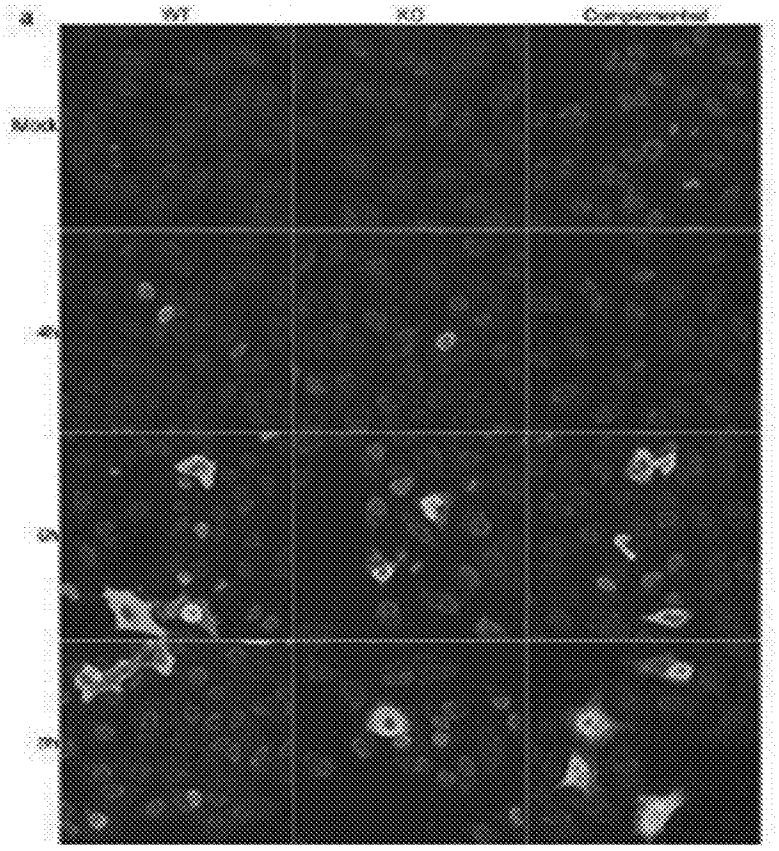


Fig. 22A

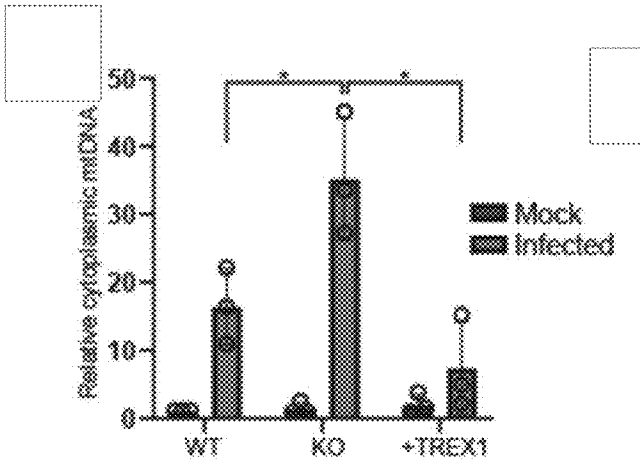


Fig. 22B

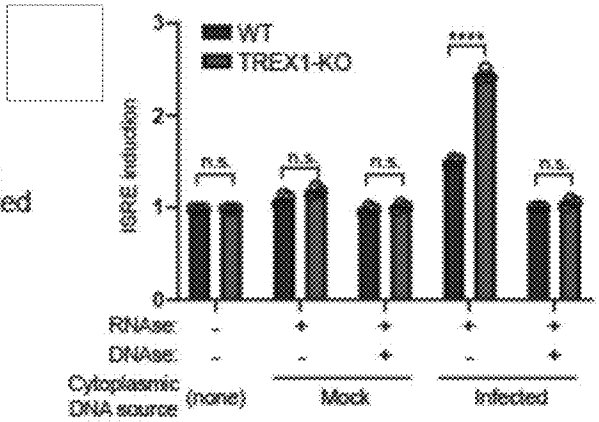


Fig. 22C

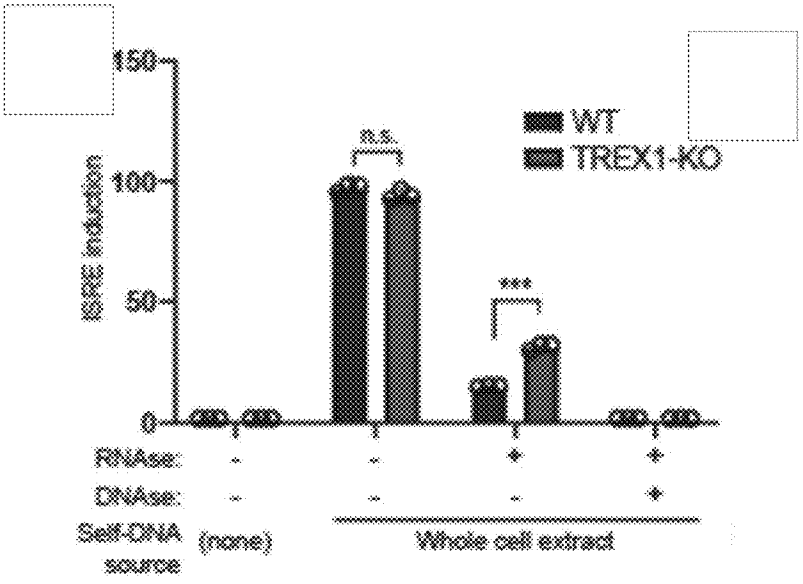


Fig. 23A

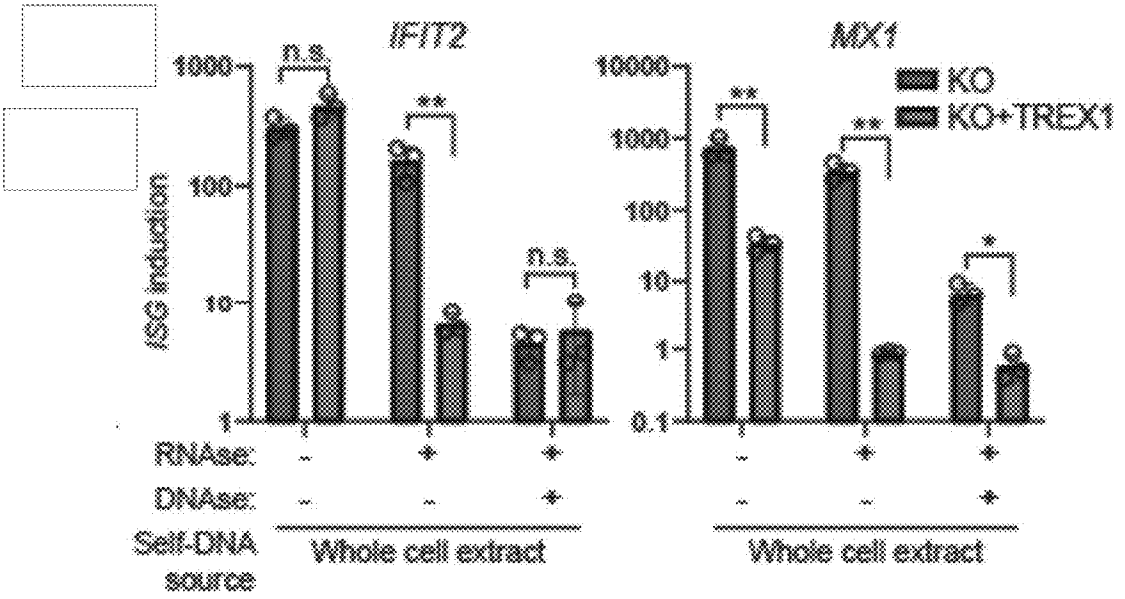


Fig. 23B

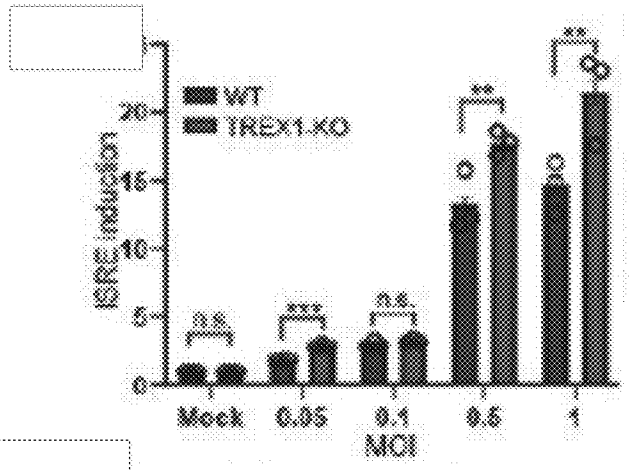


Fig. 23C

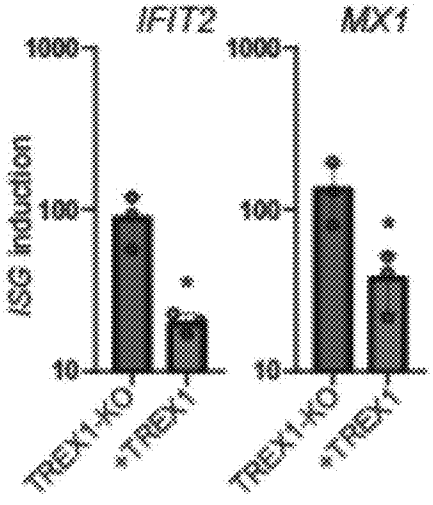


Fig. 23D

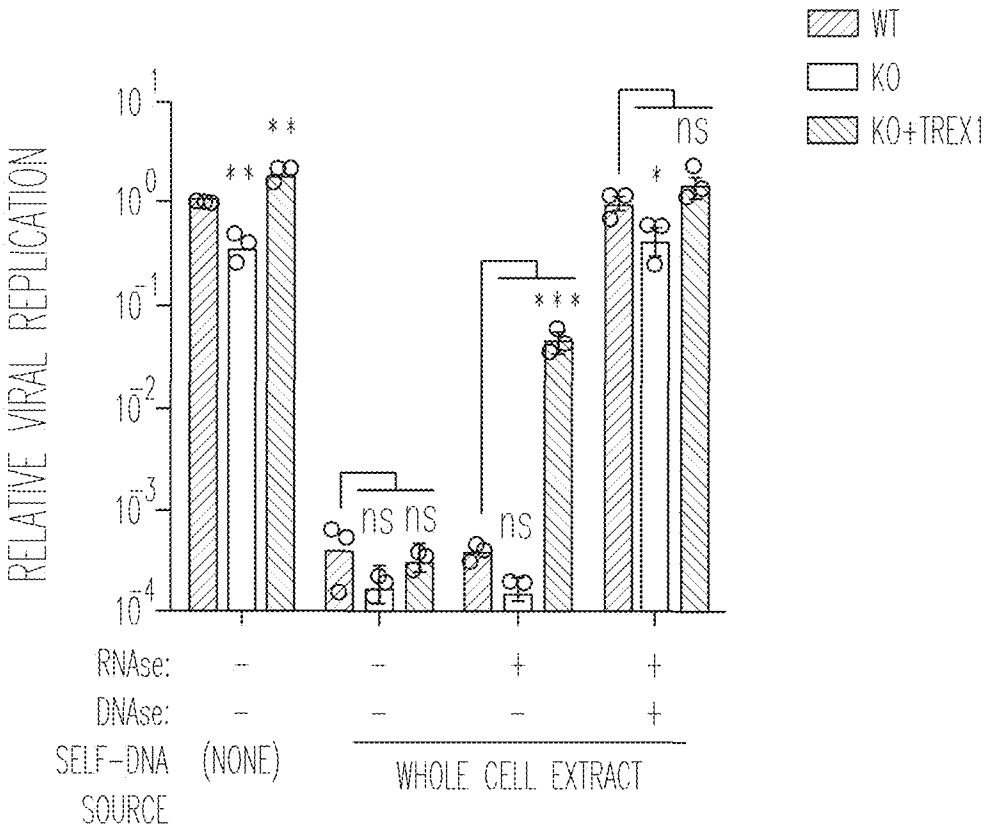

WT
KO
KO+TREX1
RELATIVE VIRAL REPLICATION
10^{1}
10^{0}
10^{-1}
10^{-2}
10^{-3}
10^{-4}
**
**
ns ns
ns
***
*
ns
RNAse: - - + +
DNAse: - - - +
SELF-DNA SOURCE (NONE)
WHOLE CELL EXTRACT

Fig.23E

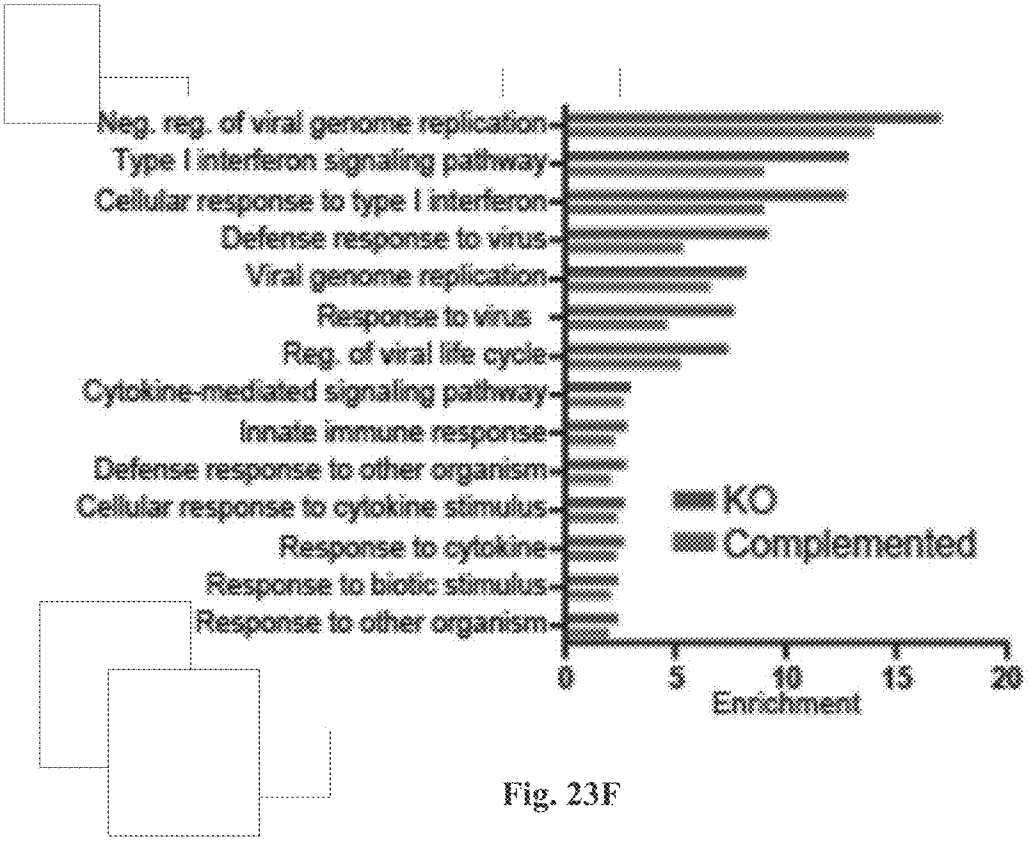

Neg. reg. of viral genome replication
Type I interferon signaling pathway
Cellular response to type I interferon
Defense response to virus
Viral genome replication
Response to virus
Reg. of viral life cycle
Cytokine-mediated signaling pathway
Innate immune response
Defense response to other organism
Cellular response to cytokine stimulus
Response to cytokine
Response to biotic stimulus
Response to other organism
KO
Complemented
0
5
10
15
20
Enrichment

Fig. 23F

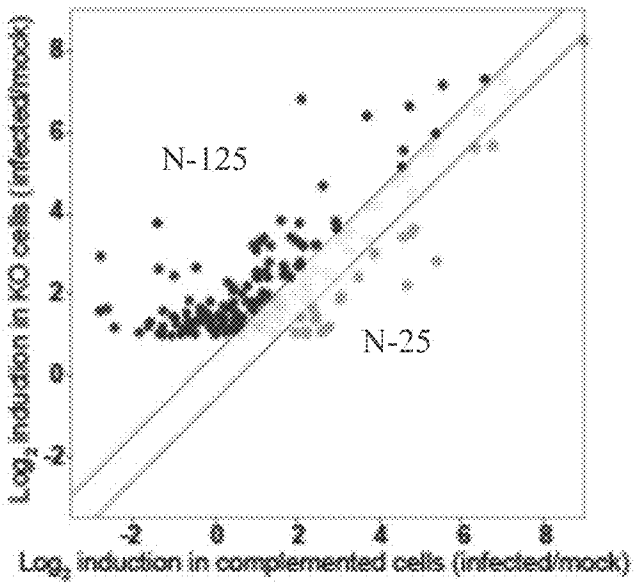


Fig. 23G

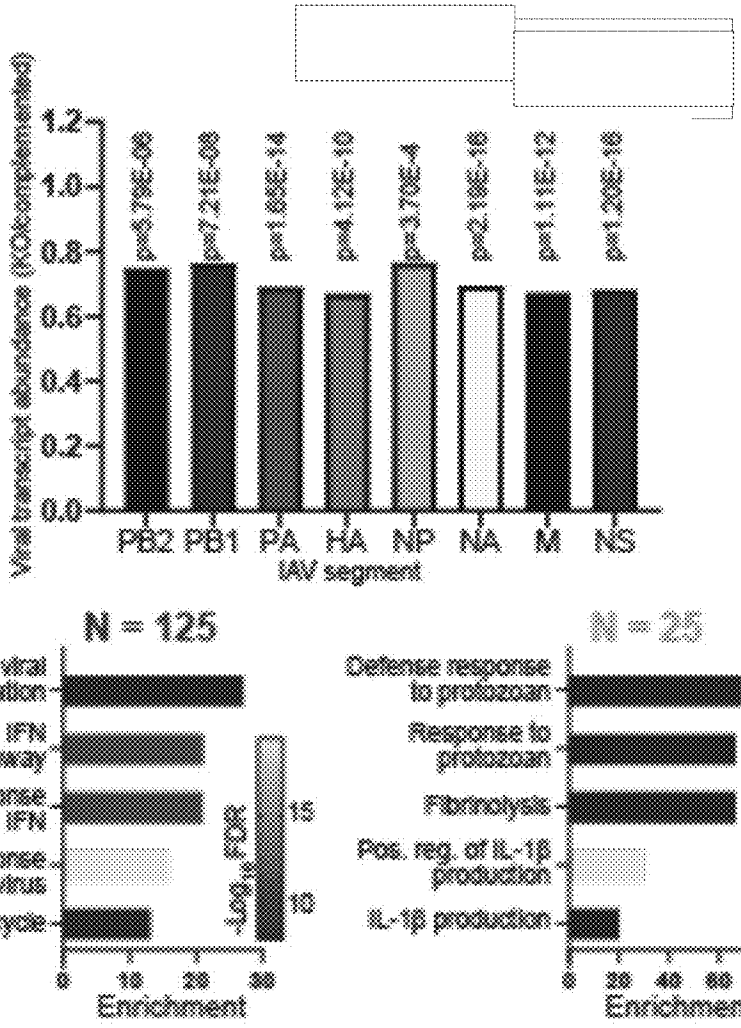


Fig. 23H

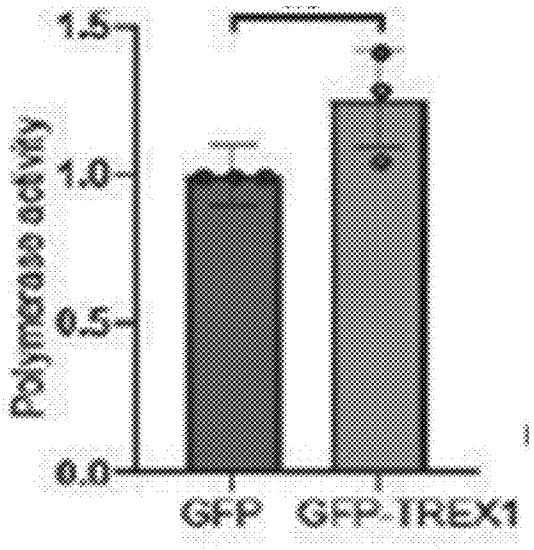


Fig. 24A

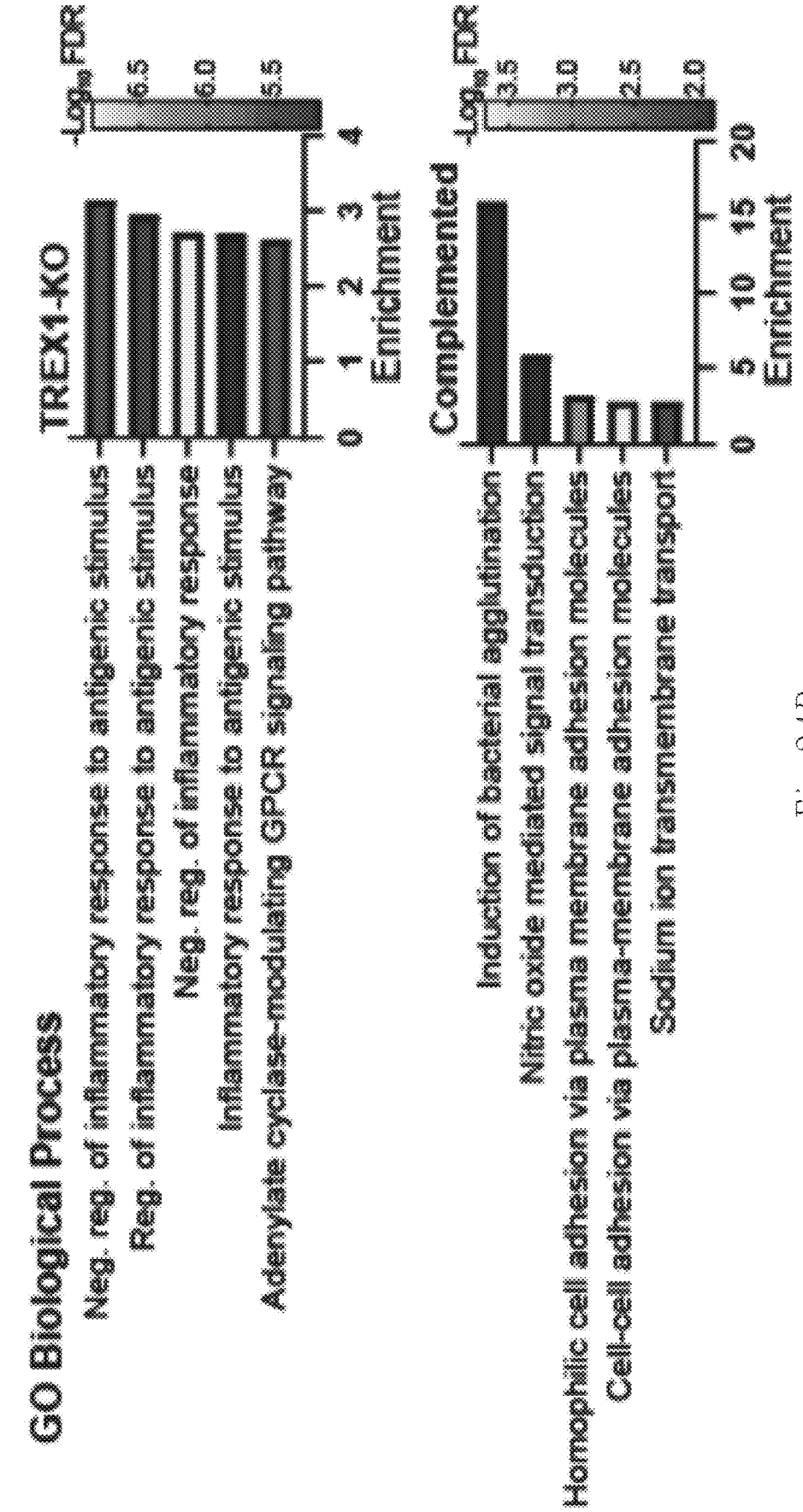

GO Biological Process
TREX1-KO
-Log10 FDR
6.5
6.0
5.5
Neg. reg. of inflammatory response to antigenic stimulus
Reg. of inflammatory response to antigenic stimulus
Neg. reg. of inflammatory response
Inflammatory response to antigenic stimulus
Adenylate cyclase-modulating GPCR signaling pathway
0 1 2 3 4
Enrichment
Complemented
-Log10 FDR
3.5
3.0
2.5
2.0
Induction of bacterial agglutination
Nitric oxide mediated signal transduction
Homophilic cell adhesion via plasma membrane adhesion molecules
Cell-cell adhesion via plasma-membrane adhesion molecules
Sodium ion transmembrane transport
0 5 10 15 20
Enrichment

Fig.24B

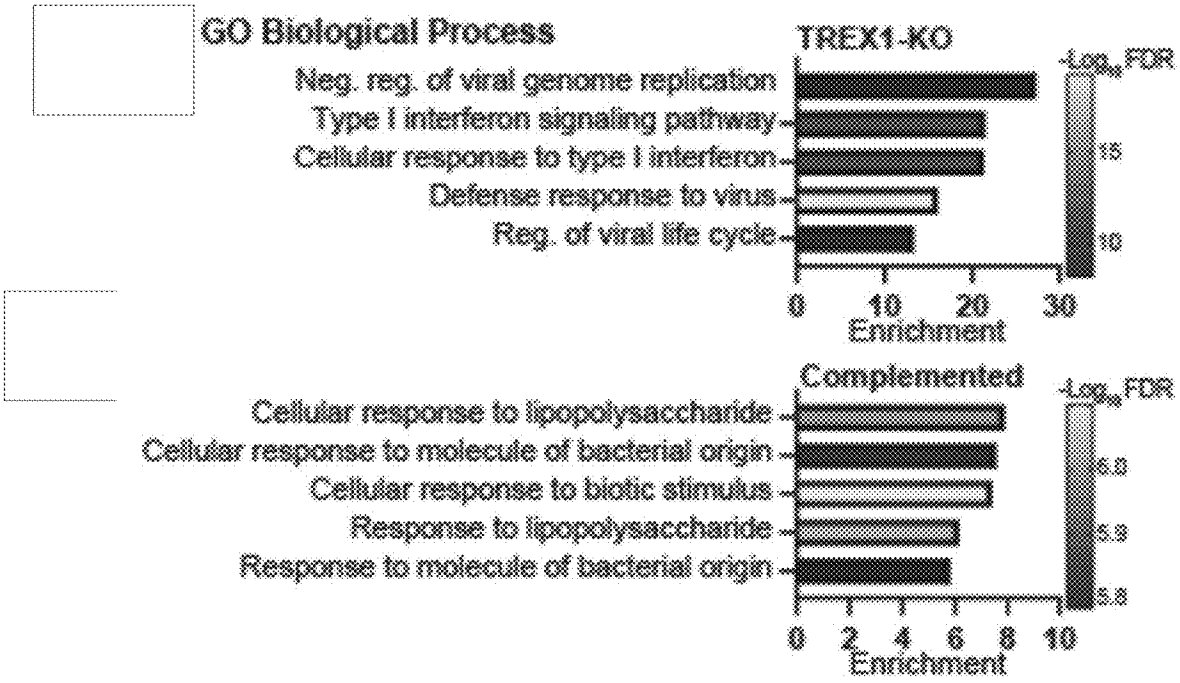

GO Biological Process
TREX1-KO
Neg. reg. of viral genome replication
Type I interferon signaling pathway
Cellular response to type I interferon
Defense response to virus
Reg. of viral life cycle
0
10
20
30
Enrichment
-Log10 FDR
15
10
Complemented
Cellular response to lipopolysaccharide
Cellular response to molecule of bacterial origin
Cellular response to biotic stimulus
Response to lipopolysaccharide
Response to molecule of bacterial origin
0
2
4
6
8
10
Enrichment
-Log10 FDR
6.0
5.9
5.8

Fig. 24C

Fig. 25

(SEQ ID NO:74) NP_002480.1 cytochrome c oxidase subunit NDUFA4 [Homo sapiens]

MLRQIIGQAKKHPSLIPLFVFIGTGATGATLYLLRLALFNPDVCWDRNNPEPWNKLGPNDQYKFYS
VNVD YSKLKKERPDF

(SEQ ID NO:75) NP_003542.1 nucleoside diphosphate kinase homolog 5 [Homo sapiens]

MEISMPPPQIYVEKTLAIIKPDIVDKEEEIQDIILRSGFTIVQRRKLRLSPEQCSNFYVEKYGKMFFPNL
TAYMSSGPLVAMILARHKAISYWLELLGPNNSLVAKETHPDSLRAIYGTDDLRNALHGSNDFAAA
EREIRFMFPEVIVEPIPIGQAAKDYLNLHIMPTLLEGLTELCKQKPADPLIWLADWLLKNNPNKPKL
CHHPIVEEPY

(SEQ ID NO:76) NP_036452.1 phospholipase A2 group XV isoform 1 precursor [Homo sapiens]

MGLHLRPYRVGLLPDGLLFLLLLLMLLADPALPAGRHPPVVLVPGDLGNQLEAKLDKPTVVHYLC
SKKTESYFTIWLNLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDVRVPGFGKTFSLEFLDPSKSS
VGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREMIEEMYQLYGGPVVLVA
HSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVLASGDNNRIPVIGPLKIREQQR
SAVSTSWLLPYNYTWSPEKVFVQTPTINYTLRDYRKFFQDIGFEDGWLMRQDTEGLVEATMPPGV
QLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGDGTVNLKSALQCQAWQSRQEHQVLLQELPGSE
HIEMLANATTLAYLKRVLLGP

(SEQ ID NO:77) NP_057625.1 guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-13 [Homo sapiens]

MEEWDVPQMKKEVESLKYQLAFQREMASKTIPELLKWIEDGIPKDPFLNPDLMKNNPWVEKGKC
TIL

(SEQ ID NO:78) NP_058640.1 taste receptor type 2 member 4 [Homo sapiens]

MLRLFYFSAIIASVILNFVGIIMNLFITVVNCKTWVKSHRISSSDRILFSLGITRFLMLGLFLVNTIYFV
SSNTERSVYLSAFFVLCFMFLDSSSVWFVTLLNILYCVKITNFQHSVFLLLKRNISPKIPRLLLACVLI
SAFTTCLYITLSQASPFPELVTTRNNTSFNISEGILSLVVSLVLSSSLQFIINVTSASLLIHSLRRHIQKM
QKNATGFWNPQTEAHVGAMKLMVYFLILYIPYSVATLVQYLPFYAGMDMGTKSICLIFATLYSPG
HSVLIIITHPKLKTTAKKILCFKK

Fig. 25 cont'd

(SEQ ID NO:79) NP_000604.1 hemopexin precursor [Homo sapiens]

MARVLGAPVALGLWSLCWSLAIATPLPPTSAHGNVAEGETKPDPDVTERCSDGWSFDAT
TLDDNGTMLFFKGEFVWKSHKWDRELISERWKNFPSPVDAAFRQGHNSVFLIKGDKVWV
YPPEKKEKGYPKLLQDEFPGIPSPLDAAVECHRGECQAEGVLFFQGDREWFWDLATGTM
KERSWPAVGNCSSALRWLGRYYCFQGNQFLRFDPVRGEVPPRYPRDVRDYFMPCPGRGH
GHRNGTGHGNSTHHGPEYMRCSPHLVLSALTSDNHGATYAFSGTHYWRLDTSRDGWHS
WPIAHQWPQGPSAVDAAFSWEEKLYLVQGTQVYVFLTKGGYTLVSGYPKRLEKEVGTPH
GIILDSVDAAFICPGSSRLHIMAGRRLWWLDLKSGAQATWTELPWPHEKVDGALCMEKSL
GPNSCSANGPGLYLIHGPNLYCYSDVEKLNAAKALPQPQNVTSLLGCTH

(SEQ ID NO:80) NP_443194.1 interleukin-22 receptor subunit alpha-2 isoform 1 precursor [Homo sapiens]

MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVYF
VQYKIMFSCSMKSSHQKPSGCWQHISCNFPGCRTLAKYGQRQWKNKEDCWGTQELSCDL
TSETSDIQEPYYGRVRAASAGSYSEWSMTPRFTPWWETKIDPPVMNITQVNGSLLVILHAP
NLPYRYQKEKNVSIEDYYELLYRVFIINNSLEKEQKVYEGAHRAVEIEALTPHSSYCVVAEI
YQPMLDRRSQRSEERCVEIP

(SEQ ID NO:81) NP_998785.1 V-type proton ATPase subunit H isoform 1 [Homo sapiens]

MTKMDIRGAVDAAVPTNIIAAKAAEVRANKVNWQSYLQGQMISAEDCEFIQRFEMKRSP
EEKQEMLQTEGSQCAKTFINLMTHICKEQTVQYILTMVDDMLQENHQRVSIFFDYARCSK
NTAWPYFLPMLNRQDPFTVHMAARIIAKLAAWGKELMEGSDLNYYFNWIKTQLSSQKLR
GSGVAVETGTVSSSDSSQYVQCVAGCLQLMLRVNEYRFAWVEADGVNCIMGVLSNKCG
FQLQYQMIFSIWLLAFSPQMCEHLRRYNIIPVLSDILQESVKEKVTRIILAAFRNFLEKSTER
ETRQEYALAMIQCKVLKQLENLEQQKYDDEDISEDIKFLLEKLGESVQDLSSFDEYSSELK
SGRLEWSPVHKSEKFWRENAVRLNEKNYELLKILTKLLEVSDDPQVLAVAAHDVGEYVR
HYPRGKRVIEQLGGKQLVMNHMHHEDQQVRYNALLAVQKLMVHNWEYLGKQLQSEQP
QTAAARS

(SEQ ID NO:82) NP_055043.2 sodium-dependent proline transporter [Homo sapiens]

MKKLQGAHLRKPVTPDLLMTPSDQGDVDLDVDFAAHRGNWTGKLDFLLSCIGYCVGLG
NVWRFPYRAYTNGGGAFLVPYFLMLAICGIPLFFLELSLGQFSSLGPLAVWKISPLFKGAG
AAMLLIVGLVAIYYNMIIAYVLFYLFASLTSDLPWEHCGNWWNTELCLEHRVSKDGNGA
LPLNLTCTVSPSEEYWSRYVLHIQGSQGIGSPGEIRWNLCLCLLLAWVIVFLCILKGVKSSG
KVVYFTATFPYLILLMLLVRGVTLPGAWKGIQFYLTPQFHHLLSSKVWIEAALQIFYSLGV
GFGGLLTFASYNTFHQNIYRDTFIVTLGNAITSILAGFAIFSVLGYMSQELGVPVDQVAKAG
PGLAFVVYPQAMTMLPLSPFWSFLFFFMLLTLGLDSQFAFLETIVTAVTDEFPYYLRPKKA
VFSGLICVAMYLMGLILTTDGGMYWLVLLDDYSASFGLMVVVITTCLAVTRVYGIQRFCR
DIHMMLGFKPGLYFRACWLFLSPATLLALMVYSIVKYQPSEYGSYRFPPWAELLGILMGL
LSCLMIPAGMLVAVLREEGSLWERLQQASRPAMDWGPSLEENRTGMYVATLAGSQSPKP
LMVHMRKYGGITSFENTAIEVDREIAEEEESMM

Fig. 25 cont'd

(SEQ ID NO:83) NP_056126.1 obscurin-like protein 1 isoform 1 precursor [Homo sapiens]

MKASSGDQGSPPCFLRFPRPVRVVSGAEAELKCVVLGEPPPVVVWEKGGQQLAASERLSFPADGAE
HGLLLTAALPTDAGVYVCRARNAAGEAYAAAAVTVLEPPASDPELQPAERPLPSPGSGEGAPVFLT
GPRSQWVLRGAEVVLTCRAGGLPEPTLYWEKDGMALDEVWDSSHFALQPGRAEDGPGASLALRIL
AARLPDSGVYVCHARNAHGHAQAGALLQVHQPPESPPADPDEAPAPVVEPLKCAPKTFWVNEGKH
AKFRCYVMGKPEPEIEWHWEGRPLLPDRRRLMYRDRDGGFVLKVLYCQAKDRGLYVCAARNSAG
QTLSAVQLHVKEPRLRFTRPLQDVEGREHGIAVLECKVPNSRIPTAWFREDQRLLPCRKYEQIEEGT
VRRLIIHRLKADDDGIYLCEMRGRVRTVANVTVKGPILKRLPRKLDVLEGENAVLLVETLEAGVEG
RWSRDGEELPVICQSSSGHMHALVLPGVTREDAGEVTFSLGNSRTTTLLRVKCVKHSPPGPPILAEM
FKGHKNTVLLTWKPPEPAPETPFIYRLERQEVGSEDWIQCFSIEKAGAVEVPGDCVPSEGDYRFRICT
VSGHGRSPHVVFHGSAHLVPTARLVAGLEDVQVYDGEDAVFSLDLSTIIQGTWFLNGEELKSNEPE
GQVEPGALRYRIEQKGLQHRLILHAVKHQDSGALVGFSCPGVQDSAALTIQESPVHILSPQDRVSLTF
TTSERVVLTCELSRVDFPATWYKDGQKVEESELLVVKMDGRKHRLILPEAKVQDSGEFECRTEGVS
AFFGVTVQDPPVHIVDPREHVFVHAITSECVMLACEVDREDAPVRWYKDGQEVEESDFVVLENEGP
HRRLVLPATQPSDGGEFQCVAGDECAYFTVTITDVSSWIVYPSGKVYVAAVRLERVVLTCELCRPW
AEVRWTKDGEEVVESPALLLQKEDTVRRLVLPAVQLEDSGEYLCEIDDESASFTVTVTEPPVRIIYPR
DEVTLIAVTLECVVLMCELSREDAPVRWYKDGLEVEESEALVLERDGPRCRLVLPAAQPEDGGEFV
CDAGDDSAFFTVTVTAPPERIVHPAARSLDLHFGAPGRVELRCEVAPAGSQVRWYKDGLEVEASDA
LQLGAEGPTRTLTLPHAQPEDAGEYVCETRHEAITFNVILAEPPVQFLALETTPSPLCVAPGEPVVLS
CELSRAGAPVVWSHNGRPVQEGEGLELHAEGPRRVLCIQAAGPAHAGLYTCQSGAAPGAPSLSFTV
QVAEPPVRVVAPEAAQTRVRSTPGGDLELVVHLSGPGGPVRWYKDGERLASQGRVQLEQAGARQ
VLRVQGARSGDAGEYLCDAPQDSRIFLVSVEEPLLVKLVSELTPLTVHEGDDATFRCEVSPPDADVT
WLRNGAVVTPGPQVEMAQNGSSRILTLRGCQLGDAGTVTLRAGSTATSARLHVRETELLFLRRLQD
VRAEEGQDVCLEVETGRVGAAGAVRWVRGGQPLPHDSRLSMAQDGHIHRLFIHGVILADQGTYGC
ESHHDRTLARLSVRPRQLRVLRPLEDVTISEGGSATFQLELSQEGVTGEWARGGVQLYPGPKCHIHS
DGHRHRLVLNGLGLADSGCVSFTADSLRCAARLIVREVPVTIVRGPHDLEVTEGDTATFECELSQAL
ADVTWEKDGNALTPSPRLRLQALGTRRLLQLRRCGPSDAGTYSCAVGTARAGPVRLTVRERTVAV
LSELRSVSAREGDGATFECTVSEVETTGRWELGGRPLRPGARVRIRQEGKKHILVLSELRAEDAGEV
RFQAGPAQSLALLEVEALPLQMCRHPPREKTVLVGRRAVLEVTVSRSGGHVCWLREGAELCPGDK
YEMRSHGPTHSLVIHDVRPEDQGTYCCQAGQDSTHTRLLVEGN

(SEQ ID NO:84) NP_001116848.1 transmembrane protein 72 isoform 1 [Homo sapiens]

MQLQVFWTGLEYTCRLLGITTAAVLIGVGTETFLQGQFKSLAFYLLFTGAAVSICEGAYFVAQLLAI
CFQCQPGSLADRVREKAHWLGCFQKFLAYLLLSVACFLHPVLVWHVTIPGSMLIITGLAYFLLSKRK
KRKAAPEVLASPEQYTDPSSSAVSTTGSGDTEQTYTFHGALKEGPSSLFIHMKSILKGTKKPSALQPP
NTLMELSLEPADSLAKKKQVHFEDNLVRIVPSLAEGLDDGDSEPEETTSDTTPIIPPPQAPLFLSSLTA
TGLF

Fig. 25 cont'd

(SEQ ID NO:85) NP_001139133.1 endothelial transcription factor GATA-2 isoform 1 [Homo sapiens]

MEVAPEQPRWMAHPAVLNAQHPDSHHPGLAHNYMEPAQLLPPDEVDVFFNHLDSQGNPYYA
NPAHARARVSYSPAHARLTGGQMCRPHLLHSPGLPWLDGGKAALSAAAAHHHNPWTVSPFSK
TPLHPSAAGGPGGPLSVYPGAGGGSGGGSGSSVASLTPTAAHSGSHLFGFPPTPPKEVSPDPSTT
GAASPASSSAGGSAARGEDKDGVKYQVSLTESMKMESGSPLRPGLATMGTQPATHHPIPTYPS
YVPAAAHDYSSGLFHPGGFLGGPASSFTPKQRSKARSCSEGRECVNCGATATPLWRRDGTGHY
LCNACGLYHKMNGQNRPLIKPKRRLSAARRAGTCCANCQTTTTTLWRRNANGDPVCNACGL
YYKLHNVNRPLTMKKEGIQTRNRKMSNKSKKSKKGAECFEELSKCMQEKSSPFSAAALAGHM
APVGHLPPFSHSGHILPTPTPIHPSSSLSFGHPHPSSMVTAMG

(SEQ ID NO:86) NP_001243781.1 ubiquitin carboxyl-terminal hydrolase 17-like protein 10 [Homo sapiens]

MEDDSLYLGGEWQFNHFSKLTSSRPDAAFAEIQRTSLPEKSPLSCETRVDLCDDLAPVARQLAP
REKPPLSSRRPAAVGAGLQNMGNTCYVNASLQCLTYKPPLANYMLFREHSQTCHRHKGCMLC
TMQAHITRALHIPGHVIQPSQALAAGFHRGKQEDAHEFLMFTVDAMRKACLPGHKQVDRHSK
DTTLIHQIFGGYWRSQIKCLHCHGISDTFDPYLDIALDIQAAQSVQQALEQLVKPEELNGENAY
HCGVCLQRAPASKTLTLHNSAKVLILVLKRFPDVTGNKIAKNVQYPECLDMQPYMSQQNTGPL
VYVLYAVLVHAGWSCHNGHYSSYVKAQEGQWYKMDDAEVTASSITSVLSQQAYVLFYIQKS
EWERHSESVSRGREPRALGVEDTDRRATQGELKRDHPCLQAPELDEHLVERATQESTLDHWK
FLQEQNKTKPEFNVRRVEGTVPPDVLVIHQSKYKCRMKNHHPEQQSSLLNLSSTTPTDQESMN
TGTLASLRGRTRRSKGKNKHSKRALLVCQ

(SEQ ID NO:87) NP_001243798.1 inactive ubiquitin carboxyl-terminal hydrolase 17-like protein 7 [Homo sapiens]

MEDDSLYLGGDWQFNHFSKLTSSRLDAAFAEIQRTSLSEKSPLSSETRFDLCDDLAPVARQLAP
REKLPLSSRRPAAVGAGLQKIGNTFYVNVSLQCLTYTLPLSNYMLSREDSQTCHLHKCCMFCT
MQAHITWALHSPGHVIQPSQVLAAGFHRGEQEDAHEFLMFTVDAMKKACLPGHKQLDHHSK
DTTLIHQIFGAYWRSQIKYLHCHGVSDTFDPYLDIALDIQAAQSVKQALEQLVKPKELNGENAY
HCGLCLQKAPASKTLTLPTSAKVLILVLKRFSDVTGNKLAKNVQYPKCRDMQPYMSQQNTGP
LVYVLYAVLVHAGWSCHNGHYFSYVKAQEGQWYKMDDAEVTASGITSVLSQQAYVLFYIQK
SEWERHSESVSRGREPRALGAEDTDRPATQGELKRDHPCLQVPELDEHLVERATQESTLDHWK
FPQEQNKTKPEFNVRKVEGTLPPNVLVIHQSKYKCGMKNHHPEQQSSLLNLSSTKPTDQESMN
TGTLASLQGSTRRSKGNNKHSKRSLLVCQ

(SEQ ID NO:88) NP_001305432.1 dual specificity protein phosphatase 9 [Homo sapiens]

MEGLGRSCLWLRRELSPPRPRLLLLDCRSRELYESARIGGALSVALPALLLRRLRRGSLSVRAL
LPGPPLQPPPPAPVLLYDQGGGRRRRGEAEAEAEEWEAESVLGTLLQKLREEGYLAYYLQGGF
SRFQAECPHLCETSLAGRAGSSMAPVPGPVPVVGLGSLCLGSDCSDAESEADRDSMSCGLDSE
GATPPPVGLRASFPVQILPNLYLGSARDSANLESLAKLGIRYILNVTPNLPNFFEKNGDFHYKQIP
ISDHWSQNLSRFFPEAIEFIDEALSQNCGVLVHCLAGVSRSVTVTVAYLMQKLHLSLNDAYDLV
KRKKSNISPNFNFMGQLLDFERSLRLEERHSQEQGSGGQASAASNPPSFFTTPTSDGAFELAPT

Fig. 25 cont'd

(SEQ ID NO:89) NP_001341698.1 neural retina-specific leucine zipper protein isoform 1 [Homo sapiens]
MALPPSPLAMEYVNDFDLMKFEVKREPSEGRPGPPTASLGSTPYSSVPPSPTFSEPGMVGATEGTRP
GLEELYWLATLQQQLGAGEALGLSPEEAMELLQGQGPVPVDGPHGYYPGSPEETGAQHVQLAER
FSDAALVSMSVRELNRQLRGCGRDEALRLKQRRRTLKNRGYAQACRSKRLQQRRGLEAERARLA
AQLDALRAEVARLARERDLYKARCDRLTSSGPGSGDPSHLFL

(SEQ ID NO:90) NP_001349881.1 nuclear receptor coactivator 1 isoform 2 [Homo sapiens]
MSGLGDSSSDPANPDSHKRKGSPCDTLASSTEKRRREQENKYLEELAELLSANISDIDSLSVKPDKC
KILKKTVDQIQLMKRMEQEKSTTDDDVQKSDISSSSQGVIEKESLGPLLLEALDGFFFVVNCEGRIV
FVSENVTSYLGYNQEELMNTSVYSILHVGDHAEFVKNLLPKSLVNGVPWPQEATRRNSHTFNCRM
LIHPPDEPGTENQEACQRYEVMQCFTVSQPKSIQEDGEDFQSCLICIARRLPRPPAITGVESFMTKQD
TTGKIISIDTSSLRAAGRTGWEDLVRKCIYAFFQPQGREPSYARQLFQEVMTRGTASSPSYRFILNDG
TMLSAHTKCKLCYPQSPDMQPFIMGIHIIDREHSGLSPQDDTNSGMSIPRVNPSVNPSISPAHGVARS
STLPPSNSNMVSTRINRQQSSDLHSSSHSNSSNSQGSFGCSPGSQIVANVALNQGQASSQSSNPSLNL
NNSPMEGTGISLAQFMSPRRQVTSGLATRPRMPNNSFPPNISTLSSPVGMTSSACNNNNRSYSNIPV
TSLQGMNEGPNNSVGFSASSPVLRQMSSQNSPSRLNIQPAKAESKDNKEIASILNEMIQSDNSSSDG
KPLDSGLLHNNDRLSDGDSKYSQTSHKLVQLLTTTAEQQLRHADIDTSCKDVLSCTGTSNSASANS
SGGSCPSSHSSLTERHKILHRLLQEGSPSDITTLSVEPDKKDSASTSVSVTGQVQGNSSIKLELDASK
KKESKDHQLLRYLLDKDEKDLRSTPNLSLDDVKVKVEKKEQMDPCNTNPTPMTKPTPEEIKLEAQ
SQFTADLDQFDQLLPTLEKAAQLPGLCETDRMDGAVTSVTIKSEILPASLQSATARPTSRLNRLPEL
ELEAIDNQFGQPGTGDQIPWTNNTVTAINQSKSEDQCISSQLDELLCPPTTVEGRNDEKALLEQLVS
FLSGKDETELAELDRALGIDKLVQGGGLDVLSERFPPQQATPPLIMEERPNLYSQPYSSPSPTANLPS
PFQGMVRQKPSLGTMPVQVTPPRGAFSPGMGMQPRQTLNRPPAAPNQLRLQLQQRLQGQQQLIH
QNRQAILNQFAATAPVGINMRSGMQQQITPQPPLNAQMLAQRQRELYSQQHRQRQLIQQQRAML
MRQQSFGNNLPPSSGLPVQMGNPRLPQGAPQQFPYPPNYGTNPGTPPASTSPFSQLAANPEASLAN
RNSMVSRGMTGNIGGQFGTGINPQMQQNVFQYPGAGMVPQGEANFAPSLSPGSSMVPMPIPPPQSS
LLQQTPPASGYQSPDMKAWQQGAIGNNNVFSQAVQNQPTPAQPGVYNNMSITVSMAGGNTNVQ
NMNPMMAQMQMSSLQMPGMNTVCPEQINDPALRHTGLYCNQLSSTDLLKTEADGTQDKKTEEPF
SVVTTD

(SEQ ID NO:91) NP_001362339.1 protein sprouty homolog 1 [Homo sapiens]
MDPQNQHGSGSSLVVIQQPSLDSRQRLDYEREIQPTAILSLDQIKAIRGSNEYTEGPSVVKRPAPRTA
PRQEKHERTHEIIPINVNNNYEHRHTSHLGHAVLPSNARGPILSRSTSTGSAASSGSNSSASSEQGLL
GRSPPTRPVPGHRSERAIRTQPKQLIVDDLKGSLKEDLTQHKFICEQCGKCKCGECTAPRTLPSCLA
CNRQCLCSAESMVEYGTCMCLVKGIFYHCSNDDEGDSYSDNPCSCSQSHCCSRYLCMGAMSLFLP
CLLCYPPAKGCLKLCRRCYDWIHRPGCRCKNSNTVYCKLESCPSRGQGKPS

Fig. 25 cont'd

(SEQ ID NO:92) NM_001256852.1 Homo sapiens ubiquitin specific peptidase 17 like family member 10 (USP17L10), mRNA

ATGGAGGACGACTCACTCTACTTGGGAGGTGAGTGGCAGTTCAACCACTTTTCAAAACTCACATCTTCTCGGCCAG
ATGCAGCTTTTGCTGAAATCCAGCGTACTTCTCTCCCTGAGAAGTCACCACTCTCATGTGAGAC
CCGTGTCGACCTCTGTGATGATTTGGCTCCTGTGGCAAGACAGCTTGCTCCCAGGGAGAAGCCTCCTCTG
AGTAGCAGGAGACCTGCTGCGGTGGGGGCTGGGCTCCAGAATATGGGAAATACCTGCTACGTGAACGCTT
CCCTGCAGTGCCTGACATACAAACCGCCACTTGCCAACTACATGCTGTTCCGGGAGCACTCTCAAACGTG
TCATCGTCACAAGGGCTGCATGCTCTGTACTATGCAAGCTCACATCACAAGGGCCCTCCACATTCCTGGC
CATGTCATCCAGCCCTCACAGGCATTGGCTGCTGGCTTCCATAGAGGCAAGCAGGAAGATGCCCATGAAT
TTCTCATGTTCACTGTGGATGCCATGAGAAAGGCATGCCTTCCCGGGCACAAGCAGGTAGATCGTCACTC
TAAGGACACCACCCTCATCCACCAAATATTTGGAGGCTACTGGAGATCTCAAATCAAGTGTCTCCACTGC
CACGGCATTTCAGACACTTTTGACCCTTACCTGGACATCGCCCTGGATATCCAGGCAGCTCAGAGTGTCC
AGCAAGCTTTGGAACAGTTGGTGAAGCCCGAAGAACTCAATGGAGAGAATGCCTATCATTGTGGTGTTTG
TCTCCAGAGGGCGCCGGCCTCCAAGACGTTAACTTTACACAACTCTGCCAAGGTCCTCATCCTTGTATTG
AAGAGATTCCCCGATGTCACAGGCAACAAAATTGCCAAGAATGTGCAATATCCTGAGTGCCTTGACATGC
AGCCATACATGTCTCAGCAGAACACAGGACCTCTCGTCTATGTCCTCTATGCTGTGCTGGTCCACGCTGG
GTGGAGTTGTCACAACGGACATTACTCCTCTTATGTCAAAGCTCAAGAAGGCCAGTGGTATAAAATGGAT
GATGCCGAGGTCACCGCCTCTAGCATCACTTCTGTCCTGAGTCAACAGGCCTACGTCCTCTTTTACATCC
AGAAGAGTGAATGGGAAAGACACAGTGAGAGTGTGTCAAGAGGCAGGGAACCAAGAGCCCTTGGCGTAGA
AGACACAGACAGGCGAGCAACGCAAGGAGAGCTCAAGAGAGACCACCCCTGCCTCCAGGCCCCCGAGTTG
GACGAGCACTTGGTGGAAAGAGCCACTCAGGAAAGCACCTTAGACCACTGGAAATTCCTTCAAGAGCAAA
ACAAAACGAAGCCTGAGTTCAACGTCAGAAGAGTCGAAGGTACGGTGCCTCCCGACGTACTTGTGATTCA
TCAATCAAAATACAAGTGTCGGATGAAGAACCATCATCCTGAACAGCAAAGCTCCCTGCTAAACCTCTCT
TCGACGACCCCGACAGATCAGGAGTCCATGAACACTGGCACACTCGCTTCCCTACGAGGGAGGACCAGGA
GATCCAAAGGGAAGAACAAACACAGCAAGAGGGCTCTGCTTGTGTGCCAGTGA

Fig. 25 cont'd

(SEQ ID NO:93) NR_038883.2 Homo sapiens long intergenic non-protein coding RNA 649 (LINC00649), transcript variant 1, long non-coding RNA

AGCTTCCCGGCTGCTTTGTTTACCTAATCAAGCCTGGGCAATGGCGGGCTCCCCTCCCCCAGCCTCGCTG
CTGCCTTGCAGTTTGATCTCAGACTGCTGTGCTAGCAATCAGCGAGACTCCGTGGGCGTAGGACCCTCCG
AGCCAGGTGTGGGATATAGTCTCGTGGTGCGCCGTTTTTTAAGCCCGTCGGAAAAGCGCAGTATTCGGGT
GGGAGTGACCCGATTTTCCAGGTGCGTCCGTCACCCCTTTCTTTGACTCGGAAAGGGAACTCCCTGACCC
CTTGCGCTTCCCAAGTGAGGCAATGCCTCGCCCTGCTTCGGCTCGCGCACGGTGCGCGCACCCACTGACC
TGCGCCCACTGTCTGGCACTCCCTAGAGAGATGAACCCGGTACCTCAGATGGAAATGCAGAAATCACCGT
CTTCTGCGTCGCTCACGCTGGGAGCTGTAGACCAGAGCTGTTCCTATTCGGCCATCTTGGCTCCTTATTC
TCATTACCTTCTTGAGTTGTGGCTCAGACACTACAACAGAGCTCTGTCACCTCTTTCTAAAAGCTGGGAA
ATGGTTATTGTCAACGCCAGCCCCATTTTGGAGGCACCTGGTTGCAGGGGACCACAGCTAGCTGGGTGCG
GTGGCTCAGGACTGTAATTCCAGCTACATGAGAGGATTGCCTGAGGCCAGGAGTTTGAGACCAGCCTGAA
CAACATAATAGACTGGGAGCTCCATGAGGTCCGAGACAACCTGAAGACGCCCAGCTCAGCAGAGACTGGC
TACGGCAATCACTCAGTAACTATTTGTTGAATTGGACATAATAGAAGAGCTGAAGAATTTTAAACAAGTC
ACCATCAGTGCAGTGGATTCCTCAAAGCAAACCTGGAAATCTCGGCATGAGTTGGATTTAAGGCAGTACA
TTTTCAGCTCCTGAAAATTTGAACAGTTTCTCAAGAGAACAACTTGAAACAGAAAGGCAAGGATGTAGAT
GTGGTTGTAGAAGATGATGTCTGCGGCCACCAAACTGTCCACTGTGAAGACAAACCATGCATGTTTAGTA
GGCAGTGGCTCCTCTTCCCTGTGGGGAGTCCCACTGCTTCCCTGGCCTGGGTGTTCTCTGCCGGTAGATG
TTATTGACAAAATAAGCAAAGTCCTCTGATTCTGAGAATTAGAGTTAATGATAGCTCTAGATTGCCTCTG
CCATGCTATTTAAAGTCCTGCTTTATTGTCTGACATGAGTTCGGCATCTATGAGGACTTGTCCAGTGCAA
AGTACAATCTCCACTGAAAGATATCACCAGCACATCTTGTCACTGTGCTGTAGCAAGCTGGGCAGTACAA
TGATGTTGGCAGGATCCTGTTTAGGTGGAGGATGGCCACCTGGGCATCAAGAATCTTCTACCCTGATTCC
ACATTGACTCCCCAAAGTGGGCTTCAGACAGCTCTTTACTTACGTCTTCTGATTAAAGCAGCAGACAGGG
TCCCAGCTAGAGAAAAGTTCTGGGAGCAGGAGAGGTGTTGGTGGCTTTAAAACCAGGGGTGAAGATTGAA
TTAGGAGGTTAGGCAGGAGTAGGATCAAAGACTTAGAAAATGCTTGTTTCCTCCTATTATTCTTATGAGA
GCTGATACGGGGCTTTCAGTTTTGGGGGAGAGCCTTGGAAGAGAATGAGGGAATTTAATCAACTAGCGGG
ACCTTTCCAACTTACATTTCCCAGTGTTTGTTGGATGATACGTTTGCCTAATAAGTTAAAGCTTCCAAAA
ATAGAAAGGAAAGCTTGGTGACACTAAGCTCTGGCATGCTGTCATCTTCTGGCTAGGGGTCTTGTGCTTC
TGTTTTTCTATTCTGACCAAAGACATAAAATGTGTTGTGACCTCTCAGGTAATGCTGTGGTATCATGTC
CAAGCAGTAACTAACCAGAGTGGAGTTTTTACAGGTAAAAAAGTATTGAATAGCTCAGCAACAGGGAGGA
CTTAATGATAAATTGCTTTTTCAGAAAATGACAAGGGGACAGACACTTGCGGTTCTTCCATTGAGAGCCT
TAAGGAAGTTAAGCGAAGCCTCTGCTCACCCCTTCAAGTAACGATGACCCATCAGATCGTGGTCATAACC
AGTAGCATCTGAGGCACCCCTAAGCTCTCTGGGCCCCAGATTCCTTGTTAAGTTAAATGAGGTGACTTCC
CAGTTTACCATTCTAGGGGTTCCTGAGGAGTTAAAAATGAAGGAGAAAATGCAACATGTACCAAGTGAGC
AAGAGCTCAAGGCTTATCTCTGGCACGAAAGTGACCGCTGTCCGTTAGAGATGTGATTGCCCTAGATTTC
CTTTAGGAAATGCAAACATTGAACTCTGGCCTTCAGGACCCAAGTCCCGGCTTGCATCTATTCTATACAC
TTTCTGTTATTTGTTAGGGCTCACAAGGAACAGTTATTTATCTTTTATTTTCTATTTTTTTTTTAGAGAT
GGAGTCTCACTCTGTCTCCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTCACTGCAACCTCCACCTCCC
GGGTTCAAGCAATTCTCCTGTCTCAGCCTCCTGAGTAGCTGGGACTACAGGCGTGTGCCATCATGCCCGG
CTAATTTTTAGTATTTTTAGTAGAGGCAGGGTTTCACCATATTGGCCAGGCTGGTCTTGAACTCCTG

Fig. 25 cont'd

(SEQ ID NO:94) NM_001354769.1 Homo sapiens neural retina leucine zipper (NRL), transcript variant 3, mRNA

GCCTCAGAGAATAAATAGGAGACTAAGAGGACAGGCAGACAAACAGGACGAGCCTGGGGGCTCCAGGCCT
GGACGGAGGAAGAAGCCAGCTATACGGGGTTTCTCCATGCTGGCCAAGCTGGTCTCCAACTCCTGACCTC
GTGATCCGCCTGCCTTGGCCTCCCAAAGTGCTGGAATTTACAGGCGTGAGCCACCACGCCCGGCCTGGTC
ATTCTTTCTCTCCACAATCCAATGAGGAAACTCATCTGCCCACCCAACTACCATCATAAAGTCCTCAGGT
GATTTCTCAAGCTATACCTCCATTGGGACATCTCTCTCCAACCTGAGACCACTGGATATCACCCACAATG
CTATATAGCACCTCAAACTCAGCATATCTATGATGGGTGTCTGCTCAGCATCCACTCGCCTTTTCTGGTG
CACTCCTCCCAGCCCAGCTCCAGAATGGCCCTGCCCCCCAGCCCCCTGGCCATGGAATATGTCAATGACT
TTGACTTGATGAAGTTTGAGGTAAAGCGGGAACCCTCTGAGGGCCGACCTGGCCCCCCTACAGCCTCACT
GGGCTCCACACCTTACAGCTCAGTGCCTCCTTCACCCACCTTCAGTGAACCAGGCATGGTGGGGGCAACC
GAGGGCACCCGGCCAGGCCTGGAGGAGCTGTACTGGCTGGCTACCCTGCAGCAGCAGCTGGGGGCTGGGG
AGGCATTGGGGCTGAGTCCTGAAGAGGCCATGGAGCTGCTGCAGGGTCAGGGCCCAGTCCCTGTTGATGG
GCCCCATGGCTACTACCCAGGGAGCCCAGAGGAGACAGGAGCCCAGCACGTCCAGCTGGCAGAGCGGTTT
TCCGACGCGGCGCTGGTCTCGATGTCTGTGCGGGAGCTAAACCGGCAGCTGCGGGGCTGCGGGCGCGACG
AGGCGCTGCGGCTGAAGCAGAGGCGCCGCACGCTGAAGAACCGCGGCTACGCGCAGGCCTGTCGCTCCAA
GCGGCTGCAGCAGCGGCGCGGGCTGGAGGCCGAGCGCGCCCGCCTGGCCGCCCAGCTGGACGCGCTGCGG
GCCGAGGTGGCCCGCCTGGCCCGGGAGCGCGATCTCTACAAGGCTCGCTGTGACCGGCTAACCTCGAGCG
GCCCCGGGTCCGGGGACCCCTCCCACCTCTTCCTCTGAGCCGTTCAGAGCACCTTGTGGTGTAGTGGGGG
CTGGGTGGGGTGGCTCCGCCCAGGAGGCGGCTGCACGGTTCTCTGCATCGTTACCAGAGCGCCTTCTGGT
CCTAGCCACGCCCTGTATGACCGCGCAAATATCCCCAAAGCTTTTGGGTCCTCAAGTCATGCCCGAATTT
AGATGCTGGTCATTTTCTGGAGAGGGGTCCCCTCCCCTTACGAACACAGAAACCCAGCCCACATGACTAG
CACGCTGAGCTCTGCAGGGACCAGTGCCAGGCACTGGGGGGTGGAAGTGTGGTGACACAGTGAATGGGAG
GTGGAGGAGGGTTGCAGCTCCCACCTCAGTTTAGTTTTTAATTCAGGGTTTTCAACCTGTAACACATTAA
AGCTGTAATTAGCAATGAGGCTGTATTTTCATTCTGAAGCTTGTAACCTCCCCATTTTAGCACTACAGAA
TTTTCAAGATTTCAATATCCAACAACTAGATAGATTAGGACCTCTATCCGAGATGCTTTTTCCCTGCCCA
ACCCTGTGGCCTTCAGGGCTCAGAGCAGCAAAGGCCTGAAGAGTGAGCTCTGGGGGTTGTTGGTGTGGGT
TGGGAGAGAGCTGTGTGCAGAAGTCTGGAAACCTGGGTCCTAGTCCCAGCTCTTCCATGGGATCCCCCTG
TCACCCTGAGCAAATCAGTTGCTTCCTGGACTTGTGTTACTTCATCTAATTCTCATGTGGATTGGACGAC
TTCTGCTCCCTTTCCAGTTCTGGCATCTCCCCAGTATGGAAGTCCCGGTGGTCTCCCCAAGAAGTCCCCA
AGACAATCTCGCCAAAGGCACCTCCTATCCTGCTGCAGTTTCCCAGCTGCAGCCTAGGCAGGGGATGCAC
AGCCCAGGCGAGGAAGCCTGGCTTCTCTGTGAGCACATACGTGGGTCCTCGGCAGCTCCCTCCAGGCTGT
CTGGGCCTCCAGACCTGCACAGGGTGCTCCTGCCACCTCCCACCTCTCTGAGGGCTGAGGTGAGACTTCT
CCTGGGATGACAATTTGCTGAGAGAGTGCAGCTTTTGTGAATTAAACTTGAAGTCCAGGCAGAATTCTAA
TGCAATAAGCTAAATGTTCTTGCAATTTAAGAAGTGTTCATTCTTTATCCCTGCTTCAGGCTACTGTTTG
TGTGTCTGTGTGTGGGAGAGGGAGAGAGAGGGAGAGAGAGAGAGAGCAAGAAAAAGGGAAGTCCCCACCT
GGAGCTGGGTGGCACATCTGTTATGGAGAGCCAATGGAAATGGGGTGGAGGGGCAGGCATTGGAACAGAT
GGATCCTCCCCCTCTCACCACCACCACCACCAAACTCAGAAGCCTCAGTGGCCCAGCTCGGCCTGTCAGT
GGCTATCCAGGTCTCACAGTTTCCATGGTAACCCAGTCCTCCAGTTCAGCAGGCTAAGGGGAGGGCAGAT
GGGGCCTCTGGGCAGAGCACAGGCGTTGTGCTGGGAGCAGCCGCCTCACGAGTTACTGTCATCTGTCCTC
TACCGGACATAATAAATGGGAGAAGCTTTCGGGCATGGGGGAAGAGGCTCCCATATGTCCCTCTTCCTTT
CTACCCCCTCTCTCCACCCCCTCCCCAGCTGTCTCTTCTCTTCCCATCACAGTTCTTGCTCCCTCTTTCC
CCTCCTCTATCCCAGCTCATCCCTCCTCCGCTTAGGAGCCTGCAATGGGAGTCCTCTCCTCCATCGCTCT
CAGAATTTCTCTCGTCTCCTCTCCCTTCCCCACCATTGGCCACTGGCCATCCTCTCTGGCTCTGGATTCT
CTCTCTGAGGGGCTCACAGAACCTTTAGCTTCTCTTTCTTCATCCCCTTCCACACTCATTGTTGAAGGGA
GAGGATGGGGCAGGGAGGGTCCTTCCGGGAGCCCAGCTCTTTTTCTCTCACTCTAAATTTCACCTGTGTC
TATCCTTGCCTGCCCTGGAGCTGTAATTCAGACCCACTACTTTTCTTGTTCACTTTTCTCACCTGCATGG
CACACAAAGACAGACAGAACCATCCATAGACACCTGAGCACACAACTAGGCCACATATACAGTACCATAC
CTGGGTCTCAAAATGATACTCCTGGGTTACCTGAGTATACTTAAAAAAACAAAGTTGCACACTGTGGTGA
TTAAGAGTAGTGCTTTAGGTGGGGCGCAGTGGTTCCTGCCTGTAATCCCAACACTTTGGGAGGCCAAGGA
GGAAGTTTGAGACCAGCCTGGGCAACATAGCGAGAACCCTGTCACTACAAAAAAATAAAATAAAATAAAT
TCAGATGTAATGGCATGCACCTGGAGTCCCACCTACCCAGGAGGCTAAGGTGGAAGGATAACTTGAGCCC
AGGAGTTCGGGGATGCAGTGAGCCATAATCGTGCCACTGCATTCCAGCCTGGGTGGCAGAGTGAGACCCT
GTTTCAAGTTGCAGTTCTACCAGTTTTTTGACCATGGGTGGGTTAAAATCAAGCCTCACTTGATTGTCAG
AAAAATGGTGAAAATAATGGTAACCACCTACTGAGAATAAATGCATTTAAATAAGCACTTAGCATAAA

Fig. 25 cont'd

(SEQ ID NO:110) NM_001362952.1 Homo sapiens nuclear receptor coactivator 1 (NCOA1), transcript variant 5, mRNA
AGTTGCCCTAGTTAGCGCGGAGAGGGCGAGCATCCGCGGAGGGGGTGCGAGCTGCGCGGCCGCCTGCCCG
GCGTGGGGAGCGGGCGCCCCGGGCCGCCGCCGAGAGGGGGAGCCGGAAGTCGGCGCGGGCGCCCCTCGGC
CCCGACGACGCCGTGACCTTGGCCGGCCCGCTCACCTCTCGGAATCTCGCCTGCCGGGACCGCGAAATGG
GGGCGACCGCGGCGTCCCTCTCCGTCGGCGCAGCCCTCGACGGCGCTTGGGTTTGACCCCGGCGCGCTTG
CTCGCCCCTTCTCCCGAGAAGGGGTTTCGGAGATCTATCCATACTAATGGAAATGTAACTGGAACTGACT
CTGATGATAAAATCAAGGACCATCAAGCAAGATCATGCAGTAGGCAACTTTGCTTCCAAAAGAAGTTACC
AACATTTAGAATTTCTACTTATTCTGAGGTTCCAGTTACAGCTATATCAGAGAATGAGTTAATCTCCTCA
GAAATCACTAAATACTACTCTGAGGGGCTTAGAAATTAACAGGTTGTTTATATAATTGGCCTTAAATGAG
GTGAGAGTGAAGAGACTAGAGCCATCTCTGGAAAACATCATTATCCCATTCCCCGGGAAGCTACCCTCTG
GAACTCAAGATTTGACCATATCTGTTTTGAGGATTCATTATGAACAAAGAAGTCTCCCAGGTGTGAAGTT
TTTCAACATGAGTGGCCTCGGGGACAGTTCATCCGACCCTGCTAACCCAGACTCACATAAGAGGAAAGGA
TCGCCATGTGACACACTGGCATCAAGCACGGAAAAGAGGCGCAGGGAGCAAGAAAATAAATATTTAGAAG
AACTAGCTGAGTTACTGTCTGCCAACATTAGTGACATTGACAGCTTGAGTGTAAAACCAGACAAATGCAA
GATTTTGAAGAAAACAGTCGATCAGATACAGCTAATGAAGAGAATGGAACAAGAGAAATCAACAACTGAT
GACGATGTACAGAAATCAGACATCTCATCAAGTAGTCAAGGAGTGATAGAAAAGGAATCCTTGGGACCTC
TTCTTTTGGAGGCTTTGGATGGATTTTTCTTTGTTGTGAACTGTGAAGGGAGAATTGTATTTGTGTCAGA
GAATGTAACCAGCTACTTAGGTTACAATCAGGAGGAATTAATGAATACGAGCGTCTACAGCATACTGCAC
GTGGGGGATCATGCAGAATTTGTGAAGAATCTGCTACCAAAATCACTAGTAAATGGAGTTCCTTGGCCTC
AAGAGGCAACACGACGAAATAGCCATACCTTTAACTGCAGGATGCTAATTCACCCTCCAGATGAGCCAGG
GACCGAGAACCAAGAAGCTTGCCAGCGTTATGAAGTAATGCAGTGTTTCACTGTGTCACAGCCAAAATCA
ATTCAAGAGGATGGAGAAGATTTCCAGTCATGTCTGATTTGTATTGCACGGCGATTACCTCGGCCTCCAG
CTATTACGGGTGTAGAATCCTTTATGACCAAGCAAGATACTACAGGTAAAATCATCTCTATTGATACTAG
TTCCCTGAGAGCTGCTGGCAGAACTGGTTGGGAAGATTTAGTGAGGAAGTGCATTTATGCTTTTTTCCAA
CCTCAGGGCAGAGAACCATCTTATGCCAGACAGCTGTTCCAAGAAGTGATGACTCGTGGCACTGCCTCCA
GCCCCTCCTATAGATTCATATTGAATGATGGGACAATGCTTAGCGCCCACACCAAGTGTAAACTTTGCTA
CCCTCAAAGTCCAGACATGCAACCTTTCATCATGGGAATTCATATCATCGACAGGGAGCACAGTGGGCTT
TCTCCTCAAGATGACACTAATTCTGGAATGTCAATTCCCCGAGTAAATCCCTCGGTCAATCCTAGTATCT
CTCCAGCTCATGGTGTGGCTCGTTCATCCACATTGCCACCATCCAACAGCAACATGGTATCCACCAGAAT
AAACCGCCAGCAGAGCTCAGACCTTCATAGCAGCAGTCATAGTAATTCTAGCAACAGCCAAGGAAGTTTC
GGATGCTCACCCGGAAGTCAGATTGTAGCCAATGTTGCCTTAAACCAAGGACAGGCCAGTTCACAGAGCA
GTAATCCCTCTTTAAACCTCAATAATTCTCCTATGGAAGGTACAGGAATATCCCTAGCACAGTTCATGTC
TCCAAGGAGACAGGTTACTTCTGGATTGGCAACAAGGCCCAGGATGCCAAACAATTCCTTTCCTCCTAAT
ATTTCGACATTAAGCTCTCCCGTTGGCATGACAAGTAGTGCCTGTAATAATAATAACCGATCTTATTCAA
ACATCCCAGTAACATCTTTACAGGGTATGAATGAAGGACCCAATAACTCCGTTGGCTTCTCTGCCAGTTC
TCCAGTCCTCAGGCAGATGAGCTCACAGAATTCACCTAGCAGATTAAATATACAACCAGCAAAAGCTGAG
TCCAAAGATAACAAAGAGATTGCCTCAATTTTAAATGAAATGATTCAATCTGACAACAGCTCTAGTGATG
GCAAACCTCTGGATTCAGGGCTTCTGCATAACAATGACAGACTTTCAGATGGAGACAGTAAATACTCTCA
AACCAGTCACAAACTAGTGCAGCTTTTGACAACAACTGCCGAACAGCAGTTACGGCATGCTGATATAGAC
ACAAGCTGCAAAGATGTCCTGTCTTGCACAGGCACTTCCAACTCTGCCTCTGCTAACTCTTCAGGAGGTT
CTTGTCCCTCTTCTCATAGCTCATTGACAGAACGGCATAAAATTCTACACCGGCTCTTACAGGAGGGTAG
CCCCTCAGATATCACCACTTTGTCTGTCGAGCCTGATAAAAAGGACAGTGCATCTACTTCTGTGTCAGTG
ACTGGACAGGTACAAGGAAACTCCAGTATAAAACTAGAACTGGATGCTTCAAAGAAAAAAGAATCAAAAG
ACCATCAGCTCCTACGCTATCTTTTAGATAAAGATGAGAAAGATTTAAGATCAACTCCAAACCTGAGCCT
GGATGATGTAAAGGTGAAAGTGGAAAAGAAAGAACAGATGGATCCATGTAATACAAACCCAACCCCAATG
ACCAAACCCACTCCTGAGGAAATAAAACTGGAGGCCCAGAGCCAGTTTACAGCTGACCTTGACCAGTTTG
ATCAGTTACTGCCCACGCTGGAGAAGGCAGCACAGTTGCCAGGCTTATGTGAGACAGACAGGATGGATGG
TGCGGTCACCAGTGTAACCATCAAATCGGAGATCCTGCCAGCTTCACTTCAGTCCGCCACTGCCAGACCC
ACTTCCAGGCTAAATAGATTACCTGAGCTGGAATTGGAAGCAATTGATAACCAATTTGGACAACCAGGAA
CAGGCGATCAGATTCCATGGACAAATAATACAGTGACAGCTATAAATCAGAGTAAATCAGAAGACCAGTG
TATTAGCTCACAATTAGATGAGCTTCTCTGTCCACCCACAACAGTAGAAGGGAGAAATGATGAGAAGGCT

Fig. 25 cont'd

(SEQ ID NO:110) Cont'd:

CTTCTTGAACAGCTGGTATCCTTCCTTAGTGGCAAAGATGAAACTGAGCTAGCTGAACTAGACAGAGCTC
TGGGAATTGACAAACTTGTTCAGGGGGGTGGATTAGATGTATTATCAGAGAGATTTCCACCACAACAAGC
AACGCCACCTTTGATCATGGAAGAAAGACCCAACCTTTATTCCCAGCCTTACTCTTCTCCTTCTCCTACT
GCCAATCTCCCTAGCCCTTTCCAAGGCATGGTCAGGCAAAAACCTTCACTGGGGACGATGCCTGTTCAAG
TAACACCTCCCCGAGGTGCTTTTTCACCTGGCATGGGCATGCAGCCCAGGCAAACTCTAAACAGACCTCC
GGCTGCACCTAACCAGCTTCGACTTCAACTACAGCAGCGATTACAGGGACAACAGCAGTTGATACACCAA
AATCGGCAAGCTATCTTAAACCAGTTTGCAGCAACTGCTCCTGTTGGCATCAATATGAGATCAGGCATGC
AACAGCAAATTACACCTCAGCCACCCCTGAATGCTCAAATGTTGGCACAACGTCAGCGGGAACTGTACAG
TCAACAGCACCGACAGAGGCAGCTAATACAGCAGCAAAGAGCCATGCTTATGAGGCAGCAAAGCTTTGGG
AACAACCTCCCTCCCTCATCTGGACTACCAGTTCAAATGGGGAACCCCCGTCTTCCTCAGGGTGCTCCAC
AGCAATTCCCCTATCCACCAAACTATGGTACAAATCCAGGAACCCCACCTGCTTCTACCAGCCCGTTTTC
ACAACTAGCAGCAAATCCTGAAGCATCCTTGGCCAACCGCAACAGCATGGTGAGCAGAGGCATGACAGGA
AACATAGGAGGACAGTTTGGCACTGGAATCAATCCTCAGATGCAGCAGAATGTCTTCCAGTATCCAGGAG
CAGGAATGGTTCCCCAAGGTGAGGCCAACTTTGCTCCATCTCTAAGCCCTGGGAGCTCCATGGTGCCGAT
GCCAATCCCTCCTCCTCAGAGTTCTCTTCTCCAGCAAACTCCACCTGCCTCCGGGTATCAGTCACCAGAC
ATGAAGGCCTGGCAGCAAGGAGCGATAGGAAACAACAATGTGTTCAGTCAAGCTGTCCAGAACCAGCCCA
CGCCTGCACAGCCAGGAGTATACAACAACATGAGCATCACCGTTTCCATGGCAGGTGGAAATACGAATGT
TCAGAACATGAACCCAATGATGGCCCAGATGCAGATGAGCTCTTTGCAGATGCCAGGAATGAACACTGTG
TGCCCTGAGCAGATAAATGATCCCGCACTGAGACACACAGGCCTCTACTGCAACCAGCTCTCATCCACTG
ACCTTCTCAAAACAGAAGCAGATGGAACCCAGGACAAGAAGACAGAAGAGTTCTTCTCTGTGGTGACTAC
AGACTAGAGGAATGCTCTACAGGTGCAACAGGTTCAGGTGTTTGCTGACGTCCAGTGTACAGTGAATCTG
GTAGGCGGGGACCCTTACCTGAACCAGCCTGGTCCACTGGGAACTCAAAAGCCCACGTCAGGACCACAGA
CCCCCCAGGCCCAGCAGAAGAGCCTCCTTCAGCAGCTACTGACTGAATAACCACTTTTAAAGGAATGTGA
AATTTAAATAATAGACATACAGAGATATACAAATATATTATATATTTTTCTGAGATTTTTGATATCTCAA
TCTGCAGCCATTCTTCAGGTCGTAGCATTTGGAGCAAAAAAAAAAAAAAAAAAAAAAAAAGGAGTTTGCT
TTTGTCGGGAGATTGAAAGATGTTTTTGTTTCTTTCTTTGTAAAGGCCTTGGATATTGAAAAAATACCAA
GGCAGAACAGTTGGACAATCTATTTCTTGAGCCAAATTTAATTATTCTTATTTTTGTAATCAGTCATTGG
CTTCTTATCTGGATGAAGGCTTTTGGAGGAGAACCAAAACGACAAGTTCCAAGAAGAAGATGAAGCTCCG
CCTCCGCCGCTTAGTCCCAACCCTGCCCAGGAAGAAGGGCCCGTGGGGCTTTGCCTGTGCCCGTCCACCA
AAGGCTGTCATGTGTCTCGAAATCAGCAGCCCTCCCCATCCCAATCCCAGGCAGCTTGTGTGTACAATCA
GCTTCTCTAGCAACTCTGTATCTGTTGGCTTCAAGAGAATATTTTGCCTCCACATATGTACCCCTTCTCC
TTTTTTTAAAGATGGATTTAAACCAAGATGCCTCCAGGAAAGAGGACGAAATGAGTATATTCACAGAGGA
ATCCAAAAAATACAGTTTGGGGGAAAATGCAATAATTTTTGATGAGATGGGTGAAGGACAAGAAGTGAGT
TGTGTCAATTATTGTAGATACAATTTTCTGATTAAATCTGGAAAAATAAAAGGCAGCCTGTTTTTTCTGC
TTTTATTGTATTAACAGCTGAGGTAGCTAAAGTTATTTAAAATAAAATTAAATTTATGATCCAAGTAGCT
TATTTTTCCCTTTAAATCTCATTGTAAATATATTTGATTTCTTGTAGAAATTGATTTCCTTCTGTTTAAT
TTTATGCTTTTATTATACTCTTGATTTTTCTAAATTTGTGTGTGAAATATAACATTGATTGAATTGCAGT
TACATTTGGTTAGTAATATTTCATTATTTTAATAACTGTGATGTCATGTATGGATTTACTTTGGGGTTCA
AATCAAAATGTCACTGCCAGAAAGAGCTGTTCCAGCTGATCTAGAGCATACTGCCCTAGAGTGTCCCTGG
GATCATCTGAACAGAAGTGCACAGGCTACTTGTACAGAGAAAAAATTAATACTCAAAGGAAATCTTCATT
TTTTAGATTGACTTTGGGAATTTGAATTTTCATCAGTGCAAATATAAATTTCTCTATCCTGCTCTGAGGC
TAATTGGTACCATATTTTCCCTTTGTGTCTTGTGACTCTGCCACATCCCATCTCATCCTGGCCTCTGAGT
CAAGAACCCAGTGAACTGACTTTCTAGTTCTAGAAGTTCCGCTGCAAGGCCAGGAAAGCTTGAGAAAGGT
ATTGTGGAAGAAGCAAAGGTAGACCCCCATCACTCACCTTTGTCTGCATCCCTGGGCCTGTGAATGATGA
CAGCACCTGACATTCTGCACCAGCTACCTCTGCCTCCATGGCAGAGAAAAGGCCATAAGAACAGTGGAAG
AGGAGCATGGACTCAGACTTCAAGGAAGAAGCCATTTCCCCAGGTCCTTCCTTCTGCATCTCACCACCCC
TAGTTACAAATAACTCCATTGAACAGCATCTATTCAGAAACTATGCCGAATAAAAAGATTGGTGGAAGGG
CTCATGTGGTTAGCAACTATGAAACAGAAATAGGACACTCAGTTACAAACATTATCTCCTTTAGTTTTTC
AGAAAATGCATCCCTGATTTCATTCATTTCCAGCTTGAAAGCCAGCCATATTACTCTAGTCCCTACCAAA
CTGCTCTAGAAGGTCATTTCCATTTTGTTTGTGATATTTAGACGCGCAGACTTCAGGAAGTTCACCTTTA
ACTTCAGCATTCCAGATGAAGTTTCCTGACTCAGTGCTTTTGCATAAGGAACTAGAAAAAAAAAAGTAAGG
AAAATTGGAGATGCTAACATCCTCCCCCATCCCAACTGCACCTTAAAATATGCATGTCACCTTCAAGGTT
TTATAATTGCACTGTTTGTTTTATGTATGTACAGATTAAAATTATTGCTACATTTGAGGAAAATAAAATT
GCTTGCTTCTATGTAATTCCTGTCATTCCACAGGAAATTCACTTTTCCAGCTACTGAATAGAATTTGTTT
AACAACCTCATGGGTTGCCTCTTCATTTACAGGGAAGAAATGAAATGTACATCTGCAGAAATTGCCAAAG
CCCAAATTAACGAGTATTATAAAAGGATAATAAAGCATCCCTGAAGCCAAA

Fig. 25 cont'd

(SEQ ID NO:95) NM_001123376.3 Homo sapiens transmembrane protein 72 (TMEM72), transcript variant 1, mRNA
GAGCCCTATTCACACCTCGGCCAGGCTGCGGTGGCCAGGACTGGTTTGGGAAGGCAGGGCCCCGGTGTGC
AGCCACAGCCAGCAGCCTCCTACCTACACAAGGGTGTTCGGGAGCATCTCAGGGCCGAAGACTTTGCTGC
CTGCCCTGCCAGGACTTTGTCCTCACCCCTGGCACCATGCAGCTCCAGGTGTTCTGGACTGGGCTGGAAT
ACACCTGCCGGCTCCTGGGCATCACCACTGCTGCAGTGTTGATCGGCGTGGGCACTGAGACCTTCCTCCA
GGGCCAGTTCAAAAGCCTGGCTTTCTATCTGCTGTTTACAGGAGCCGCTGTCTCCATATGTGAAGGGGCC
TACTTTGTGGCTCAGCTGCTGGCCATCTGCTTCCAGTGTCAACCAGGGTCCCTGGCAGACAGAGTAAGGG
AGAAAGCCCACTGGCTGGGCTGCTTCCAGAAGTTCCTGGCCTACCTGCTGCTGTCGGTGGCCTGCTTCCT
CCACCCGGTCCTGGTCTGGCACGTGACCATCCCAGGCTCCATGCTCATCATCACCGGCCTGGCCTACTTC
CTTCTGAGCAAGCGGAAGAAGAGGAAAGCTGCCCCCGAGGTGCTGGCCTCCCCAGAGCAGTACACAGACC
CCTCTAGCAGCGCTGTGAGCACCACCGGCTCTGGGGACACAGAGCAAACCTACACTTTCCATGGGGCCCT
CAAGGAGGGGCCCAGCTCCCTTTTCATCCACATGAAGAGTATCCTGAAGGGGACTAAGAAGCCCAGTGCC
CTCCAGCCCCCCAACACCCTGATGGAGCTGAGCCTGGAGCCAGCCGACTCCCTGGCCAAGAAGAAGCAGG
TGCACTTTGAAGACAACTTGGTCCGCATAGTCCCCTCCCTCGCCGAAGGTCTGGATGATGGGGACAGTGA
GCCAGAGGAGACCACCTCTGACACGACACCCATCATTCCCCCTCCCCAGGCCCCACTCTTCCTGTCATCT
CTTACAGCCACCGGCCTGTTCTGAGCGCTTGCTCCAGCCTGGAGGACGCTCAGTGAGGGGTCTACCTAGC
TCAATGGCCCTCCCTGGAGTTTCAGGGTCTTCTCTGGTCAGCTTTTCAAGGGGTAACCAGACACCCCCAC
ACTGGCTGGGCCCCTGAGGCCATCAGGAGGTGTGACTGGCCAGCATTTCTGGAGAGGCCTCGAGGGAGGC
ACAAACAAGGCTCACGCCACCTCAAGCCAGCACAAGCTCCTTCCTCCTGGCCACAGGTGGGGAAACCCTT
ATGCTTCCCCAACAAGACCATCACTGCCACTGCGCACGAGGCTGCAGGTGCCATTGACTCAGCCCAGAAG
GGACAGAGGATGTCTGCCCAGCAAAAGCCTCTGGGCTTTTCTTACTCCCAACCCAGGGCACAACACTCAG
TGAGGAACCTATGGTCCACCCATCTCTGCAGGCCCAGGGAAGTGTCAGTAACTTAAGCATCTCTAAGGCA
GAGAAGGTGGCTGTGGGTCTTGACCAACCAAGACTGCTCAGGGTCGGGAGGGGAGGCTGCAGGCCTCTGG
TGGGAGCAGCCGGGCCGTGGGCCACATTCTCTGCATGCTCTAGGGCTGGGGCTGAGCTGCTCAGGAAAAC
AATGCCGCTCTGTGCTCACTGTGGGAAAGCCAGGCCAGATGAGCAAAGCTCATTCCAGAAACATGGCTGG
GGACTTCCAGCCTCCTTACCACATGGCCTTTCCAAGATTCCAGGTTGATGATGCAAACTGAACGCAGTGA
ATGCCAGGGCCCAGAAGGCAATGTCTGCTGTGGGCAGGACCACAGAGGCTGCCCAGGGGTGGCACAGCAC
AGAGAAGTGTCAGTGCCGTGTTTAGGCACTTGGTAGCAGAATAGGTGATAAATATAAATGTCTTCAAAAT
GAAAGGAAGTGAGGGGGGAAGAAGAGGAGGGAAAATGGGAGGATAGGAGGAAGTGGGCAGGCAGGCAAGT
TCTCTGCCATGGGGCCACGGAAGTGACAGTTAACCCAGAAGGAACAAAGACATCTGAATCAGATATTCCT
TTGTAAATCTGTAAAGGATTTGCAATATAGGCTTTACTTCTAAAAATTGTTGTCGGGTCCATGAGGCTGT
TGCCAGGAAGAGCACACACACCATTCTTCATGGCAACTGCAGTGAGGGAGCAGTCAGGAGGAAGAGTCCT
GTGGCTTCTCAGTCCCTGTGGAGGCTAACGCAAAGCTCTGTAGAACAAGCCTTAGAGTGCATGCTCTATG
GTCTAATGAGAAACTTGTGTTTGTGCTTGCACACGTTTCAATGTTCCCTACAGGATATTTTACAAAGGTA
TGAAAATAATGGCCAACCAGAAGCTAGTATCAGTTTGGGGCCTAAATGCAGCAGGTGTTCCTGATAAGCA
GATAAGCAGAGCTCTTCCTGCAGTAGCCCAGGTCTCACCAAATGACAAATGGCTAATCAAGACACTCCTG
CAAGCCCTTGATGGTGAGAGCTGCAGAGCTGTTTCTTCAGCTGCCATCAAGGCAGGACCTCAGGACCTGA
CTGTCTACAGTCAGGGAATAGTGAACAATATGGGATATGGGTATAGGTAGGTGGTAGACAAGGATCGTGC
CCCATGGCTGATGGGCCGGGTGTCTCAGGCAGGCCCCCTGTGCACAGAAAGAGCCTAAGTGCAGAGAAGC
CAGGCATCTTTCCCCTGTCAACTGTGGAAGGGGAATGTGATGGCCACAGACACCCTCATGGCACAGACAT
GGCCAGCCTCTGACGTTCCTCTGCATCAGAGTAGTTCTGTCCTCGAAGCCCCAGTCAGCAGAGCTGGATG
ACCAGATCGCAAGAAGCAAACCAGAAAGTGTGATGGCAGAGATGTCAGATCCCGTTTAATAAACACTTCA
GTAAACCCAA

Fig. 25 cont'd

(SEQ ID NO:96) NM_014228.5 Homo sapiens solute carrier family 6 member 7 (SLC6A7), mRNA

GTCAGCTGTCTGTCTGGGTGTCTATGCGGGCGCAGCAGTGCACCCTTCCCCAGCCTCGGGCGCTGCGCAG
GGACAGACAAGGCATTCGCAGCGCCCTGCCCGCGCTCCACGCCCGCAGCCGCCAGACGGCAGCGCCTGCG
TCCGTGCCCGCCCCAGCCGGTGCGCGGGAGCCGCGGGGGCAAAGGCGCAGTGGCCAGCGGACCATCTCTC
GTGCCCTCGCTCTCTGCGCTCCGGGGCAGCTGAGCCCCGGCCACCCGCTCTCCAAGATGAAGAAGCTCCA
GGGAGCTCACCTCCGCAAGCCTGTCACCCCAGACCTGCTGATGACCCCCAGTGACCAGGGCGATGTCGAC
CTGGATGTGGACTTTGCTGCACACCGGGGGAACTGGACAGGCAAGCTGGACTTCCTGCTGTCCTGCATTG
GCTACTGTGTAGGCCTGGGGAATGTCTGGCGCTTCCCCTATCGAGCGTACACCAATGGAGGAGGCGCCTT
CCTCGTGCCCTACTTCCTCATGCTGGCCATCTGTGGCATCCCCCTCTTCTTCCTGGAGCTCTCCCTGGGC
CAGTTCTCCAGCCTAGGGCCCCTGGCTGTCTGGAAAATCAGCCCTCTCTTCAAAGGCGCCGGCGCAGCCA
TGCTGCTCATCGTGGGCTTGGTGGCCATCTACTACAACATGATCATCGCCTACGTGCTCTTCTACCTCTT
CGCCTCCCTCACCAGCGACCTACCCTGGGAGCACTGTGGCAACTGGTGGAACACAGAACTCTGCCTGGAG
CACAGAGTCTCCAAGGACGGCAACGGGGCCCTGCCCCTCAACCTCACCTGCACCGTCAGCCCCAGCGAGG
AGTACTGGAGCCGCTACGTCCTCCACATCCAAGGCAGCCAGGGCATCGGCAGCCCTGGGGAGATCCGCTG
GAACCTCTGCCTCTGCCTGCTGCTGGCCTGGGTCATCGTGTTCCTCTGTATCCTCAAGGGTGTGAAGTCT
TCGGGCAAGGTGGTGTATTTCACGGCCACGTTCCCCTACCTCATCCTGCTCATGCTGCTGGTCCGCGGAG
TCACCCTCCCAGGGGCCTGGAAGGGCATCCAGTTCTATCTCACCCCCCAGTTCCACCACTTGTTGTCTTC
CAAGGTGTGGATTGAAGCTGCTCTTCAGATCTTCTATTCCCTGGGTGTGGGCTTCGGGGGGCTCCTCACC
TTTGCCTCCTACAACACGTTTCACCAGAACATCTATAGAGACACTTTCATCGTCACTCTGGGCAACGCCA
TCACCAGCATCCTGGCTGGCTTTGCCATCTTCTCCGTGCTGGGCTACATGTCTCAGGAGCTGGGCGTGCC
TGTGGACCAAGTAGCCAAAGCAGGCCCTGGCCTGGCCTTTGTCGTCTACCCACAGGCCATGACCATGCTG
CCTCTGTCACCCTTCTGGTCCTTTCTCTTCTTCTTCATGCTTCTGACTCTCGGCCTAGATAGCCAGTTTG
CTTTTCTGGAGACCATTGTGACAGCTGTGACAGATGAGTTCCCATACTACCTGCGGCCCAAGAAGGCGGT
GTTCTCAGGGCTCATCTGCGTGGCCATGTACCTGATGGGGCTGATCCTCACCACTGATGGGGGCATGTAC
TGGCTGGTCCTTCTGGATGACTACAGCGCCAGCTTCGGGCTGATGGTGGTGGTTATCACCACGTGCCTTG
CCGTGACACGGGTGTATGGCATTCAGAGGTTCTGCCGAGACATCCACATGATGCTGGGCTTCAAGCCGGG
CCTCTACTTCAGGGCCTGCTGGCTGTTCCTGTCCCCAGCCACGCTCTTGGCCCTCATGGTGTATAGCATC
GTCAAGTACCAGCCCTCGGAGTATGGCAGTTACCGCTTCCCGCCCTGGGCTGAGCTGCTGGGCATCCTGA
TGGGCCTGCTGTCCTGCCTCATGATCCCAGCTGGCATGCTGGTGGCTGTGCTTCGAGAAGAGGGCTCACT
CTGGGAGCGGCTCCAACAGGCCAGCCGGCCGGCCATGGACTGGGGACCATCGCTGGAGGAGAACCGGACG
GGCATGTATGTGGCCACGCTGGCTGGGAGCCAGTCACCAAAGCCACTGATGGTGCACATGCGCAAGTACG
GGGGCATCACCAGCTTCGAGAACACGGCCATCGAGGTGGACCGTGAGATTGCAGAGGAGGAGGAGTCGAT
GATGTGAGGCAGGAGGCAGGCGGGCAGAAGGCCCTGCCCGGGACCTCACAGTCCCTTCTTAGAAGCCTGC
AAAGGTCAGCTGTGCCCTCTGGGATTCTGAGAGGCTATGGGGGGGCCTGCCATAGGGATGCCAGTCCCCC
AGTGGGGGTCCCTTCTGCAGCCTCTGCCTCTCCTGAAACCTCTGACAACCCCCTACACACACACACAGGC
ATACTCAGACCCACTCAAAGCTGAGAATGATCCAACTCAGCCCTACTTTGCGGATGGACATATTAAGGCC
AGGAGGGGAGGGACTTGCCCCAGGTCGCATGGCAGAGGGGACTTGAACCCACGCCTCCTGACCAGCCAGC
TCCCTTTCCCATGGGGCAGCCGGCACCACCTTCTCATCTCTATTCAGGGCCTACACCCCTCCCTTTTTGG
GGGGAGCCTGTCCCCACACACCTTAGCACAACCAGAATCTTGAGTTGGGCAGGGAAGGTCAGGGCTACAG
AGGCTCTTGAGGCTCCGAGGCCCTGGGGATCAAAGGTCAATGAGTTAGGTGGGGAGAAAGATCCCTGGGG
GCTCCTGTATGCAGGACTCCTGAAGGAGGTGGGAGCTGAGGGCCCTGGAGGATGGGGAAGGTTTGCAGAG
AGAGGAAGAAGAGGGCAGGGTGGGGAGGAGCTCTGGGCCAGAGGATGCTGAGCTGCCTGGGCAGAGACCA
AGAGGGTTGGAGACACTAGTTTTACCAGGTTACAGGAGGGTTCAAGACAGAAGGAAAACTAACAGAGGGG
GAGCCAGGGATGATGGGGTGGGCAGGGGATTTGCATGATGAGGAGTATCATTCCAGATCTGTGCAGAGCG
GATCGGACGGGACAGGGTGGAGCGGGGAGGCCTGTGCAAAGTGGGAAAGAGCTGCCGGTGGCCTGAGCCA
GGGTGCTGGGGCTGCGGGTGGGGAAAGGAGGCCCCAGCACTTCAGACAAAGACCACCCCTTCACCCACTG
GACCCCAAGCCGCAAAAGCTGGGGAGGTAGGAAGGGTCACTGTGAGGGCCCAGGGCCCCTCTCTTCCCAT
CTCCCTTGTCCTGGTGGCCTTCAGTGTCTCTTCCAGTTCCAGGAGCTGCTGGGAAGCTGGCCTTCATTGT
TGGTGACAGGGCAACCATGGGACTAGGAGGTGGCCCATACACATGGCTGGCTGGTCCTGAGGCCACCCAC
CTTGTTCCAGGACATGGGCCCGGGCCCGGTGTGGGGGTAGACGCAGAGGGCAGAGGGTAGCCCTTGGTAC
TGTGGGTCCCTCAAAGAGGAGAGTGGGGTGCAGAAATGCCTCAGCATGGCTCATGCACACAGCATTCTCC
CGTGGGGCAGGGTTCCCTCATGCAACAGGCCTCCCTGTGGCCAGCCTCTCTGCCTGTCTCTCGCTGCGTC
CCCCCAACCCCTTGTGTTCTATTGGTTCATTGTTAATAAATATCAAATGAGGTCA

Fig. 25 cont'd

(SEQ ID NO:97) NM_003551.3 Homo sapiens NME/NM23 family member 5 (NME5), mRNA
ACGCTGGGGCTTCAGGTCTCCTAGCAACAAGTTGTACCATATGAGGACGGCCGCTGAGCCATAATGGAGA
TATCAATGCCTCCACCTCAGATATATGTAGAAAAAACTCTGGCCATTATCAAACCAGATATTGTTGACAA
AGAGGAGGAGATACAAGATATTATTCTTAGATCCGGATTCACCATTGTTCAGAGAAGAAAACTACGCCTC
AGCCCTGAGCAATGTAGTAACTTTTATGTGGAAAAGTATGGAAAAATGTTTTTCCCCAACTTAACAGCTT
ACATGAGTTCTGGACCACTTGTCGCCATGATATTAGCTAGACATAAAGCCATCTCTTATTGGTTAGAACT
TTTGGGACCAAATAATAGCTTAGTAGCGAAGGAGACACATCCAGACAGTCTGAGGGCAATTTATGGCACA
GATGACCTAAGGAATGCACTTCATGGGAGTAATGACTTTGCTGCTGCGGAAAGAGAAATACGTTTTATGT
TTCCTGAAGTGATTGTTGAGCCCATTCCAATTGGACAAGCTGCTAAGGACTATTTAAATTTACATATAAT
GCCAACTCTGCTTGAAGGACTCACAGAGCTTTGTAAGCAAAAACCAGCAGATCCTTTGATTTGGCTAGCT
GATTGGCTGCTGAAAAATAATCCTAACAAACCCAAACTTTGTCACCATCCAATTGTAGAAGAACCTTATT
AAAAAAAAAATCCTCGAAAGAACAAATCATGAACTATCTTATTATAAAAGGCTGTACTTCTACTGTTTGA
AAAAATTATTTCTAGGGTTTAAGTAACTACAAGTAAAATAAATTTATTTCTTAAAAATAAGTGTTAAAGG
AATAACTATTCTATGAAGCAGATAACATTAAGGTAAAATATAGGCTTAGAGTATGATTTTAACAATGATG
TAACACTAGGTAATGGAAAACTCATGTAAGATGTTGCTAGATGTTTTTGTTTTTCTTAAGTTTGAGAAGT
AAGACATAAAGTTTAGTTATACATTTTCCCAAGCACATATCCTATATCTAAATACATAATTAATGCACAG
TTGAGACAGTCTAGTTTAAAAGGCTTAGGTCCTTTTGTAGTCCATAAGCATGGTGATTTGGTTTCATGCT
CATGTGTCAGATATGCTTCCCTCAAACCTTGTTACAGCATCATCACATTACCTGTTTGATGTAAAAAATA
AAAAATAGAAAGGTGTAA

(SEQ ID NO:98) NM_016541.3 Homo sapiens G protein subunit gamma 13 (GNG13), mRNA
ACTTGGCCCTCGCTCTCACTCGCGGTCGCCTGGCCGTTGTCATTGTCCCTCCGCTGTCACCTTTTCAAGC
CCCAGGCTGGCTGCTTCAGAAGCCCCTGACCCCATGGAGGAGTGGGACGTGCCACAGATGAAGAAAGAGG
TGGAGAGCCTCAAGTACCAGCTGGCCTTCCAGCGGGAGATGGCGTCCAAGACCATCCCCGAGCTGCTGAA
GTGGATCGAGGACGGGATCCCCAAGGACCCCTTCCTGAACCCCGACCTGATGAAGAACAACCCATGGGTG
GAAAAGGGCAAATGCACCATCCTGTGAGCCCCGCACCCGGCCCCTCTCACACCATCCTGTGAGACCACGC
CCGGCCCCACTCCCACCATCTTGTAAGACTGTGCCCAGCCCCACTCACTCCATCCTGTGAGTCCCACTCC
CAGCCCCACTCCCACCATCCTGTGAGCCCATGCCCGGCCCCACTCACACCAACCTGTGAGCCCCACTCCC
GGCCCCACTCACTCCATCTTGTAAGACTATGCCCAGCCCCATTCACTCCATCCTGTGAGTCCCACTCCCA
GCCCCACTCCCACCATCCTGTGAGCCCCACTTCCAGCCCCACTCCCACCATCCTGTGAGCCCCACTCCCA
GCCCCACTCCCACCATCCTGTGAGCCCCACTCCCGGCCCCACTCACTCCATCCTGTGAGCCCCACTCCCA
GCCCCACTCACACCAACCTGTGAGCCCCACTCCCGGCCCCACTCACAACATCTTGTAAGACTGTGCCCGG
CCCCATTCACTCCATCCTGTGAGACCACGCCCGGCCCCACTCACTCTATCCTGTGAGACCACGCCTGGCC
CCACTCCCACCATCCTGTGAGCCCCACTCCTGGCCCCACTCACACCATCCTATGAGCCCACGCCCGGCCC
CACTCCCACCATCCTGTGAACCCCACTCCACTCGCACGTGATTACAGTCTGTAAAGGTGTGACTTTATAA
AGACA

(SEQ ID NO:99) NM_015311.3 Homo sapiens obscurin like cytoskeletal adaptor 1 (OBSL1), transcript variant 1, mRNA
AAGAGCAGGAAGCCAGGCAGCGGGCAGGGGAGGCTGCGGGGCCACTCGCTGGAGAGGCAAACAGGAAGGA
CTGCCCCCTGAGCGCCAGGCTTCGGGCCCGGGAATCGCCGCCGCCGCCGCCGCAGAGCTGCAGCTCGGGG
CCGAGGGTAAGGAGGCGAGCCGGGAGCGGGAGGCCCGGGAGAGCTCCGCGGGTCCCCGCGCCCAGTCCCC
AGCCGCGCCCCGACCCCGCCGCCCCGGGCCTCGGCTCGCCCTCCGCACCCCCCCCTGCCCCCCCACCGTT
CGCCGCTGCAGGCGGTCGGCCGCCGCGATGAAGGCGAGCTCGGGGGATCAGGGGAGCCCCCCGTGCTTCC
TGCGCTTCCCGCGGCCTGTGCGGGTGGTAAGTGGCGCCGAGGCCGAGCTCAAGTGCGTGGTCCTGGGGGA
GCCGCCGCCTGTAGTGGTGTGGGAGAAGGGCGGGCAGCAGCTGGCGGCCTCGGAACGCCTGAGCTTCCCG
GCGGACGGCGCGGAGCACGGCCTGCTGCTGACCGCCGCACTGCCCACCGACGCGGGGGTCTACGTGTGCC
GCGCCCGCAACGCGGCCGGCGAGGCCTACGCGGCGGCCGCCGTCACCGTGCTGGAGCCGCCGGCCTCCGA
CCCCGAGCTGCAGCCCGCCGAGCGCCCGCTGCCATCGCCGGGGTCCGGGGAGGGCGCCCCGGTCTTCCTC
ACGGGGCCTCGATCCCAGTGGGTGCTGCGGGGGGCGGAGGTGGTGCTGACGTGCCGGGCGGGGGGCCTCC
CCGAGCCCACACTGTACTGGGAGAAGGACGGGATGGCCCTGGACGAAGTGTGGGACAGCAGCCACTTCGC
GCTCCAGCCGGGCCGCGCCGAGGACGGCCCCGGCGCGAGCCTGGCACTGCGCATCCTGGCGGCTCGGCTG
CCGGATTCCGGCGTCTACGTGTGCCACGCCCGCAACGCGCACGGCCACGCGCAGGCGGGGGCGCTGCTCC
AGGTGCACCAGCCCCCCGAGAGCCCGCCCGCGGACCCCGACGAGGCCCCCGCGCCGGTGGTGGAGCCGCT
CAAGTGCGCGCCTAAGACCTTCTGGGTGAACGAGGGCAAGCACGCCAAGTTCCGCTGCTACGTGATGGGC
AAGCCCGAGCCCGAGATCGAATGGCACTGGGAGGGCCGCCCGCTGCTCCCGGACCGCCGCCGCCTCATGT
ACCGCGACCGCGACGGCGGCTTCGTGCTCAAGGTGCTTTACTGCCAGGCCAAGGATCGTGGGCTCTACGT
CTGCGCCGCGCGCAACTCGGCGGGCCAGACGCTCAGTGCCGTGCAGCTGCACGTGAAAGAGCCCCGCCTC

Fig. 25 cont'd

(SEQ ID NO:99) cont'd

CGGTTCACACGGCCCCTGCAGGACGTGGAGGGCCGTGAGCACGGGATTGCCGTGCTGGAATGTAAAGTAC
CCAACTCCCGCATCCCCACGGCCTGGTTCCGTGAGGACCAGCGGCTGCTGCCCTGCCGCAAGTACGAGCA
GATCGAAGAGGGCACTGTCCGGCGCCTCATCATCCACAGGCTGAAGGCAGACGATGATGGTATCTACCTG
TGCGAGATGCGGGGCCGGGTGCGCACCGTGGCCAACGTCACAGTCAAAGGGCCCATCCTGAAGCGCCTGC
CCCGGAAGCTCGACGTCCTGGAAGGAGAGAATGCTGTGCTGCTAGTGGAAACTCTAGAGGCCGGGGTCGA
GGGACGCTGGAGCCGTGATGGGGAGGAGCTGCCGGTCATCTGCCAGAGCAGCTCAGGCCACATGCATGCC
CTGGTCCTTCCAGGGGTCACCCGAGAGGATGCTGGCGAGGTCACCTTTAGCCTGGGCAACTCCCGTACCA
CTACGCTTCTCAGAGTAAAATGTGTCAAGCACAGTCCCCCAGGACCCCCCATATTGGCAGAGATGTTCAA
GGGCCACAAGAACACGGTCCTGTTGACCTGGAAGCCTCCCGAGCCAGCTCCCGAGACCCCATTCATCTAC
CGGCTGGAGCGGCAGGAAGTGGGCTCTGAAGACTGGATTCAGTGCTTCAGCATCGAGAAAGCCGGAGCCG
TGGAGGTGCCGGGCGACTGTGTGCCCTCCGAGGGTGACTACCGCTTCCGCATCTGCACAGTCAGCGGACA
TGGCCGTAGTCCCCACGTGGTGTTCCACGGTTCTGCTCACCTTGTGCCCACAGCTCGCCTGGTGGCAGGT
CTGGAGGATGTGCAGGTATACGACGGGGAAGATGCCGTCTTCTCCCTCGATCTCTCCACCATCATCCAGG
GTACCTGGTTCCTTAATGGGGAAGAGCTCAAGAGTAACGAGCCGGAGGGCCAGGTGGAACCTGGGGCCCT
GCGGTACCGTATAGAGCAGAAGGGTCTGCAGCACAGACTCATCCTGCATGCCGTCAAGCACCAGGACAGC
GGTGCCCTGGTCGGCTTCAGCTGCCCCGGCGTGCAGGACTCAGCTGCCCTCACAATCCAAGAGAGCCCGG
TGCACATCCTGAGCCCCCAGGACAGGGTGTCGTTGACCTTCACAACCTCAGAGCGGGTGGTGCTGACTTG
TGAGCTCTCAAGGGTGGACTTCCCGGCAACCTGGTACAAGGATGGGCAGAAGGTGGAGGAGAGCGAGTTG
CTGGTGGTGAAGATGGATGGGCGCAAACACCGTCTGATCCTGCCTGAGGCCAAAGTCCAGGACAGTGGCG
AGTTTGAGTGCAGGACAGAAGGGGTCTCGGCCTTCTTCGGCGTCACTGTCCAAGATCCTCCCGTGCACAT
CGTGGACCCCCGAGAACATGTGTTCGTGCATGCCATAACTTCCGAGTGTGTCATGCTGGCCTGTGAGGTG
GACCGAGAGGACGCCCCTGTGCGTTGGTACAAGGACGGGCAGGAGGTGGAGGAGAGTGACTTCGTGGTGC
TGGAGAATGAGGGGCCCCATCGCCGCCTGGTGCTGCCCGCCACCCAGCCCTCAGACGGGGGCGAGTTTCA
GTGCGTCGCTGGAGATGAGTGTGCCTACTTCACTGTCACCATCACAGACGTCTCCTCGTGGATCGTGTAT
CCCAGCGGCAAGGTGTATGTGGCAGCCGTGCGCCTGGAGCGTGTGGTGCTGACCTGTGAGCTATGCCGGC
CCTGGGCAGAGGTGCGCTGGACCAAGGATGGAGAGGAGGTGGTGGAGAGCCCCGCGCTGCTCCTGCAGAA
GGAAGACACTGTCCGCCGCCTGGTGCTGCCCGCTGTCCAGCTCGAGGACTCCGGCGAGTACTTGTGTGAA
ATTGACGATGAGTCGGCCTCCTTCACTGTCACCGTCACAGAACCCCCAGTGCGGATCATATACCCTCGCG
ATGAGGTGACCTTGATCGCCGTGACCTTGGAGTGTGTGGTGCTGATGTGTGAACTGTCTCGGGAGGATGC
CCCTGTGCGCTGGTACAAGGATGGGCTGGAAGTGGAGGAGAGCGAGGCCCTGGTGCTGGAGAGGGATGGG
CCACGCTGCCGCCTGGTGCTACCTGCTGCTCAGCCCGAGGACGGGGGCGAGTTTGTATGTGATGCTGGAG
ATGACTCGGCCTTCTTCACTGTCACTGTCACAGCCCCACCAGAGAGGATTGTGCACCCGGCAGCCCGCTC
CCTGGATCTGCATTTTGGGGCTCCAGGGCGCGTGGAGCTGCGCTGTGAGGTGGCCCCAGCTGGGTCTCAG
GTGCGCTGGTACAAGGACGGGCTGGAAGTGGAGGCATCAGATGCCCTGCAGCTGGGTGCCGAGGGGCCCA
CCCGCACCCTGACCCTGCCCCACGCCCAGCCTGAGGACGCCGGGGAGTATGTGTGTGAGACCCGGCATGA
GGCCATCACCTTCAATGTCATCCTGGCTGAGCCTCCAGTGCAGTTCCTTGCTCTAGAGACAACTCCAAGC
CCGCTCTGTGTGGCCCCTGGGGAGCCAGTGGTGCTGAGCTGTGAACTGTCCCGGGCTGGCGCCCCCGTGG
TCTGGAGCCACAATGGGAGGCCCGTGCAGGAGGGCGAGGGCCTAGAGCTCCATGCCGAGGGCCCCCGCCG
AGTCCTCTGCATCCAGGCTGCAGGCCCAGCCCATGCAGGGCTCTACACCTGCCAGTCTGGAGCAGCCCCC
GGAGCCCCAAGCCTCAGCTTCACCGTCCAGGTGGCTGAGCCCCCTGTGCGGGTGGTAGCTCCCGAGGCAG
CCCAGACGAGGGTTCGGAGCACCCCAGGCGGGGACCTAGAGCTGGTGGTGCACCTCTCCGGGCCAGGGGG
CCCTGTACGCTGGTACAAGGACGGGGAGCGACTGGCAAGCCAGGGGCGGGTGCAGCTGGAGCAGGCCGGG
GCCAGGCAGGTGCTGCGGGTGCAGGGGGCACGGAGCGGGGACGCTGGGGAGTACCTGTGCGATGCGCCCC
AGGACAGCCGCATCTTCCTTGTCAGCGTGGAAGAGCCACTGCTGGTGAAGCTGGTCTCGGAGCTGACACC
ACTCACTGTCCACGAGGGCGATGATGCCACGTTCCGGTGTGAAGTCTCCCCACCAGATGCCGATGTCACC
TGGCTGCGCAATGGGGCCGTCGTCACTCCAGGGCCCCAGGTGGAGATGGCCCAGAATGGTTCAAGCCGCA
TCTTAACCTTGCGAGGCTGCCAACTGGGGGATGCAGGGACCGTGACTTTGCGGGCAGGGAGCACGGCCAC
AAGTGCCCGGCTCCATGTTCGAGAGACAGAGCTGCTGTTCCTACGGCGGTTGCAGGATGTGCGGGCAGAG
GAAGGCCAGGATGTGTGTCTCGAAGTGGAGACAGGCCGAGTGGGTGCAGCGGGGGCCGTGCGCTGGGTGC
GAGGTGGGCAGCCCCTGCCCCACGACTCTCGCCTGTCCATGGCCCAGGATGGGCACATCCACCGCCTCTT
CATCCATGGTGTCATACTGGCCGACCAGGGCACCTACGGCTGCGAGAGCCACCACGATCGCACCCTGGCC
AGGCTCAGCGTGAGGCCGAGGCAGCTGAGGGTGCTGCGGCCTCTGGAGGACGTGACCATCAGTGAGGGGG
GCAGTGCCACCTTCCAGCTGGAGCTGTCCCAGGAAGGTGTGACCGGGGAGTGGGCCCGGGGTGGAGTACA
GCTGTATCCAGGACCCAAGTGTCACATCCACTCGGACGGCCACCGTCACCGACTGGTACTCAATGGCCTG
GGCCTGGCCGACTCAGGCTGTGTCTCCTTCACAGCGGATTCCCTGCGCTGCGCAGCCAGACTCATTGTGA

Fig. 25 cont'd

(SEQ ID NO:99) cont'd

GAGAGGTCCCAGTGACCATCGTGCGGGGGCCACACGACCTAGAGGTGACCGAGGGCGACACAGCTACGTT
CGAGTGCGAGCTTTCCCAAGCTTTGGCTGATGTTACCTGGGAGAAGGACGGGAACGCGCTTACGCCTAGC
CCGCGGCTCCGGCTCCAGGCCCTCGGCACGCGCCGCCTTCTCCAGCTGCGACGCTGCGGCCCCTCGGACG
CCGGGACCTACAGCTGCGCGGTGGGGACGGCCCGCGCCGGACCGGTCCGCCTGACCGTGCGCGAGCGTAC
TGTGGCGGTACTCTCCGAGCTGCGGTCGGTGAGCGCCCGCGAAGGCGACGGCGCTACGTTCGAGTGCACC
GTGTCGGAGGTCGAGACCACGGGGCGCTGGGAGCTCGGAGGCCGCCCGCTGAGACCCGGAGCCCGCGTCC
GCATCCGACAGGAAGGGAAGAAACACATTCTGGTGCTTAGCGAGCTGCGCGCCGAGGACGCCGGTGAAGT
CCGCTTCCAGGCGGGGCCCGCCCAGTCCCTGGCTCTACTGGAAGTGGAGGCATTGCCTCTCCAGATGTGC
CGCCACCCCCCTCGCGAGAAGACCGTTCTGGTGGGCCGCCGGGCGGTGCTGGAGGTGACTGTGTCCCGCT
CGGGGGGCCACGTGTGCTGGCTGCGGGAGGGGGCCGAGCTGTGCCCGGGAGATAAGTATGAGATGCGCAG
CCACGGCCCCACCCACAGCCTGGTCATCCATGACGTTCGACCTGAGGACCAAGGCACTTACTGCTGCCAG
GCCGGCCAGGACAGCACCCACACACGGCTGCTGGTAGAGGGCAACTAGGAGAACCTAACCAGGCCAGGCG
GGTGCCCTTGGACAGCTTGGAAGGCGTTTGCCCTTACCCTGGGCAGGGGTAGAGAGACAAGGAACAATAA
AAGTGCTACAGCTCA

(SEQ ID NO:100) NM_000613.3 Homo sapiens hemopexin (HPX), mRNA
GTCCTGTGGCCTCTGCAGCTCAGCATGGCTAGGGTACTGGGAGCACCCGTTGCACTGGGGTTGTGGAGCC
TATGCTGGTCTCTGGCCATTGCCACCCCTCTTCCTCCGACTAGTGCCCATGGGAATGTTGCTGAAGGCGA
GACCAAGCCAGACCCAGACGTGACTGAACGCTGCTCAGATGGCTGGAGCTTTGATGCTACCACCCTGGAT
GACAATGGAACCATGCTGTTTTTTAAAGGGGAGTTTGTGTGGAAGAGTCACAAATGGGACCGGGAGTTAA
TCTCAGAGAGATGGAAGAATTTCCCCAGCCCTGTGGATGCTGCATTCCGTCAAGGTCACAACAGTGTCTT
TCTGATCAAGGGGGACAAAGTCTGGGTATACCCTCCTGAAAAGAAGGAGAAAGGATACCCAAAGTTGCTC
CAAGATGAATTTCCTGGAATCCCATCCCCACTGGATGCAGCTGTGGAATGTCACCGTGGAGAATGTCAAG
CTGAAGGCGTCCTCTTCTTCCAAGGTGACCGCGAGTGGTTCTGGGACTTGGCTACGGGAACCATGAAGGA
GCGTTCCTGGCCAGCTGTTGGGAACTGCTCCTCTGCCCTGAGATGGCTGGGCCGCTACTACTGCTTCCAG
GGTAACCAATTCCTGCGCTTCGACCCTGTCAGGGGAGAGGTGCCTCCCAGGTACCCGCGGGATGTCCGAG
ACTACTTCATGCCCTGCCCTGGCAGAGGCCATGGACACAGGAATGGGACTGGCCATGGGAACAGTACCCA
CCATGGCCCTGAGTATATGCGCTGTAGCCCACATCTAGTCTTGTCTGCACTGACGTCTGACAACCATGGT
GCCACCTATGCCTTCAGTGGGACCCACTACTGGCGTCTGGACACCAGCCGGGATGGCTGGCATAGCTGGC
CCATTGCTCATCAGTGGCCCCAGGGTCCTTCAGCAGTGGATGCTGCCTTTTCCTGGGAAGAAAAACTCTA
TCTGGTCCAGGGCACCCAGGTATATGTCTTCCTGACAAAGGGAGGCTATACCCTAGTAAGCGGTTATCCG
AAGCGGCTGGAGAAGGAAGTCGGGACCCCTCATGGGATTATCCTGGACTCTGTGGATGCGGCCTTTATCT
GCCCTGGGTCTTCTCGGCTCCATATCATGGCAGGACGGCGGCTGTGGTGGCTGGACCTGAAGTCAGGAGC
CCAAGCCACGTGGACAGAGCTTCCTTGGCCCCATGAGAAGGTAGACGGAGCCTTGTGTATGGAAAAGTCC
CTTGGCCCTAACTCATGTTCCGCCAATGGTCCCGGCTTGTACCTCATCCATGGTCCCAATTTGTACTGCT
ACAGTGATGTGGAGAAACTGAATGCAGCCAAGGCCCTTCCGCAACCCCAGAATGTGACCAGTCTCCTGGG
CTGCACTCACTGAGGGGCCTTCTGACATGAGTCTGGCCTGGCCCCACCTCCTAGTTCCTCATAATAAAGA
CAGATTGCTTCTTCGCTTCTCACTGAGGGGCCTTCTGACATGAGTCTGGCCTGGCCCCACCTCCCCAGTT
TCTCATAATAAAGACAGATTGCTTCTTCACTTGAA

Fig. 25 cont'd

(SEQ ID NO:101) NM_002489.4 Homo sapiens NDUFA4 mitochondrial complex associated (NDUFA4), mRNA
GGAAGTCCGTAGTGTCTCATTGCAGATAATTTTTAGCTTAGGGCCTGGTGGCTAGGTCGGTTCTCTCCTT
TCCAGTCGGAGACCTCTGCCGCAAACATGCTCCGCCAGATCATCGGTCAGGCCAAGAAGCATCCGAGCTT
GATCCCCCTCTTTGTATTTATTGGAACTGGAGCTACTGGAGCAACACTGTATCTCTTGCGTCTGGCATTG
TTCAATCCAGATGTTTGTTGGGACAGAAATAACCCAGAGCCCTGGAACAAACTGGGTCCCAATGATCAAT
ACAAGTTCTACTCAGTGAATGTGGATTACAGCAAGCTGAAGAAGGAACGTCCAGATTTCTAAATGAAATG
TTTCACTATAACGCTGCTTTAGAATGAAGGTCTTCCAGAAGCCACATCCGCACAATTTTCCACTTAACCA
GGAAATATTTCTCCTCTAAATGCATGAAATCATGTTGGAGATCTCTATTGTAATCTCTATTGGAGATTAC
AATGATTAAATCAATAAATAACTGAAACTTGATATGTGTCACTTTTTTATGCTGAAAGTATGCTCTGAAC
TTTAGAGTATAGGAAATTAACTATTAGAATTTAAAGAATTTCTTGAATTTCTGTAGTTTGAAAATACGAC
TTTAAGCTGCTTTAGTAAAACACTTCCATTTTGTGTATAGACTGTTGGTAACTTCACTAGAGCATACATA
ACAACTGGAACTGGAAATTATACAAAAGTAAATTGGGAAGGATACTCCAGCATCTGACACTGGCAAAATG
GAAACCTTTGAGTTTCTCTTACTGGCTGTTGAAGTGTGTGCAGTTTTTAACAATGGTTTTTACTTGGCAT
CTCTTTGTTGTGATTTTCAAGGTTATAAGTTGCTTTGGTCCTAGGATTGAAGTTGAAATCTGAGTTTATC
AGTGCTAACCATGGTGCTAGTAGTCAAGAGATCTTGAGAATTTTGGCTGCTGAGTCTTGGTGCAGGGTGC
AGGTTTTCTTTTCTTTTTTCTTTTTTTTTTTTTTGAGATAGTCTCTGTCACCCAGGCTGGAGTGCAGTGG
TACAAACATGGATCACTGCAGCCTCTACCTCCCGGGCTTAAGTGATCCTCCTGCCTCAGCCCCTAAGTAG
CCGGGACTACAGGTATGTGCCACCATGCCCAGTTAATTTTTGTAATTTTTTTTAGAGACAGGGTTTTGCC
ATGTTGCCCAGGCTGGTCTCAAACTCTTGAGCTCAAGCGATCCATTCTCCTCAGCCTCCCAGGGTGCTGG
GATTACAGGCGTGAGCCATTGCGCTTAGCCATGGTGCAGGTTTTCAAAGGCCAGGAAGTATATTCATAAT
TTTAAGATGGGGAATATAGCAAGTTTTCACATAGGTGTGTGTAAGTCATCACATCATAGAAACTTGAGGA
ATTCAGTGACATTAATTTTGGATTTTCATACGTAAGTATACAATTAAATGTTTACAGGGTAGTAGAAGCA
CATTTTAAATGTCAGGAACTGAACTAAGTATTTGAATTACGTGGATTATCTCAAAAATTTTGAAATTGTT
AAACGAGTTGAATTACTTGAATTCATTCTGTTAGTCAAATGGTGGATATTTACACCCATGTAGTTTTGAA
TTTAGAGTGTGTAGAGTGTTTTCAGTTACCAGACTCCATGCTTTTACCTCCTATGTGTCAGGTATAATTT
GAACCTCTAAGAACAGGGTTTCTCAACCTTGCCACTGTTGACTATTTCTGAAAGACAGTTTGGTTTAGCA
GACCATCCCATGCGCTTTAGCTTGTTTAGTAGCTAACTTGGGCTCTGCCACTACAGACAAAAAGCACTCT
TTCCCTCCAATTCCCACAGGCTATGAGAAGAATGGAGACATTACCAAATGTCCATTGGTGGGCAAAATTG
CTTCATTCCTACCTCTGTTGAGAATTACTCTAGATCCTTTGGCACAAATTACCTCAAAGTTTAAAATTGT
GTAAACAAACAGTGTGTCATGTAATTGAAAAACATTAAGCAACTCCAAATAAATGCTACATTAAGAAATT
AGTAA

(SEQ ID NO:102) NM_012320.4 Homo sapiens phospholipase A2 group XV (PLA2G15), transcript variant 1, mRNA
GAGAGCCCAGAGAGCTGAACCTGCATCCCGGACCTGCGGCGACCGTCGTACACCATGGGCCTCCACCTCC
GCCCCTACCGTGTGGGGCTGCTCCCGGATGGCCTCCTGTTCCTCTTGCTGCTGCTAATGCTGCTCGCGGA
CCCAGCGCTCCCGGCCGGACGTCACCCCCCAGTGGTGCTGGTCCCTGGTGATTTGGGTAACCAACTGGAA
GCCAAGCTGGACAAGCCGACAGTGGTGCACTACCTCTGCTCCAAGAAGACCGAAAGCTACTTCACAATCT
GGCTGAACCTGGAACTGCTGCTGCCTGTCATCATTGACTGCTGGATTGACAATATCAGGCTGGTTTACAA
CAAAACATCCAGGGCCACCCAGTTTCCTGATGGTGTGGATGTACGTGTCCCTGGCTTTGGGAAGACCTTC
TCACTGGAGTTCCTGGACCCCAGCAAAAGCAGCGTGGGTTCCTATTTCCACACCATGGTGGAGAGCCTTG
TGGGCTGGGGCTACACACGGGGTGAGGATGTCCGAGGGGCTCCCTATGACTGGCGCCGAGCCCCAAATGA
AAACGGGCCCTACTTCCTGGCCCTCCGCGAGATGATCGAGGAGATGTACCAGCTGTATGGGGGCCCCGTG
GTGCTGGTTGCCCACAGTATGGGCAACATGTACACGCTCTACTTTCTGCAGCGGCAGCCGCAGGCCTGGA
AGGACAAGTATATCCGGGCCTTCGTGTCACTGGGTGCGCCCTGGGGGGGCGTGGCCAAGACCCTGCGCGT
CCTGGCTTCAGGAGACAACAACCGGATCCCAGTCATCGGGCCCCTGAAGATCCGGGAGCAGCAGCGGTCA
GCTGTCTCCACCAGCTGGCTGCTGCCCTACAACTACACATGGTCACCTGAGAAGGTGTTCGTGCAGACAC
CCACAATCAACTACACACTGCGGGACTACCGCAAGTTCTTCCAGGACATCGGCTTTGAAGATGGCTGGCT
CATGCGGCAGGACACAGAAGGGCTGGTGGAAGCCACGATGCCACCTGGCGTGCAGCTGCACTGCCTCTAT
GGTACTGGCGTCCCCACACCAGACTCCTTCTACTATGAGAGCTTCCCTGACCGTGACCCTAAAATCTGCT
TTGGTGACGGCGATGGTACTGTGAACTTGAAGAGTGCCCTGCAGTGCCAGGCCTGGCAGAGCCGCCAGGA

Fig. 25 cont'd

(SEQ ID NO:102) cont'd

GCACCAAGTGTTGCTGCAGGAGCTGCCAGGCAGCGAGCACATCGAGATGCTGGCCAACGCCACCACCCTG
GCCTATCTGAAACGTGTGCTCCTTGGGCCCTGACTCCTGTGCCACAGGACTCCTGTGGCTCGGCCGTGGA
CCTGCTGTTGGCCTCTGGGGCTGTCATGGCCCACGCGTTTTGCAAAGTTTGTGACTCACCATTCAAGGCC
CCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGCTGTTTGTTATCCTTTCTCTGTGGCAGTGAA
GAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAATGCTGCTGATGGTGGAACTGCT
GTGACCTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGCCCTGGTCCCAGTCCCTGCCTGGGGCCATGT
GTCCCCCCTATTCCTGTGGGCTTTTCATACTTGCCTACTGGGCCCTGGCCCCGCAGCCTTCCTATGAGGG
ATGTTACTGGGCTGTGGTCCTGTACCCAGAGGTCCCAGGGATCGGCTCCTGGCCCCTCGGGTGACCCTTC
CCACACACCAGCCACAGATAGGCCTGCCACTGGTCATGGGTAGCTAGAGCTGCTGGCTTCCCTGTGGCTT
AGCTGGTGGCCAGCCTGACTGGCTTCCTGGGCGAGCCTAGTAGCTCCTGCAGGCAGGGGCAGTTTGTTGC
GTTCTTCGTGGTTCCCAGGCCCTGGGACATCTCACTCCACTCCTACCTCCCTTACCACCAGGAGCATTCA
AGCTCTGGATTGGGCAGCAGATGTGCCCCCAGTCCCGCAGGCTGTGTTCCAGGGGCCCTGATTTCCTCGG
ATGTGCTATTGGCCCCAGGACTGAAGCTGCCTCCCTTCACCCTGGGACTGTGGTTCCAAGGATGAGAGCA
GGGGTTGGAGCCATGGCCTTCTGGGAACCTATGGAGAAAGGGAATCCAAGGAAGCAGCCAAGGCTGCTCG
CAGCTTCCCTGAGCTGCACCTCTTGCTAACCCCACCATCACACTGCCACCCTGCCCTAGGGTCTCACTAG
TACCAAGTGGGTCAGCACAGGGCTGAGGATGGGGCTCCTATCCACCCTGGCCAGCACCCAGCTTAGTGCT
GGGACTAGCCCAGAAACTTGAATGGGACCCTGAGAGAGCCCAGGGGTCCCCTGAGGCCCCCCTAGGGGCTT
TCTGTCTGCCCCAGGGTGCTCCATGGATCTCCCTGTGGCAGCAGGCATGGAGAGTCAGGGCTGCCTTCAT
GGCAGTAGGCTCTAAGTGGGTGACTGGCCACAGGCCGAGAAAAGGGTACAGCCTCTAGGTGGGGTTCCCA
AAGACGCCTTCACGCTGGACTGAGCTGCTCTCCCACAGGGTTTCTGTGCAGCTGGATTTTCTCTGTTGCA
TACATGCCTGGCATCTGTCTCCCCTTGTTCCTGAGTGGCCCCACATGGGGCTCTGAGCAGGCTGTATCTG
GATTCTGGCAATAAAAGTACTCTGGATGCTGTAA

(SEQ ID NO:103) NM_001318503.2 Homo sapiens dual specificity phosphatase 9 (DUSP9), transcript variant 1, mRNA
AAGGTGGAAGCTGGGTCCGGCTGCCAGGAAGCGGCCGGTGCGCGGGCTGCGCGGGGCTCGG
CTTCCACGTGCGAGCCTGCACCGCCGCCCCGCCCTCTCCTGGCGGCCAGGCCTGGGGACTCTCTGCCGCG
GGACGGCGCCTCGCGTTCCGCCGTGGCAGTGGCCGTGGCCAGAACGTCCACGCGCGGTCGTCCACCGCCG
GATCTCGCTCCAGCGCCCGTGGTCCAGCGTGTAGGGAGCCGATCGCCCATGGAGGGTCTGGGCCGCTCGT
GCCTGTGGCTGCGTCGGGAGCTGTCGCCCCCGCGGCCGCGGCTCCTGCTCCTGGACTGCCGCAGCCGCGA
GCTGTACGAGTCGGCGCGCATCGGTGGGGCGCTGAGCGTGGCCCTGCCGGCGCTCCTGCTGCGCCGCCTG
CGGAGGGGCAGCCTGTCGGTGCGCGCGCTCCTGCCTGGGCCGCCGCTGCAGCCGCCCCCGCCTGCCCCCG
TGCTCCTGTACGACCAGGGCGGGGGCCGGCGCCGGCGCGGGGAGGCCGAGGCCGAGGCCGAGGAGTGGGA
GGCCGAGTCGGTGCTGGGCACCCTGCTGCAGAAGCTGCGAGAGGAAGGCTACCTGGCCTACTACCTCCAG
GGAGGCTTCAGCAGATTCCAGGCCGAGTGCCCTCACCTGTGTGAGACCAGCCTTGCTGGCCGTGCCGGCT
CCAGCATGGCGCCGGTGCCCGGTCCAGTGCCCGTGGTGGGGTTGGGCAGCCTGTGCCTGGGCTCCGACTG
CTCTGATGCGGAATCCGAGGCTGACCGCGACTCCATGAGCTGTGGCCTGGATTCGGAGGGTGCCACACCC
CCACCAGTGGGGCTGCGGGCATCCTTCCCTGTCCAGATCCTGCCCAACCTCTATCTGGGCAGTGCCCGGG
ATTCCGCCAATTTGGAGAGCCTGGCCAAACTGGGCATCCGCTACATCCTCAATGTCACCCCCAACCTCCC
AAACTTCTTCGAGAAGAATGGTGACTTTCACTACAAGCAGATCCCCATCTCCGACCACTGGAGCCAGAAC
CTGTCGCGGTTCTTTCCGGAGGCCATTGAGTTCATTGATGAGGCCTTGTCCCAGAACTGCGGGGTGCTCG
TCCACTGCTTGGCGGGGGTCAGCCGTTCTGTCACCGTCACTGTGGCCTACCTCATGCAGAAGCTCCACCT
CTCTCTCAACGATGCCTATGACCTGGTCAAGAGGAAGAAGTCTAACATCTCCCCCAACTTCAACTTCATG
GGGCAGTTGCTGGACTTTGAGCGCAGCTTGCGGCTGGAGGAGCGCCACTCGCAGGAGCAGGGCAGTGGGG
GGCAGGCATCTGCGGCCTCCAACCCGCCCTCCTTCTTCACCACCCCCACCAGTGATGGCGCCTTCGAGCT
GGCCCCCACCTAGGGCCCCGTGGCCGGCAGGCCGGCCCCTGCCCCACCCCCACCCACGGGTGTCCCTGCC
CACTCGTGTGGCAAGGGAGGGGAGGGCAGGAGGGCTCGGCCTGAGCAGGGTGCTGGGGGGAGAGCGCAAT
ACCTCACGCGGGCTGCCGTCCTAATCAACGTGCCTATGGCGGGACCACGCTCGGAGCCTGCCTCTTCTGC
GACTGTTACTTTTTCTTTGCGGGATGGGGGTGGGGGTTCCCTCTCCAGGTGGTTGTCCAGGCCCAGGTCC
CGGCCCTGGGTGCTCAGCCAGCTCGGCTAGGCCCTGCGCCTCCCTGCGCTTCCCCCTTCAGGAAGGGTGT
GTGCCACCTCGTTGCACTGGATCCCAGTGGCTGCTTGGGGGAGAGGCGTTTGCCATCACTGGTGTTGTCA
CCTCCCTGTTTCTCCACCAAGGGCTTGGGCCTCTCGGGGCTGGGGCCTCCCAGGGGATGGGGACCCAGAG
TGCAGTGGCCGCCCACATCCATGGCCTAGGAGCTACTGGGCAGGTTCCCGGCCACACATCTGGTGGGCTG
TTTTGTTTTTTTTTTTTCCTCTTCCCCCAGATGTCTTGACGGGATCACTGGGGCTCTTTGTGAGTGAGGG
TGGCCAAACTACCGCCGGAGGAGATGGGGTCTCAGAGCGAGAGCTGCGGAGGGGGAGGGGAAGAAGAAGG
CCTCACTTTTGCTGCTGCCGGGCCCACACAGCCGCTGCTACTTTGGGGGGTGGGGAAGGGGCCAAGCTGC
AGACACACACAGTCATTCATTTCTGTCCACACCCCTGTGGGTGGCGGGTGTGCGTGTGTGTGCTTGTGTG
TGCGCACGTGTCGGCGCTCACACACACATGCTAGCCCACTGATGCACCCAGCCCAGGGCTGGCAGTCTTT
GCAGCGTGGGGCCGTCTCACCCTGGAGCCTGGAGAGGATCTATGCTTGTTTGTTTTTGTAATCCATATCA
TAGTTGCTTTCTTTAATTGTTCCTTCTGAATAAACAGTTTATTTAAGATACTGA

Fig. 25 cont'd

(SEQ ID NO:104) NM_052962.3 Homo sapiens interleukin 22 receptor subunit alpha 2 (IL22RA2), transcript variant 1, mRNA

CTTTACCACTACTCGCTATAGAGCCCTGGTCAAGTTCTCTCCACCTCTCTATCTATGTCTCAGTTTCTTC
ATCTGTAACATCAAATGAATAATAATACCAATCTCCTAGACTTCATAAGAGGATTAACAAAGACAAAATA
TGGGAAAAACATAACATGGCGTCCCATAATTATTAGATCTTATTATTGACACTAAAATGGCATTAAAATT
ACCAAAAGGAAGACAGCATCTGTTTCCTCTTTGGTCCTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAA
CAGTCACACTTGCAACCATGATGCCTAAACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGG
TGTAGCAGGAACTCAGTCAACGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTT
CACAACATTTTGCAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTTGTGCAGTACA
AAATCATGTTCTCATGCAGCATGAAAAGCTCTCACCAGAAGCCAAGTGGATGCTGGCAGCACATTTCTTG
TAACTTCCCAGGCTGCAGAACATTGGCTAAATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGG
GGTACTCAAGAACTCTCTTGTGACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGG
TGAGGGCGGCCTCGGCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAAC
AAAAATAGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTCCA
AATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAACTACTATACCGAG
TTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGGGCTCACAGAGCGGTTGAAAT
TGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCTGAAATATATCAGCCCATGTTAGACAGAAGA
AGTCAGAGAAGTGAAGAGAGATGTGTGGAAATTCCATGACTTGTGGAATTTGGCATTCAGCAATGTGGAA
ATTCTAAAGCTCCCTGAGAACAGGATGACTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTT
CTTAAAGCAATATTCACTGTTACACCTTGGGGACTTCTTTGTTTATCCATTCTTTTATCCTTTATATTTC
ATTTGTAAACTATATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCAGAGAATAAAG
TGTTCTATGAAATTCAGAACTTTATTTCTGAATGTAACATCCCTAATAACAACCTTCATTCTTCTAATAC
AGCAAAATAAAAATTTAACAACCAAGGAATAGTATTTAAGAAAATGTTGAAATAATTTTTTTAAAATAGC
ATTACAGACTGAGGCGGTCCTGAAGCAATGGTTTTTCACTCTCTTATTGAGCCAATTAAATTGACATTGC
TTTGACAATTTAAAACTTCTATAAAGGTGAATATTTTTCATACATTTCTATTTTATATGAATATACTTTT
TATATATTTATTATTATTAAATATTTCTACTTAATGAATCAAAATTTTGTTTTAAAGTCTACTTTATGTA
AATAAGAACAGGTTTTGGGGAAAAAAATCTTATGATTTCTGGATTGATATCTGAATTAAAACTATCAACA
ACAAGGAAGTCTGCTCTGTACAATTGTCCCTCATTTAAAAGATATATTAAGCTTTTCTTTTCTGTTTGTT
TTTGTTTTGTTTAGTTTTTAATCCTGTCTTAGAAGAACTTATCTTTATTCTCAAAATTAAATGTAATTTT
TTTAGTGACAAAGAAGAAAGGAAACCTCATTACTCAATCCTTCTGGCCAAGAGTGTCTTGCTTGTGGCGC
CTTCCTCATCTCTATATAGGAGGATCCCATGAATGATGGTTTATTGGGAACTGCTGGGGTCGACCCCATA
CAGAGAACTCAGCTTGAAGCTGGAAGCACACAGTGGGTAGCAGGAGAAGGACCGGTGTTGGTAGGTGCCT
ACAGAGACTATAGAGCTAGACAAAGCCCTCCAAACTGGCCCCTCCTGCTCACTGCCTCTCCTGAGTAGAA
ATCTGGTGACCTAAGGCTCAGTGTGGTCAACAGAAAGCTGCCTTCTTCACTTGAGGCTAAGTCTTCATAT
ATGTTTAAGGTTGTCTTTCTAGTGAGGAGATACATATCAGAGAACATTTGTACAATTCCCCATGAAAATT
GCTCCAAAGTTGATAACAATATAGTCGGTGCTTCTAGTTATATGCAAGTACTCAGTGATAAATGGATTAA
AAAATATTCAGAAATGTATTGGGGGGTGGAGGAGAATAAGAGGCAGAGCAAGAGCTAGAGAATTGGTTTC
CTTGCTTCCCTGTATGCTCAGAAAACATTGATTTGAGCATAGACGCAGAGACTGAAAAAAAAATTTACTT
TGATCTCTGTTTTTGAATTCTTATTATTTATATTTTGCTTACTACCTTTTTTGCCTTTTGTCCTTTTGTG
GAGAGGGCGATGAATTAAGAGTAGTGGGGTGGGTGGCGAGTAAGTAAAATTTCAAATAGCATTTTAGTGA
ATGCAATTCAGTAGTCCTGAAGCCTGACTTAATAAAACAAAATTCATTTATGGTTGTTTCATGAAAGTTA
TTAGATAGGATCAAGTTTTGTTTGTATATTGTTTGCCTTGCTCTGTTTTTGCTTTTGTGCTTAGGCAAGT
GCAAAATACTCTATGGAAATCATAATTGTCATCTTCTTCATGGTGTTAGGGATATATTGTCACATGATTT
CAATAAATCCTTTTTTTGCTTTA

Fig. 25 cont'd

(SEQ ID NO:105) NM_001145661.2 Homo sapiens GATA binding protein 2 (GATA2), transcript variant 1, mRNA

ACTGGGTCAAGCACAGCCCTGAGCGGCCGCGTGTCCGAGGCCCAGGTGCCCTCTAGAGCCCTGTAGTTCC
TGCCCCTCTCTGCCCCTCTCGGCTCCTGCTGTTCCGCCGCTGTCGTCCGAACCATCCCAACCCCCAGTCC
ACCCAGACAGCGCCCGAGCTAGGGGAGGGAACGGTCTGGGAGTCGGCAGCTGGCGCCAGGGCGGCCGGAG
GATGCCGAGGGGCCGGAGCCGGGAGGGCCCGAGGCCGAGGCGCACTCTACCCCCAGCTCCTACCCTGTAA
GCCCCGCCAGCCTCCGGACGTGCTGTCCCTGGGCCCGTCGCCCTCGGGGCTCCCGCCGGAACTCCTTCAC
TCTCAGAGGCCGAGTCCCTCCCCTCCCCACGGCTGCGTGTGGCCGTTGCCGTCTGCACCCAGACCCTGAG
CCGCCGCCGCCGGCCATGGAGGTGGCGCCCGAGCAGCCGCGCTGGATGGCGCACCCGGCCGTGCTGAATG
CGCAGCACCCCGACTCACACCACCCCGGGCCTGGCGCACAACTACATGGAACCCGCGCAGCTGCTGCCTCC
AGACGAGGTGGACGTCTTCTTCAATCACCTCGACTCGCAGGGCAACCCCTACTATGCCAACCCCGCTCAC
GCGCGGGCGCGCGTCTCCTACAGCCCCGCGCACGCCCGCCTGACCGGAGGCCAGATGTGCCGCCCACACT
TGTTGCACAGCCCGGGTTTGCCCTGGCTGGACGGGGGCAAAGCAGCCCTCTCTGCCGCTGCGGCCCACCA
CCACAACCCCTGGACCGTGAGCCCCTTCTCCAAGACGCCACTGCACCCCTCAGCTGCTGGAGGCCCTGGA
GGCCCACTCTCTGTGTACCCAGGGGCTGGGGGTGGGAGCGGGGGAGGCAGCGGGAGCTCAGTGGCCTCCC
TCACCCCTACAGCAGCCCACTCTGGCTCCCACCTTTTCGGCTTCCCACCCACGCCACCCAAAGAAGTGTC
TCCTGACCCTAGCACCACGGGGGCTGCGTCTCCAGCCTCATCTTCCGCGGGGGGGTAGTGCAGCCCGAGGA
GAGGACAAGGACGGCGTCAAGTACCAGGTGTCACTGACGGAGAGCATGAAGATGGAAAGTGGCAGTCCCC
TGCGCCCAGGCCTAGCTACTATGGGCACCCAGCCTGCTACACACCACCCCATCCCCACCTACCCCTCCTA
TGTGCCGGCGGCTGCCCACGACTACAGCAGCGGACTCTTCCACCCCGGAGGCTTCCTGGGGGGACCGGCC
TCCAGCTTCACCCCTAAGCAGCGCAGCAAGGCTCGTTCCTGTTCAGAAGGCCGGGAGTGTGTCAACTGTG
GGGCCACAGCCACCCCTCTCTGGCGGCGGGACGGCACCGGCCACTACCTGTGCAATGCCTGTGGCCTCTA
CCACAAGATGAATGGGCAGAACCGACCACTCATCAAGCCCAAGCGAAGACTGTCGGCCGCCAGAAGAGCC
GGCACCTGTTGTGCAAATTGTCAGACGACAACCACCACCTTATGGCGCCGAAACGCCAACGGGGACCCTG
TCTGCAACGCCTGTGGCCTCTACTACAAGCTGCACAATGTTAACAGGCCACTGACCATGAAGAAGGAAGG
GATCCAGACTCGGAACCGGAAGATGTCCAACAAGTCCAAGAAGAGCAAGAAAGGGGCGGAGTGCTTCGAG
GAGCTGTCAAAGTGCATGCAGGAGAAGTCATCCCCCTTCAGTGCAGCTGCCCTGGCTGGACACATGGCAC
CTGTGGGCCACCTCCCGCCCTTCAGCCACTCCGGACACATCCTGCCCACTCCGACGCCCATCCACCCCTC
CTCCAGCCTCTCCTTCGGCCACCCCCACCCGTCCAGCATGGTGACCGCCATGGGCTAGGGAACAGATGGA
CGTCGAGGACCGGGCACTCCCGGGATGGGTGGACCAAACCCTTAGCAGCCCAGCATTTCCCGAAGGCCGA
CACCACTCCTGCCAGCCCGGCTCGGCCCAGCACCCCCTCTCCTGGAGGGCGCCCAGCAGCCTGCCAGCAG
TTACTGTGAATGTTCCCCACCGCTGAGAGGCTGCCTCCGCACCTGACCGCTGCCCAGGTGGGGTTTCCTG
CATGGACAGTTGTTTGGAGAACAACAAGGACAACTTTATGTAGAGAAAAGGAGGGGACGGGACAGACGAA
GGCAACCATTTTTAGAAGGAAAAAGGATTAGGCAAAAATAATTTATTTTGCTCTTGTTTCTAACAAGGAC
TTGGAGACTTGGTGGTCTGAGCTGTCCCAAGTCCTCCGGTTCTTCCTCGGGATTGGCGGGTCCACTTGCC
AGGGCTCTGGGGGCAGATTTGTGGGGACCTCAGCCTGCACCCTCTTCTCCTCTGGCTTCCCTCTCTGAAA
TAGCCGAACTCCAGGCTGGGCTGAGCCAAAGCCAGAGTGGCCACGGCCCAGGGAGGGTGAGCTGGTGCCT
GCTTTGACGGGCCAGGCCCTGGAGGGCAGAGACAATCACGGGCGGTCCTGCACAGATTCCCAGGCCAGGG
CTGGGTCACAGGAAGGAAACAACATTTTCTTGAAAGGGGAAACGTCTCCCAGATCGCTCCCTTGGCTTTG
AGGCCGAAGCTGCTGTGACTGTGTCCCCTTACTGAGCGCAAGCCACAGCCTGTCTTGTCAGGTGGACCCT
GTAAATACATCCTTTTTCTGCTAACCCTTCAACCCCCTCGCCTCCTACTCTGAGACAAAAGAAAAAATAT
TAAAAAAATGCATAGGCTTAACTCGCTGATGAGTTAATTGTTTTATTTTTAAACTCTTTTTGGGTCCAGT
TGATTGTACGTAGCCACAGGAGCCCTGCTATGAAAGGAATAAAACCTACACACAAGGTTGGAGCTTTGCA
ATTCTTTTTGGAAAAGAGCTGGGATCCCACAGCCCTAGTATGAAAGCTGGGGGTGGGGAGGGGCCTTTGC
TGCCCTTGGTTTCTGGGGGCTGGTTGGCATTTGCTGGCCTGGCAGGGGGTGAAGGCAGGAGTTGGGGGCA
GGTCAGGACCAGGACCCAGGGAGAGGCTGTGTCCCTGCTGGGGTCTCAGGTCCAGCTTTACTGTGGCTGT
CTGGATCCTTCCCAAGGTACAGCTGTATATAAACGTGTCCCGAGCTTAGATTCTGTATGCGGTGACGGCG
GGGTGTGGTGGCCTGTGAGGGGCCCCTGGCCCAGGAGGAGGATTGTGCTGATGTAGTGACCAAGTGCAAT
ATGGGCGGGCAGTCGCTGCAGGGAGCACCACGGCCAGAAGTAACTTATTTTGTACTAGTGTCCGCATAAG
AAAAAGAATCGGCAGTATTTTCTGTTTTTATGTTTTATTTGGCTTGTTTTATTTTGGATTAGTGAACTAA
GTTATTGTTAATTATGTACAACATTTATATATTGTCTGTAAAAAATGTATGCTATCCTCTTATTCCTTTA
AAGTGAGTACTGTTAAGAATAATAAAATACTTTTTGTGAA

Fig. 25 cont'd

(SEQ ID NO:106) NM_001375410.1 Homo sapiens sprouty RTK signaling antagonist 1 (SPRY1), transcript variant 5, mRNA

GTAGCCGGAGTGAGACCGCTCTGCAAACCACTGCGTGCTTTGCAGAGTGATTATCAGCACAGTTCCCTGC
CCTGGATAAGGAACAGCTACAGTCGCTGTTAAATGTGCCTGAAAAGCAATTTGCAATCTTTGCATTAGGC
ATTTCGGCCGTGGAACCCCAGGCTCGGAGGACTGGGTGTGAGCGCTGCCCGGGAGAGGCTGACCTGCCGG
GACCGGAGTGCCCGGGGACGCTGTGCCCCCACTTGCCCAACGTGCGGAATCGGCTAAGCGCGTCGGCCTG
CGCGGGGCACAAGGGACGACGCCCGCCTTTCTCTCTCCGAGAAGGATCCCCAAACCTCACTCTCTTCACT
CCTCCCCGCTAAAAAAAAAAAAAAAAAGAAAAGGGTAAAAAAATCCCCCTCCCCCTCCCGGCCGCGGCAG
CCTCTGCCTGGCAGGCGCGTGCTCCGAGGTTTCGCCGGGGTACTGCGCGGCTCCGTGACCCACCCGCCGA
CGGCGGTTCGGGCCCCGACCCGGGCGCTGCGGAGTCTCGAACGCCCGTGACGTGGATTTTTCGCTCGTCA
GGAAGCCGCCATCCCTTCCTTCGTTCCTTGCGAGGAGCGACTAGAACCCGAGTTCTCTGAGCACACCGTG
CCGTCAGCTGGCCCGTCACGCACTCGACTCCGCCACTCCCCTACTTGTTTTTCTGAGACTTGGGAAGCCT
TCCTGAAAGGATTTGTAAAAACTGGTTCTTGGAAAGGGGCTGCAGAAGACCTCCCGAGGTGGATGTTACT
GAGCCGCCCGGCGAGCACCAGCCGTGACAGGTCCGGGCCCGGCCGCGCGGAGCCGCGGGAGAACTGCCCT
CCGCAGCCGGAAGGGGGCCGCGGGGAGCGCTCCTGGCCGGTGGCGGCGGGGGCGGGGGAGGCCGCGAGCC
GAGGCGCTCCAACTCCGGCGATGCCGCCTCGCCCTCCCCGCCGCGGTTGATGCGGCACGTGCACGCCGCC
GCCCGCACCAGGACCTGGGCCGGGTCGCACGGCTTGGCCCCCGGCCACCGCTTCGGCCTAGGATTTCAGA
TGCATGCCAGGTTTCCACTGATTGCCAGAACTCGAGATCACTACACATGGATCCCCAAAATCAACATGGC
AGTGGCAGTTCGTTAGTTGTGATCCAGCAGCCTTCTTTGGATAGCCGTCAGAGATTAGACTATGAGAGAG
AGATTCAGCCTACTGCTATTTTGTCCTTAGACCAGATCAAGGCCATAAGAGGCAGCAATGAATACACAGA
AGGGCCTTCGGTGGTGAAAAGACCTGCTCCTCGGACAGCACCAAGACAAGAAAAGCATGAAAGGACTCAT
GAAATCATACCAATTAATGTGAATAATAACTACGAGCACAGACACACAAGCCACCTGGGACATGCAGTAC
TCCCAAGTAATGCCAGGGGCCCCATTTTGAGCAGATCAACCAGCACTGGAAGTGCAGCCAGCTCTGGGAG
CAACAGCAGTGCCTCTTCTGAACAGGGACTGTTAGGAAGGTCACCACCAACCAGACCAGTCCCTGGTCAT
AGGTCTGAAAGGGCAATCCGGACCCAGCCCAAGCAACTGATTGTGGATGACTTGAAGGGTTCCTTGAAAG
AGGACCTGACACAGCACAAGTTCATTTGTGAACAGTGTGGGAAGTGCAAGTGTGGAGAATGCACTGCTCC
CAGGACCCTACCATCCTGTTTGGCCTGTAACCGGCAGTGCCTTTGCTCTGCTGAGAGCATGGTGGAATAT
GGAACCTGCATGTGCTTAGTCAAGGGCATCTTCTACCACTGCTCCAATGACGACGAAGGGGATTCCTATT
CAGATAATCCTTGCTCCTGTTCACAATCACACTGCTGCTCTAGATACCTGTGTATGGGAGCCATGTCTTT
ATTTTTACCTTGCTTACTCTGTTATCCTCCTGCTAAAGGATGCCTGAAGCTGTGCAGGAGGTGTTATGAC
TGGATCCATCGCCCAGGGTGCAGATGTAAGAACTCCAACACTGTCTATTGTAAGCTGGAGAGCTGCCCCT
CCCGGGGTCAGGGTAAACCATCATGATTTTTGGAGGTGGGTTGTACCTCCTGAACTTTTAGCTTTCAAGT
TGTGGCTGTTTTTTGTTTTTGTTTTTGTTTTTGTTTTCTTTAGAATTTTTCCCTGTTTCCCACCTTCTCT
TCCCCTGTTGCCAAGGTCTAACTCATGGATTTTTCTCTTTCCTCATGGATGATCTTCAGCAAGAGTGGAC
TGGGAAGCTGCACCTGGCTCCCACTTTCAACAAGAGCCTCTGCCATCCACTTGAGGGTATTGAGAGCCAG
TGGGCTTTTGTGTAGCCTTTTTGTTCTGCAAGCAACTTTCTAAAGTTGTGTACATGAACATACACCCACA
TCCAGACTACAGTGATTTAGAGTTGTTTTGATTGGGTACCGTGGGAGCAGGGAAATTGGTTTTTTAAAAA
GCAACTGTTTAATTGCTTAAATAAGCTATGTATTAAATCTGTCTCCAGTTAGGGCTATCTTCCTAGCATA
GGCCCCTTAAGTAGCATGGGGGATATATTTTTGCTATAACGTAAAAATTTTCCTTTAACCACTGCCCTC
TCCTTCTTTCTCCTTCAAGGTTCTTTCCCCCTCAGTTTTGTTGTTGTCTTACTCTGGAGATGCCAAGTGT
ATTTTTTCTTTCTATGTAATTTTAGATTCGCCTTACAATGTAAATCTTCACATTGGAGATAATATTGGTT
GGACCTTGCCCATCTTCACTCTAGCCTTCGTATTTGTGAAGGACTCAGCCACCTTCCTTCTTCACCCCAT
GCTTCTCACCAAATTTTTGTTGTCATTGAGGGCACTTGGATAACTCAAGTTGATATTTATAGCTGATCAA
TCTATATGTGTCACAGAACTATGCTGCCTAAAGTGATCTTGGCTCCTTAATGGTCCTTTTGGCCCCTTGG
ATAGTTAACAGCTGAGTAATTCTAATCTCTTCTGTGTTTTCCTTGCCTTAACCACAAATTGTGGTGCTTT
TTGTATATTTTATGTATAAATCACAAAGTTGAATTCTGACTATTTTTAAGACAAAAGTCTGTTAAACTTT
TTTATTGTAAAGAATATTTATTATGCGAATCTCTATTATTTTATGGTATTTATTGCAAAAGACTGTTGAA
ATGTACTCATGTTTGAATATAACAAAATATCAATACTTAACGGAAAATAAGGTGACACGAAGAAAGTACA
TATGTTAACTATAATGCAGAAAATATATTAATTAATGAAA

Fig. 25 cont'd

(SEQ ID NO:107) NM_016944.2 Homo sapiens taste 2 receptor member 4 (TAS2R4), mRNA
CTAGAAACATAGTTGATGTTCTTACCCTTATCATATAAGGATAAGATTATCCTTATCATCCTTATCATCA
TGATAAGGAAAACAGCTAGGAAGTTTAACCATAGGTCAAATTCTCATGCATAGGGAGAAAGGGTTCTGCT
AACACTTTTCCTATACTGACCCTTGTGGAAATAACTTCTAACTGAATGAGCTCATTCATTGATTGTGCTA
GCCAACCTTATCACATCTTAATTATAGCACTTCCTCCTACAGAGAACCCAACAATTTGGTATAGTACATT
CTAGATAGAGTTTGTTACTATCTAATTCTGGGATTCCTGCTCTTTTGGCCACATTTATCTGTTATGGCTT
ACTCTATATCATTTATTCTATTTAAATGTGATGTTAGTAATATTTCAACTTCACCACTTTAATGCAGCCA
TCTATGGATAAGTAATTGGAAATCTGTGCTATAATTTTCCTTTTAGTCATAGTCTTCCTGGCTCATTCTG
TTTGCCTGCTTACCTGATGTGGGCATGCCTCTATCAGTGCCTGTTAGTTTTGAATAAAAAGCTTCTGTAA
GCACCTGGGCACCAGGTCAGAGAATTTCTCCAGGCTAGGCTTCCTGTCATCTGTCTTAAAGGGCCTCATG
AATGTATTCCCCTCTTCTGGACCTGATTATTATTAAATCTTAGCTCCTTTTTCTTGTCTGTTTCTATTTG
GACTTGGCAGTAGGACTTTGTGCTGTACCTTGATGCTACTTTGGTAACATCTGTGGCTGCATCCAGGATT
GCACCTTGGTTTCATTCAGCTGCTAGAGAAGATAAGAGATGCCATACTCTTACATTCACCTATGGGCCTC
CATAATATCATTTGCCAGGGATATTTTGCCATTTCCCATCTGAGCAAGTACAGAGAAATCCAGCAATGAG
ATGCCTAGCTGTTTGGCTCACAAAACTACAACTAATGCATTACTGTGTATCTCATTCCAGGGTACCTGGA
TTGACAGTTAAATGCCTAAGAGAAAATAGCCACATATGATCTAAACATAAACCCAGATTTATAAAGGAAA
CACCTACAAGGGCTGACTTAATTTTTTCTAAGGAAAACCAGAACATAGCAAATGGTTATGGCACAAATCT
ATGTATGTAGATAGAGAAGGCAAAGCAAAGGGCATCAGAAAGAATGGGATTAATTGAGAAAGGTTTTCTC
AAGGAGGTATTGGGTCTTTGAACTTGATCTATTAGATCACTGTAAATCGCTATAGGTGAATCACTGAGGT
TGAAAGAGTGGCATTGGCATGGCCAATTGGTGAAACTTGTTGTGGCAGCAACAGATTAGAGGGGAGAGAG
AAATTGGATTCTGGTCATCCATGAATATGTGGCTAGGAGGTGGGTGGGTAGGAGTGAGGAATTAGGATTT
CCACCATATTCTGGCATTTTTATGAAGAAAAACTTTACCGTAAAACATTGACAGAAACATTGCTGGACTC
AAGCTCTCTGGTTTGGATTCTAAGTTTTTGGAGCCTGCTGTGACTCTTCCCTCTCGCCCTCCTGCTCTTG
GAGGAGTGGACTCCCAGCATCACCTAGGCTTGCTGTAATTAGGCATTTCTAAGGAGAACAGGATACTAAT
GAAGAAATAGTAATGTAATCCTTGGAAGATTTGCATCTCAGTAAAATCAGGTGGCCCTTGATCATGAATG
GCTCATTTGCCATGCTGGGAAAAATTAAAAAGGAGATGTCCTTCCTGGCTGGATACTGGTGTCTGCTTAT
ACATTTTGGTATTTCTTCTGCCTCCACTATCAGCACCACAACTGCTGAATCCTCAATGAGTAAAGATGCT
TCGGTTATTCTATTTCTCTGCTATTATTGCCTCAGTTATTTTAAATTTTGTAGGAATCATTATGAATCTG
TTTATTACAGTGGTCAATTGCAAAACTTGGGTCAAAAGCCATAGAATCTCCTCTTCTGATAGGATTCTGT
TCAGCCTGGGCATCACCAGGTTTCTTATGCTGGGACTATTTCTGGTGAACACCATCTACTTCGTCTCTTC
AAATACGGAAAGGTCAGTCTACCTGTCTGCTTTTTTTGTGTTGTGTTTCATGTTTTTGGACTCGAGCAGT
GTCTGGTTTGTGACCTTGCTCAATATCTTGTACTGTGTGAAGATTACTAACTTCCAACACTCAGTGTTTC
TCCTGCTGAAGCGGAATATCTCCCCAAAGATCCCCAGGCTGCTGCTGGCCTGTGTGCTGATTTCTGCTTT
CACCACTTGCCTGTACATCACGCTTAGCCAGGCATCACCTTTTCCTGAACTTGTGACTACGAGAAATAAC
ACATCATTTAATATCAGTGAGGGCATCTTGTCTTTAGTGGTTTCTTTGGTCTTGAGCTCATCTCTCCAGT
TCATCATTAATGTGACTTCTGCTTCCTTGCTAATACACTCCTTGAGGAGACATATACAGAAGATGCAGAA
AAATGCCACTGGTTTCTGGAATCCCCAGACGGAAGCTCATGTAGGTGCTATGAAGCTGATGGTCTATTTC
CTCATCCTCTACATTCCATATTCAGTTGCTACCCTGGTCCAGTATCTCCCCTTTTATGCAGGGATGGATA
TGGGGACCAAATCCATTTGTCTGATTTTTGCCACCCTTTACTCTCCAGGACATTCTGTTCTCATTATTAT
CACACATCCTAAACTGAAAACAACAGCAAAGAAGATTCTTTGTTTCAAAAAATAGTGGAATTTCAGTAAA
CAATACCTAGATTTACCTGATGGTTTGGGGGCAAGATTTTCTGTTTGCAGTTTTCCCAGTGATCTGGGGA
ATTCAGTTTTGTGATTGCTGATCTGACATCATAGGCTTTTGAGTGCCTGAATTTCAGTTCATTCTGTAAT
TTTTTTTTTTTGGTATGTAAGTATTTTAAAATAAGGCACATTCTGTAAGAAACTTTTTTGAGGCATTATT
TGTCATGTATTTTGCATGGCCATTGAATCCATGTATAATGGAAATCATCACATTGTTTCATTGTCTATTG
AAGTATAATGGGAAATTCTTCCAAATTAGAGAACACATTGGGGTGCACGTGATGAGTTAGATATTTGTGG
TTTAGCTGAGGAGCCCTGAGTAAGGGCTCAGCAGTGGATAGGTGGTCACTGGGAGCCACTGGACTGACCG
AAAGCAGAGGAAGGGGGTTCAGTGCAAAGAGAAAAGGAAAAAAGGAAGGTTTCAGAGAGAAAAGAAGGAA
AGAGAAAGGTGAAGAGAAATAGGCGTACACTGGGCCAGGCGCGGTGGCTCATGCTTGTAATCCCAGCTCT

Fig. 25 cont'd

(SEQ ID NO:107) cont'd
TTGGGAGGCCGAGGCAGGTGAATCGTGAGGTCAGGAGATCGAGACCATCCTGGCTAACACGGTGAAACCC
TGTCTCTACTAAAAATACAAAAAAATTAGCTGGGCGTGGTGGCGGGCACCTGTAGTCCCAGCTACTCGGG
AGGCTGAGGCAGGAGAATGGCTTCAACCCAGGAGGCGGAGCTTGCAGTGAGATGAGATCGCGCCACTGCA
CTCCAGTCTGGGCGACAGAGCAAGACTCTGTCTCAAAAAAAGAAATAGACGTACACTCTGGGACAAGACA
GAAAAAGTATCCTCACACTTGCTGGGTAATAGTAACTGTGCTATTCCTAGCAAGAAACCCTAAGGTTTCT
AGGCTTGTTCTGGAAAAGAGGATATTGCCAGAGTTGGTAAGTAGAGGAAAGTGATTAGTATTTAAGAAAC
TGAATCAAGAATGGTTCCAAAAATCTTAAAATCCAGGGAAACCAGCTTAAGGTCAAAGGCAAGTGCTAGA
TAATGAAATTAACACCATATGAGTACAAATTTACAAAATACTGTACTTCACCATAGGCTATGGAACTCAG
TGGAAAGCCAAAAAAGCACTGGACAGGTGGTGGGAGTGCTTGACTTGTGGTGAATTTATTTCATCTGCTT
ATACATTTGTACACAGCACAGTTCTTCTCCAGAATGTTGTTTCTGTGGCTGGGACCATTGGACTGTGGCT
CCAAAAGAACAACAGTCTGAAGATGGGATGTTGACAAGTTTTGGAATGTCAATTGGGGAATCATAATTTG
TATTTATTTAGGTTTTTTTTGGTGTTCATAAAATGCTTATGTAATATTTACATATGTCAAATAAATCTTA
AAATTTTATAAATTACATGACTTTTCTCATTCTGGCCACCAGAATCTTGACTGCAATATTCAGTAAAAAT
TACCCAAGCCAATATTTTGTGCTATGAAACCTGGAGGTATTCATCATGTTAAATCCTAAGAGAGATAAAA
GGATTACTGAGAGTGATTAAATGCATACTATGTCTTAAGAACTCTAAATGAGTGGCAGAAACCCTCATTG
GTCCCTCAGTATCTGTTCTTTCTCCTCTCTTCCATAGTAATCAAATCATTAGCTGTTCAGAATTTTGGCA
GCAAATTCCATTATTGCCATGTATGTGAGCAGAAAAGATGTATATAATTTCTGGGTGGTACTTCGGAGCA
GTCCTACCTTCCCTTCTTTAATCTTTTCTTTGTTACTCCCTCCATGAGCTGGAATGCTGACATCATGATT
GTCTATCTTGGACAATGCAGATGAGGTGAATGCTTGGGATAGTGAAGTAATTCTCCATCCTAGAGCTGGC
TCCATGGTTCTTCACACTGTGGACTTGTAACACCAGCTCTGGACTGCTCAAGCCTGAACTCCAGGACTGT
TGATGAGAAATCAGTGTCTCCATTCTTTCAGGTGCTGGAGTTTTGGTCTCTGTTACCTTAGTCAAATAAC
CTATGCTATACCTTAAATATACACAATAATATATATCTTTATGATGAAATAGTATGTATTTACCATCTTA
TTAGTCAAAGAACCTTTTTTATATGACCTACTAAGTGAAATTGAAATAAAACCTGTACATGTGGTATAATA
CCATTTTTTTTGGTAAAAATGTGTACATATGAAGAAAAGTCTAAAAGGAAATATATAAAAATGTAAACAG
TAATTATTTTAGGTGGGAGGAATCAATAAATTTTTTTGTGTATTTCAA

(SEQ ID NO:108) NM_001256869.2 Homo sapiens ubiquitin specific peptidase 17 like family member 7 (USP17L7), mRNA
GGTCATTTGAAGACTCTCTCGGAAGAGATAGCGTCTTGCTGCAACCTGCGGTCCCAGCAGAAAAACCTTG
TGATCCTTGTTGCGGGCGACATGGAAGACGACTCACTCTATTTGGGAGGTGACTGGCAGTTCAATCACTT
TTCAAAACTCACATCTTCTCGGCTAGATGCAGCTTTTGCTGAAATCCAGCGGACTTCTCTCTCTGAAAAG
TCACCACTCTCATCTGAGACCCGTTTCGACCTCTGTGATGATTTGGCTCCTGTGGCAAGACAGCTTGCTC
CCAGGGAGAAGCTTCCTCTGAGTAGCAGGAGACCTGCTGCGGTGGGGGCTGGGCTCCAGAAGATAGGAAA
TACCTTCTATGTGAACGTTTCCCTGCAGTGCCTGACATACACACTGCCGCTTTCCAACTACATGCTGTCC
CGGGAGGACTCTCAAACGTGTCATCTTCACAAGTGCTGCATGTTCTGTACTATGCAAGCTCACATCACAT
GGGCCCTCCACAGTCCTGGCCATGTCATCCAGCCCTCACAGGTATTGGCTGCTGGCTTCCATAGAGGTGA
GCAGGAGGATGCCCATGAATTTCTCATGTTTACTGTGGATGCCATGAAAAAGGCATGCCTTCCCGGGCAC
AAGCAGCTAGATCATCACTCCAAGGACACCACCCTCATCCACCAAATATTTGGAGCGTATTGGAGATCTC
AAATCAAGTATCTCCACTGCCACGGCGTTTCAGACACCTTTGACCCTTACCTGGACATCGCCCTGGATAT
CCAGGCAGCTCAGAGTGTCAAGCAAGCTTTGGAACAGTTGGTGAAGCCCAAAGAACTCAATGGAGAGAAT
GCCTATCATTGTGGTCTTTGTCTCCAGAAGGCGCCTGCCTCCAAGACGTTAACTTTACCCACTTCTGCCA
AGGTCCTCATTCTTGTATTGAAGAGATTCTCCGATGTCACAGGCAACAAACTTGCCAAGAATGTGCAATA
TCCTAAGTGCCGTGACATGCAGCCATACATGTCTCAGCAGAACACAGGACCTCTTGTCTATGTCCTCTAT
GCTGTGCTGGTCCACGCTGGGTGGAGTTGTCACAACGGACATTACTTCTCTTATGTCAAAGCTCAAGAAG
GCCAGTGGTATAAAATGGATGATGCCGAGGTCACTGCCTCTGGCATCACCTCTGTCCTGAGTCAACAGGC
CTATGTCCTCTTTTACATCCAGAAGAGTGAATGGGAAAGACACAGTGAGAGTGTGTCAAGAGGCAGGGAA
CCAAGAGCCCTTGGTGCTGAAGACACAGACAGGCCAGCAACGCAAGGAGAGCTCAAGAGAGACCACCCTT
GCCTCCAGGTACCCGAGTTGGACGAGCACTTGGTGGAAAGAGCCACTCAGGAAAGCACCTTAGACCACTG
GAAATTCCCCCAAGAGCAAAACAAAACGAAGCCTGAGTTCAACGTCAGAAAAGTTGAAGGTACCCTGCCT
CCCAACGTACTTGTGATTCATCAATCAAAATACAAGTGTGGTATGAAAAACCATCATCCTGAACAGCAAA
GCTCCCTGCTAAACCTCTCTTCGACGAAACCGACAGATCAGGAGTCCATGAACACTGGCACACTCGCTTC
TCTGCAAGGGAGCACCAGGAGATCCAAAGGGAATAACAAACACAGCAAGAGATCTCTGCTTGTGTGCCAG
TGA

Fig. 25 cont'd

(SEQ ID NO:109) NM_213620.3 Homo sapiens ATPase H+ transporting V1 subunit H (ATP6V1H), transcript variant 3, mRNA

CTTCTACCTGTGCGGCCCTCAACGTCTCCTTGGTGCGGGACCCGCTTCACTTTCGGCTCCCGGAGTCTCC
CTCCACTGCTCAGACCTCTGGACCTGACAGGAGACGCCTACTTGGCTCTGACGCGGCGCCCCAGCCCGGC
TGTGTCCCCGGCGCCCCGGACCACCCTCCCTGCCGGCTTTGGGTGCGTTGTGGGGTCCCGAGGATTCGCG
AGGTAAGGCCGCCCTCGCGTTGTTTGGTCTCAGGCTGCAGACCAGGTCAGGCGACTCTTGCAGTTTCTCC
AGCTTGCCTGGTGCGTGCTGGTGTCTCGCCGCTTGGTCCTCTCCTGTTCTTCGGCCCCCGGTTGCCAGAT
TGCTTTTCTTCCAGGCCTCAACCAGATTTGTTGAAAGACATTCAAGATTACGAAGTTTAGATGACCAAAA
TGGATATCCGAGGTGCTGTGGATGCTGCTGTCCCCACCAATATTATTGCTGCCAAGGCTGCAGAAGTTCG
TGCAAACAAAGTCAACTGGCAATCCTATCTTCAGGGACAGATGATTTCTGCTGAAGATTGTGAGTTTATT
CAGAGGTTTGAAATGAAACGAAGCCCTGAAGAGAAGCAAGAGATGCTTCAAACTGAAGGCAGCCAGTGTG
CTAAAACATTTATAAATCTGATGACTCATATCTGCAAAGAACAGACCGTTCAGTATATACTAACTATGGT
GGATGATATGCTGCAGGAAAATCATCAGCGTGTTAGCATTTTCTTTGACTATGCAAGATGTAGCAAGAAC
ACTGCGTGGCCCTACTTTCTGCCAATGTTGAATCGCCAGGATCCCTTCACTGTTCATATGGCAGCAAGAA
TTATTGCCAAGTTAGCAGCTTGGGGAAAAGAACTGATGGAAGGCAGTGACTTAAATTACTATTTCAATTG
GATAAAAACTCAGCTGAGTTCACAGAAACTGCGTGGTAGCGGTGTTGCTGTTGAAACAGGAACAGTCTCT
TCAAGTGATAGTTCGCAGTATGTGCAGTGCGTGGCCGGGTGTTTGCAGCTGATGCTCCGGGTCAATGAGT
ACCGCTTTGCTTGGGTGGAAGCAGATGGGGTAAATTGCATAATGGGAGTGTTGAGTAACAAGTGTGGCTT
TCAGCTCCAGTATCAAATGATTTTTTCAATATGGCTCCTGGCATTCAGTCCTCAAATGTGTGAACACCTG
CGGCGCTATAATATCATTCCAGTTCTGTCTGATATCCTTCAGGAGTCTGTCAAAGAGAAAGTAACAAGAA
TCATTCTTGCAGCATTTCGTAACTTTTTAGAAAAATCAACTGAAAGAGAAACTCGCCAAGAATATGCCCT
GGCTATGATTCAGTGCAAAGTTCTGAAACAGTTGGAGAACTTGGAACAGCAGAAGTACGATGATGAAGAT
ATCAGCGAAGATATCAAATTTCTTTTGGAAAAACTTGGAGAGAGTGTCCAGGACCTTAGTTCATTTGATG
AATACAGTTCAGAACTTAAATCTGGAAGGTTGGAATGGAGTCCTGTGCACAAATCTGAGAAATTTTGGAG
AGAGAATGCTGTGAGGTTAAATGAGAAGAATTATGAACTCTTGAAAATCTTGACAAAACTTTTGGAAGTG
TCAGATGATCCCCAAGTCTTAGCTGTTGCTGCTCACGATGTTGGAGAATATGTGCGGCATTATCCACGAG
GCAAACGGGTCATCGAGCAGCTCGGTGGGAAGCAGCTGGTCATGAACCACATGCATCATGAAGACCAGCA
GGTCCGCTATAATGCTCTGCTGGCCGTGCAGAAGCTCATGGTGCACAACTGGGAATACCTTGGCAAGCAG
CTCCAGTCCGAGCAGCCCCAGACCGCTGCCGCCCGAAGCTAAGCCTGCCTCTGGCCTTCCCCTCCGCCTC
AATGCAGAACCAGTAGTGGGAGCACTGTGTTTAGAGTTAAGAGTGAACACTGTTTGATTTTACTTGGAAT
TTCCTCTGTTATATAGCTTTTCCCAATGCTAATTTCCAAACAACAACAACAAAATAACATGTTTGCCTGT
TAAGTTGTATAAAAGTAGGTGATTCTGTATTTAAAGAAAATATTACTGTTACATATACTGCTTGCAATTT
CTGTATTTATTGTTCTCTGGAAATAAATATAGTTATTAAAGGATTCTCACTCCAAACATGGCCTCTCTCT
TTACTTGGACTTTGAACAAAAGTCAACTGTTGTCTCTTTTCAAACCAAATTGGGAGAATTGTTGCAAAGT
AGTGAATGGCAAATAAATGTTTTAAAATCTATCGCTCTATCAA

HOST FACTORS THAT ENHANCE VIRAL PRODUCTION VIA VIRALLY DRIVEN FITNESS-BASED CRISPR SCREENING

CROSS REFERENCE TO RELATED APPLICATIONS

[0001] This application is a continuation of U.S. Provisional Application Ser. No. 63/384,541, filed Nov. 21, 2022, the contents of which are specifically incorporated herein by reference in its entirety.

STATEMENT OF GOVERNMENT SUPPORT

[0002] This invention was made with government support under AI125897 awarded by the National Institutes of Health awarded by the National Institutes of Health. The government has certain rights in the invention.

INCORPORATION BY REFERENCE OF SEQUENCE LISTING

[0003] This application contains a Sequence Listing which has been submitted electronically in ST26 format and is hereby incorporated by reference in its entirety. Said ST26 file, created on Mar. 18, 2024, is named "800132US1.xml" and is 323,493 bytes in size.

BACKGROUND

[0004] Viruses are completely dependent upon the host for replication. Like all viruses, influenza virus exploits cellular processes to support its replication while simultaneously evading antiviral responses deployed by the cell in an attempt to block the infection. The balance between these pro- and anti-pathogen forces influences the outcome of an infection, the severity of disease, and even the potential to establish a pandemic outbreak.

[0005] Influenza virus is a serious public health threat causing annual epidemics and occasional pandemics with significant morbidity and mortality. Identifying cellular genes and proteins required by influenza virus is essential to understanding the viral life cycle and establishing a mechanistic foundation for the development of host-directed antiviral therapeutics. Most genetic approaches to identify host factors regulating infection have relied upon loss-of-function screens, which only probe those genes already expressed in the system under study and are limited in their ability to detect contributions from genes essential for cell viability, genes with redundant functions, or gene products needed in limited quantities. Such studies leave a large amount of genetic space unexplored and raises the possibility that entirely new classes of viral co-factors have yet to be discovered.

SUMMARY

[0006] Employing a screening approach for identifying host factors that impact influenza viral production after the initial infection, host factors that enhance influenza virus production were identified. Those factors are useful to study the regulation of the expression of viral genes and replication of the viral genome. Screening described herein include variations of the Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)/Cas9 system, termed CRISPR activation (CRISPRa) and CRISPR inhibition (CRISPRi). In those methods, the sequence of a single guide RNA ("sgRNA") directs Cas9 to a specific location, and the catalytically inactive Cas9 has been modified to recruit transcriptional activators or repressors to modify gene expression at that location.

[0007] An influenza virus was used to express the CRISPR sgRNA, in a technique referred to as transcriptional regulation by pathogen-programmed Cas9 (TRPPC). This way, the construct is inactive until after a virus infects a host cell and begins to be transcribed, and only the Cas9-expressing and influenza-infected cells are affected. To thoroughly blanket the genome, a library of 70,000 sequences (about 3 targeting sequences for each human gene) was prepared, which incorporated the sgRNA sequences into the influenza genome in between the two coding regions of the influenza NS gene segment and ensured proper cleavage via insertion of a microRNA sequence. In embodiments, the M gene segment may be employed. The library was used to perform a genetic selection by allowing all viruses to compete with each other through multiple rounds of replication in human lung cells. Viruses that activated pro-viral host factors gained a replicative advantage and came to quickly dominate the viral population, and those viruses and their host gene targets were easily determined by deep sequencing. This process can be adapted to any pathogen capable of delivering the targeting RNA.

[0008] In embodiments, a nucleic acid vector comprises a heterologous promoter operably linked to an open reading frame encoding a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91. In embodiments, the promoter is a viral promoter. In embodiments the promoter is a CMV promotes, retroviral LTRs (e g., HIV, MLV), or an adenovirus promoter like E1A. In embodiments, the polypeptide has at least 90% or 95% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or the portion thereof. In embodiments, the vector is a viral vector. In embodiments, the vector is a plasmid.

[0009] Further provided is a host cell having the vector or the genome of which is augmented with nucleic acid encoding a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91 or comprising a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91. In embodiments, the host cells can comprise eukaryotic cells. In embodiments, the host cells can comprise prokaryotic cells. The vector or nucleic acid can be maintained extrachromosomally or stably integrated into the genome of the host cell. In embodiments, the host cell can comprise an insect cell, a plant cell, or a mammalian cell. In embodiments, the host cell is a MDCK cell or derivatives thereof, MDBK, VERO, A549, 293T, CaLu3, MRC5, avian eggs such as chicken eggs. In embodiments, the host cell comprises transgenic eggs expressing a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91.

[0010] Also provided is method to increase influenza virus yield in cells, comprising: contacting influenza virus and cells comprising the vector comprising a nucleic acid encoding a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91 or

contacted with a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91; and collecting progeny influenza virus. The cells can be human, canine, or non-human primate cells. In embodiments, the cells are Vero cells, MDCK cells, 293T or PER C6® cells, or MvLu1 cells. The cells can be contacted with the vector or the polypeptide before contacting the cells with the influenza virus. In embodiments, the cell is contacted with the vector or the polypeptide after contacting the cells with the influenza virus. The yield of influenza virus in cells contacted with the vector or the polypeptide can be increased at least two-fold relative to the corresponding yield in host cells not contacted with the vector or the polypeptide.

[0011] In embodiments, a method to detect influenza virus in a sample is provided, comprising: contacting cells having the vector comprising a nucleic acid encoding a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91 and a biological sample; and determining whether the sample comprises influenza virus. In embodiments, the cells are human, canine or non-human primate cells. In embodiments, the cells are Vero cells, MDCK cells, 293T or PER.C6® cells, or MvLu1 cells. In embodiments, the sample is a physiological sample. In embodiments, the sample is a nasal sample. In embodiments, the sample is a physiological fluid sample. In embodiments, the method does not include employing nucleic acid amplification.

[0012] A method to decrease influenza virus replication in a mammal is provided, comprising: administering to the mammal a composition that inhibits or prevents expression of a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91.

[0013] Further provided is a method to screen for compounds that alter the activity of a pathogen, comprising contacting cells expressing a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91 or an isolated polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91 and a sample having a pathogen; and determining whether the polypeptide alters the activity of the pathogen. In embodiments, the pathogen is a virus. In embodiments, the cells are mammalian cells. For example, the cells can be canine, non-human primate, or human cells. In embodiments, the cells are MDCK cells. Any cell, e.g., any avian or mammalian cell, such as a human, e.g., 293T or PER.C6® cells, or canine, e.g., MDCK, bovine, equine, feline, swine, ovine, rodent, for instance mink, e.g., MvLu1 cells, or hamster, e.g., CHO cells, or non-human primate, e.g., Vero cells, including mutant cells, which supports efficient replication of influenza virus can be employed.

[0014] In embodiments, a method to inhibit expression of pro-viral genes in a mammal is provided, comprising administering to the mammal an effective amount a composition that specifically inhibits the expression of a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91. In embodiments, the composition comprises RNA. In embodiments, the RNA comprises RNAi. In embodiments, the RNA comprises siRNA. In embodiments, the amount prevents or inhibits influenza virus replication.

[0015] In embodiments, a method to screen for inhibitory compounds is provided, comprising combining cells expressing a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91 or isolated nucleic acid that encodes a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91 and one or more test compounds; and determining whether the one or more test compounds inhibit expression of the polypeptide or inhibit transcription or translation of the isolated nucleic acid. Any cell, e.g., any avian or mammalian cell, such as a human, e.g., 293T or PER.C6® cells, or canine, e.g., MDCK, bovine, equine, feline, swine, ovine, rodent, for instance mink, e.g., MvLu1 cells, or hamster, e.g., CHO cells, or non-human primate, e.g., Vero cells, including mutant cells, which supports efficient replication of influenza virus can be employed.

[0016] In addition, disclosed herein are methods to prevent, inhibit, or treat influenza virus infection in an avian or a mammal is provided, comprising administering to the avian or mammal an effective amount of RNA that triggers RNA interference (RNAi), wherein the RNA encodes a polypeptide having at least 80% amino acid sequence identity to SEQ ID Nos. 1-36 or 74-91 or an antibody or antibody fragment thereof specific for one of SEQ ID Nos. 1-36 or 74-91. In embodiments, the mammal is a primate. In embodiments, the primate is a human. In embodiments, the RNA that triggers RNAi comprises small interfering RNAs (siRNA). In embodiments, the siRNA comprises microRNA (miRNA) or a binding site for miRNA. In embodiments, the miRNA binds to the S'UTR of RNA encoding one of SEQ ID Nos. 1-36 or 74-91. In embodiments, the RNAi binds to the 3'UTR of RNA encoding a polypeptide having at least 80% amino acid sequence identity to SEQ ID Nos. 1-36 or 74-91. In embodiments, the composition is locally administered, e.g., to the lungs. In embodiments, the composition is systemically administered or intranasally administered. The composition can comprise liposomes or nanoparticles comprising the siRNA. The antibody fragment can comprise Fab', F(ab')2, scFv or a single domain, e.g., of a heavy chain or light chain.

[0017] Described herein are methods to detect influenza virus in a sample, comprising: detecting in a biological sample the presence or amount of a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91.

BRIEF DESCRIPTION OF FIGURES

[0018] FIG. **1** illustrates host factors that influence influenza virus replication.

[0019] FIG. **2** illustrates loss of function using CRISPRi and gain of function using CRISPRa.

[0020] FIG. **3** illustrates constructs in the NS gene segment for CRISPRa.

[0021] FIG. **4** illustrates screening.

[0022] FIG. **5** illustrates sequentially passaging.

[0023] FIG. **6** illustrates enrichment of TRIPC viruses.

[0024] FIG. **7** illustrates changes in the population over sequential passages.

[0025] FIG. **8** shows identification of a host factor that promotes viral replication.

[0026] FIG. **9** compares knock out screens versus virus driven selections.

[0027] FIG. **10** illustrates CRISPRa and CRISPRi.

[0028] FIG. **11** illustrates use of CRISPRa and CRISPRi and sgRNAs.

[0029] FIG. **12** illustrates use of an example CRISPRa and sgRNA.

[0030] FIG. **13** illustrates virus driven selection of host modifiers.

[0031] FIGS. **14**A-**14**H illustrate how transcriptional regulation by influenza-programmed Cas9

[0032] (TRIPC) manipulates host gene expression to enable fitness-based screening. FIG. **14**A: Engineering influenza A virus (IAV) to express an sgRNA. Cartoon detailing engineering of the NS genome segment to encode and process the sgRNA needed to program Cas9 for CRISPR activation (CRISPRa)-mediated gene expression. FIG. **14**B: Validation of TRIPC in transfected cells. TRIPC activation (TRIPCa) of a luciferase reporter targeted by sgRNA expressed from transfected NS (left). Inclusion of the viral polymerase and NP (+RNP), which amplify NS transcription and replication, boosts TRIPCa (right). FIG. **14**C: TRIPC virus replicates similar to WT. Multicycle replication in A549 cells inoculated with IAV harboring a WT or engineered NS segment (MOI=0.01). Viral titers were determined by plaque assay. Example plaque morphologies are shown. Engineered NS segment integrity over serial passaging was confirmed by RT-PCR. FIG. **14**D: Virally delivered sgRNA activates reporter gene expression. A549-CR cells expressing dCas9-VP64 and MS2-p65-HSF1 were inoculated with WT, split-NS or a TRIPCa-NS virus (MOI=0.05) targeting the reporter promoter. Activation of the luciferase reporter was measured over the course of infection. FIG. **14**E: Virally delivered sgRNAs activate expression of host genes from the endogenous locus. A549-CR cells were inoculated with TRIPC viruses (MOI=5) targeting the indicated gene, a non-targeting control (NT) or mock. Host gene expression was measured at 8 hpi via RT-qPCR. FIG. **14**F: TRIPCa is suitable for fitness-based screening. A pool of 34 TRIPC viruses targeting a collection of 10 potential pro- or antiviral host genes were subject to 4 rounds of selection in A549-CR cells. Viruses present at each stage of selection were quantified by deep-sequencing and normalized sgRNA composition is depicted. Viruses activating proviral genes were enriched, with those >3x enriched colored green, while viruses activating antiviral genes drop out, with those >3x depleted colored red. Graph is representative of mean values for 2 replicate screens.

[0033] FIG. **14**G: TRIPCa screens are highly reproducible. Comparison of two biological replications shows nearly identical relative enrichment of TRIPC viruses targeting the indicated host genes after 4 rounds of selection. FIG. **14**H: TRIPC results reflect changes in viral replication. Multicycle replication in A549-CR cells of TRIPC viruses targeting specific host genes (MOI=0.01). Data are shown as means of 2 (f) or 3 (b-e, h) replicates±SEM (b, d) or s.d. (c, e, h). Pairwise T-tests or one-way ANOVA with post-hoc Tukey's tests were performed (*$p<0.05$, ** $p<0.01$, *** $p<0.001$, **** $p<0.0001$).

[0034] FIG. **15**A: TRIPCa functions in NS from primary isolates of IAV and IBV. TRIPCa of a luciferase reporter targeted by sgRNA expressed from transfected CA04 or IBV TRIPC-NS in the presence of the viral polymerase and NP. FIG. **15**B: TRIPC-inhibition (TRIPCi) suppresses gene expression. PR8 TRIPC-NS suppressed reporter gene expression when transfected into cells with the viral polymerase, NP, and dCas9-KRAB. FIG. **15**C: TRIPC viruses replicate like WT in multiple cell lines. Multicycle replication kinetics of WT, split-NS, or TRIPCa-NS with a non-targeting sgRNA in MDCK and A549-CR cells (MOI=0.01). FIG. **15**D: A549-CR cells support TRIPCa. Luciferase reporter expression was measured in A549-CR cells expressing split-NS or TRIPC-NS targeting the reporter promoter. FIG. **15**E: TRIPC targeting does not affect replication in cells lacking the CRISPRa machinery. Multicycle replication of TRIPC viruses targeting specified host genes in WT A549 cells inoculated at MOI=0.01. Data are shown as means of 3 replicates=SEM (a-b, d) or s.d. (c, c). Pairwise T-tests or one-way ANOVA with post-hoc Tukey's tests were performed (*$p<0.05$, ** $p<0.01$, *** $p<0.001$, **** $p<0.0001$).

[0035] FIGS. **16**A-**16**G illustrate genome-wide TRIPC screens identify new pro-IAV host factors. FIG. **16**A: Experimental design of a genome-wide TRIPC screen in CRISPRa cells. FIG. **16**B: TRIPCa selects viruses that replicate at higher levels. Viral titers (left Y-axis) and number of unique TRIPC viruses (right Y-axis) over the course of 5 rounds of selection for replicates A, B and C. FIG. **16**C: TRIPCa enriches specific viruses. Stack plot of the abundance of individual TRIPC viruses. Viruses enriched >4-fold at passage 5 are plotted for each replicate. FIG. **16**D: Final abundance is independent of starting abundance. Final abundance of individual TRIPC viruses at passage 5 as a function of their abundance at passage 0 for all replicates. Colors represent viruses >4-fold enriched (green) or >4-fold depleted (red) or unchanged (grey). FIG. **16**E: Robust ranking aggregation for top hits. MAGeCK gene scores for the top 30 genes in the TRIPC screens. FIG. **16**F: High reproducibility of top hits. Venn diagram of genes enriched >4-fold in the 3 screen replicates. FIG. **16**G: Enrichment of top hits. Bubble plot depicting positive selection values for all genes in the screen. Bubble size indicates the number of replicate screens in which that gene was detected. Colored dots represent genes >10-fold enriched, with labelled dots representing genes >20-fold enriched. Genes are randomly positions along the X-axis.

[0036] FIGS. **17**A-**17**D illustrate characterization of TRIPC library and gene enrichment analysis. FIG. **17**A: Experimental workflow for the creation of a genome-wide TRIPC virus library. FIG. **17**B: Individual members in the TRIPC library are evenly distributed. Distribution histogram and cumulative frequency plot of members of the TRIPC virus library. FIG. **17**C: Population diversity decreases during selection. Shannon's diversity indices of the viral populations across the 3 TRIPC screens. FIG. **17**D: High reproducibility of top hits. Venn diagram of TRIPC viruses that were >4-fold enriched at passage 5 across 3 screen replicates. Some viruses target activation of the same gene. GO analysis highlighting the enriched molecular function pathways among the top 100 genes (above). Groupings of high-level gene functions conferred by the top 100 genes (below).

[0037] FIGS. **18**A-**18**I illustrates methods to determine the activity of the identified factors employing the 3'-S' DNA exonuclease TREX1 as an example. FIGS. **18**A and **18**B: Multiple TRIPC viruses with distinct targeting sequences activate TREX1. A549-CR cells were inoculated at an MOI =1 with viruses targeting different sites in the TREX1 promoter or a non-targeting control. TREX1 expression was measured by RT-qPCR (FIG. **18**A) at 10 hpi and western blotting (FIG. **18**B) at 12 hpi. FIG. **18**C: TREX1 activation enhances viral growth. Multicycle replication of TREX1- or non-targeting TRIPC viruses in A549-CR cells (MOI=0.01). Titers were determined by plaque assay.

[0038] FIG. **18**D: TRIPC viruses activating TREX1 gain a fitness advantage. A pool of TRIPC viruses were allowed to compete for 48 h during replication in A549-CR cells (pooled MOI=0.05). Relative abundances at the start (input) and end (output) of the infection for each virus are shown for 2 independent replicates. FIG. **18**E: TREX1 over-expression increases replication. Multicycle replication of an influenza A reporter virus was performed in WT A549 cells or those stably expressing TREX1 or the catalytic mutant $TREX1^{D18N}$. FIGS. **18**F-**18**H: TREX1 knockout (KO) reduces viral replication. FIG. **18**F: Viral replication was measure at 48 hpi (MOI=0.05) in 3 distinct TREX1-KO clones. Clones were complemented with TREX1 or TREXID18N, where indicated. Values are compared to replication in parental WT A549 cells. FIG. **18**G: Multicycle replication in WT A549 cells, TREX1-KO cells, or complemented cell lines. FIG. **18**H: Loss of TREX1 decreases viral protein levels. NP protein levels at 24 hpi (above) and titers at 48 hpi (below) in the indicated cells inoculated with PR8 (MOI=0.01). FIG. **18**I: TREX1 stimulates replication of multiple primary influenza virus isolates and VSV. Replication of reporter viruses based on CA04 (MOI=0.5), S009 (MOI=0.05), B/Bris (MOI=0.2) at 48 h, and VSV (MOI=0. 001) at 24 h Cells are as described in H). Data are shown as means of 3 replicates #SEM (e-g, i) or s.d. (a, c, h-i). Pairwise T-tests or one-way ANOVA with post-hoc Tukey's tests were performed (*p<0.05, ** p<0.01, *** p<0.001, **** p<0.0001, ns=not significant).

[0039] FIGS. **19**A-**19**G illustrates methods to determine the activity of the identified factors employing TREX1 as an example. FIGS. **19**A-**19**B: TRIPC viruses do not activate TREX1 in WT A549 cells. TREX1 expression was measured in WT A549 inoculated with TREX1-targeting TRIPC viruses by RT-qPCR (MOI=1, 10 h) (FIG. **19**A) and protein expression (MOI=1, 12 h) (FIG. **19**B). FIG. **19**C: TRIPC viruses have no growth advantage in WT A549 cells. Multicycle replication of TREX1- or non-targeting TRIPC viruses in WT A549 cells (MOI=0.01). Titers determined by plaque assay FIG. **19**D: Transient expression of TREX1 boosts viral replication. Multicycle replication of a reporter IAV (MOI=0.05) in A549 cells transfected with GFP-tagged TREX1, TREXID18N or a GFP-alone control. FIG. **19**E: Multicycle replication of a reporter IAV (MOI=0.05) in polyclonal TREX1-KO cells. FIG. **19**F: TREX1 genotype of knockout cells. Sanger sequencing traces display CRISPR-Cas9 editing at the TREX1 locus for 3 selected knockout clones. Edits compared to the WT genome are shown for 2 homozygous (B6, C8) and 1 heterozygous (G11) clones. FIG. **19**G: Western blot demonstrating TREX1 protein levels in WT, clonal KO, and complemented A549 lines utilized throughout. Endogenous TREX1 and recombinant TREX1-V5-2A are indicated. *=non-specific bands. Data are shown as means of 3 replicates±SEM (d-e) or s.d. (a-c). Pairwise T-tests or one-way ANOVA with post-hoc Tukey's tests were performed (*p<0.05, ** p<0.01, *** p<0.001, **** p<0.0001, ns=not significant).

[0040] FIGS. **20**A-**20**G illustrate TREX1 moderates DNA sensing to regulate RNA virus replication. FIG. **20**A: TREX1 controls sensing of foreign immunogenic DNA. WT and TREX1-KO reporter cells were transfected with indicated amounts of salmon sperm DNA and innate immune activation was measure with an IFN-stimulated response element (ISRE) reporter. Values are normalized to untransfected cells. FIG. **20**B: TREX1 regulates activation of endogenous IFN-stimulated genes (ISGs). WT, TREX-KO, or complemented cells were transfected with salmon sperm DNA. ISG expression was measure by RT-qPCR and normalized to untransfected controls. FIG. **20**C: Sensing of foreign DNA suppresses IAV replication. Replication of IAV (MOI=0.05) at 24 hpi in WT, TREX1-KO, or complemented cells transfected with salmon sperm DNA or mock treated. FIG. **20**D: IAV replicates better in cells lacking DNA sensing. Multicycle replication of IAV (MOI=0.05) in WT or STING-KO A549 cells. FIG. **20**E: Chemical activation of the cGAS/STING pathways blunts IAV replication. Multicycle replication of IAV (MOI=0.05) in A549 cells treated with a STING agonist (diABZI) or a DMSO control. FIG. **20**F: Activation of the DNA sensing pathway blocks replication of multiple primary influenza virus isolates and VSV A549 cells were treated with diABZI or control and inoculated with reporter viruses based on CA04 (MOI=0.5), S009 (MOI=0.05), B/Bris (MOI=0.2), or VSV (MOI=0.001). Relative replication was measured at 48 hpi for influenza viruses and 24 hpi for VSV. FIG. **20**G: The cGAS/STING pathway is not the only DNA sensor regulating infection. Replication of IAV (MOI=0.05) at 48 hpi in WT and STING-KO A549 cells stably expressing TREX1 where indicated. Data are shown as means of 3 replicates±SEM (a, c-g) or s.d. (b). Pairwise T-tests or one-way ANOVA with post-hoc Tukey's tests were performed (*p<0.05, ** p<0.01, *** p<0.001, **** p<0.0001, ns=not significant).

[0041] FIGS. **21**A-**21**D illustrate reporter cell line and IAV replication in MAVS-knockout. FIGS. **21**A-**21**B show IFN signaling and RNA sensing remain intact in TREX1-KO cells. ISRE induction in WT and TREX1-KO reporter cells treated with IFNβ (FIG. **21**A) or transfected with poly(I:C). ISRE activation is normalized to untreated and mock-transfected cells, respectively. C. Sensing of foreign nucleic acids blocks IAV replication. Replication of IAV (MOI=0.05) on WT A549 cells treated with the indicated nucleic acid ligands. D. Infection in cells lacking RNA sensing for comparison. Multicycle replication of IAV (MOI=0.05) in MAVSKO cells. Data are shown as means of 3 replicates±SEM. One-way ANOVA with post-hoc Tukey's tests were performed (*p<0.05, ** p<0.01, *** p<0.001, **** p<0.0001, ns=not significant).

[0042] FIGS. **22**A-**22**C illustrate TREX1 degrades self-DNA released during IAV infection. FIG. **22**A: IAV infection releases dsDNA into the cytoplasm. Immunofluorescence staining of WT, TREX1-KO and complemented A549 cells inoculated with PR8 (MOI=1). Blue=DAPI (nucleus), green=viral NP, red=dsDNA. FIG. **22**B: mtDNA release into the cytoplasm is exacerbarted in TEK1-KO cells. Cytosolic fractions were prepared from mock- or PR8-infected (MOI=1) cells. mtDNA was detected and quantified by qPCR and shown relative to mock-infected WT cells. FIG.

22C: Cytosolic DNA activates innate immune sensing. Cytosolic extracts were prepared from mock or infected A549 cells and re-introduced into WT or TREX1-KO ISRE reporter cells. Where indicated, extracts were pretreated with nucleases prior to transfection. ISRE activation is normalized to untransfected cells. Data are shown as means of 3 replicates±SEM (c) or s.d. (b). One-way ANOVA with post-hoc Tukey's tests were performed (*p<0.05, ** p<0.01, *** p<0.001, **** p<0.0001, ns=not significant).

[0043] FIGS. **23**A-**23**H illustrate TREX1 tempers the antiviral host response to IAV infection. A-B. TREX1 dampens DNA sensing FIG. **23**A: ISRE induction in WT and TREX1-KO reporter cells transfected with nucleic acids from A549 whole cell extracts±nuclease treatments. ISRE induction was normalized to untransfected cells. FIG. **23**B: Activation of endogenous ISGs measured by RT-qPCR in TREX-KO or complemented cell lines transfected with self nucleic acids ±nuclease treatments. Induction values are relative to untransfected cells. FIGS. **23**C-**23**D show TREX1 knockout boosts innate immune activation during infection. FIG. **23**C: ISRE induction in WT and TREX1-KO reporter cells infected with increasing amounts of IAV. ISRE induction was normalized to uninfected cells. FIG. **23**D: Activation of endogenous ISGs measured by RT-qPCR in cell lines infected with PR8 (MOI=0.5). Induction values are relative to uninfected cells. FIG. **23**E: Self-DNA sensing antagonizes IAV replication. IAV replication (MOI=0.05) in WT, TREX1-KO, and complemented A549 cells at 48 hpi. Cells were transfected with self nucleic acids and treated with nucleases where indicated. Viral replication values are relative to untreated WT cells. FIGS. **23**F-**23**H: Loss of TREX1 amplifies innate immune responses. FIG. **23**F: Gene enrichment analysis of all host genes upregulated >4-fold as gauged by RNA-seq in TREX1-KO and complemented cells 24 hpi with PR8 (MOI=0.5). FIG. **23**G: ISG induction in TREX-KO versus complemented cells following infection with PR8. Only ISGs induced >2-fold are shown, with diagonal lines separating ISGs where the induction level differs by at least 50% between cell lines. Gene enrichment analysis is shown for ISGs with higher induction in TREX1-KO cells (lower left) and ISGs with higher induction in complemented cells (lower right). FIG. **23**H: Abundance of IAV transcripts in infected TREX1-KO cells relative to infected complemented cells. Values were compiled from 3 RNA-seq experiments with p-values for each gene segment annotated. Data are shown as means of 3 replicates #SEM (A, C, E) or s.d. (B, D). Pairwise T-tests or one-way ANOVA with post-hoc Tukey's tests were performed (*p<0.05. ** p<0.01, *** p<0.001, **** p<0.0001, ns =not significant).

[0044] FIGS. **24**A-**24**C illustrate TREX1 modulates host gene expression but does not alter viral polymerase activity. FIG. **24**A: Viral polymerase activity is unchanged by TREX1 expression. IAV polymerase activity was measured in a mini-replicon assay in the presence of exogenous GFP-TREX1 or vector control. Data are shown as means of 3 replicates±SEM. Pairwise T-tests tests were performed (ns=not significant). FIG. **24**B: TREX1-KO cells exhibit a chronic inflammatory state. Differential expression analysis of RNA-seq data from uninfected TREX1-KO and complemented cells were subject to gene enrichment analysis for all host genes differentially upregulated >4-fold. Significantly enriched biological processes are shown along with their enrichment values. FIG. **24**C: Gene enrichment analysis of all ISGs with >2-fold induction in either TREX1-KO cells or complemented cells. Significantly enriched biological processes are shown along with their enrichment values.

[0045] FIG. **25** shows the amino acid sequences for the polypeptides of SEQ ID NOS: 74-91 and the corresponding nucleic acid sequences of SEQ ID NOs: 92-110 that encode the polypeptides of SEQ ID NOS: 74-91.

DETAILED DESCRIPTION

[0046] Many approaches to identify host factors regulating infection have relied upon loss-of-function screens, which leaves a large amount of genetic space unexplored and raises the possibility that entirely new classes of viral co-factors have yet to be discovered. CRISPR activation (CRISPRa) and CRISPR inhibition (CRISPRi) may be used to exploit the programmable nature of Cas9 to recruit transcriptional activators or repressor to discrete genomic loci, respectively. CRISPRa and CRISPRi permit both gain- and loss-of-function screens, something not achievable in prior genome-wide surveys of viral host factors.

[0047] As disclosed herein, CRISPR-Cas9 technology was adapted to be programmed by the pathogen itself. The pathogen encodes and expresses the targeting RNA that places Cas9 as specific sites in the host genome, termed transcriptional regulation by pathogen-programmed Cas9 (TRPPC). Using the RNA virus influenza virus as an exemplar, TRPPC viruses were shown to modulate host gene expression. Thus, influenza virus can be engineered to specifically and potently modulate expression of discrete host genes. This process can be adapted to any pathogen capable of delivering the targeting RNA. Given that the pathogen expresses essential components of the TRPPC platform, the screen itself only begins during infection, and only in infected cells, which results in the identification of host regulators in the middle-to-late stages of replication.

[0048] A pool of TRPPC influenza viruses was prepared targeting the entire genome and a genetic selection was performed allowing all viruses to compete with each other through multiple rounds of replication in human lung cells. Viruses within that population that activated pro-viral factors gained a replicative advantage and came to quickly dominate the viral population. Because the RNA programming Cas9 is encoded in the viral genome, the viruses with an advantage and their host gene targets are easily determined by deep sequencing. Moreover, as this is a fitness-based screen, TRPPC selections identify and inherently rank-order the most potent host regulators of viral replication. In short, the virus itself does the "heavy lifting" to pinpoint the cellular regulators of viral replication.

[0049] As an example, 36 host regulators of influenza virus replication whose expression enhances influenza virus replication, that were identified in a genome wide screen are disclosed herein. Several of these host regulators were individually tested for pro-viral properties for influenza virus. In embodiments, the host factor may increase viral yields ~10-fold, e.g., in human lung cells. Importantly, over-expression of the host factors results in higher levels of virus replication. These are targets to generate cell lines to increase virus yields.

Definitions

[0050] A "vector" or "delivery" vehicle refers to a macromolecule or association of macromolecules that comprises or associates with a polynucleotide or polypeptide, and

which can be used to mediate delivery of the polynucleotide or polypeptide to a cell or intercellular space, either in vitro or in vivo. Illustrative vectors include, for example, plasmids, viral vectors, liposomes, nanoparticles, or microparticles and other delivery vehicles. In embodiments, a polynucleotide to be delivered, sometimes referred to as a "target polynucleotide" or "transgene," may comprise a coding sequence of interest in gene therapy (such as a gene encoding a protein of therapeutic interest), a coding sequence of interest and/or a selectable or detectable marker.

[0051] "Transduction," "transfection," "transformation" or "transducing" as used herein, are terms referring to a process for the introduction of an exogenous polynucleotide into a host cell leading to expression of the polynucleotide, e.g., the transgene in the cell, and includes the use of recombinant virus to introduce the exogenous polynucleotide to the host cell. Transduction, transfection or transformation of a polynucleotide in a cell may be determined by methods well known to the art including, but not limited to, protein expression (including steady state levels), e.g., by ELISA, flow cytometry and Western blot, measurement of DNA and RNA by hybridization assays, e.g., Northern blots, Southern blots and gel shift mobility assays. Methods used for the introduction of the exogenous polynucleotide include well-known techniques such as viral infection or transfection, lipofection, transformation and electroporation, as well as other non-viral gene delivery techniques. The introduced polynucleotide may be stably or transiently maintained in the host cell.

[0052] "Gene delivery" refers to the introduction of an exogenous polynucleotide into a cell for gene transfer, and may encompass targeting, binding, uptake, transport, localization, replicon integration and expression.

[0053] "Gene transfer" refers to the introduction of an exogenous polynucleotide into a cell which may encompass targeting, binding, uptake, transport, localization and replicon integration, but is distinct from and does not imply subsequent expression of the gene.

[0054] "Gene expression" or "expression" refers to the process of gene transcription, translation, and post-translational modification.

[0055] An "infectious" virus or viral particle is one that comprises a polynucleotide component which is capable of delivering into a cell for which the viral species is trophic. The term does not necessarily imply any replication capacity of the virus.

[0056] The term "polynucleotide" refers to a polymeric form of nucleotides of any length, including deoxyribonucleotides or ribonucleotides, or analogs thereof. A polynucleotide may comprise modified nucleotides, such as methylated or capped nucleotides and nucleotide analogs, and may be interrupted by non-nucleotide components. If present, modifications to the nucleotide structure may be imparted before or after assembly of the polymer. The term polynucleotide, as used herein, refers interchangeably to double- and single-stranded molecules. Unless otherwise specified or required, any embodiment described herein 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.

[0057] A "transcriptional regulatory sequence" refers to a genomic region that controls the transcription of a gene or coding sequence to which it is operably linked. Transcriptional regulatory sequences of use generally include at least one transcriptional promoter and may also include one or more enhancers and/or terminators of transcription.

[0058] "Operably linked" refers to an arrangement of two or more components, wherein the components so described are in a relationship permitting them to function in a coordinated manner. By way of illustration, a transcriptional regulatory sequence or a promoter is operably linked to a coding sequence if the TRS or promoter promotes transcription of the coding sequence. An operably linked TRS is generally joined in cis with the coding sequence, but it is not necessarily directly adjacent to it.

[0059] "Heterologous" means derived from a genotypically distinct entity from the entity to which it is compared. For example, a polynucleotide introduced by genetic engineering techniques into a different cell type is a heterologous polynucleotide (and, when expressed, can encode a heterologous polypeptide). Similarly, a transcriptional regulatory element such as a promoter that is removed from its native coding sequence and operably linked to a different coding sequence is a heterologous transcriptional regulatory element.

[0060] A "terminator" refers to a polynucleotide sequence that tends to diminish or prevent read-through transcription (i.e., it diminishes or prevent transcription originating on one side of the terminator from continuing through to the other side of the terminator). The degree to which transcription is disrupted is typically a function of the base sequence and/or the length of the terminator sequence. In particular, as is well known in numerous molecular biological systems, particular DNA sequences, generally referred to as "transcriptional termination sequences" are specific sequences that tend to disrupt read-through transcription by RNA polymerase, presumably by causing the RNA polymerase molecule to stop and/or disengage from the DNA being transcribed. Typical example of such sequence-specific terminators include polyadenylation ("polyA") sequences, e.g., SV40 polyA. In addition to or in place of such sequence-specific terminators, insertions of relatively long DNA sequences between a promoter and a coding region also tend to disrupt transcription of the coding region, generally in proportion to the length of the intervening sequence. This effect presumably arises because there is always some tendency for an RNA polymerase molecule to become disengaged from the DNA being transcribed, and increasing the length of the sequence to be traversed before reaching the coding region would generally increase the likelihood that disengagement would occur before transcription of the coding region was completed or possibly even initiated. Terminators may thus prevent transcription from only one direction ("uni-directional" terminators) or from both directions ("bi-directional" terminators), and may be comprised of sequence-specific termination sequences or sequence-non-specific terminators or both. A variety of such terminator sequences are known in the art, and illustrative uses of such sequences within the context of the present disclosure are provided below.

[0061] "Host cells," "cell lines," "cell cultures," "packaging cell line" and other such terms denote higher eukaryotic cells, such as mammalian cells including human cells, useful in the present disclosure, e.g., to produce recombinant virus or recombinant polypeptide. These cells include the progeny of the original cell that was transduced. It is understood that

the progeny of a single cell may not necessarily be completely identical (in morphology or in genomic complement) to the original parent cell.

[0062] "Recombinant," as applied to a polynucleotide means that the polynucleotide is the product of various combinations of cloning, restriction and/or ligation steps, and other procedures that result in a construct that is distinct from a polynucleotide found in nature. A recombinant virus is a viral particle comprising a recombinant polynucleotide. The terms respectively include replicates of the original polynucleotide construct and progeny of the original virus construct.

[0063] A "control element" or "control sequence" is a nucleotide sequence involved in an interaction of molecules that contributes to the functional regulation of a polynucleotide, including replication, duplication, transcription, splicing, translation, or degradation of the polynucleotide. The regulation may affect the frequency, speed, or specificity of the process, and may be enhancing or inhibitory in nature. Control elements known in the art include, for example, transcriptional regulatory sequences such as promoters and enhancers. A promoter is a DNA region capable under certain conditions of binding RNA polymerase and initiating transcription of a coding region usually located downstream (in the 3' direction) from the promoter. Promoters include AAV promoters, e.g., P5, P19, P40 and AAV ITR promoters, as well as heterologous promoters.

[0064] An "expression vector" is a vector comprising a region which encodes a gene product of interest, and is used for effecting the expression of the gene product in an intended target cell. An expression vector also comprises control elements operatively linked to the encoding region to facilitate expression of the protein in the target. The combination of control elements and a gene or genes to which they are operably linked for expression is sometimes referred to as an "expression cassette," a large number of which are known and available in the art or can be readily constructed from components that are available in the art.

[0065] The terms "polypeptide" and "protein" are used interchangeably herein to refer to polymers of amino acids of any length. The terms also encompass an amino acid polymer that has been modified; for example, disulfide bond formation, glycosylation, acetylation, phosphorylation, lipidation, or conjugation with a labeling component.

[0066] An "isolated" polynucleotide, e.g., plasmid, virus, polypeptide or other substance refers to a preparation of the substance devoid of at least some of the other components that may also be present where the substance or a similar substance naturally occurs or is initially prepared from. Thus, for example, an isolated substance may be prepared by using a purification technique to enrich it from a source mixture. Isolated nucleic acid, peptide or polypeptide is present in a form or setting that is different from that in which it is found in nature. For example, a given DNA sequence (e g., a gene) is found on the host cell chromosome in proximity to neighboring genes; RNA sequences, such as a specific mRNA sequence encoding a specific protein, are found in the cell as a mixture with numerous other mRNAs that encode a multitude of proteins. The isolated nucleic acid molecule may be present in single-stranded or double-stranded form. When an isolated nucleic acid molecule is to be utilized to express a protein, the molecule will contain at a minimum the sense or coding strand (i.e., the molecule may single-stranded), but may contain both the sense and anti-sense strands (i.e., the molecule may be double-stranded). Enrichment can be measured on an absolute basis, such as weight per volume of solution, or it can be measured in relation to a second, potentially interfering substance present in the source mixture. For example, a 2-fold enrichment, 10-fold enrichment, 100-fold enrichment, or a 1000-fold enrichment.

[0067] A "transcriptional regulatory sequence" refers to a genomic region that controls the transcription of a gene or coding sequence to which it is operably linked. Transcriptional regulatory sequences of use generally include at least one transcriptional promoter and may also include one or more enhancers and/or terminators of transcription.

[0068] "Operably linked" refers to an arrangement of two or more components, wherein the components so described are in a relationship permitting them to function in a coordinated manner. By way of illustration, a transcriptional regulatory sequence or a promoter is operably linked to a coding sequence if the TRS or promoter promotes transcription of the coding sequence. An operably linked TRS is generally joined in cis with the coding sequence, but it is not necessarily directly adjacent to it.

[0069] "Conservative" amino acid substitutions are, for example, aspartic-glutamic as polar acidic amino acids; lysine/arginine/histidine as polar basic amino acids; leucine/isoleucine/methionine/valine/alanine/glycine/proline as non-polar or hydrophobic amino acids; serine/threonine as polar or uncharged hydrophilic amino acids. Conservative amino acid substitution also includes groupings based on side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. For example, it is reasonable to expect that replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid will not have a major effect on the properties of the resulting polypeptide. Whether an amino acid change results in a functional polypeptide can readily be determined by assaying the specific activity of the polypeptide. Naturally occurring residues are divided into groups based on common side-chain properties: (1) hydrophobic: norleucine, met, ala, val, leu, ile; (2) neutral hydrophilic: cys, ser, thr; (3) acidic: asp, glu; (4) basic: asn, gln, his, lys, arg; (5) residues that influence chain orientation: gly, pro, and (6) aromatic; trp, tyr, phe.

[0070] The disclosure also envisions polypeptides with non-conservative substitutions. Non-conservative substitutions entail exchanging a member of one of the classes described above for another.

[0071] As used herein, "individual" (as in the subject of the treatment) means a mammal. Mammals include, for example, humans; non-human primates, e.g., apes and monkeys; and non-primates, e.g., dogs, cats, rats, mice, cattle, horses, sheep, and goats. Non-mammals include, for example, fish and birds.

[0072] "Substantially" as the term is used herein means completely or almost completely; for example, a composition that is "substantially free" of a component either has none of the component or contains such a trace amount that any relevant functional property of the composition is unaffected by the presence of the trace amount, or a compound is "substantially pure" is there are only negligible traces of impurities present.

[0073] "Treating" or "treatment" within the meaning herein refers to an alleviation of symptoms associated with a disorder or disease, "inhibiting" means inhibition of further progression or worsening of the symptoms associated with the disorder or disease, and "preventing" refers to prevention of the symptoms associated with the disorder or disease.

[0074] As used herein, an "effective amount" or a "therapeutically effective amount" of an agent, refers to an amount of the agent that alleviates, in whole or in part, symptoms associated with the disorder or condition, or halts or slows further progression or worsening of those symptoms, or prevents or provides prophylaxis for the disorder or condition, e.g., an amount that is effective to prevent, inhibit or treat in the individual one or more symptoms.

[0075] In particular, a "therapeutically effective amount" refers to an amount effective, at dosages and for periods of time necessary, to achieve the desired therapeutic result A therapeutically effective amount is also one in which any toxic or detrimental effects of the agent(s)are outweighed by the therapeutically beneficial effects.

[0076] The term "sequence" refers to a nucleotide sequence of any length, which can be DNA or RNA; can be linear, circular or branched and can be either single-stranded or double stranded. The term "donor sequence" refers to a nucleotide sequence that is inserted into a genome. A donor sequence can be of any length, for example between 2 and 10,000 nucleotides in length (or any integer value therebetween or thereabove), e.g., between about 100 and 1,000 nucleotides in length (or any integer therebetween), e.g., between about 200 and 500 nucleotides in length. For example, an exogenous nucleic acid can comprise an infecting viral genome, a plasmid or episome introduced into a cell, or a chromosome that is not normally present in the cell. Methods for the introduction of exogenous molecules into cells are known to those of skill in the art and include, but are not limited to, lipid-mediated transfer (e.g., liposomes, including neutral and cationic lipids), electroporation, direct injection, cell fusion, particle bombardment, calcium phosphate co-precipitation, DEAE-dextran-mediated transfer and viral vector-mediated transfer. An exogenous molecule can also be the same type of molecule as an endogenous molecule but derived from a different species than the cell is derived from. For example, a human nucleic acid sequence may be introduced into a cell line originally derived from a mouse or hamster.

[0077] The term "exogenous," when used in relation to a protein, gene, nucleic acid, or polynucleotide in a cell or organism refers to a protein, gene, nucleic acid, or polynucleotide which has been introduced into the cell or organism by artificial or natural means. An exogenous nucleic acid may be from a different organism or cell, or it may be one or more additional copies of a nucleic acid which occurs naturally within the organism or cell. By way of a non-limiting example, an exogenous nucleic acid is in a chromosomal location different from that of natural cells, or is otherwise flanked by a different nucleic acid sequence than that found in nature, e.g., an expression cassette which links a promoter from one gene to an open reading frame for a gene product from a different gene.

[0078] "Transformed" or "transgenic" is used herein to include any host cell or cell line, which has been altered or augmented by the presence of at least one recombinant DNA sequence. The host cells are typically produced by transfection with a DNA sequence in a plasmid expression vector, as an isolated linear DNA sequence, or infection with a recombinant viral vector.

[0079] The term "sequence homology" means the proportion of base matches between two nucleic acid sequences or the proportion amino acid matches between two amino acid sequences. When sequence homology is expressed as a percentage, e.g., 50%, the percentage denotes the proportion of matches over the length of a selected sequence that is compared to some other sequence. Gaps (in either of the two sequences) are permitted to maximize matching; gap lengths of 15 bases or less are usually used, or 6 bases or less or 2 bases or less. When using oligonucleotides as probes or treatments, the sequence homology between the target nucleic acid and the oligonucleotide sequence is generally not less than 17 target base matches out of 20 possible oligonucleotide base pair matches (85%); not less than 9 matches out of 10 possible base pair matches (90%), or not less than 19 matches out of 20 possible base pair matches (95%).

[0080] Two amino acid sequences are homologous if there is a partial or complete identity between their sequences. For example, 85% homology means that 85% of the amino acids are identical when the two sequences are aligned for maximum matching. Gaps (in either of the two sequences being matched) are allowed in maximizing matching; gap lengths of 5 or less or 2 or less. Alternatively, two protein sequences (or polypeptide sequences derived from them of at least 30 amino acids in length) are homologous, as this term is used herein, if they have an alignment score of at more than 5 (in standard deviation units) using the program ALIGN with the mutation data matrix and a gap penalty of 6 or greater. The two sequences or parts thereof are more homologous if their amino acids are greater than or equal to 50% identical when optimally aligned using the ALIGN program.

[0081] The term "corresponds to" is used herein to mean that a polynucleotide sequence is structurally related to all or a portion of a reference polynucleotide sequence, or that a polypeptide sequence is structurally related to all or a portion of a reference polypeptide sequence, e.g., they have at least 80%, 82%, 85%, 87%, 90%, 92%, 95%, 97% or more, e.g., 99% or 100%, sequence identity. In contradistinction, the term "complementary to" is used herein to mean that the complementary sequence is homologous to all or a portion of a reference polynucleotide sequence. For illustration, the nucleotide sequence "TATAC" corresponds to a reference sequence "TATAC" and is complementary to a reference sequence "GTATA".

[0082] The term "sequence identity" means that two polynucleotide sequences are identical (i.e., on a nucleotide-by-nucleotide basis) over the window of comparison. The term "percentage of sequence identity" means that two polynucleotide sequences are identical (i.e., on a nucleotide-by-nucleotide basis) over the window of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over the window of comparison, determining the number of positions at which the identical nucleic acid base (e.g., A. T, C, G, U, or I) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison (i.e., the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The terms "substantial identity" as used herein denote a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 85 percent sequence identity, e.g., at least 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison window of at least 20 nucleotide positions, frequently over a window of at least 20-50 nucleotides, wherein the percentage of sequence identity is calculated by comparing the reference sequence to the polynucleotide sequence which may include deletions or additions which total 20 percent or less of the reference sequence over the window of comparison.

[0083] As used herein, "substantially pure" or "purified" means an object species is the predominant species present (i.e., on a molar basis it is more abundant than any other individual species in the composition), for instance, a substantially purified fraction is a composition wherein the object species comprises at least about 50 percent (on a molar basis) of all macromolecular species present. Generally, a substantially pure composition will comprise more than about 80 percent of all macromolecular species present in the composition, or more than about 85%, about 90%,

about 95%, and about 99%. The object species may be purified to essential homogeneity (contaminant species cannot be detected in the composition by conventional detection methods) wherein the composition consists essentially of a single macromolecular species.

Preparation of Expression Cassettes

[0084] To prepare expression cassettes encoding one of SEQ ID Nos. 1-36 or 74-91 or truncated forms thereof (a "portion"), a peptide thereof, or a fusion thereof, for transformation, the recombinant DNA sequence or segment may be circular or linear, double-stranded or single-stranded. A DNA sequence which encodes an RNA sequence that is substantially complementary to a mRNA sequence encoding a gene product of interest is typically a "sense" DNA sequence cloned into a cassette in the opposite orientation (i.e., 3' to 5' rather than 5' to 3'). Generally, the DNA sequence or segment is in the form of chimeric DNA, such as plasmid DNA, that can also contain coding regions flanked by control sequences which promote the expression of the DNA in a cell. As used herein, "chimeric" means that a vector comprises DNA from at least two different species, or comprises DNA from the same species, which is linked or associated in a manner which does not occur in the "native" or wild-type of the species.

[0085] Aside from DNA sequences that serve as transcription units, or portions thereof, a portion of the DNA may be untranscribed, serving a regulatory or a structural function. For example, the DNA may itself comprise a promoter that is active in eukaryotic cells, e.g., mammalian cells, or in certain cell types, or may utilize a promoter already present in the genome that is the transformation target of the lymphotrophic virus. Such promoters include the CMV promoter, as well as the SV40 late promoter and retroviral LTRs (long terminal repeat elements), although many other promoter elements well known to the art may be employed, e.g., the MMTV, RSV, MLV or HIV LTR. In embodiments, expression is inducible. In embodiments, a tissue-specific promoter (or enhancer) is employed.

[0086] Other elements functional in the host cells, such as introns, enhancers, polyadenylation sequences and the like, may also be a part of the recombinant DNA. Such elements may or may not be necessary for the function of the DNA but may provide improved expression of the DNA by affecting transcription, stability of the mRNA, or the like. Such elements may be included in the DNA as desired to obtain the optimal performance of the transforming DNA in the cell. The recombinant DNA to be introduced into the cells may contain either a selectable marker gene or a reporter gene or both to facilitate identification and selection of transformed cells from the population of cells sought to be transformed. Alternatively, the selectable marker may be carried on a separate piece of DNA and used in a co-transformation procedure. Both selectable markers and reporter genes may be flanked with appropriate regulatory sequences to enable expression in the host cells. Useful selectable markers are well known in the art and include, for example, antibiotic and herbicide-resistance genes, such as neo, hpt, dhfr, bar, aroA, puro, hyg, dapA and the like. See also, the genes listed on Table 1 of Lundquist et. al. (U.S. Pat. No. 5,848,956).

[0087] Reporter genes are used for identifying potentially transformed cells and for evaluating the functionality of regulatory sequences. Reporter genes which encode for easily assayable proteins are well known in the art. In general, a reporter gene is a gene which is not present in or expressed by the recipient organism or tissue and which encodes a protein whose expression is manifested by some easily detectable property, e.g., enzymatic activity. Example reporter genes include the chloramphenicol acetyl transferase gene (cat) from Tn9 of *E. coli*, the beta-glucuronidase gene (gus) of the uidA locus of *E. coli*, the green, red, or blue fluorescent protein gene, and the luciferase gene. Expression of the reporter gene is assayed at a suitable time after the DNA has been introduced into the recipient cells.

[0088] The general methods for constructing recombinant DNA which can transform target cells are well known to those skilled in the art, and the same compositions and methods of construction may be utilized to produce the DNA useful herein.

[0089] The recombinant DNA can be readily introduced into the host cells, e.g., mammalian, bacterial, yeast or insect cells, or prokaryotic cells, by transfection with an expression vector comprising the recombinant DNA by any procedure useful for the introduction into a particular cell, e.g., physical or biological methods, to yield a transformed (transgenic) cell having the recombinant DNA so that the DNA sequence of interest is expressed by the host cell. In embodiments, the recombinant DNA is stably integrated into the genome of the cell.

[0090] Physical methods to introduce a recombinant DNA into a host cell include calcium-mediated methods, lipofection, particle bombardment, microinjection, electroporation, and the like. Biological methods to introduce the DNA of interest into a host cell include the use of DNA and RNA viral vectors. Viral vectors, e.g., retroviral or lentiviral vectors, have become a widely used method for inserting genes into eukaryotic cells, such as mammalian, e.g., human cells. Other viral vectors can be derived from poxviruses, e.g., vaccinia viruses, herpes viruses, adenoviruses, adeno-associated viruses, baculoviruses, and the like.

[0091] To confirm the presence of the recombinant DNA sequence in the host cell, a variety of assays may be performed. Such assays include, for example, molecular biological assays well known to those of skill in the art, such as Southern and Northern blotting, RT-PCR and PCR; biochemical assays, such as detecting the presence or absence of a particular gene product, e.g., by immunological means (ELISAs and Western blots) or by other molecular assays.

[0092] To detect and quantitate RNA produced from introduced recombinant DNA segments, RT-PCR may be employed. In this application of PCR, it is first necessary to reverse transcribe RNA into DNA, using enzymes such as reverse transcriptase, and then through the use of conventional PCR techniques amplify the DNA. In most instances PCR techniques, while useful, will not demonstrate integrity of the RNA product. Further information about the nature of the RNA product may be obtained by Northern blotting. This technique demonstrates the presence of an RNA species and gives information about the integrity of that RNA. The presence or absence of an RNA species can also be determined using dot or slot blot Northern hybridizations. These techniques are modifications of Northern blotting and only demonstrate the presence or absence of an RNA species.

[0093] While Southern blotting and PCR may be used to detect the recombinant DNA segment in question, they do not provide information as to whether the recombinant DNA segment is being expressed. Expression may be evaluated by specifically identifying the peptide products of the introduced DNA sequences or evaluating the phenotypic changes brought about by the expression of the introduced DNA segment in the host cell.

Vectors or Vehicles for Delivery

[0094] Delivery vectors or vehicles include, for example, viral vectors, microparticles, nanoparticles, liposomes and other lipid-containing complexes, and other macromolecular complexes capable of mediating delivery of a gene or a protein to a host cell, e.g., a gene to provide for recombinant expression of a polypeptide encoded by the gene. Vectors or vehicles can also comprise other components or function-

alities that further modulate gene delivery and/or gene expression, or that otherwise provide beneficial properties. Such other components include, for example, components that influence binding or targeting to cells (including components that mediate cell-type or tissue-specific binding); components that influence uptake of the vector by the cell; components that influence localization of the transferred gene within the cell after uptake (such as agents mediating nuclear localization); and components that influence expression of the gene. Such components also might include markers, such as detectable and/or selectable markers that can be used to detect or select for cells that have taken up and are expressing the nucleic acid delivered by the vector or have taken up protein delivered by a vehicle. Such components can be provided as a natural feature of the vector (such as the use of certain viral vectors which have components or functionalities mediating binding and uptake), or vectors can be modified to provide such functionalities. Selectable markers can be positive, negative or bifunctional. Positive selectable markers allow selection for cells carrying the marker, whereas negative selectable markers allow cells carrying the marker to be selectively eliminated. A variety of such marker genes have been described, including bifunctional (i.e., positive/negative) markers (see, e.g., WO 92/08796; and WO 94/28143). Such marker genes can provide an added measure of control that can be advantageous in gene therapy contexts. A large variety of such vectors are known in the art and are generally available.

[0095] Vectors or vehicles within the scope of the disclosure include, but are not limited to, isolated nucleic acid, e.g., plasmid-based vectors which may be extrachromosomally maintained, and viral vectors, e.g., recombinant adenovirus, retrovirus, lentivirus, herpesvirus, poxvirus, papilloma virus, or adeno-associated virus, including viral and non-viral vectors, or proteins which are present in liposomes, e.g., neutral or cationic liposomes, such as DOSPA/DOPE, DOGS/DOPE or DMRIE/DOPE liposomes, and/or associated with other molecules such as DNA-anti-DNA antibody-cationic lipid (DOTMA/DOPE) complexes. Vectors or vehicles may be administered via any route including, but not limited to, intramuscular, buccal, rectal, intravenous or intracoronary administration, and transfer to cells may be enhanced using electroporation and/or iontophoresis. In embodiments, vectors are locally administered.

[0096] In embodiments, an isolated polynucleotide or vector having that polynucleotide, encoding a polypeptide or fusion protein that has substantial identity, e.g., at least 80% or more, e.g., 85%, 87%, 90%, 92%, 95%, 97%, 98%, 99% and up to 100%, amino acid sequence identity to one of SEQ ID NOs. 1-36 or 74-91, or a portion thereof, is envisioned.

Retroviral Vectors

[0097] Retroviral vectors exhibit several distinctive features including their ability to stably and precisely integrate into the host genome providing long-term transgene expression. These vectors can be manipulated ex vivo to eliminate infectious gene particles to minimize the risk of systemic infection and patient-to-patient transmission. Pseudotyped retroviral vectors can alter host cell tropism.

Lentiviruses

[0098] Lentiviruses are derived from a family of retroviruses that include human immunodeficiency virus and feline immunodeficiency virus. However, unlike retroviruses that only infect dividing cells, lentiviruses can infect both dividing and nondividing cells. Although lentiviruses have specific tropisms, pseudotyping the viral envelope with vesicular stomatitis virus yields virus with a broader range (Schnepp et al., Meth. Mol. Med., 69:427 (2002)).

Adenoviral Vectors

[0099] Adenoviral vectors may be rendered replication-incompetent by deleting the early (E1A and E1B) genes responsible for viral gene expression from the genome and are stably maintained into the host cells in an extrachromosomal form. These vectors have the ability to transfect both replicating and nonreplicating cells and, in particular, these vectors have been shown to efficiently infect cardiac myocytes in vivo, e.g., after direction injection or perfusion. Adenoviral vectors have been shown to result in transient expression of therapeutic genes in vivo, peaking at 7 days and lasting approximately 4 weeks. The duration of transgene expression may be improved in systems utilizing neural specific promoters. In addition, adenoviral vectors can be produced at very high titers, allowing efficient gene transfer with small volumes of virus.

Adeno-Associated Virus Vectors

[0100] Recombinant adeno-associated viruses (rAAV) are derived from nonpathogenic parvoviruses, evoke essentially no cellular immune response, and produce transgene expression lasting months in most systems. Moreover, like adenovirus, adeno-associated virus vectors also have the capability to infect replicating and nonreplicating cells and are believed to be nonpathogenic to humans.

[0101] AAV vectors include but are not limited to AAV1, AAV2, AAV5, AAV7, AAV8, AAV9 or AAVrh. 10.

Plasmid DNA Vectors

[0102] Plasmid DNA is often referred to as "naked DNA" to indicate the absence of a more elaborate packaging system. Direct injection of plasmid DNA to myocardial cells in vivo has been accomplished. Plasmid-based vectors are relatively nonimmunogenic and nonpathogenic, with the potential to stably integrate in the cellular genome, resulting in long-term gene expression in postmitotic cells in vivo. Plasmid DNA may be delivered to cells as part of a macromolecular complex, e.g., a liposome or DNA-protein complex, and delivery may be enhanced using techniques including electroporation.

Peptides, Polypeptides and Fusion Proteins

[0103] The peptide, polypeptide or fusion proteins can be synthesized in vitro, e.g., by the solid phase peptide synthetic method or by recombinant DNA approaches (see above). The solid phase peptide synthetic method is an established and widely used method. These polypeptides can be further purified by fractionation on immunoaffinity or ion-exchange columns; ethanol precipitation; reverse phase HPLC; chromatography on silica or on an anion-exchange resin such as DEAE; chromatofocusing, SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; or ligand affinity chromatography.

[0104] Once isolated and characterized, chemically modified derivatives of a given peptide, polypeptide or fusion thereof, can be readily prepared. For example, amides of the peptide, polypeptide or fusion thereof may also be prepared by techniques well known in the art for converting a carboxylic acid group or precursor, to an amide. One method for amide formation at the C-terminal carboxyl group is to cleave the peptide, polypeptide or fusion thereof from a solid support with an appropriate amine, or to cleave in the presence of an alcohol, yielding an ester, followed by aminolysis with the desired amine.

[0105] Salts of carboxyl groups of a peptide, polypeptide or fusion thereof may be prepared in the usual manner by contacting the peptide, polypeptide, or fusion thereof with one or more equivalents of a desired base such as, for example, a metallic hydroxide base, e.g., sodium hydroxide;

a metal carbonate or bicarbonate base such as, for example, sodium carbonate or sodium bicarbonate; or an amine base such as, for example, triethylamine, triethanolamine, and the like.

[0106] N-acyl derivatives of an amino group of the peptide, polypeptide or fusion thereof may be prepared by utilizing an N-acyl protected amino acid for the final condensation, or by acylating a protected or unprotected peptide, polypeptide, or fusion thereof. O-acyl derivatives may be prepared, for example, by acylation of a free hydroxy polypeptide or polypeptide resin. Either acylation may be carried out using standard acylating reagents such as acyl halides, anhydrides, acyl imidazoles, and the like. Both N- and O-acylation may be carried out together, if desired.

[0107] Formyl-methionine, pyroglutamine and trimethyl-alanine may be substituted at the N-terminal residue of the polypeptide. Other amino-terminal modifications include aminooxypentane modifications.

[0108] In embodiments, an isolated peptide, polypeptide or fusion protein has substantial identity, e.g., at least 80% or more, e.g., 85%, 87%, 90%, 92%, 95%, 97%, 98%, 99% and up to 100%, amino acid sequence identity to one of SEQ ID NOs. 1-36 or 74-91 or portion thereof, is envisioned.

[0109] Substitutions may include substitutions which utilize the D rather than L form, as well as other well known amino acid analogs, e.g., unnatural amino acids such as a, a-disubstituted amino acids, N-alkyl amino acids, lactic acid, and the like. These analogs include phosphoserine, phosphothreonine, phosphotyrosine, hydroxyproline, gamma-carboxyglutamate; hippuric acid, octahydroindole-2-carboxylic acid, statine, 1,2,3,4,-tetrahydroisoquinoline-3-carboxylic acid, penicillamine, ornithine, citruline, α-methyl-alanine, para-benzoyl-phenylalanine, phenylglycine, propargylglycine, sarcosine, ε-N,N,N-trimethyllysine, ε-N-acetyllysine, N-acetylserine, N-formylmethionine, 3-methylhistidine, 5-hydroxylysine, w-N-methylarginine, and other similar amino acids and imino acids and tert-butylglycine.

[0110] Conservative amino acid substitutions may be employed—that is, for example, aspartic-glutamic as acidic amino acids; lysine/arginine/histidine as polar basic amino acids; leucine/isoleucine/methionine/valine/alanine/proline/glycine non-polar or hydrophobic amino acids; serine/threonine as polar or hydrophilic amino acids Conservative amino acid substitution also includes groupings based on side chains. For example, a group of amino acids having aliphatic side chains is glycine, alanine, valine, leucine, and isoleucine; a group of amino acids having aliphatic-hydroxyl side chains is serine and threonine; a group of amino acids having amide-containing side chains is asparagine and glutamine; a group of amino acids having aromatic side chains is phenylalanine, tyrosine, and tryptophan; a group of amino acids having basic side chains is lysine, arginine, and histidine; and a group of amino acids having sulfur-containing side chains is cysteine and methionine. For example, it is reasonable to expect that replacement of a leucine with an isoleucine or valine, an aspartate with a glutamate, a threonine with a serine, or a similar replacement of an amino acid with a structurally related amino acid will not have a major effect on the properties of the resulting peptide, polypeptide or fusion polypeptide. Whether an amino acid change results in a functional peptide, polypeptide or fusion polypeptide can readily be determined by assaying the specific activity of the peptide, polypeptide or fusion polypeptide.

[0111] Amino acid substitutions are, in general, accomplished by selecting substitutions that do not differ significantly in their effect on maintaining (a) the structure of the peptide backbone in the area of the substitution, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

[0112] (1) hydrophobic: norleucine, met, ala, val, leu, ile;

[0113] (2) neutral hydrophilic: cys, ser, thr;

[0114] (3) acidic: asp, glu;

[0115] (4) basic: asn, gln, his, lys, arg;

[0116] (5) residues that influence chain orientation: gly, pro; and

[0117] (6) aromatic; trp, tyr, phe.

[0118] The disclosure also envisions a peptide, polypeptide or fusion polypeptide with non-conservative substitutions. Non-conservative substitutions entail exchanging a member of one of the classes described above for another.

[0119] Acid addition salts of the peptide, polypeptide or fusion polypeptide or of amino residues of the peptide, polypeptide or fusion polypeptide may be prepared by contacting the polypeptide or amine with one or more equivalents of the desired inorganic or organic acid, such as, for example, hydrochloric acid. Esters of carboxyl groups of the polypeptides may also be prepared by any of the usual methods known in the art.

Formulations and Dosages

[0120] The polypeptides or fusions thereof, or nucleic acid encoding the polypeptide or fusion or the complement thereof, e.g., RNAi, can be formulated as pharmaceutical compositions and administered to a mammalian host, such as a human patient in a variety of forms adapted to the chosen route of administration, e.g., orally or parenterally, by intravenous, intramuscular, topical or subcutaneous routes.

[0121] In embodiments, the polypeptides or fusions thereof, or nucleic acid encoding the polypeptide or fusion, or the complement thereof, may be administered by infusion or injection. Solutions of the polypeptides or fusions thereof, or nucleic acid encoding the polypeptide or fusion or the complement thereof, or its salts can be prepared in water, optionally mixed with a nontoxic surfactant. Dispersions can also be prepared in glycerol, liquid polyethylene glycols, triacetin, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations contain a preservative to prevent the growth of microorganisms.

[0122] The pharmaceutical dosage forms suitable for injection or infusion may include sterile aqueous solutions or dispersions or sterile powders comprising the active ingredient which are adapted for the extemporaneous preparation of sterile injectable or infusible solutions or dispersions, optionally encapsulated in liposomes. In all cases, the ultimate dosage form should be sterile, fluid and stable under the conditions of manufacture and storage. The liquid carrier or vehicle can be a solvent or liquid dispersion medium comprising, for example, water, ethanol, a polyol (for example, glycerol, propylene glycol, liquid polyethylene glycols, and the like), vegetable oils, nontoxic glyceryl esters, and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the formation of liposomes, by the maintenance of the required particle size in the case of dispersions or by the use of surfactants. The prevention of the action of microorganisms can be brought about by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it may be preferable to include isotonic agents, for example, sugars, buffers or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate and gelatin.

[0123] Sterile injectable solutions are prepared by incorporating the active agent in the required amount in the

appropriate solvent with various of the other ingredients enumerated above, as required, followed by filter sterilization. In the case of sterile powders for the preparation of sterile injectable solutions, the methods of preparation include vacuum drying and the freeze drying techniques, which yield a powder of the active ingredient plus any additional desired ingredient present in the previously sterile-filtered solutions.

[0124] Useful solid carriers may include finely divided solids such as tale, clay, microcrystalline cellulose, silica, alumina and the like. Useful liquid carriers include water, alcohols or glycols or water-alcohol/glycol blends, in which the present compounds can be dissolved or dispersed at effective levels, optionally with the aid of non-toxic surfactants. Adjuvants such as antimicrobial agents can be added to optimize the properties for a given use. Thickeners such as synthetic polymers, fatty acids, fatty acid salts and esters, fatty alcohols, modified celluloses or modified mineral materials can also be employed with liquid carriers to form spreadable pastes, gels, ointments, soaps, and the like, for application directly to the skin of the user.

[0125] Useful dosages of the polypeptides or fusions thereof, or nucleic acid encoding the polypeptide or fusion, can be determined by comparing their in vitro activity and in vivo activity in animal models thereof. Methods for the extrapolation of effective dosages in mice, and other animals, to humans are known to the art; for example, see U.S. Pat. No. 4,938,949.

[0126] Generally, the concentration of the polypeptides or fusions thereof, or nucleic acid encoding the polypeptide or fusion, or the complement thereof, in a liquid composition, may be from about 0.1-25 wt-%, e.g., from about 0.5-10 wt-%. The concentration in a semi-solid or solid composition such as a gel or a powder may be about 0.1-5 wt-%, e.g., about 0.5-2.5 wt-%.

[0127] The amount of the polypeptides or fusions thereof, or nucleic acid encoding the polypeptide or fusion required for use alone or with other agents will vary with the route of administration, the nature of the condition being treated and the age and condition of the patient and will be ultimately at the discretion of the attendant physician or clinician.

[0128] The polypeptides or fusions thereof, or nucleic acid encoding the polypeptide or fusion, or the complement thereof, may be conveniently administered in unit dosage form; for example, containing 5 to 1000 mg, conveniently 10 to 750 mg, or conveniently 50 to 500 mg of active ingredient per unit dosage form.

[0129] In general, however, a suitable dose may be in the range of from about 0.5 to about 100 mg/kg, e.g., from about 10 to about 75 mg/kg of body weight per day, such as 3 to about 50 mg per kilogram body weight of the recipient per day, for example in the range of 6 to 90 mg/kg/day, e.g., in the range of 15 to 60 mg/kg/day.

Example Pro-Influenza Virus Host Cell Factors

[0130] In embodiments, the pro-viral factor comprises a sodium/hydrogen exchanger 10 isoform 1 (SLC9C1) [*Homo sapiens*]

(NCBI Reference Sequence NP_898884.1) having the following amino acid sequence (SEQ ID NO: 1):
MAGIFKEFFESTEDLPEVILTLSLISSIGAFLNRHLEDFPIPVPVI

LFLLGCSFEVLSFTSSQVQRYANAIQWMSPDLFFRIFTPVVFFTT

AFDMDTYMLQKLFWQILLISIPGFLVNYILVLWHLASVNQLLLKP

TQWLLFSAILVSSDPMLTAAAIRDLGLSRSLISLINGESLMTSVI

-continued

SLITFTSIMDEDQRLQSKRNHTLAEEIVGGICSYIIASFLFGILS

SKLIQFWMSTVEGDDVNHISLIFSILYLIFYICELVGMSGIFTLA

IVGLLLNSTSFKAAIEETLLLEFWTFLSRIAFLMVFTFFGLLIPA

HTYLYIEFVDIYYSLNIYLTLIVLRFLTLLLISPVLSRVGHEFSW

RWIFIMVCSEMKGMPNINMALLLAYSDLYEGSDKEKSQILFHGVL

VCLITLVVNRFILPVAVTILGLRDATSTKYKSVCCTFQHFQELTK

SAASALKFDKDLANADWNMIEKAITLENPYMLNEEETTEHQKVKC

PHCNKEIDEIENTEAMELANRRLLSAQIASYQRQYRNEILSQSAV

QVLVGAAESFGEKKGKCMSLDTIKNYSESQKTVTFARKLLLNWVY

NTRKEKEGPSKYFFFRICHTIVFTEEFEHVGYLVILMNIFPFIIS

WISQLNVIYHSELKHTNYCFLTLYILEALLKIAAMRKDFFSHAWN

IFELAITLIGILHVILIEIDTIKYIFNETEVIVFIKVVQFFRILR

IFKLIAPKLLQIIDKRMSHQKTFWYGILKGYVQGEADIMTIIDQI

TSSKQIKQMLLKQVIRNMEHAIKELGYLEYDHPEIAVTVKTKEEI

NVMLNMATEILKAFGLKGIISKTEGAGINKLIMAKKKEVLDSQSI

IRPLTVEEVLYHIPWLDKNKDYINFIQEKAKVVTFDCGNDIFEEG

DEPKGIYIIISGMVKLEKSKPGLGIDQMVESKEKDFPIIDTDYML

SGEIIGEINCLINEPMKYSATCKTVVETCFIPKTHLYDAFEQCSP

LIKQKMWLKLGLAITARKIREHLSYEDWNYNMQLKLSNIYVVDIP

MSTKTDIYDENLIYVILIHGAVEDCLLRKTYRAPFLIPITCHQIQ

SIEDFTKVVIIQTPINMKTFRRNIRKFVPKHKSYLTPGLIGSVGT

LEEGIQEERNVKEDGAHSAATARSPQPCSLIGTKENCKESPRINL

RKVRKE

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0131] In embodiments, the pro-viral factor comprises a treslin isoform 1 (TICRR) [*Homo sapiens*]

(NCBI Reference Sequence NP_001294954.1) having the following amino acid sequence (SEQ ID NO: 2):
MACCHKVMLL LDTAGGAARH SRVRRAALRL LTYLSCREGL

ARVHWAFKFF DSQGARSRPS RVSDFRELGS RSWEDFEEEL

EARLEDRAHL PGPAPRATHT HGALMETLLD YQWDRPEITS

PTKPILRSSG RRLLDVESEA KEAEAALGGL VNAVFLLAPC

PHSQRELLQF VSGCEAQAQR LPPTPKQVME KLLPKRVREV

MVARKITFYW VDTTEWSKLW ESPDHLGYWT VCELLHHGGG

TVLPSESFSW DFAQAGEMLL RSGIKLSSEP HLSPWISMLP

TDATLNRLLY NSPEYEASFP RMEGMLFLPV EGKEIQETWT

VTLEPLAMHQ RHFQKPVRIF LKGSVAQWSL PTSSTLGTDS

WMLGSPEEST ATQRLLFQQL VSRLTAEELH LVADVDPGEG

-continued

RPPITGVISP LSASAMILTV CRTKEAEFQR HVLQTAVADS

PRDTASLESD VVDSILNQTH DSLADTASAA SPVPEWAQQE

LGHTTPWSPA VVEKWFPFCN ISGASSDLME SEGLLQAASA

NKEESSKTEG ELIHCLAELY QRKSREESTI AHQEDSKKKR

GVPRTPVRQK MNTMCRSLKM LNVARLNVKA QKLHPDGSPD

VAGEKGIQKI PSGRTVDKLE DRGRTLRSSK PKDFKTEEEL

LSYIRENYQK TVATGEIMLY ACARNMISTV KMELKSKGTK

ELEVNCLNQV KSSLIKTSKS LRQNLGKKLD KEDKVRECQL

QVFLRLEMCL QCPSINESTD DMEQVVEEVT DLLRMVCLTE

DSAYLAEFLE EILRLYIDSI PKTLGNLYNS LGFVIPQKLA

GVLPTDFFSD DSMTQENKSP LLSVPFLSSA RRSVSGSPES

DELQELRTRS AKKRRKNALI RHKSIAEVSQ NLRQIEIPKV

SKRATKKENS HPAPQQPSQP VKDTVQEVTK VRRNLENQEL

LSPSKRSLKR GLPRSHSVSA VDGLEDKLDN FKKNKGYHKL

LTKSVAETPV HKQISKRLLH RQIKGRSSDP GPDIGVVEES

PEKGDEISLR RSPRIKQLSF SRTHSASFYS VSQPKSRSVQ

RVHSFQQDKS DQRENSPVQS IRSPKSLLFG AMSEMISPSE

KGSARMKKRS RNTLDSEVPA AYQTPKKSHQ KSLSESKTTP

PRISHTPQTP LYTPERLQKS PAKMTPTKQA AFKESIKDSS

SPGHDSPLDS KITPQKRHTQ AGEGTSLETK TPRTPKRQGT

QPPGFLPNCT WPHSVNSSPE SPSCPAPPTS STAQPRRECL

TPIRDPLRTP PRAAAFMGTP QNQTHQQPHV LRAARAEEPA

QKLKDKAIKT PKRPGNSTVT SSPPVTPKKL FTSPLCDVSK

KSPFRKSKIE CPSPGELDQK EPQMSPSVAA SLSCPVPSTP

PELSQRATLD TVPPPPPSKV GKRCRKTSDP RRSIVECQPD

ASATPGVGTA DSPAAPTDSR DDQKGLSLSP QSPPERRGYP

GPGLRSDWHA SSPLLITSDT EHVTLLSEAE HHGIGDLKSN

VLSVEEGEGL RTADAEKSSL SHPGIPPSPP SCGPGSPLMP

SRDVHCTTDG RQCQASAQLD NLPASAWHST DSASPQTYEV

ELEMQASGLP KLRIKKIDPS SSLEAEPLSK EESSLGEESF

LPALSMPRAS RSLSKPEPTY VSPPCPRLSH STPGKSRGQT

YICQACTPTH GPSSTPSPFQ TDGVPWTPSP KHSGKTTPDI

IKDWPRRKRA VGCGAGSSSG RGEVGADLPG SLSLLESEGK

DHGLELSIHR TPILEDFELE GVCQLPDQSP PRNSMPKAEE

ASSWGQFGLS SRKRVLLAKE EADRGAKRIC DLREDSEVSK

SKEGSPSWSA WQLPSTGDEE VEVSGSTPPP SCAVRSCLSA

SALQALTQSP LLFQGKTPSS QSKDPRDEDV DVLPSTVEDS

PFSRAFSRRR PISRTYTRKK IMGTWLEDL

a different isoform of the protein, a polypeptide having the sequence in NP_689472.3, which is incorporated by reference herein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0132] In embodiments, the pro-viral factor comprises an olfactory receptor 4C6 (OR4C6) [*Homo sapiens*]

(NCBI Reference Sequence NP_001004704.1) having the following amino acid sequence (SEQ ID NO: 3):
MENQNNVTEF ILLGLIENLE LWKIFSAVEL VMYVATVLEN

LLIVVTIITS QSLRSPMYFF LTFLSLLDVM FSSVVAPKVI

VDTLSKSTTI SLKGCLTQLF VEHFFGGVGI ILLTVMAYDR

YVAICKPLHY TIIMSPRVCC LMVGGAWVGG FMHAMIQLLF

MYQIPFCGPN IIDHFICDLE QLLTLACTDT HILGLLVTLN

SGMMCVAIFL ILIASYTVIL CSLKSYSSKG RHKALSTCSS

HLTVVVLFFV PCIFLYMRPV VTHPIDKAMA VSDSIITPML

NPLIYTLRNA EVKSAMKKLW MKWEALAGK

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0133] In embodiments, the pro-viral factor comprises a C-type lectin domain family 4 member C isoform 1 (CLEC4C) [*Homo sapiens*]

(NCBI Reference Sequence NP_001358319.1) having the following amino acid sequence (SEQ ID NO: 4):
MVPEEEPQDR EKGLWWFQLK VWSMAVVSIL LLSVCFTVSS

VVPHNEMYSK TVKRLSKLRE YQQYHPSLTC VMEGKDIEDW

SCCPTPWTSF QSSCYFISTG MQSWIKSQKN CSVMGADLVV

INTREEQDFI IQNLKRNSSY FLGLSDPGGR RHWQWVDQTP

YNENVTFWHS GEPNNLDERC AIINFRSSEE WGWNDIHCHV

PQKSICKMKK IYI

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0134] In embodiments, the pro-viral factor comprises a NADH dehydrogenase [ubiquinone] 1 alpha subcomplex subunit 7(NDUFA7) [*Homo sapiens*]

(NCBI Reference Sequence: NP_004992.2) having the following amino acid sequence (SEQ ID NO: 5):
MASATRLIQR LRNWASGHDL QGKLQLRYQE ISKRTQPPPK

LPVGPSHKLS NNYYCTRDGR RESVPPSIIM SSQKALVSGK

PAESSAVAAT EKKAVTPAPP IKRWELSSDQ PYL

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0135] In embodiments, the pro-viral factor comprises an olfactory receptor 51A7 (OR51A7) [*Homo sapiens*]

(NCBI Reference Sequence: NP_001004749.1) having the following amino acid sequence (SEQ ID NO: 6):

MSVLNNSEVK LFLLIGIPGL EHAHIWFSIP ICLMYLLAIM

GNCTILFIIK TEPSLHEPMY YFLAMLAVSD MGLSLSSLPT

MLRVFLFNAM GISPNACFAQ EFFIHGFTVM ESSVLLIMSL

DRFLAIHNPL RYSSILTSNR VAKMGLILAI RSILLVIPFP

FTLRRLKYCQ KNLLSHSYCL HQDTMKLACS DNKINVIYGF

FIALCTMLDL ALIVLSYVLI LKTILSIASL AERLKALNTC

VSHICAVLTF YVPIITLAAM HHFAKHKSPL VVILIADMEL

LVPPLMNPIV YCVKTRQIWE KILGKLLNVC GR

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0136] In embodiments, the pro-viral factor comprises a chloride channel protein CIC-Kb isoform 1 (CLCNKB) [*Homo sapiens*]

(NCBI Reference Sequence: NP_000076.2) having the following amino acid sequence (SEQ ID NO: 7):

MEEFVGLREG SSGNPVTLQE LWGPCPRIRR GIRGGLEWLK

QKLFRLGEDW YELMTLGVLM ALVSCAMDLA VESVVRAHQW

LYREIGDSHL LRYLSWTVYP VALVSFSSGF SQSITPSSGG

SGIPEVKTML AGVVLEDYLD IKNEGAKVVG LSCTLACGST

LFLGKVGPFV HLSVMMAAYL GRVRTTTIGE PENKSKQNEM

LVAAAAVGVA TVEAAPESGV LFSIEVMSSH FSVWDYWRGF

FAATCGAFMF RLLAVENSEQ ETITSLYKTS FRVDVPEDLP

-continued

EIFFFVALGG LCGILGSAYL FCQRIFFGFI RNNRFSSKLL

ATSKPVYSAL ATLVLASITY PPSAGRFLAS RLSMKQHLDS

LEDNHSWALM TQNSSPPWPE ELDPQHLWWE WYHPRFTIFG

TLAFFLVMKF WMLILATTIP MPAGYEMPIF VYGAAIGRLF

GETLSFIFPE GIVAGGITNP IMPGGYALAG AAAFSGAVTH

TISTALLAFE VTGQIVHALP VLMAVLAANA IAQSCQPSFY

DGTVIVKKLP YLPRILGRNI GSHRVRVEHF MNHSITTLAK

DMPLEEVVKV VISTDVAKYP LVESTESQIL VGIVRRAQLV

QALKAEPPSW APGHQQCLQD ILAAGCPTEP VILKLSPETS

LHEAHNLFEL LNLHSLEVTS RGRAVGCVSW VEMKKAISNL

TNPPAPK

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0137] In embodiments, the pro-viral factor comprises a guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-5 (GNG5) [*Homo sapiens*]

(NCBI Reference Sequence: NP_005265.1) having the following amino acid sequence (SEQ ID NO: 8):

MSGSSSVAAM KKVVQQLRLE AGLNRVKVSQ AAADLKQFCL

QNAQHDPLLT GVSSSTNPER PQKVCSEL

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0138] In embodiments, the pro-viral factor comprises a S-adenosyl-L-methionine-dependent tRNA 4-demethyl-wyosine synthase (TYW1) [*Homo sapiens*]

(NCBI Reference Sequence: NP_060734.2) having the following amino acid sequence (SEQ ID NO: 9):

MDPSADTWDL FSPLISLWIN RFYIYLGFAV SISLWICVQI VIKTQGKNLQ EKSVPKAAQD

LMINGYVSLQ EKDIFVSGVK IFYGSQTGTA KGFATVLAEA VTSLDLPVAI INLKEYDPDD

HLIEEVTSKN VCVELVATYT DGLPTESAEW FCKWLEEASI DEREGKTYLK GMRYAVFGLG

NSAYASHENK VGKNVDKWLW MLGAHRVMSR GEGDCDVVKS KHGSIEADER AWKTKFISQL

QALQKGERKK SCGGHCKKGK CESHQHGSEE REEGSHEQDE LHHRDTEEEE PFESSSEEEF

GGEDHQSLNS IVDVEDLGKI MDHVKKEKRE KEQQEEKSGL FRNMGRNEDG ERRAMITPAL

REALTKQGYQ LIGSHSGVKL CRWTKSMLRG RGGCYKHTFY GIESHRCMET TPSLACANKC

VFCWRHHTNP VGTEWRWKMD QPEMILKEAI ENHQNMIKQF KGVPGVKAER FEEGMTVKHC

ALSLVGEPIM YPEINRFLKL LHQCKISSEL VTNAQFPAEI RNLEPVTQLY VSVDASTKDS

LKKIDRPLEK DEWQRFLDSL KALAVKQQRT VYRLTLVKAW NVDELQAYAQ LVSLGNPDFI

EVKGVTYCGE SSASSLTMAH VPWHEEVVQF VHELVDLIPE YEIACEHEHS NCLLIAHRKE

KIGGEWWTWI DYNRFQELIQ EYEDSGGSKT FSAKDYMART PHWALFGASE RGFDPKDTRH

QRKNKSKAIS GC

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0139] In embodiments, the pro-viral factor comprises a ras-related protein Rab-42 isoform 1 (RAB42) [*Homo sapiens*]

(NCBI Reference Sequence: NP_001180461.1) having the following amino acid sequence (SEQ ID NO: 10):

MEAEGCRYQF RVALLGDAAV GKTSLLRSYV

AGAPGAPEPE PEPEPTVGAE CYRRALQLRA

GPRVKLQLWD TAGHERFRCI TRSFYRNVVG

-continued

VLLVEDVINR KSFEHIQDWH QEVMATQGPD

KVIFLLVGHK SDLQSTRCVS AQEAEELAAS

LGMAFVETSV KNNCNVDLAF DTLADAIQQA

LQQGDIKLEE GWGGVRLIHK TQIPRSPSRK

QHSGPCQC

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0140] In embodiments, the pro-viral factor comprises a potassium/sodium hyperpolarization-activated cyclic nucleotide-gated channel 3 (HCN3) [*Homo sapiens*]

(NCBI Reference Sequence: NP_065948.1) having the following amino acid sequence (SEQ ID NO: 11):

MEAEQRPAAG ASEGATPGLE AVPPVAPPPA TAASGPIPKS GPEPKRRHLG TLLQPTVNKE

SLRVFGSHKA VEIEQERVKS AGAWITHPYS DERFYWDLIM LLLMVGNLIV LPVGITFFKE

ENSPPWIVEN VISDIFFLLD LVLNFRTGIV VEEGAEILLA PRAIRTRYLR TWELVDLISS

IPVDYIFLVV ELEPRLDAEV YKTARALRIV RFTKILSLLR LLRLSRLIRY IHQWEEIFHM

TYDLASAVVR IFNLIGMMLL LCHWDGCLQF LVPMLQDFPP DCWVSINHMV NHSWGRQYSH

ALFKAMSHML CIGYGQQAPV GMPDVWLTML SMIVGATCYA MFIGHATALI QSLDSSRRQY

QEKYKQVEQY MSFHKLPADT RQRIHEYYEH RYQGKMEDEE SILGELSEPL REEIINFTCR

GLVAHMPLFA HADPSFVTAV LTKLRFEVFQ PGDLVVREGS VGRKMYFIQH GLLSVLARGA

RDTRLTDGSY FGEICLLTRG RRTASVRADT YCRLYSLSVD HFNAVLEEFP MMRRAFETVA

MDRLLRIGKK NSILQRKRSE PSPGSSGGIM EQHLVQHDRD MARGVRGRAP STGAQLSGKP

VLWEPLVHAP LQAAAVTSNV AIALTHQRGP LPLSPDSPAT LLARSAWRSA GSPASPLVPV

RAGPWASTSR LPAPPARTLH ASLSRAGRSQ VSLLGPPPGG GGRRLGPRGR PLSASQPSLP

QRATGDGSPG RKGSGSERLP PSGLLAKPPR TAQPPRPPVP EPATPRGLQL SANM

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0141] In embodiments, the pro-viral factor comprises a rasGAP-activating-like protein 1 isoform 1 (RASAL1) [*Homo sapiens*]

(NCBI Reference Sequence: NP_001180449.1) having the following amino acid sequence (SEQ ID NO: 12):

MAKSSSLNVR VVEGRALPAK DVSGSSDPYC LVKVDDEVVA RTATVWRSLG PFWGEEYTVH

LPLDFHQLAF YVLDEDTVGH DDIIGKISLS REAITADPRG IDSWINLSRV DPDAEVQGEI

CLSVQMLEDG QGRCLRCHVL QARDLAPRDI SGTSDPFARV FWGSQSLETS TIKKTREPHW

DEVLELREMP GAPSPLRVEL WDWDMVGKND FLGMVEFSPK TLQQKPPKGW FRLLPFPRAE

EDSGGNLGAL RVKVRLIEDR VLPSQCYQPL MELLMESVQG PAEEDTASPL ALLEELTLGD

CRQDLATKLV KLFLGRGLAG RFLDYLTRRE VARTMDPNTL FRSNSLASKS MEQFMKLVGM

PYLHEVLKPV ISRVFEEKKY MELDPCKMDL GRTRRISEKG ALSEEQMRET SLGLLTGYLG

PIVDAIVGSV GRCPPAMRLA FKQLHRRVEE RFPQAEHQQD VKYLAISGFL FLRFFAPAIL

TPKLFDLRDQ HADPQTSRSL LLLAKAVQSI GNLGQQLGQG KELWMAPLHP FLLQCVSRVR

-continued

DFLDRLVDVD GDEEAGVPAR ALFPPSAIVR EGYLLKRKEE PAGLATREAF KKRYVWLSGE

TLSFSKSPEW QMCHSIPVSH IRAVERVDEG AFQLPHVMQV VTQDGTGALH TTYLQCKNVN

ELNQWLSALR KASAPNPNKL AACHPGAFRS ARWTCCLQAE RSAAGCSRTH SAVTLGDWSD

PLDPDAEAQT VYRQLLLGRD QLRLKLLEDS NMDTTLEADT GACPEVLARQ RAATARLLEV

LADLDRAHEE FQQQERGKAA LGPLGP

a different isoform of the protein, a polypeptide having the sequence in NP_001288131.1, which is incorporated by reference herein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0142] In embodiments, the pro-viral factor comprises a UL16-binding protein 1 isoform 1 precursor (ULBP1) [*Homo sapiens*]

(NCBI Reference Sequence: NP_079494.1) having the following amino acid sequence (SEQ ID NO: 13):
MAAAASPAFL LCLPLLHLLS GWSRAGWVDT HCLCYDFIIT PKSRPEPQWC EVQGLVDERP

FLHYDCVNHK AKAFASLGKK VNVTKTWEEQ TETLRDVVDF LKGQLLDIQV ENLIPIEPLT

LQARMSCEHE AHGHGRGSWQ FLENGQKELL FDSNNRKWTA LHPGAKKMTE KWEKNRDVTM

FFQKISLGDC KMWLEEFLMY WEQMLDPTKP PSLAPGTTQP KAMATTLSPW SLLIIFLCFI

LAGR

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0143] In embodiments, the pro-viral factor comprises a macrophage immunometabolism regulator (C5orf30) [*Homo sapiens*]

(NCBI Reference Sequence: NP_149988.1) having the following amino acid sequence (SEQ ID NO: 14):
MEVDINGESR STLITLPFPG AEANSPGKAE AEKPRCSSTP CSPMRRTVSG YQILHMDSNY

LVGFTTGEEL LKLAQKCTGG EESKAEAMPS LRSKQLDAGL ARSSRLYKTR SRYYQPYEIP

AVNGRRRRRM PSSGDKCTKS LPYEPYKALH GPLPLCLLKG KRAHSKSLDY LNLDKMIKEP

ADTEVLQYQL QHLTLRGDRV FARNNT

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0144] In embodiments, the pro-viral factor comprises a protein mono-ADP-ribosyltransferase PARP15 isoform 1 [*Homo sapiens*]

(NCBI Reference Sequence: NP_001106995.1)
having the following amino acid sequence (SEQ ID NO: 15):
MAAPGPLPAA ALSPGAPTPR ELMHGVAGVT SRAGRDREAG SVIPAGNRGA RKASRRSSSR

SMSRDNKFSK KDCLSIRNVV ASIQTKEGLN LKLISGDVLY IWADVIVNSV PMNLQLGGGP

LSRAFLQKAG PMLQKELDDR RRETEEKVGN IFMTSGCNLD CKAVLHAVAP YWNNGAETSW

QIMANIIKKC LTTVEVLSES SITFPMIGTG SLQFPKAVFA KLILSEVFEY SSSTRPITSP

LQEVHELVYT NDDEGCQAFL DEFINWSRIN PNKARIPMAG DTQGVVGTVS KPCFTAYEMK

IGAITFQVAT GDIATEQVDV IVNSTARTEN RKSGVSRAIL EGAGQAVESE CAVLAAQPHR

DFIITPGGCL KCKIIIHVPG GKDVRKTVTS VLEECEQRKY TSVSLPAIGT GNAGKNPITV

-continued

ADNIIDAIVD FSSQHSTPSL KTVKVVIFQP ELLNIFYDSM KKRDLSASIN FQSTFSMTTC

NLPEHWIDMN HQLFCMVQLE PGQSEYNTIK DKFTRTCSSY AIEKIERIQN AFLWQSYQVK

KRQMDIKNDH KNNERLLFHG TDADSVPYVN QHGENRSCAG KNAVSYGKGT YFAVDASYSA

KDTYSKPDSN GRKHMYVVRV LTGVFTKGRA GLVTPPPKNP HNPTDLEDSV INNTRSPKLF

VVFFDNQAYP EYLITFTA

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0145] In embodiments, the pro-viral factor comprises a neuroligin-4, X-linked (NLGN4X) [*Homo sapiens*]

MSRPQGLLWL PLLFTPVCVM LNSNVLLWLT ALAIKFTLID SQAQYPVVNT NYGKIRGLRT

PLPNEILGPV EQYLGVPYAS PPTGERRFQP PEPPSSWTGI RNTTQFAAVC PQHLDERSLL

HDMLPIWFTA NLDTLMTYVQ DQNEDCLYLN IYVPTEDDIH DQNSKKPVMV YIHGGSYMEG

TGNMIDGSIL ASYGNVIVIT INYRLGILGF LSTGDQAAKG NYGLLDQIQA LRWIEENVGA

FGGDPKRVTI FGSGAGASCV SLLTLSHYSE GLFQKAIIQS GTALSSWAVN YQPAKYTRIL

ADKVGCNMLD TIDMVECLRN KNYKELIQQT ITPATYHIAF GPVIDGDVIP DDPQILMEQG

EFLNYDIMLG VNQGEGLKFV DGIVDNEDGV TPNDEDFSVS NFVDNLYGYP EGKDTLRETI

KEMYTDWADK ENPETRRKTL VALFTDHQWV APAVATADLH AQYGSPTYFY AFYHHCQSEM

KPSWADSAHG DEVPYVFGIP MIGPTELFSC NFSKNDVMLS AVVMTYWTNF AKTGDPNQPV

PQDTKFIHTK PNRFEEVAWS KYNPKDQLYL HIGLKPRVRD HYRATKVAFW LELVPHLHNL

NEIFQYVSTT TKVPPPDMTS FPYGTRRSPA KIWPTTKRPA ITPANNPKHS KDPHKTGPED

TTVLIETKRD YSTELSVTIA VGASLLELNI LAFAALYYKK DKRRHETHRR PSPQRNITND

IAHIQNEEIM SLQMKQLEHD HECESLQAHD TLRLTCPPDY TLTLRRSPDD IPLMTPNTIT

MIPNTLTGMQ PLHTENTFSG GQNSTNLPHG HSTTRV

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0146] In embodiments, the pro-viral factor comprises a CD59 glycoprotein preproprotein (CD59) [*Homo sapiens*]

(NCBI Reference Sequence: NP_000602.1) having the following amino acid sequence (SEQ ID NO: 17):
MGIQGGSVLF GLLLVLAVFC HSGHSLQCYN

CPNPTADCKT AVNCSSDFDA CLITKAGLQV

YNKCWKFEHC NENDVTTRLR ENELTYYCCK

KDLCNENEQL ENGGTSLSEK TVLLLVTPFL

AAAWSLHP

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0147] In embodiments, the pro-viral factor comprises a cofilin-2 isoform 1 (CFL2) [*Homo sapiens*]

(NCBI Reference Sequence: NP_619579.1) having the following amino acid sequence (SEQ ID NO: 18):
MASGVTVNDE VIKVENDMKV RKSSTQEEIK

KRKKAVLFCL SDDKRQIIVE EAKQILVGDI

GDTVEDPYTS FVKLLPLNDC RYALYDATYE

TKESKKEDLV FIFWAPESAP LKSKMIYASS

KDAIKKKFTG IKHEWQVNGL DDIKDRSTLG

EKLGGNVVVS LEGKPL

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0148] In embodiments, the pro-viral factor comprises a gasdermin-B isoform 1 (GSDMB) [*Homo sapiens*]

(NCBI Reference Sequence: NP_001035936.1) having the following amino acid sequence (SEQ ID NO: 19):

MFSVFEEITR IVVKEMDAGG DMIAVRSLVD ADRFRCFHLV GEKRTFFGCR HYTTGLILMD

ILDTDGDKWL DELDSGLQGQ KAEFQILDNV DSTGELIVRL PKEITISGSF QGFHHQKIKI

SENRISQQYL ATLENRKLKR ELPFSERSIN TRENLYLVTE TLETVKEETL KSDRQYKEWS

QISQGHLSYK HKGQREVTIP PNRVLSYRVK QLVEPNKETM KKDGASSCLG KSLGSEDSRN

MKEKLEDMES VLKDLTEEKR KDVLNSLAKC LGKEDIRQDL EQRVSEVLIS GELHMEDPDK

PLLSSLFNAA GVLVEARAKA ILDFLDALLE LSEEQQFVAE ALEKGTLPLL KDQVKSVMEQ

NWDELASSPP DMDYDPEARI LCALYVVVSI LLELAEGPTS VSS

a different isoform of the protein, a polypeptide having the sequence in NP_001159430.1, which is incorporated by reference herein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0149] In embodiments, the pro-viral factor comprises a bromodomain-containing protein 4 isoform long (BRD4) [*Homo sapiens*]

(NCBI Reference Sequence: NP_001366220.1) having the following amino acid sequence (SEQ ID NO: 20):

MSAESGPGTR LRNLPVMGDG LETSQMSTTQ AQAQPQPANA ASTNPPPPET SNPNKPKRQT

NQLQYLLRVV LKTLWKHQFA WPFQQPVDAV KLNLPDYYKI IKTPMDMGTI KKRLENNYYW

NAQECIQDEN TMFTNCYTYN KPGDDIVLMA EALEKLFLQK INELPTEETE IMIVQAKGRG

RGRKETGTAK PGVSTVPNTT QASTPPQTQT PQPNPPPVQA TPHPFPAVTP DLIVQTPVMT

VVPPQPLQTP PPVPPQPQPP PAPAPQPVQS HPPIIAATPQ PVKTKKGVKR KADTTTPTTI

DPIHEPPSLP PEPKTIKLGQ RRESSRPVKP PKKDVPDSQQ HPAPEKSSKV SEQLKCCSGI

LKEMFAKKHA AYAWPFYKPV DVEALGLADY CDIIKHPMDM STIKSKLEAR EYRDAQEFGA

DVRLMFSNCY KYNPPDHEVV AMARKLQDVE EMRFAKMPDE PEEPVVAVSS PAVPPPTKVV

APPSSSDSSS DSSSDSDSST DDSEEERAQR LAELQEQLKA VHEQLAALSQ PQQNKPKKKE

KDKKEKKKEK HKRKEEVEEN KKSKAKEPPP KKTKKNNSSN SNVSKKEPAP MKSKPPPTYE

SEEEDKCKPM SYEEKRQLSL DINKLPGEKL GRVVHIIQSR EPSLKNSNPD EIEIDFETLK

PSTLRELERY VTSCLRKKRK PQAEKVDVIA GSSKMKGFSS SESESSSESS SSDSEDSETE

MAPKSKKKGH PGREQKKHHH HHHQQMQQAP APVPQQPPPP PQQPPPPPPP QQQQQPPPPP

PPPSMPQQAA PAMKSSPPPF IATQVPVLEP QLPGSVEDPI GHFTQPILHL PQPELPPHLP

QPPEHSTPPH LNQHAVVSPP ALHNALPQQP SRPSNRAAAL PPKPARPPAV SPALTQTPLL

PQPPMAQPPQ VLLEDEEPPA PPLTSMQMQL YLQQLQKVQP PTPLLPSVKV QSQPPPPLPP

PPHPSVQQQL QQQPPPPPPP QPQPPPQQQH QPPPRPVHLQ PMQFSTHIQQ PPPPQGQQPP

HPPPGQQPPP PQPAKPQQVI QHHHSPRHHK SDPYSTGHLR EAPSPLMIHS PQMSQFQSLT

HQSPPQQNVQ PKKQELRAAS VVQPQPLVVV KEEKIHSPII RSEPFSPSLR PEPPKHPESI

KAPVHLPQRP EMKPVDVGRP VIRPPEQNAP PPGAPDKDKQ KQEPKTPVAP KKDLKIKNMG

SWASLVQKHP TTPSSTAKSS SDSFEQFRRA AREKEEREKA LKAQAEHAEK EKERLRQERM

RSREDEDALE QARRAHEEAR RRQEQQQQQR QEQQQQQQQQ AAAVAAAATP QAQSSQPQSM

LDQQRELARK REQERRRREA MAATIDMNFQ SDLLSIFEEN LF

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0150] In embodiments, the pro-viral factor comprises an interferon-induced protein with tetratricopeptide repeats 3 isoform a (IFIT3) [*Homo sapiens*]

(NCBI Reference Sequence: NP_001540.2) having the following amino acid sequence (SEQ ID NO: 21):

MSEVIKNSLE KILPQLKCHF TWNLFKEDSV SRDLEDRVCN QIEFLNTEFK ATMYNLLAYI

KHLDGNNEAA LECLRQAEEL IQQEHADQAE IRSIVIWGNY AWVYYHLGRL SDAQIYVDKV

KQTCKKESNP YSIEYSELDC EEGWTQLKCG RNERAKVCFE KALEEKPNNP EFSSGLAIAM

YHLDNHPEKQ FSTDVLKQAI ELSPDNQYVK VLLGLKLQKM NKEAEGEQFV EEALEKSPCQ

TDVLRSAAKF YRRKGDLDKA IELFQRVLES TPNNGYLYHQ IGCCYKAKVR QMQNTGESEA

SGNKEMIEAL KQYAMDYSNK ALEKGLNPLN AYSDLAEFLE TECYQTPENK EVPDAEKQQS

HQRYCNLQKY NGKSEDTAVQ HGLEGLSISK KSTDKEEIKD QPQNVSENLL PQNAPNYWYL

QGLIHKQNGD LLQAAKCYEK ELGRLLRDAP SGIGSIFLSA SELEDGSEEM GQGAVSSSPR

ELLSNSEQLN

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0151] In embodiments, the pro-viral factor comprises an opioid growth factor receptor (OGFR) [*Homo sapiens*]

(NCBI Reference Sequence: NP_031372.2) having the following amino acid sequence (SEQ ID NO: 22):

MDDPDCDSTW EEDEEDAEDA EDEDCEDGEA AGARDADAGD EDEESEEPRA ARPSSFQSRM

TGSRNWRATR DMCRYRHNYP DLVERDCNGD TPNLSFYRNE IRFLPNGCFI EDILQNWTDN

YDLLEDNHSY IQWLFPLREP GVNWHAKPLT LREVEVEKSS QEIQERLVRA YELMLGFYGI

RLEDRGTGTV GRAQNYQKRF QNLNWRSHNN LRITRILKSL GELGLEHFQA PLVRFFLEET

LVRRELPGVR QSALDYEMEA VRCRHQRRQL VHEAWEHFRP RCKFVWGPQD KLRRFKPSSL

PHPLEGSRKV EEEGSPGDPD HEASTQGRTC GPEHSKGGGR VDEGPQPRSV EPQDAGPLER

SQGDEAGGHG EDRPEPLSPK ESKKRKLELS RREQPPTEPG PQSASEVEKI ALNLEGCALS

QGSLRTGTQE VGGQDPGEAV QPCRQPLGAR VADKVRKRRK VDEGAGDSAA VASGGAQTLA

LAGSPAPSGH PKAGHSENGV EEDTEGRTGP KEGTPGSPSE TPGPSPAGPA GDEPAESPSE

TPGPRPAGPA GDEPAESPSE TPGPRPAGPA GDEPAESPSE TPGPSPAGPT RDEPAESPSE

TPGPRPAGPA GDEPAESPSE TPGPRPAGPA GDEPAESPSE TPGPSPAGPT RDEPAKAGEA

AELQDAEVES SAKSGKP

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0152] In embodiments, the pro-viral factor comprises an epimerase family protein SDR39U1 isoform 1 (SDR39U1) [*Homo sapiens*]

(NCBI Reference Sequence: NP_064580.2) having the following amino acid sequence (SEQ ID NO: 23):

MRVLVGGGTG FIGTALTQLL NARGHEVTLV SRKPGPGRIT WDELAASGLP SCDAAVNLAG

ENILNPLRRW NETFQKEVIG SRLETTQLLA KAITKAPQPP KAWVLVTGVA YYQPSLTAEY

DEDSPGGDFD FFSNLVTKWE AAARLPGDST RQVVVRSGVV LGRGGGAMGH MLLPERLGLG

-continued

GPIGSGHQFF PWIHIGDLAG ILTHALEANH VHGVLNGVAP SSATNAEFAQ TLGAALGRRA

FIPLPSAVVQ AVEGRQRAIM LLEGQKVIPQ RTLATGYQYS FPELGAALKE IVA

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0153] In embodiments, the pro-viral factor comprises a regulating synaptic membrane exocytosis protein 2 isoform a (RIMS2) [*Homo sapiens*]

(NCBI Reference Sequence: NP_001093587.1) having the following amino acid sequence (SEQ ID NO: 24):

MSAPVGPRGR LAPIPAASQP PLQPEMPDLS HLTEEERKII LAVMDRQKKE EEKEQSVLKK

LHQQFEMYKE QVKKMGEESQ QQQEQKGDAP TCGICHKTKF ADGCGHNCSY CQTKFCARCG

GRVSLRSNKV MWVCNLCRKQ QEILTKSGAW FYNSGSNTPQ QPDQKVLRGL RNEEAPQEKK

PKLHEQTQFQ GPSGDLSVPA VEKSRSHGLT RQHSIKNGSG VKHHIASDIA SDRKRSPSVS

RDQNRRYDQR EEREEYSQYA TSDTAMPRSP SDYADRRSQH EPQFYEDSDH LSYRDSNRRS

HRHSKEYIVD DEDVESRDEY ERQRREEEYQ SRYRSDPNLA RYPVKPQPYE EQMRIHAEVS

RARHERRHSD VSLANADLED SRISMLRMDR PSRQRSISER RAAMENQRSY SMERTREAQG

PSSYAQRTTN HSPPTPRRSP LPIDRPDLRR TDSLRKQHHL DPSSAVRKTK REKMETMLRN

DSLSSDQSES VRPPPPKPHK SKKGGKMRQI SLSSSEEELA STPEYTSCDD VEIESESVSE

KGDMDYNWLD HTSWHSSEAS PMSLHPVTWQ PSKDGDRLIG RILLNKRLKD GSVPRDSGAM

LGLKVVGGKM TESGRLCAFI TKVKKGSLAD TVGHLRPGDE VLEWNGRLLQ GATFEEVYNI

ILESKPEPQV ELVVSRPIGD IPRIPDSTHA QLESSSSSFE SQKMDRPSIS VTSPMSPGML

RDVPQFLSGQ LSSQSLSRRT TPEVPRVQIK LWEDKVGHQL IVTILGAKDL PSREDGRPRN

PYVKIYFLPD RSDKNKRRTK TVKKTLEPKW NQTFIYSPVH RREFRERMLE ITLWDQARVR

EEESEFLGEI LIELETALLD DEPHWYKLQT HDVSSLPLPH PSPYMPRRQL HGESPERRLQ

RSKRISDSEV SDYDCDDGIG VVSDYRHDGR DLQSSTLSVP EQVMSSNHCS PSGSPHRVDV

IGRTRSWSPS VPPPQSRNVE QGLRGTRTMT GHYNTISRMD RHRVMDDHYS PDRDRDCEAA

DRQPYHRSRS TEQRPLLERT TTRSRSTERP DTNLMRSMPS LMTGRSAPPS PALSRSHPRT

GSVQTSPSST PVAGRRGRQL PQLPPKGTLD RKAGGKKLRS TVQRSTETGL AVEMRNWMTR

QASRESTDGS MNSYSSEGNL IFPGVRLASD SQFSDELDGL GPAQLVGRQT LATPAMGDIQ

VGMMDKKGQL EVEIIRARGL VVKPGSKTLP APYVKVYLLD NGVCIAKKKT KVARKTLEPL

YQQLLSFEES PQGKVLQIIV WGDYGRMDHK SEMGVAQILL DELELSNMVI GWFKLEPPSS

LVDPTLAPLT RRASQSSLES STGPSYSRS

a different isoform of the protein, or a polypeptide having the sequence in NP_001335413.1, which is incorporated by reference herein or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0154] In embodiments, the pro-viral factor comprises a sia-alpha-2,3-Gal-beta-1,4-G1cNAc-R:alpha 2,8-sialyl-transferase (ST8SIA3) [*Homo sapiens*]

(NCBI Reference Sequence: NP_056963.2) having the following amino acid sequence (SEQ ID NO: 25):

MRNCKMARVA SVLGLVMLSV ALLILSLISY VSLKKENIFT TPKYASPGAP RMYMFHAGER

SQFALKFLDP SFVPITNSLT QELQEKPSKW KENRTAFLHQ RQEILQHVDV IKNFSLTKNS

-continued

VRIGQLMHYD YSSHKYVFSI SNNFRSLLPD VSPIMNKHYN ICAVVGNSGI LTGSQCGQEI

DKSDFVFRCN FAPTEAFQRD VGRKTNLTTF NPSILEKYYN NLLTIQDRNN FFLSLKKLDG

AILWIPAFFF HTSATVTRTL VDFFVEHRGQ LKVQLAWPGN IMQHVNRYWK NKHLSPKRLS

TGILMYTLAS AICEEIHLYG FWPFGEDPNT REDLPYHYYD KKGTKFTTKW QESHQLPAEF

QLLYRMHGEG LTKLTLSHCA

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0155] In embodiments, the pro-viral factor comprises a cyclin-dependent kinase inhibitor 3 isoform 1 (CDKN3) [*Homo sapiens*]

(NCBI Reference Sequence: NP_005183.2) having the following amino acid sequence (SEQ ID NO: 26):

MKPPSSIQTS EFDSSDEEPI EDEQTPIHIS WLSLSRVNCS QFLGICALPG CKEKDVRRNV

QKDTEELKSC GIQDIFVECT RGELSKYRVP NLLDLYQQCG IITHHHPIAD GGTPDIASCC

EIMEELTTCL KNYRKTLIHC YGGLGRSCLV AACLLLYLSD TISPEQAIDS LRDLRGSGAI

QTIKQYNYLH EFRDKLAAHL SSRDSQSRSV SR

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0156] In embodiments, the pro-viral factor comprises a T-cell immunoglobulin and mucin domain-containing protein 4 isoform 1 precursor (TIMD4) [*Homo sapiens*]

(NCBI Reference Sequence: NP_612388.2) having the following amino acid sequence (SEQ ID NO: 27):

MSKEPLILWL MIEFWWLYLT PVTSETVVTE VLGHRVTLPC LYSSWSHNSN SMCWGKDQCP

YSGCKEALIR TDGMRVTSRK SAKYRLQGTI PRGDVSLTIL NPSESDSGVY CCRIEVPGWE

NDVKINVREN LQRASTTTHR TATTTTRRTT TTSPTTTRQM TTTPAALPTT VVTTPDLTTG

TPLQMTTIAV FTTANTCISL TPSTLPEEAT GLLTPEPSKE GPILTAESET VLPSDSWSSV

ESTSADTVLL TSKESKVWDL PSTSHVSMWK TSDSVSSPQP GASDTAVPEQ NKTTKTGQMD

GIPMSMKNEM PISQLLMIIA PSLGFVLFAL FVAFLLRGKL METYCSQKHT RLDYIGDSKN

VLNDVQHGRE DEDGLFTL

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0157] In embodiments, the pro-viral factor comprises a protein SYS1 homolog isoform a (SYS1) [*Homo sapiens*]

(NCBI Reference Sequence: NP_291020.1) having the following amino acid sequence (SEQ ID NO: 28):

MAGQFRSYVW DPLLILSQIV LMQTVYYGSL GLWLALVDGL VRSSPSLDQM FDAEILGEST

PPGRLSMMSF ILNALTCALG LLYFIRRGKQ CLDFTVTVHF FHLLGCWFYS SRFPSALTWW

LVQAVCIALM AVIGEYLCMR TELKEIPLNS APKSNV

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0158] In embodiments, the pro-viral factor comprises an ubiquitin D (UBD) [*Homo sapiens*]

(NCBI Reference Sequence: NP_006389.2) having the following amino acid sequence (SEQ ID NO: 29):
MAPNASCLCV HVRSEEWDLM TFDANPYDSV KKIKEHVRSK TKVPVQDQVL LLGSKILKPR

RSLSSYGIDK EKTIHLTLKV VKPSDEELPL ELVESGDEAK RHLLQVRRSS SVAQVKAMIE

TIKTGIIPETQ IVTCNGKRLE DGKMMADYGI RKGNLLFLAC YCIGG

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0159] In embodiments, the pro-viral factor comprises a mediator of RNA polymerase II transcription subunit 17 (MED17) [*Homo sapiens*]

(NCBI Reference Sequence: NP_004259.3)
having the following amino acid
sequence (SEQ ID NO: 30):
MSGVRAVRIS IESACEKQVH EVGLDGTETY LPPLSMSQNL ARLAQRIDES QGSGSEEEEA

AGTEGDAQEW PGAGSSADQD DEEGVVKFQP SLWPWDSVRN NLRSALTEMC VLYDVLSIVR

DKKEMTLDPV SQDALPPKQN PQTLQLISKK KSLAGAAQIL LKGAERLIKS VTENQENKLQ

RDENSELLRL RQHWKLRKVG DKILGDLSYR SAGSLFPHHG TFEVIKNTDL DLDKKIPEDY

CPLDVQIPSD LEGSAYIKVS IQKQAPDIGD LGTVNLFKRP LPKSKPGSPH WQTKLEAAQN

VLLCKEIFAQ LSREAVQIKS QVPHIVVKNQ IISQPFPSLQ LSISLCHSSN DKKSQKFATE

KQCPEDHLYV LEHNLHLLIR EPHKQTLSSI MMPHPASAPF GHKRMRLSGP QAFDKNEINS

LQSSEGLLEK IIKQAKHIFL RSRAAATIDS LASRIEDPQI QAHWSNINDV YESSVKVLIT

SQGYEQICKS IQLQLNIGVE QIRVVHRDGR VITLSYQEQE LQDELLSQMS QHQVHAVQQL

AKVMGWQVLS FSNHVGLGPI ESIGNASAIT VASPSGDYAI SVRNGPESGS KIMVQFPRNQ

CKDLPKSDVL QDNKWSHLRG PFKEVQWNKM EGRNEVYKME LLMSALSPCL L

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0160] In embodiments, the pro-viral factor comprises a peroxisome biogenesis factor 13 (PEX13) [*Homo sapiens*]

(NCBI Reference Sequence: NP_002609.1) having the following amino acid sequence (SEQ ID NO: 31):
MASQPPPPPK PWETRRIPGA GPGPGPGPTF QSADLGPTLM TRPGQPALTR VPPPILPRPS

QQTGSSSVNT FRPAYSSESS GYGAYGNSFY GGYSPYSYGY NGLGYNRLRV DDLPPSREVQ

QAEESSRGAF QSIESIVHAF ASVSMMMDAT FSAVYNSFRA VLDVANHESR LKIHFTKVES

AFALVRTIRY LYRRLQRMLG LRRGSENEDL WAESEGTVAC LGAEDRAATS AKSWPIFLFF

AVILGGPYLI WKLLSTHSDE VIDSINWASG EDDHVVARAE YDFAAVSEEE ISFRAGDMLN

LALKEQQPKV RGWLLASLDG QTTGLIPANY VKILGKRKGR KTVESSKVSK QQQSFTNPTL

TKGATVADSL DEQEAAFESV FVETNKVPVA PDSIGKDGEK QDL

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0161] In embodiments, the pro-viral factor comprises an ubiquitin carboxyl-terminal hydrolase 17-like protein 13 (USP17L13) [*Homo sapiens*]

(NCBI Reference Sequence: NP_001243784.1)
having the following amino acid sequence (SEQ ID NO: 32):
MEEDSLYLGG EWQFNHESKL TSSRLDAAFA EIQRTSLPEK SPLSCETRVD LCDDLVPEAR

QLAPREKLPL SSRRPAAVGA GLQNMGNTCY VNASLQCITY TPPLANYMLS REHSQTCHRH

KGCMLCTMQA HITRALHNPG HVIQPSQALA AGFHRGKQED AHEFLMFTVD AMKKACLPGH

KQVDHPSKDT TLIHQIFGGY WRSQIKCLHC HGISDTEDPY LDIALDIQAA QSVQQALEQL

VKPEELNGEN AYHCGVCLQR APASKILTLH TSAKVLILVL KRESDVTGNK IAKNVQYPEC

LDMQPYMSQQ NTGPLVYVLY AVLVHAGWSC HNGHYFSYVK AQEGQWYKMD DAEVTAASIT

SVLSQQAYVL FYIQKSEWER HSESVSRGRE PRALGAEDTD RRATQGELKR DHPCLQAPEL

DEHLVERATQ ESTLDRWKEL QEQNKTKPEF NVRKVEGTLP PDVLVIHQSK YKCGMKNHHP

EQQSSLINLS SSTPTHQESM NTGTLASLRG RARRSKGKNK HSKRALLVCQ

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0162] In embodiments, the pro-viral factor comprises a mirror-image polydactyly gene 1 protein isoform 1 (MIPOL1) [*Homo sapiens*]

(NCBI Reference Sequence: NP_001374996.1) having the
following amino acid sequence (SEQ ID NO: 33):
MENWSKDITH SYLEQETTGI NKSTQPDEQL TMNSEKSMHR KSTELVNEIT CENTEWPGQR

STNFQIISSY PDDESVYCTT EKYNVMEHRH NDMHYECMTP CQVTSDSDKE KTIAFLLKED

DILRTSNKKL QQKLAKEDKE QRKLKFKLEL QEKETEAKIA EKTAALVEEV YFAQKERDEA

VMSRLQLAIE ERDEAIARAK HMEMSLKVLE NINPEENDMT LQELLNRINN ADTGIAIQKN

GAIIVDRIYK TKECKMRITA EEMSALIEER DAALSKCKRL EQELHHVKEQ NQTSANNMRH

LTAENNQERA LKAKLLSMQQ ARETAVQQYK KLEEEIQTLR VYYSLHKSLS QEENLKDQEN

YILSTYEEAL KNRENIVSIT QQQNEELATQ LQQALTERAN MELQLQHARE ASQVANEKVQ

KLERLVDVLR KKVGTGTMRT VI

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0163] In embodiments, the pro-viral factor comprises a ribokinase isoform 1 (RBKS) [*Homo sapiens*]

(NCBI Reference Sequence: NP_071411.1)
having the following amino acid sequence
(SEQ ID NO: 34):
MAASGEPQRQ WQEEVAAVVV VGSCMTDLVS LTSRLPKTGE TIHGHKFFIG FGGKGANQCV

QAARLGAMTS MVCKVGKDSF GNDYIENLKQ NDISTEFTYQ TKDAATGTAS IIVNNEGQNI

IVIVAGANLL INTEDLRAAA NVISRAKVMV CQLEITPATS LEALTMARRS GVKTLENPAP

AIADLDPQFY TLSDVFCCNE SEAEILTGLI VGSAADAGEA ALVLLKRGCQ VVIITLGAEG

CVVLSQTEPE PKHIPTEKVK AVDITGAGDS FVGALAFYLA YYPNLSLEDM LNRSNFIAAV

SVQAAGTQSS YPYKKDLPLT LF

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0164] In embodiments, the pro-viral factor comprises an ubiquitin carboxyl-terminal hydrolase 17 (USP17L2) [*Homo sapiens*]

(NCBI Reference Sequence: NP_958804.2) having the following amino acid sequence (SEQ ID NO: 35):

MEDDSLYLGG EWQFNHESKL TSSRPDAAFA EIQRTSLPEK SPLSSEARVD LCDDLAPVAR

QLAPRKKLPL SSRRPAAVGA GLQNMGNTCY ENASLQCITY TPPLANYMLS REHSQTCQRP

KCCMLCTMQA HITWALHSPG HVIQPSQALA AGFHRGKQED AHEFLMFTVD AMKKACLPGH

KQVDHHSKDT TLIHQIFGGC WRSQIKCLHC HGISDTEDPY LDIALDIQAA QSVKQALEQL

VKPEELNGEN AYHCGLCLQR APASKTLTLH TSAKVLILVL KRFSDVIGNK LAKNVQYPEC

LDMQPYMSQQ NTGPLVYVLY AVLVHAGWSC HDGHYFSYVK AQEGQWYKMD DAKVTACSIT

SVLSQQAYVL FYIQKSEWER HSESVSRGRE PRALGAEDTD RRATQGELKR DHPCLQAPEL

DERLVERATQ ESTLDHWKFP QEQNKTKPEF NVRKVEGTLP PNVLVIHQSK YKCGMKNHHP

EQQSSLINLS STTRTDQESV NTGTLASLQG RTRRSKGKNK HSKRALLVCQ

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

[0165] In embodiments, the pro-viral factor comprises a dystrophin isoform Dp427m (DMD) [*Homo sapiens*]

(NCBI Reference Sequence: NP_003997.2) having the following amino acid sequence (SEQ ID NO: 36):

MLWWEEVEDC YEREDVQKKT FTKWVNAQFS KFGKQHIENL FSDLQDGRRL LDLLEGLTGQ

KLPKEKGSTR VHALNNVNKA LRVLQNNNVD LVNIGSTDIV DGNHKLILGL IWNIILHWQV

KNVMKNIMAG LQQTNSEKIL LSWVRQSTRN YPQVNVINFT TSWSDGLALN ALIHSHRPDL

FDWNSVVCQQ SATQRLEHAF NIARYQLGIE KLLDPEDVDT TYPDKKSILM YITSLFQVLP

QQVSIEAIQE VEMLPRPPKV TKEEHFQLHH QMHYSQQITV SLAQGYERTS SPKPRFKSYA

YTQAAYVTTS DPTRSPFPSQ HLEAPEDKSF GSSIMESEVN LDRYQTALEE VLSWLLSAED

TLQAQGEISN DVEVVKDQFH THEGYMMDLT AHQGRVGNIL QLGSKLIGTG KLSEDEETEV

QEQMNLLNSR WECLRVASME KQSNLHRVLM DLQNQKLKEL NDWLIKTEER TRKMEEEPLG

PDLEDLKRQV QQHKVLQEDL EQEQVRVNSL THMVVVVDES SGDHATAALE EQLKVLGDRW

ANICRWTEDR WVLLQDILLK WQRLTEEQCL FSAWLSEKED AVNKIHTTGF KDQNEMLSSL

QKLAVLKADL EKKKQSMGKL YSLKQDLLST LKNKSVTQKT EAWLDNFARC WDNLVQKLEK

STAQISQAVT TTQPSLTQTT VMETVTTVTT REQILVKHAQ EELPPPPPQK KRQITVDSEI

RKRLDVDITE LHSWITRSEA VLQSPEFAIF RKEGNFSDLK EKVNAIEREK AEKFRKLQDA

SRSAQALVEQ MVNEGVNADS IKQASEQLNS RWIEFCQLLS ERLNWLEYQN NIIAFYNQLQ

QLEQMTTTAE NWLKIQPTTP SEPTAIKSQL KICKDEVNRL SDLQPQIERL KIQSIALKEK

GQGPMFLDAD FVAFTNHFKQ VESDVQAREK ELQTIFDTLP PMRYQETMSA IRTWVQQSET

KLSIPQLSVT DYEIMEQRLG ELQALQSSLQ EQQSGLYYLS TIVKEMSKKA PSEISRKYQS

EFEEIEGRWK KLSSQLVEHC QKLEEQMNKL RKIQNHIQTL KKWMAEVDVF LKEEWPALGD

SEILKKQLKQ CRLLVSDIQT IQPSLNSVNE GGQKIKNEAE PEFASRLETE LKELNTQWDH

MCQQVYARKE ALKGGLEKTV SLQKDLSEMH EWMTQAEEEY LERDFEYKTP DELQKAVEEM

KRAKEEAQQK EAKVKLLTES VNSVIAQAPP VAQEALKKEL ETLITNYQWL CTRLNGKCKT

-continued

LEEVWACWHE LLSYLEKANK WLNEVEFKLK TTENIPGGAE EISEVLDSLE NLMRHSEDNP

NQIRILAQTL TDGGVMDELI NEELETENSR WRELHEEAVR RQKLLEQSIQ SAQETEKSLH

LIQESLTFID KQLAAYIADK VDAAQMPQEA QKIQSDLISH EISLEEMKKH NQGKEAAQRV

LSQIDVAQKK LQDVSMKERL FQKPANFEQR LQESKMILDE VKMHLPALET KSVEQEVVQS

QLNHCVNLYK SLSEVKSEVE MVIKTGRQIV QKKQTENPKE LDERVTALKL HYNELGAKVT

ERKQQLEKCL KLSRKMRKEM NVLTEWLAAT DMELTKRSAV EGMPSNLDSE VAWGKATQKE

TEKQKVHLKS ITEVGEALKT VLGKKETLVE DKLSLINSNW IAVTSRAEEW LNLLLEYQKH

METFDQNVDH ITKWIIQADT LLDESEKKKP QQKEDVLKRL KAELNDIRPK VDSTRDQAAN

LMANRGDHCR KLVEPQISEL NHRFAAISHR IKTGKASIPL KELEQFNSDI QKLLEPLEAE

IQQGVNLKEE DENKDMNEDN EGTVKELLQR GDNLQQRITD ERKREEIKIK QQLLQTKHNA

LKDLRSQRRK KALEISHQWY QYKRQADDLL KCLDDIEKKL ASLPEPRDER KIKEIDRELQ

KKKEELNAVR RQAEGLSEDG AAMAVEPTQI QLSKRWREIE SKFAQFRRLN FAQIHTVREE

TMMVMTEDMP LEISYVPSTY LTEITHVSQA LLEVEQLLNA PDLCAKDFED LFKQEESLKN

IKDSLQQSSG RIDIIHSKKT AALQSATPVE RVKLQEALSQ LDFQWEKVNK MYKDRQGRED

RSVEKWRRFH YDIKIFNQWL TEAEQFLRKT QIPENWEHAK YKWYLKELQD GIGQRQTVVR

TLNATGEEII QQSSKTDASI LQEKLGSLNL RWQEVCKQLS DRKKRLEEQK NILSEFQRDL

NEFVLWLEEA DNIASIPLEP GKEQQLKEKL EQVKLLVEEL PLRQGILKQL NETGGPVLVS

APISPEEQDK LENKLKQTNL QWIKVSRALP EKQGEIEAQI KDLGQLEKKL EDLEEQLNHL

LLWLSPIRNQ LEIYNQPNQE GPEDVKETEI AVQAKQPDVE EILSKGQHLY KEKPATQPVK

RKLEDLSSEW KAVNRLLQEL RAKQPDLAPG LITIGASPTQ TVTLVTQPVV TKETAISKLE

MPSSLMLEVP ALADFNRAWT ELTDWLSLLD QVIKSQRVMV GDLEDINEMI IKQKATMQDL

EQRRPQLEEL ITAAQNLKNK TSNQEARTII TDRIERIQNQ WDEVQEHLQN RRQQLNEMLK

DSTQWLEAKE EAEQVLGQAR AKLESWKEGP YTVDAIQKKI TETKQLAKDL RQWQTNVDVA

NDLALKLLRD YSADDTRKVH MITENINASW RSIHKRVSER EAALEETHRL LQQFPLDLEK

FLAWLTEAET TANVLQDATR KERLLEDSKG VKELMKQWQD LQGEIEAHTD VYHNLDENSQ

KILRSLEGSD DAVLLQRRLD NMNEKWSELR KKSLNIRSHL EASSDQWKRL HLSLQELLVW

LQLKDDELSR QAPIGGDEPA VQKQNDVHRA FKRELKTKEP VIMSTLETVR IFLTEQPLEG

LEKLYQEPRE LPPEERAQNV TRLLRKQAEE VNTEWEKLNL HSADWQRKID ETLERLRELQ

EATDELDLKL RQAEVIKGSW QPVGDLLIDS LQDHLEKVKA LRGEIAPLKE NVSHVNDLAR

QLTTLGIQLS PYNLSTLEDL NTRWKLLQVA VEDRVRQLHE AHRDFGPASQ HELSTSVQGP

WERAISPNKV PYYINHETQT TCWDHPKMTE LYQSLADINN VRESAYRTAM KLRRLQKALC

LDLLSLSAAC DALDQHNLKQ NDQPMDILQI INCLTTIYDR LEQEHNNLVN VPLCVDMCLN

WLLNVYDTGR TGRIRVLSEK TGIISLCKAH LEDKYRYLFK QVASSTGFCD QRRLGLLLHD

SIQIPRQLGE VASEGGSNIE PSVRSCFQFA NNKPEIEAAL FLDWMRLEPQ SMVWLPVLHR

VAAAETAKHQ AKCNICKECP IIGFRYRSLK HENYDICQSC FFSGRVAKGH KMHYPMVEYC

TPTTSGEDVR DFAKVLKNKF RTKRYFAKHP RMGYLPVQTV LEGDNMETPV TLINFWPVDS

APASSPQLSH DDTHSRIEHY ASRLAEMENS NGSYLNDSIS PNESIDDEHL LIQHYCQSLN

QDSPLSQPRS PAQILISLES EERGELERIL ADLEEENRNL QAEYDRLKQQ HEHKGLSPLP

SPPEMMPTSP QSPRDAELIA EAKLLRQHKG RLEARMQILE DHNKQLESQL HRLRQLLEQP

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QAEAKVNGTT VSSPSTSLQR SDSSQPMLLR VVGSQTSDSM GEEDLLSPPQ DTSTGLEEVM

EQLNNSFPSS RGRNTPGKPM REDTM

a different isoform of the protein, or a polypeptide having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity thereto.

Example Host Cell Factors for Inhibition.

[0166] In embodiments, the disclosure provides for nucleic acid sequences useful to inhibit transcription or translation of mRNA in a host organism, e.g., useful to inhibit RNA, or to enhance viral production. The nucleic acid sequences encode a polypeptides having at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91.

[0167] In embodiments, the nucleic acid inhibits expression of a *Homo sapiens* solute carrier family 9 member C1 (SLC9C1), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_183061.3 (SEQ ID NO: 37):

gagtttggag caagtaactg tcagtgaggt tgcagttggt ctgggctgtt tggctgtgag

cgaaatagct gccccccact tctcacttgc acaccacggg atactectcc tgaggctccg

gatgattcag atggactgtg aaaaacaaca agatggatga tcatatggag attgcttcta

acataaatct gcataaaaat ttttctgaaa catggctgga atatttaagg agtttttttt

cagtactgag gacctccctg aagtcattct aacattgtct ttgatcagct ccattggagc

atttttgaac cggcacttgg aagactttcc aattcctgtc cctgtgatat tatttttact

tggatgcagt tttgaagtat taagctttac atcttcacag gtccaaagat acgcaaacgc

catacaatgg atgagtccag acttatttttt tcgtatattt acaccagtag ttttctttac

tactgcattt gacatggata cgtacatget tcaaaagtta ttttggcaga tacttttaat

ttcaattccc ggctttttgg ttaattatat cttagttctt tggcatctgg catctgtaaa

tcaattactt ttgaagccta cccaatggtt attattttca gctatccttg tgagttcaga

tcccatgcta accgcagctg ctataagaga ccttgggctt tctagaagcc tcatcagttt

aattaatgga gaaagtctga tgacctctgt tatatcatta attacattta ctagtattat

ggattttgac caaagactac aaagtaaaag aaaccatacc ttagctgaag agatcgtggg

tggaatttgt tcatatatta tagcaagttt cttgtttgga attctaagtt caaaactgat

tcaattttgg atgtcaactg tttttggtga tgatgtcaat catataagte tcatcttttc

aattctgtat ctcatctttt atatttgtga gttagttgga atgtcaggaa tatttactct

ggccattgtg ggacttcttt taaattctac aagttttaaa gcagcaattg aagaaacact

tcttcttgaa ttctggactt ttctatcacg tattgctttt ctcatggtgt ttactttett

tggacttcta attcctgcac atacatattt gtatatagaa tttgttgata tatactattc

attaaatatc tacttaacat tgattgtttt aagatttctg accettcttt taataagccc

tyttttgtet cgagttggtc atgagttcag tiggcgctgg atattcataa tggtctgtag

tgaaatgaag gggatgccta atataaacat ggcccttctg cttgcctact ctgatcttta

ttttggatct gacaaagaaa aatctcaaat attatttcat ggagtgttag tatgcctaat

aacccttgtt gtcaatagat ttattttgcc agtggcagtt actatactag gtcttcgtga

tgccacatca acaaaatata aatcggtttg ttgcacattt caacacttte aagagctaac

caagtctgca gectctgccc ttaaatttga caaagatctt gctaatgctg attggaacat

gattgagaaa gcaattacac ttgaaaaccc atacatgttg aacgaagaag aaacaacaga

acatcagaag gtgaaatgtc cacactgtaa caaggaaata gatgagatct ttaacactga

agcaatggag ctggccaaca ggcgtctctt gtcagcacaa atagcaagct accagagaca

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atacaggaat gagattctgt cccagagtgc tgtccaggtg ttggttggtg cagcagaaag

ttttggtgag aagaagggaa aatgtatgag tcttgataca ataaagaatt attctgaaag

ccaaaaaaca gttacctttg ctagaaaact actacttaat tgggtgtata ataccagaaa

ggaaaaagag ggcccatcaa aatacttctt ttttcgtata tgccatacaa tagtatttac

tgaggaattt gaacatgttg gataccttgt gatattaatg aatatatttc cctttataat

ctcttggata tcccagttaa atgtaatcta ccacagcgaa ttaaaacaca ctaactactg

ttttcttaca ctttatattc tagaggcact acttaagata gcagcaatga ggaaggactt

tttttcacat gcctggaaca tattcgagtt agcaattaca ttaattggca tcttacatgt

aatacttatt gaaatagaca ccattaagta tatttttaat gagactgaag taatagtctt

tataaaagtt gttcaatttt ttcgtatact acgcattttc aagctcatag caccaaagtt

gctgcaaata atagataaaa gaatgagtca tcagaagacc ttttggtatg gaatactaaa

aggctatgtc caaggcgaag cagacataat gaccataatt gatcagatta caagttctaa

acagattaaa cagatgttat taaagcaagt gataaggaat atggaacatg ctataaaaga

gctaggctac ttagagtatg atcacccaga aattgctgtc actgtgaaaa caaaggaaga

aattaatgtt atgctcaata tcgctacaga aattcttaag gcttttggct taaaaggaat

tattagtaaa actgaaggtg ctggaattaa taagttaatc atggccaaaa agaaagaggt

gcttgattct caatctatta tcaggcctct tactgttgaa gaagttctat atcatattcc

gtggctagat aaaaacaaag attatataaa cttcattcag gaaaaagcca aagttgtaac

atttgattgt ggaaatgata tatttgaaga aggtgatgag cccaaaggaa tctatatcat

tatttcagge atggtaaage ttgaaaaatc aaagccaggt ttagggattg atcaaatggt

ggagtcaaag gagaaagatt ttccgataat tgacacagac tatatgctca gtggagaaat

aataggagag ataaactget taactaatga acctatgaaa tattctgcca cctgcaaaac

tgtagtggag acatgtttta ttcccaaaac tcacttgtat gatgcttttg agcaatgctc

tcctctcatt aaacaaaaaa tgtggctaaa acttggactc gctattacag ccagaaaaat

cagagaacac ttatcttatg aggattggaa ctacaatatg caactaaage tctctaatat

ttatgtagta gatataccaa tgagtaccaa aactgatatt tatgatgaaa atctaatcta

tgttatcctc atacatggag ctgtagaaga ttgtctgtta cgaaaaactt atagagcacc

tttcttaatt cctataacat gccatcagat acaaagtatt gaagatttca caaaagtagt

gattattcaa actccgatta acatgaaaac attcagaagg aatattagaa agtttgttcc

taaacataaa agttatctta caccaggatt aataggttca gttggaacat tggaagaagg

cattcaagaa gaaagaaatg ttaaggagga tggagcacac agtgccgcca ctgccaggag

tccccagcct tgctccctgc tggggacaaa gttcaactgt aaggagtccc ctagaataaa

cctaaggaaa gtcaggaaag agtaagactg ttaagaagac cgaagcatgt attaatgctg

tggctatgag aggectcctg ctgcagaaac acacttccct acatcaagaa ggagtaactt

caggttggat cctgtgtgga tgatcttggt gctaagcaga aaagaaattt ggaccttgaa

accagcagtt caacatatat actttttgca aaatttcctt gatttaaaat atttgttatt

ttaaatatac aaaacatttt agaaaatctt agagtaaatt ttagtcttaa agccagaaaa

taagtttata gccatctaga tattttgcat attgctctta cagcaataat ggtttggttc

actttatgaa aaataaaatg tattaaaata tagtttaaa

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0168] In embodiments, the nucleic acid inhibits expression of an *Homo sapiens* olfactory receptor family 4 subfamily C member 6 (OR4C6), mRNA having NCBI Reference Sequence:

NM_001004704.2 (SEQ ID NO: 38):
catgaaggtg gctgatggtg tgattcaaga ttgaactgga agttcaagga ttctcaactc

tcagctggaa ctcatatcaa cacctgagaa atggaaaatc aaaacaatgt gactgaattc

attcttctgg gtctcacaga gaacctggag ctgtggaaaa tattttctgc tgtgtttctt

gtcatgtatg tagccacagt gctggaaaat ctacttattg tggtaactat tatcacaagt

cagagtctga ggtcacctat gtatttttt cttaccttct tgtccctttt ggatgtcatg

ttctcatctg tcgttgcccc caaggtgatt gtagacaccc tctccaagag cactaccatc

tctctcaaag gctgcctcac ccagctgttt gtggagcatt tctttggtgg tgtggggatc

atcctcctca ctgtgatggc ctatgaccgc tacgtggcca tctgtaagcc cctgcactac

acgatcatca tgagtccacg ggtgtgctgc ctaatggtag gaggggcttg ggtgggggga

tttatgcacg caatgataca acttctcttc atgtatcaaa tacccttctg tggtcctaat

atcatagatc actttatatg tgatttgttt cagttgttga cacttgcctg cacggacacc

cacatcctgg gcctcttagt taccctcaac agtgggatga tgtgtgtggc catctttctt

atcttaattg cgtcctacac ggtcatccta tgctccctga agtcttacag ctctaaaggg

cggcacaaag ccctctctac ctgcagctcc cacctcacgg tggttgtatt gttctttgtc

ccctgtattt tcttgtacat gaggcctgtg gtcactcacc ccatagacaa ggcaatggct

gtgtcagact caatcatcac acccatgtta aatcccttga tctatacact gaggaatgca

gaggtgaaaa gtgccatgaa gaaactctgg atgaaatggg aggctttggc tgggaaataa

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0169] In embodiments, the nucleic acid inhibits expression of a *Homo sapiens* C-type lectin domain family 4 member C (CLEC4C), transcript variant 1, mRNA NCBI Reference Sequence:

NM 130441.3 (SEQ ID NO: 39):
actctgtcac ccaggctgga gtgaagtggt acgattacgg ctcactgcaa tccctgcctc

ccaaattcca gtgattctcg tgcctcagcc tcctgagtag ccgaaattac agacgtgtgc

caccatgctt ggctaatttt ttggattttt agtagagatg gggtttcact atgttggcca

ggctagtctt gaactcctgg cctgaagcaa tccgcccacc tcagcctccc aaagtgctga

gattataggc acgagccact acacctggcc acaaaattct ttaaagaagc caatcccatc

ctccctcaag agccaagggg ccacctcacc ctcttgttac agcagatcct gcctcccaca

gtcaccctgc tcccaagtgc aacctctgtc tgaccctgca tggtgtgcgg tgccctcctg

cctcaggccg cgaagaagga tctaagggct tggcttgttt gaaagaacca caccccgaaa

gtaacatctt tggagaaagt gatacaagag cttctgcacc cacctgatag aggaagtcca

aagggtgtgc gcacacacaa tggtgcctga agaagagcct caagaccgag agaaaggact

ctggtggttc cagttgaagg tctggtccat ggcagtcgta tccatcttgc tcctcagtgt

ctgtttcact gtgagttctg tggtgcctca caattttatg tatagcaaaa ctgtcaagag

gctgtccaag ttacgagagt atcaacagta tcatccaagc ctgacctgcg tcatggaagg

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aaaggacata gaagattgga gctgctgccc aacccttgg acttcatttc agtctagttg

ctactttatt tctactggga tgcaatcttg gactaagagt caaaagaact gttctgtgat

gggggctgat ctggtggtga tcaacaccag ggaagaacag gatttcatca ttcagaatct

gaaaagaaat tcttcttatt ttctggggct gtcagatcca gggggtcggc gacattggca

atgggttgac cagacaccat acaatgaaaa tgtcacattc tggcactcag gtgaacccaa

taaccttgat gagcgttgtg cgataataaa tttccgttct tcagaagaat ggggctggaa

tgacattcac tgtcatgtac ctcagaagtc aatttgcaag atgaagaaga tctacatata

aatgaaatat tctccctgga aatgtgtttg ggttggcatc caccgttgta gaaagctaaa

ttgatttttt aatttatgtg taagttttgt acaaggaatg cccctaaaat gtttcagcag

gctgtcacct attacactta tgatataatc ca

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0170] In embodiments, the nucleic acid inhibits expression of an *Homo sapiens* NADH:ubiquinone oxidoreductase subunit A7 (NDUFA7),

mRNA having the nucleic acid sequence (SEQ ID NO: 40):
agtatcgcgg acggaagatg gcgtccgcca cccgtctcat ccagcggctg cggaactggg

cgtccgggca tgacctgcag gggaagctgc agctacgcta ccaggagatc tccaagcgaa

ctcagcctcc tcccaagctc cctgtgggtc ctagccacaa gctctccaac aattactatt

gcactcgcga tggccgccgg gaatctgtgc ccccttccat catcatgtcg tcgcagaagg

cgctggtgtc aggcaagcca gcagagagct ctgctgtagc tgccactgag aagaaggcgg

tgactccagc tcctcccata aagaggtggg agctgtcctc ggaccagcct tacctgtgac

actgcaccct cacggccacc cgactacttt gcctccttgg atttcctcca gggagaatgt

gacctaattt atgacaaata cgtagagctc aggtatcact tctagtttta ctttaaaaaa

taaaaaaata gagacagagt ctcaccatgt ttcccaggct gatcttgaac tcctggcctc

aagcgatcct cctgccttga cctcccaaag tgctgggatt

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0171] In embodiments, the nucleic acid inhibits expression of a *Homo sapiens* olfactory receptor family 51 subfamily A member 7 (OR51A7), mRNA having NCBI Reference Sequence:

NM_001004749.2 (SEQ ID NO: 41):
ctgagcatct ggttctggta aggttaagga gctataaatc cttttggaaa cctaaatcta

agatccggct aacgagctca tatctccctc attatgtctg ttctcaataa ctccgaagtc

aagcttttcc ttctgattgg gatcccagga ctggaacatg cccacatttg gttctccatc

cccatttgcc tcatgtacct gcttgccatc atgggcaact gcaccattct ctttattata

aagacagagc cctcgcttca tgagcccatg tattatttcc ttgccatgtt ggctgtctct

gacatgggcc tgtccctctc ctcccttcct accatgttga gggtcttctt gttcaatgcc

atgggaattt cacctaatgc ctgctttgct caagaattct tcattcatgg attcactgtc

atggaatcct cagtacttct aattatgtct ttggaccgct ttcttgccat tcacaatccc

ttaagataca gttctatcct cactagcaac agggttgcta aaatgggact tattttagcc

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attaggagca ttctcttagt gattccattt cccttcacct taaggagatt aaaatattgt

caaaagaatc ttctttctca ctcatactgt cttcatcagg ataccatgaa gctggcctgc

tctgacaaca agaccaatgt catctatggc ttcttcattg ctctctgtac tatgctggac

ttggcactga ttgttttgtc ttatgtgctg atcttgaaga ctatactcag cattgcatct

ttggcagaga ggcttaaggc cctaaatacc tgtgtctccc acatctgtgc tgtgctcacc

ttctatgtgc ccatcatcac cctggctgcc atgcatcact ttgccaagca caaaagccct

cttgttgtga tccttattgc agatatgttc ttgttggtgc cgccccttat gaaccccatt

gtgtactgtg taaagactcg acaaatctgg gagaagatct tggggaagtt gcttaatgta

tgtgggagat aagaacttga acaattaggt aataaattat caaccagtag gcatttactg

tcatttgcta tgtgcttaat gccatagaag tcactaatga aggactggat gatggaagtg

aaaagctatg tagtgcagaa tttataataa agttgagaat ataactgaac aggatagaaa

aaaaagtcaa gagatatata agatatagag gtttaattaa cattttaagg gaagttgaag

gaaaatactt ctgtgatgga gcagctggat ttgagtcaac ccataaagaa tgaatacaat

ttgggcagat tgagattacc attcagttag tatctattaa aaatacagat gatatacaaa

gtctaatctc atactgtcaa ggaaaggtaa aatagctatg aaggatgctg atctgattac

aatagaaagt gaaatttaac agatagcaag tgatattttg gataaaataa gtgaaccaga

ttttggagca cctaaaaaaa gctttgaaaa gtctaaattc aggaggtgtt ggaatgccaa

tttcttctct acatgataaa tttcatttta agaagagcgt gcctgtaaac atggattgaa

tttgggagag atgaggaagg aagattaaca ggagaaagca caataatcct gctgtgaagt

gatgactcag aataggcagg gagagaacaa gatcatttag ctgctgttgt tatttttctg

ttataaaacc aacatgtaaa ttatggaaaa ttcacaaatt taactaagtg actaaaagat

aattttaaac cccctatggt tttgctgttt agtttttttc tgtgatttag tctttccctg

cgccttaaaa aaaatcagcc cctctaatat gttcttaaaa attgattcct gcaggacacg

acatttggta ccacaataat tttcactaaa atttatattt taaacttttt ttctcatgta

tagaggaaat acatgatgga aaaatcaaaa gagtatacag ttgaaaatac aatttgaagg

ggggcaaaca agattgatat ggcaatctct ctgggattct aaggtaagag tgttgtaaac

agaaaagaaa agcttttcaa aggaactggg gacttgaatg atgggtttga attttgtctt

gaggatttgg cataggtgac tgaat

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0172] In embodiments, the nucleic acid inhibits expression of an *Homo sapiens* chloride voltage-gated channel Kb (CLCNKB), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_000085.5 (SEQ ID NO: 42):

gaggatgttg attgttggaa cacacacctg tccaggtgca ggggagctgg aggctctgtg

agaggagggc cagctcagcc acagcaggag gactgacagg ggcctgatgg aggagtttgt

ggggctgcgt gaaggctcct cagggaaccc tgtgactctg caggagctgt ggggcccctg

tccccgcatc cgccgaggca tccgaggtgg cctggagtgg ctgaagcaga agctcttccg

-continued

cctgggcgag gactggtact tcctgatgac cctcggggtg ctcatggccc tggtcagctg

tgccatggac ttggctgttg agagtgtggt ccgagcgcac cagtggctgt acagggagat

tggggacagc cacctgctcc ggtatctctc ctggactgtg taccctgtgg ccctcgtctc

tttctcttca ggcttctctc agagcatcac accctcctct ggaggttctg gaatcccgga

ggtgaagacc atgttggcgg gtgtggtctt ggaggactac ctggatatca agaactttgg

ggccaaagtg gtgggcctct cctgcaccct ggcctgtggc agcaccctct tcctcgggaa

agtgggccct ttcgtgcacc tgtctgtgat gatggctgcc tacctgggcc gtgtgcgcac

cacgaccatc ggggagcctg agaacaagag caagcaaaac gaaatgctgg tggcagcggc

ggcagtgggc gtggccacag tctttgcagc tcccttcagc ggcgtcctgt tcagcatcga

ggtcatgtct tcccacttct ctgtctggga ttactggagg ggcttctttg cggccacctg

cggggccttc atgttccggc tcctggcggt cttcaacagc gagcaggaga ccatcacctc

cctctacaag accagtttcc gggtggacgt tcccttcgac ctgcctgaga tcttcttttt

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cttctttggc ttcatcagga acaataggtt cagctccaaa ctgctggcca ccagcaagcc

tgtgtactcc gctctggcca ccttggttct cgcctccatc acctacccac ccagcgccgg

ccgcttccta gcttctcggc tgtccatgaa gcagcatctg gactcgctgt tcgacaacca

ctcctgggcg ctgatgaccc agaactccag cccaccctgg cccgaggagc tcgacccccа

gcacctgtgg tgggaatggt accacccgcg gttcaccatc tttgggaccc ttgccttctt

cctggttatg aagttctgga tgctgattct ggccaccacc atccccatgc ctgccgggta

cttcatgccc atctttgtct atggagctgc tatcgggcgc ctctttgggg agactctctc

ttttatcttc cctgagggca tcgtggctgg agggatcacc aatcccatca tgccaggggg

gtatgctctg gcaggggctg cagccttctc aggggctgtg acccacacca tctccacggc

gctgctggcc ttcgaggtga ccggccagat agtgcatgca ctgcccgtgc tgatggcggt

gctggcagcc aacgccattg cacagagctg ccagccctcc ttctatgatg gcaccgtcat

tgtcaagaag ctgccatacc tgccacggat tctgggccgc aacatcggtt cccaccgcgt

gagggtggag cacttcatga accacagcat caccacactg gccaaggaca tgccactgga

ggaggtggtc aaggttgtga cctccacaga cgtggccaag tatcccctgg tggagagcac

agagtcccag atcctggtgg gcatagtgcg aagggcccag ctggtgcagg ccctgaaggc

tgagcctcct tcctgggctc ctggacacca gcagtgtctc caggacatct tggctgcagg

ctgccccaca gaaccagtga ccctgaagct gtccccagag acttccctgc atgaggcaca

caacctcttt gagctgttga accttcattc cctctttgtg acgtcgcggg gcagagctgt

gggctgcgtg tcctgggtgg agatgaagaa agcaatttcc aacctgacaa atccgccagc

cccaaagtga gccggcccag caagatgaaa cagggcaccc cagctgacct ggtactgagg

ttgggctgag accctgcttc tcttccccca tcaccacctg cccctccctc cagcccagct

ccattctttg gcataacagg caactttaac ctagcccaga agaggatggc tcatcctggg

tgggacgatg gctcctgcct tgaaagacaa aaatcccacc ttgggcagag ctgagtgtga

gaagatggaa aaccagtatc tgccagttgc tcagtgactg gccatcacat taatgaatga

tgagattgga gtacactgtc accaagggca ggcacagatg ccttctgggg ttgtctggtt

cccagtgaga ggctcctgag aaaaataaag ctggttccca ga

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0173] In embodiments, the nucleic acid inhibits expression of an *Homo sapiens* G protein subunit gamma 5 (GNG5), mRNA having NCBI Reference Sequence:

NM_005274.3 (SEQ ID NO: 43):
ctcacttccc tcaacccttc ccacaaactg ggaggaaaac tgagacctcc tggtcacccg

ccgccgggcc ttttagaaac tcccacaagc tctgccttcc ctccctggtc ctcttcagac

cccctcttag ttcttcgcgg ctaacggctc gcgctcgggg ccgggtgtgg agctggaaca

gagggctggc aaggcgcgca tgcgcaccga gggtggagcc gctgagcaca gaaccggaaa

cttagagaca aagttcggag ccccgccccc gccgcgcgcc gctgagttgt ctggccccgc

cgacccacgg cccacgaccc accgacccac gaatcggccc ggccgtcgcg tgcaccatgt

ctggctcctc cagcgtcgcc gctatgaaga aagtggttca acagctccgg ctggaggccg

gactcaaccg cgtaaaagtt tcccaggcag ctgcagactt gaaacagttc tgtctgcaga

atgctcaaca tgaccctctg ctgactggag tatcttcaag tacaaatccc ttcagacccc

agaaagtctg ttccttttg tagtaaaatg aatctttcaa aggtttccca aaccactcct

tatgatccag tgaatattca agagagctac atttgaagcc tgtacaaaag cttatccctg

taacacatgt gccataatat acaaacttct actttcgtca gtccttaaca tctacctctc

tgaattttca tgaatttcta tttcacaagg gtaattgttt tatatacact ggcagcagca

tacaataaaa cttagtatga aacttt

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0174] In embodiments, the nucleic acid inhibits expression of an *Homo sapiens* tRNA-yW synthesizing protein 1 homolog (TYW1), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_018264.4 (SEQ ID NO: 44):
ctggcagtgt catggctgcc cacaggtctg caggcactcg gtacgccgct aacgcggcga

ggtagctcgg tgcgtctcgc ggtaccagtg cgaatcatcg ggctatccag gtccgagatc

ctagtctcct gtcggctctg aggaggatgg atccttctgc ggatacatgg gacctcttct

caccttaat atcattatgg ataaacaggt tttacattta tttgggcttt gctgttagca

ttagcctttg gatttgtgtc cagattgtca tcaagacgca gggcaagaac ttacaggaaa

aatctgttcc aaaagcagct caggatttga tgacaaatgg ttatgtctcc cttcaagaga

aagacatctt tgtgtctgga gtgaagattt tttatggttc tcagactgga acagcgaagg

gattcgcaac agttcttgct gaagcagtta catccctgga tctgcctgtg gccattatta

atctaaaaga atatgatcca gatgatcatc tgatagaaga ggtgactagt aaaaatgtct

gtgtcttcct ggttgcgaca tacactgacg gcctaccaac tgaaagtgca gagtggttct

gcaaatggtt agaggaagca tccattgatt ttcgatttgg caaaacttac ctgaagggta

tgagatatgc ggtatttggc ctgggaaatt ctgcctatgc tagccacttc aacaaggttg

gcaaaaatgt tgacaagtgg ctctggatgc ttggcgcgca tcgtgtgatg agtcgagggg

agggcgactg cgacgtggtt aaaagcaagc acggcagcat tgaggccgac ttcagagcat

ggaagaccaa gttcatctcc cagctgcagg cacttcagaa aggggagaga aagaagtcct

gtggcggcca ctgcaagaaa ggcaaatgtg aatctcacca acatggctca gaggagaggg

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ttgagagctc cagtgaagaa gagtttggtg gtgaggacca tcagagccta aattccattg

ttgatgttga agatttgggc aaaattatgg atcatgtgaa gaaagaaaag agagaaaagg

aacagcagga agagaagtct ggtttgttca ggaacatggg gaggaatgaa gatggtgaaa

gaagagctat gataactcct gctctccgag aagcccttac taaacaaggt tatcagttga

ttgggagcca ctcgggggtg aagctttgca ggtggacaaa gtccatgctc cgagggagag

gaggttgtta caaacacaca ttctatggaa ttgagagcca tcgctgcatg gaaaccaccc

cgagcttggc gtgtgctaat aaatgtgtct tctgttggcg gcaccacacc aaccccgtgg

gcactgagtg gcggtggaag atggaccagc ctgaaatgat cttgaaggaa gccattgaaa

accatcagaa catgattaag cagtttaaag gagtaccggg cgtcaaagca gaacgctttg

aagaaggaat gacggtaaag cactgtgcat tgtccctcgt gggagaacca ataatgtacc

cagagatcaa caggtttttg aagctactcc accagtgtaa aatttccagc ttcctggtca

caaacgcaca atttcctgcg gaaatcagga acctcgagcc ggttactcag ctgtatgtca

gtgtggatgc cagtaccaaa gacagcctga agaaaatcga ccgcccactc ttcaaggatt

tctggcagag attccttgac agtttaaaag ccttggcagt caagcaacaa cgaactgtct

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acgagttggt ggatctgatc cccgaatatg aaattgcatg tgaacacgaa cactctaatt

gcctcctgat agcacacaga aagtttaaaa ttggtggtga atggtggaca tggatcgatt

ataaccgctt ccaggagctc atccaggaat atgaagatag tggtggatca aaaacgttca

gcgcaaagga ttatatggcc agaactcctc actgggcatt atttggtgcc agtgaaagag

gctttgatcc caaggacaca agacatcaga gaaagaacaa atcaaaggct atttctggat

gttgagatta tctgatttca aggtactgaa ggacaaaaac ttggatggcc tcaaaaggtt

cttgaacacc actgtgattc tccaaggacg aattacgtaa attatacttt catacaaagg

agacgataag gcagtaaaca tggagacacg ggggacagcg tccacactca gagggcctgg

gccacagccc cgatgtttct tttcagaact cagccccttt cctgatttta cttctaagag

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cctgggactc ttccccttac ccggccctta gatttcatgg agcagccact tagcattgaa

ttgcactacc ctgagctaaa cgtgtctgtg ctttctaaga taagagcttg atccctttct

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gctggagcgg agtgaagctg tctgctgtaa gaggagtggc catgtgaggg catggagtca

ttagtctcac aaacacactt tggactgaag aggatcattt ctttttgttc gtgaggtcac

tgtccaggcc tctcatatca tgaccagacg gcgggtctcc atcttctttc actcctgtgg

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ccctggctgc tttacacaat ctgttctata aggttcaggt gttttcaagt tggaaagatc

ataaatactc aaaattgttt tcaagttagc aagttctttt aacagtcttt tatgcaaaaa

ttgaattaat aaaataatct tttgtaaaga

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0175] In embodiments, the nucleic acid inhibits expression of an *Homo sapiens* RAB42, member RAS oncogene family (RAB42), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_001193532.3 (SEQ ID NO: 45):

ctagtttagt ccctttatcc tgtgaagtag gggtcatcat tagccccctt ttacagagga

gagaattgag gcttcgagag agagaaactt ggccaggagt ttccactcgg tccgacgccc

tcggtgcccc gccgggtacg gtggctgggc gcggggagcg gggggcggcg ccggcggggc

cccgggcagg ggcggggtcg gggcgcggac aaaaccgccg cggggcggcg gggtggcgga

cgcggccatg gaggccgagg gctgccgcta ccaatttcgg gtcgcgctgc tgggggacgc

ggcggtgggc aagacgtcgc tgctgcggag ctacgtggca ggcgcgcctg gcgccccgga

gccggagccc gagcccgagc ccacggtggg cgccgagtgc taccgccgcg cgctgcagct

gcgggccggg ccgcgggtca agctgcaact ctgggacacc gcgggccacg agcgcttcag

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cccggacaag gtcatcttcc tgctggttgg ccacaagagt gacctgcaga gcacccgctg

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gcaggccctg cagcaggggg acatcaagct agaagagggc tgggggggtg tccggctcat

ccacaagacc caaatcccca ggtcccccag caggaagcag cactcaggcc catgccagtg

ttgactctag gagagaaagg gttaaagcag tcccagcctt agcccacctg gtgggatggg

gagtgttaat atctctctgg aggacaaatg acagaagggt tcatataaac agtatcctga

cacagtcatg cttcctggat tttggagtcg aggctttcta cagaaaagaa agttctgatg

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cacctgaggt caggggttcg agaccagcct ggccaacatg gtgaaaccct gtctctacta

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ctaaggcagg agaattgctt gaacctggga ggcagagatt gcagtgagcc aagactgcgc

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ctatcgatgg ggctcataaa agatcccacc ttgaagggag gtggtgacca caaatgagac

agtggacagg atgtgctcac ccagagcctg ccgcgctgtg aattgaatga caaaagctct

cattcccact ccctttttct tggctgcgat gtggccactc tggcagcatt cctgggctca

gacactgaga agccagcgtc aggaagctga tgcatgggca aaggcaggtg cggggaattc

caggggggagc ttggcttgga ggcttcttat gtcctcaggc taaaatgatt ctgggcatgg

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acacagtggc cactgtgatg agccaccaag atcccccttt ctggctgggg aacccatcaa

ccctctcccc agctgctgga gtgccactgg atgatggact tcagcttgcc ccactctctg

ggaaaggccc tcccttcagg gcagcttgta tccaaagttc atctcctggg gggccttaaa

ggactccctc ttgccccagc tctggacaac tctgaaagtc aaaaccaact ttatcagtct

ctgtgggctt cattgaggac actgttgtga catcatagcc aagttatccc cttgcccaat

cctgcttcct tttcttcccc aaacaggtat ccatttcaag aatatcccct aataaacatc

tgcacactca tctcca

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0176] In embodiments, the nucleic acid inhibits expression of an *Homo sapiens* hyperpolarization activated cyclic nucleotide gated potassium channel 3 (HCN3), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_020897.3 (SEQ ID NO: 46):

gattccgagc ctacgacgcc tccgctagag cccgcggggc tgcgccgact cctgctctgg

aggggttgcg ggtacctgat ggccacagag ggctctagga ggccgagcgt gtaagcgggg

tgggcgccat ggaggcagag cagcggccgg cggcgggggc cagcgaaggg gcgacccctg

gactggaggc ggtgcctccc gttgctcccc cgcctgcgac cgcggcctca ggtccgatcc

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acaagttctc ccttcgggtg ttcggcagcc acaaagcagt ggaaatcgag caggagcggg

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accaggaccc taagtctcct ttccttctgg gtggggagtt ctggggttct tggtgtgtgg

gagaagtttt ataattgctt ccaaacagct gggtttaaat ataaaataga cacactca

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0177] In embodiments, the nucleic acid inhibits expression of an *Homo sapiens* RAS protein activator like 1 (RASAL1), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_001193520.2 (SEQ ID NO: 47):

gtgtttaact ggaaactaga acgagatgga aggggatgtt caaggcccct cccttgactc

tgaacggacc cccagggaac atgcgaccct ctctctggcg acgcctccca cccaccacta

atacttgctc ctggaccggg gggcgcggag gttggagaga ggagctaccc gggtctcgga

caggcggcac tgggaccacg aggcagggag ccaggcttga agcaggtgac atgtagacgt

cccctggtcc agcctcggaa cctgagcgcc cttctgcctg gaaagtttgt ggctaggcgc

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ggaggattct ggggggaacc tgggtgccct gcgagtgaag gtacgcctga ttgaggaccg

cgtcctgccc tcccagtgct accagcctct catggagctg ctcatggagt ctgtgcaggg

gccagcagag gaggacactg ctagcccctt ggctttgctg gaagagctga ccttgggggа

ctgccgccag gaccttgcca ccaagctggt gaaactcttt cttggccggg gactggctgg

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cctgggcccc cttggcccct aaggaaatgc cagagctagc ccggaaggag gagcaagagc

caggggggccc tcttcagcgc atcctgcccc gggagtctcc tgtctccttg gacctctttg

attctgtggt ttggaggctc ccagagacgt gcctagtcct gtgtgccttg agtccagaac

tcagggcatg gaagcccttt ggcaggggcc agccttgcac tgagtgaaac ttgccctctg

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tctctacttc accaaactgg cctctatcca taccaaggag gccagcctgg ccctgagctg

ctggatacag ctggacctga attcctgatg cccatgtgat gttgttgccc cagatgggca

ctaaatggcc tcactccttc ctgttttcat gtctgctaat ccctataacc tcactgattc

ttctgtaccc tgcccttggc ctaggactcc aaccacaagc ttccagaatc aggtgccctc

aggaagaacc aaggctgggt gggggtccag tgtgccaaac tcagaccctt ggagcctggg

agaccttggg ccaggctgtt tatctctctc tgggtctcag attaccctgt ataaaaagag

gagggaaagt cta

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0178] In embodiments, the nucleic acid inhibits expression of an *Homo sapiens* UL16 binding protein 1 (ULBP1), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_025218.4 (SEQ ID NO: 48):

gtatccctgc gcgcggcggg ccgggctggg cagctttata aacagccgtg gtgtgagcct

cgaagggaac catcagcgcc tcctgtccac ggagctccag gtctacaatg gcagcggccg

ccagccccgc gttccttctg tgcctcccgc ttctgcacct gctgtctggc tggtcccggg

caggatgggt cgacacacac tgtctttgct atgacttcat catcactcct aagtccagac

ctgaaccaca gtggtgtgaa gttcaaggcc tggtggatga aaggcctttt cttcactatg

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actgtgttaa ccacaaggcc aaagcctttg cttctctggg gaagaaagtc aatgtcacaa

aaacctggga agaacaaact gaaacactaa gagacgtggt ggatttcctt aaagggcaac

tgcttgacat tcaagtggag aatttaatac ccattgagcc cctcaccctg caggccagga

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gaaagcagtt tggagatttc tccaagaact taaaatagaa ctaccattca atcccgcaat

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gcagctaaac attaaattcg catgaaccac agatgctgga gatcaccaga ccggggagag

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acccagctca aaaagataaa atctagtcat ttaagataat cataagttgt atgatgataa

ttgtataaaa atttgtatga tgataattgt ataataatta tacatgaaag tcccaaaacc

ctacaattaa acactgtata atggaattac a

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0179] In embodiments, the nucleic acid inhibits expression of an *Homo sapiens* macrophage immunometabolism regulator (MACIR), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_001316968.2 (SEQ ID NO: 49):

cccttggccg ctgttcccgc accgcggggc agcgggcctg gaggcccctt tgagaagtag

ctttccccgg ccggcggcac ctttggctgc gtgcccggcc gcgctcaggg tgcgactgcc

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gctgaattgg accacttttt atttttaaat attgagttta aatattttat aactggtttt

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tgattaaact aagtatgaag tgataccatt cagcatggca tcaggtcatt gcagttttag

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cgtgcttcta ctgttttaat gggttaatcc tggattactt aacaatttat gtcaattgca

ctggtttaat ttgttgctaa agaaataatg ccctgggttt agtaacaaat acagctcaac

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ttttctttag ccagaatgaa tggcaaactc tatttagagc aaagtaagta ttagaaaacc

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atgccaaaga gtgggatttt tatgtttaat gattaaacac cattatttat tgacaattta

ccctgtggaa ctgtattatt tctaactatg aaataaaggg gtgatgtaaa cacacattgt

tgtgtggtgc tttaaactag gtccactatc aacaggctac ttactgttca agaattccac

tgaagcactt attttaaggc cctatttttc ttaaacaaaa cagtgacaac aacaatcaaa

ccatttactt ttgatgctca ttggcatttt atgataaaag atgtattcat ggcaatgata

tgtattcacc ctattaggaa acacaactgg ttacctatga gacctgttct gtccgtgtgc

ctacgttcct taataatagc taaataaaaa tttgtagctt tt

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0180] In embodiments, the nucleic acid inhibits expression of an *Homo sapiens* poly(ADP-ribose) polymerase family member 15 (PARP15), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_001113523.3 (SEQ ID NO: 50):

agtcccagcg agctgaggat ggctgcgcca ggccccttc ctgccgctgc tctgagtcca

ggggctccga cccccagaga acttatgcac ggagttgcag gtgttacttc cagagccgga

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cattatttat agtttaataa tcagtttcat cttgcagtgt atcattttcc tcgtcattaa

atattttacg tatcattttt aa

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0181] In embodiments, the nucleic acid inhibits expression of an *Homo sapiens* neuroligin 4 X-linked (NLGN4X), transcript variant 1, mRNA having NCBI Reference Sequence.

(SEQ ID NO: 51):
NM_020742.4

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tattttctaa

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0182] In embodiments, the nucleic acid inhibits expression of an *Homo sapiens* CD59 molecule (CD59 blood group) (CD59), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_203330.2 (SEQ ID NO: 52):

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tgcgggggct gagcgcagaa gcggctcgag gctggaagag

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ttatgtgtgt cctgaaaaaa taagagcctg cccaagactt

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gctcgcatta gtttctgttg ctgccaacag atctgaacta

atgctaacag atccccctga gggattcttg atgggctgag

cagctggctg gagctagtac tgactgacat tcattgtgat

gagggcagct ttctggtaca ggattctaag ctctatgttt

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agaggaaact atgcaaagtt agctggatcg ctcaaggtca

cttaggtaag ttggcaagtc catgcttccc actcagctcc

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atccctgaag ttgccctggt ctctgcacct tctaaaccta

gttcttaaga gctttccatt acatgagctg tctcaaagcc

ctccaataaa ttctcagtgt aagcttctgt tgcttgtgga

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aggataacat gagaacgcac aacagtaagt ggtcactaag

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tgaataataa aggaaagact gttctgggct tcccagaata

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atgtgtaact gtataataac tgtagccaca ctccaatgac

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cctcctgaca gcggaacaat gactgccccg ataggtgagg

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actttctaac ctggcctcac gctgggtaag cttaaggtag

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agctacatct ttcaactgac cctgatcaac gaagagggac

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gggcgttagg aagctccaac aggatggtac ttaatggggc

atttgagtgg agaggtaggt gacatagtgc tttggagccc

agggagggaa aggttctgct gaagttgaat tcaagactgt

tctttcatca caaacttgag tttcctggac atttgtttgc

agaaacaacc gtagggtttt gccttaacct cgtgggttta

ttattacctc atagggactt tgcctcctga cagcagttta

tgggtgttca ttgtggcact tgagttttct tgcatacttg

ttagagaaac caagtttgtc atcaacttct tatttaaccc

cctggctata acttcatgga ttatgttata attaagccat

ccagagtaaa atctgtttag attatcttgg agtaaggggg

aaaaaatctg taatttttc tcctcaacta gatatataca

taaaaaatga ttgtattgct tcatttaaaa aatataacgc

aaaatctctt ttccttctaa aaaaaaaaaa aaaaaa

[0183] a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0184] In embodiments, the nucleic acid inhibits expression of an *Homo sapiens* cofilin 2 (CFL2), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_021914.8 (SEQ ID NO: 53):

ccctttcgct tccacgtcca aaccccttta agaaggatga

atgggcagga tgagttagac tccttcgctg tatcgtctac

tgattcttaa aatgtgacaa atctgattgg acgacttaca

tggcttctgg agttacagtg aatgatgaag tcatcaaagt

ttttaatgat atgaaagtaa ggaaatcttc tacacaagag

gagatcaaaa agagaaagaa agcagttctc ttctgtttaa

gcgatgacaa aagacaaata attgtagagg aagcaaagca

gatcttggtg ggtgacattg gtgatactgt agaggacccc

tacacatctt ttctgaagtt gctacctctg aatgattgcc

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gatatgcttt gtacgatgcc acatacgaaa caaaagagtc

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agtgcacctt taaaaagcaa gatgatttat gctagctcta

aagatgccat taaaaagaaa tttacaggta ttaaacatga

gtggcaagta aatggcttgg atgatattaa ggaccgttcg

acacttggag agaaattggg aggcaatgta gtagtttcac

ttgaaggaaa accattataa aatgacagtc aagtgccatc

tggatcttaa ggagcttcca tttctccagc tcagtccatt

ggaatagtat taggttttgg ttttttgttg tatttccccc

tttccactgg gcccttccaa cacaatgaat gaaggaaata

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gttgaatact gttactttta tatagaaccc aaggaatgcc

ttcctgtcat attttagcca aaacaactgg ttatatgcct

cccttgcagc aagcactaca atgtatgtga tcgtcaatgt

gaatagctta gaatactgca aaggataagc taattgaatg

ccttgaaagt attatccact ggtcagatgg tcaacttttt

tcagtattat ttatagttgg cacttgattg cagttctgtg

aggcttgagc attcatacac ctcacctgcc ttggcaagcc

tattttagtg atatggcagc acggatataa cactatgcat

taaaagcact ttttgtaata agtttaatat cctaaaagga

atgccaatta agttttgtta actgtgtcat caacttatcc

tagtacctca gtgttcattc ctgttacctg catatcttct

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tgagtgtaca ctactgaata agtgtaggag ttttatgttt

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agtcatgatg gcaatttctg tataaaagag ccttaaatgg

aacattgttt tgagatcaaa ctccccaccc tcacaaaaat

ggccacgttg caataaaaat tgtggcatat tacagaacgt

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aacaacttct agggtaaaaa cagctattac taatctctgc

actggtcatt tgagaatttt ttttgtacag cattcatgtg

tgatattttc cagatttgtt ggatctattt ggtttaaaaa

gtattctatc ttaaggccaa ctaatataaa ataccattgt

taaagaatgg tacttttata aacattagtg tatttatttc

ctatgtgtta atatgaagat cagaaattat tttttgcact

ttggcataaa tacttttcaa tatctgattt gttctctgga

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gtctaggctt ccatttaaaa ttatatgaat ggtttgggat

ctttttgcac tgagcaattt tatttcaggc ttccagctgt

ccctgtgagt tatcctggac atttcgatgg tttttggtaa

ggccaaactc tgataagcaa aacagagaat actgacgtat

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tcaatgttcc agttagcttt aaaaggtata cggtgctaat

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taaagctgtt gagatgtgtt tacttatact tcagaacatt

aaaagtttaa aaactggtat ttcagatcaa agaggcatca

ttatctttat tctgtttttc aggattttag ttggtaatac

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gttacagcaa ttaattttag cattttcaga caaatgggaa

cagttggcat gtgtcccaaa ctggctatca gctgttgttt

tccatcatta tctaaaatag tgtggccagc attgtgtatt

gaaatgtgcc tttttcgtac attggaagag aagcctctta

ctgggtttga gtttctctga tacagaacat ttgtagcagc

taatttatgg aatctggcaa ataagctttg ggaggaaatt

cttttaaaag tgttttcttg ttaaggaata atctcaacaa

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tagaggaatc atccctccac ttaaatttcc tctcataatg

caatttggca aattaaatct ctaaatctca gttttttaac

ccatagtatg ggaacggtaa tatctgttta ccatgtttcc

tgagtactaa atatggaaat ggtttttgaa aacaggaaaa

tgctatgtaa atgcaataat ctgtttaaac tattcattct

taattactgt atgtaagtag ataaatatta aatgtttttg

ttaaaagatg ta

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88% 90%. 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0185] In embodiments, the nucleic acid inhibits expression of treslin isoform 1 [*Homo sapiens*] mRNA having NCBI Reference Sequence:

NP_001294954.1 (SEQ ID NO: 54):

1 atggcatgt gtcacaaagt aatgctgctg ctggacaccg cgggcggcgc cgcccgccac

61 agccgggtcc gggggccgc cctgcgcctc ctcacctatc tgagttgccg attcggcctg

121 gccagggtcc actgggcctt caagttcttt gactcgcagg gggcgcggag ccggccgtcc

181 cgcgtgtctg acttccgcga gctggggtcc cgctcgtggg aggactttga ggaggagctg

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301 cacggcgccc tgatggagac gctgctagac taccagtggg accggcccga gatcacgtcg

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661 gaatccccag accaccttgg atactggact gtttgtgaac tgctccacca cggaggtggc

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901 cgaatggaag gaatgttatt tctccctgtt gaaggcaaag agattcaaga aacatggaca

961 gtcaccctag agcccttggc catgcatcag agacattttc agaaaccagt cagaattttt

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1081 tggatgctag gaagtccaga ggagagcaca gcaactcaaa ggctgttatt tcagcagttg

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1501 atcagtggtg ccagttccga tttgatggag tcatttgggt tactacaggc tgcctcagct

1561 aataaggaag agtcttccaa aactgaaggc gaattaatac attgccttgc cgagctctac

1621 cagagaaaat ctcgtgaaga atccactata gctcatcaag aagacagcaa aaagaaacga

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3241 aagggttcag ctcgaatgaa aaagcgttca agaaacactt tggattcgga ggtacctgca

3301 gcttaccaga ctcccaagaa gagtcaccag aaatctctga gcttttctaa aactacacca

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3421 cctgcaaaaa tgacccctac aaagcaggca gcttttaagg agtccttaaa agactcctcc

3481 tcacccggcc atgactcacc attggattca aaaatcactc ctcaaaaacg acatacccag

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3601 cagccgcctg ggtttttgcc aaactgtact tggccacatt cagtgaattc cagtccagaa

3661 agcccctcct gtccagcccc tccaacttca tcgactgccc agcccaggag agagtgtctc

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4141 gggaaacggt gtagaaagac ctctgatccc agaaggagca tcgtggagtg tcagcctgat

4201 gcctccgcta ctcctggggt tggcacagct gacagcccag ctgcccccac agactctaga

4261 gatgaccaga agggactgag cctctctcct cagtctcctc ctgaaagacg gggctaccca

4321 ggccctggtc tcaggagtga ttggcatgca tcctctcctc tgctcattac aagtgacaca

4381 gagcatgtca ctctcctcag tgaagccgaa caccatggca ttggtgactt gaaaagtaac

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4741 tcttcattag aggctgagcc cctcagcaag gaggagagct ctctgggaga agagagcttc

4801 ctccctgctc tcagcatgcc cagggccagc aggtccttaa gcaaacctga acccacctat

4861 gtgtcacccc cctgcccccg cctctcccac agcacacctg gcaagagcag ggggcaaacc

4921 tacatctgcc aggcctgtac ccccacccac ggcccttcta gtaccccctc tccatttcaa

4981 acagatgggg ttccttggac accatccccc aagcacagtg ggaagacaac tccagacata

5041 attaaagact ggcccaggag gaagagggcg gtgggctgtg gcgccggctc ctcttccggg

5101 aggggcgagg tcggtgcaga ccttcctggg agcctgtcac tgcttgagtc agagggcaag

5161 gaccacggcc ttgaactcag catccacagg acgcccatct tggaggattt tgagctcgag

5221 ggagtgtgcc agctcccaga ccagtcgcct cccaggaaca gcatgcctaa ggccgaggaa

5281 gcctcttcct ggggacagtt tgggttgagt tccaggaaga gagtcctgtt ggccaaggaa

5341 gaagctgacc gtggagccaa aaggatctgt gacctgagag aagattcaga agttagtaag

5401 agtaaagagg ggtctccaag ttggagtgca tggcagctac cctccacggg agacgaagag

5461 gtgtttgttt ccggctccac cccacctccc agctgtgccg tgcggagctg cctctctgcc

5521 agtgccctcc aggctctgac ccagtctccg ctgctgttcc aggggaaaac accttcctct

5581 cagagcaaag accccagaga tgaggatgtg gatgttcttc cctccactgt agaagactct

5641 cctttcagtc gcgctttctc caggaggcgc cccatcagca gaacttatac acggaagaag

5701 ctcatgggaa cctggctgga ggacttatag ccacaaacat tactgagccc aaaagatcaa

5761 ggagtcagcc aggaccctgt ggacataaag aagttggatg cctggtccca agcctctttt

5821 gccatggtca gtgttcagat tgccattaga atgccttagg gttttctaat tccccttatg

5881 gatccaatcc atctcctggc cctgcccctt gttggggaag ttgcaggagg agaggtggat

5941 ggcaatgtga ttggtgctat aactcaggca gcctgggagt caggaaccca gacaaggaat

6001 cccattccag cctcacccca accatgacct tggcaagtca gggggccact ctgcctcatt

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6121 ctgcgacaca ggcagcgctt tgtaaactgt gaagccatat acgtgaaact gaagagtgca

6181 ttgggcagtg gaagctattt tttgccttcc ctgtgtaaca gtaaaatcat ctctagtgac

6241 tgagcactca gtacattttt gtttaatgtt gggcctgagg ttaactgtga ccatggtcca

6301 gcttgagtgg cttctggagc agccacattt tcaaggactg tccaagagcc agccagttca

6361 gggctcaggc ctcacccatt gcccactcct ggggagacca tcacctggct catcgtttcc

6421 accaagagtg ccccacagga gtgccccaca gacccgctgg accagcctgc tgcgggtcct

6481 ggccaggggt ctggctaacg gtgagggctg actctgaact gtctctcagt ctccagaaag

6541 tgttcaagcc tgttgtgttc ccaaatctga ttcctcctat tgtcttgtaa atcaaactct

6601 aagtgaaaac ttcccatttg tcccttcaaa gatttttttt tattaaatgg ttttttaaga

6661 tcctaaaaaa aaaaaaaaaa aaaaa
```

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0186] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* macrophage immunometabolism regulator (MACIR), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_001316968.2 (SEQ ID NO: 55):

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   1 cccttggccg ctgttcccgc accgcggggc agcgggcctg gaggcccctt tgagaagtag

  61 ctttccccgg ccggcggcac ctttggctgc gtgcccggcc gcgctcaggg tgcgactgcc

 121 cgggtcagat agcacctcag ggcgagcccc ggcggtctga tctcgccgac cctcctcgtc

 181 ctggttgcaa cccgcgtgcg aggccgcccg cgccctccga gtgtctgccg gtgcagtggg

 241 ggtggactgg ccggctgtgg ccgtgtgtgc gcgtgtggat tggggcccgg tccgagccag

 301 aagcttaagc ggcagatgtc gggcattgcc accctcgccc cacctgtcgc gggtggactt

 361 tggggcagta cctggagtag aacagaaaaa ttattatgtc tgtgttccct tgggactcat

 421 tggaaattgt acagtgacat cttctgggat ttagtctgga ttgtgcagac tggtgcttaa

 481 aatggaagtc gatattaatg gagagtctag aagtaccctg accaccttgc ccttccctgg

 541 ggctgaggcc aactccccgg gaaaggcgga ggcagagaag ccccgctgct ccagcacacc

 601 ctgctccccg atgcggagga ccgtgtcagg ctaccagatc ctacacatgg actctaacta

 661 tttggttggc ttcacgactg gcgaggaact cctgaagtta gctcagaagt gcacaggagg

 721 tgaagagagc aaagcagaag ccatgccatc cttacgctcc aaacagctag atgcaggact

 781 tgcccgttcc tctcgtttgt ataaaaccag aagtaggtac taccagccat acgagattcc

 841 agctgtcaat ggcaggaggc gaaggcggat gccaagctca ggagacaagt gcactaaatc

 901 tttaccttat gaaccttaca aggccctcca tgggcctctg cctctttgtc ttcttaaagg

 961 taagagggct cactccaaat ctctggacta cctcaatcta gataaaatga tcaaggagcc

1021 agctgataca gaagtgctac agtaccagct tcaacaccta accctccgag gggaccgtgt

1081 gtttgctagg aataatacat gaatgacttg gagagagctt aaaccaattt aggtcagcct

1141 acgcttggct agaaaaaacc cactgctgta ctctgtacat gactcttcac actatagatg

1201 gttatatcag ctaagtgttc ctggaacata aaaattgttt gggtcaaatt tgaatacagg

1261 aatgaaatca caggtacttg gggggggat atcattctag agcacgcaac tgcaaagaaa
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1381 gtaatttcat ctttatgatt ctgacactca aattgggaat gttacctgct tggttgttgc

1441 tgacttgata tgattcatta gaaatttata tcttcagtac tcaagtactt cttgaatctc

1501 tgtattttac tataaaatgt atgtaatgat ttgttttatg aaatttagaa cttgaacatt

1561 gctgaattgg accacttttt atttttaaat attgagttta aatattttat aactggtttt

1621 gcactgaaaa aattaacatt tcagattgac aagagagtaa tctttcttca cttgcctcaa

1681 taatgttatt gagcaatgaa ttttttattt ccgcatggaa agttattgat ctctatggct

1741 gtaaaatatt tctttatagc gttattaaag tgtgtcttaa taaaattaaa tttgggatac

1801 aaagtattta ttttacaatg ggtgggcggg ggaaactttt ccagaaagtt tccaatatga

1861 cgttttcata agttgaaaaa actctcctta gtgcttattt tctaacttaa aattcacctg

1921 gaactttaaa tcggaaagga ttcttttaat tgtggattat aggcataata ctgtttgcat

1981 ctgaattttc tgtaagtgaa taatagttta atagaggaac tcatgatttg tactattgaa

2041 tgattaaact aagtatgaag tgataccatt cagcatggca tcaggtcatt gcagttttag

2101 ttctgtgtaa cacaagcact cactgaaatt ccagtttcta ggattagtgt aggagcctaa

2161 cgtgcttcta ctgttttaat gggttaatcc tggattactt aacaatttat gtcaattgca

2221 ctggtttaat ttgttgctaa agaaataatg ccctgggttt agtaacaaat acagctcaac

2281 tattcttgaa tatattttga aaaaaaaatg tatgtaactt acctttttgta aacgttccat

2341 ttctttttttc cctcattttt gactcttaaa ggtgcaattt attactgaat tgggatttct

2401 ggcagcacag aactgctttt tattttgggg tctgtgagtt tcttaggtat tagcaatctt

2461 gcttataaaa taagaacacc ttttaattaa tgagtgggtc attcctggtg caattgtgat

2521 ttttctttag ccagaatgaa tggcaaactc tatttagagc aaagtaagta ttagaaaacc

2581 ctaggaactc ttaatcaacg tttattacac tttcattaag gcaaactacg tgaaagagcc

2641 ttggggaagt tggcccatat cttactaagt tgatcagatt tctcgttggg ctggaaatgt

2701 ttcgctgttg tatattttaa agtaaattgc acctttgtaa catattgtat tgacgaatga

2761 tcactaagat tagctatatc tatacagtca ttagtttgac aagaaataga atcctgtcag

2821 atgccaaaga gtgggatttt tatgtttaat gattaaacac cattatttat tgacaattta

2881 ccctgtggaa ctgtattatt tctaactatg aaataaaggg gtgatgtaaa cacacattgt

2941 tgtgtggtgc tttaaactag gtccactatc aacaggctac ttactgttca agaattccac

3001 tgaagcactt attttaaggc cctatttttc ttaaacaaaa cagtgacaac aacaatcaaa

3061 ccatttactt ttgatgctca ttggcatttt atgataaaag atgtattcat ggcaatgata

3121 tgtattcacc ctattaggaa acacaactgg ttacctatga gacctgttct gtccgtgtgc

3181 ctacgttcct taataatagc taaataaaaa tttgtagctt tt

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0187] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* gasdermin B (GSDMB), transcript variant 1, mRNA having NCBI Reference Sequence:

(SEQ ID NO: 56):
NM_001042471.2

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attattttag cttcctgaga ttcagaggcc aggaactgtg

cagagatctg tggggattct cacaacttcc atttctggtg

aacagctgag gtcagagagg agttggtcca ggcgcaatgt

tcagcgtatt tgaggaaatc acaagaattg tagttaagga

gatggatgct ggaggggata tgattgccgt tagaagcctt

gttgatgctg atagattccg ctgcttccat ctggtggggg

agaagagaac tttctttgga tgccggcact acacaacagg

cctcaccctg atggacattc tggacacaga tggggacaag

tcgttagatg aactggattc tgggctccaa ggtcaaaagg

ctgagtttca aattctggat aatgtagact caacgggaga

gttgatagtg agattaccca aagaaataac aatttcaggc

agtttccagg gcttccacca tcagaaaatc aagatatcgg

agaaccggat atcccagcag tatctggcta cccttgaaaa

caggaagctg aagagggaac tacccttttc attccgatca

attaatacga gagaaaacct gtatctggtg acagaaactc

tggagacggt aaaggaggaa accctgaaaa gcgaccggca

atataaattt tggagccaga tctctcaggg ccatctcagc

tataaacaca agggccaaag ggaagtgacc atccccccaa

atcgggtcct gagctatcga gtaaagcagc ttgtcttccc

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aagtgcctcg gcaaggagga tattcggcag gatctagagc

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ggaggaccca gacaagcctc tcctaagcag ccttttaat

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ggttttccct ttaccagtct gtcctcactg ccatcgccac

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atccaaaacc agcctggatt tcatacatgg acttctgatt

aaaagtggca ggttgtgcat gttaa
```

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0188] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* bromodomain containing 4 (BRD4), transcript variant long, mRNA having NCBI Reference Sequence:

NM_058243.3 (SEQ ID NO: 57):

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attctttgga atactactgc tagaagtctg acttaagacc

cagcttatgg gccacatggc acccagctgc ttctgcagag

aaggcaggcc actgatgggt acagcaaagt gtggtgctgc

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ctacatcccc tctttttgac ctgaaaggtc ctttattgtc

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ccactcaggc actttctcat ataccactgt gccacttcaa

gtgtgacgta tttaggttct ttggggtttc ttccatctca

tcccacccac tcatttttgt tccttgtttt gttcagacac

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tctgcagctt cctgctgaag atttaactca gccatggcct

tctccacacc tccctgatgg gtgtctctct acctgggttg

taattagaac tgggatctat ttaatttctc cagccatttc

ccaacccttc ccacagtact agaaatctta gtcctatacc

agagtaagag gtgtgtacaa gcccccactg tactgtatgc

acggatcgct tggccaataa ttatgtcagt gaatctgaga

cttgtattaa acactttaga catttgtaga agggaattcg

tagacttttc acttacatac gaaaggtttt ttttttttt

tgtgcagttc tcattgcaaa aataaacatt tgtactgagt

ataaagtta

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0189] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* interferon induced protein with tetratricopeptide repeats 3 (IFIT3), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_001549.6 (SEQ ID NO: 58):

gcagacagga agacttctga agaacaaatc agcctggtca

ccagcttttc ggaacagcag agacacagag ggcagtcatg

agtgaggtca ccaagaattc cctggagaaa atccttccac

agctgaaatg ccatttcacc tggaacttat tcaaggaaga

cagtgtctca agggatctag aagatagagt gtgtaaccag

attgaatttt taaacactga gttcaaagct acaatgtaca

acttgttggc ctacataaaa cacctagatg gtaacaacga

ggcagccctg gaatgcttac ggcaagctga agagttaatc

cagcaagaac atgctgacca agcagaaatc agaagtctag

tcacttgggg aaactacgcc tgggtctact atcacttggg

cagactctca gatgctcaga tttatgtaga taaggtgaaa

caaacctgca agaaattttc aaatccatac agtattgagt

attctgaact tgactgtgag gaagggtgga cacaactgaa

gtgtggaaga aatgaaaggg cgaaggtgtg ttttgagaag

gctctggaag aaaagcccaa caacccagaa ttctcctctg

gactggcaat tgcgatgtac catctggata atcacccaga

gaaacagttc tctactgatg ttttgaagca ggccattgag

ctgagtcctg ataaccaata cgtcaaggtt ctcttgggcc

tgaaactgca gaagatgaat aaagaagctg aaggagagca

gtttgttgaa gaagccttgg aaaagtctcc ttgccaaaca

gatgtcctcc gcagtgcagc caaattttac agaagaaaag

gtgacctaga caaagctatt gaactgtttc aacgggtgtt

ggaatccaca ccaaacaatg gctacctcta tcaccagatt

gggtgctgct acaaggcaaa agtaagacaa atgcagaata

caggagaatc tgaagctagt ggaaataaag agatgattga

agcactaaag caatatgcta tggactattc gaataaagct

cttgagaagg gactgaatcc tctgaatgca tactccgatc

tcgctgagtt cctggagacg gaatgttatc agacaccatt

caataaggaa gtccctgatg ctgaaaagca acaatcccat

cagcgctact gcaaccttca gaaatataat gggaagtctg

aagacactgc tgtgcaacat gctttagagg gtttgtccat

aagcaaaaaa tcaactgaca aggaagagat caaagaccaa

ccacagaatg tatctgaaaa tctgcttcca caaaatgcac

caaattattg gtatcttcaa ggattaattc ataagcagaa

tggagatctg ctgcaagcag ccaaatgtta tgagaaggaa

ctgggccgcc tgctaaggga tgccccttca ggcataggca

gtattttcct gtcagcatct gagcttgagg atggtagtga

ggaaatgggc cagggcgcag tcagctccag tcccagagag

ctcctctcta actcagagca actgaactga gacagaggag

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gaaaacagag catcagaagc ctgcagtggt ggttgtgacg

ggtaggacga taggaagaca gggggcccca acctgggatt

gctgagcagg gaagctttgc atgttgctct aaggtacatt

tttaaagagt tgtttttgg ccgggcgcag tggctcatgc

ctgtaatccc agcactttgg gaggccgagg tgggcggatc

acgaggtctg gagtttgaga ccatcctggc taacacagtg

aaatcccgtc tctactaaaa atacaaaaaa ttagccaggc

gtggtggctg gcacctgtag tcccagctac ttgggaggct

gaggcaggag aatggcgtga acctggaagg aagaggttgc

agtgagccaa gattgcgccc ctgcactcca gcctgggcaa

cagagcaaga ctccatctca aaaaaaaaaa aaaaaaaaaa

aaagagttgt tttctcatgt tcattatagt tcattacagt

tacatagtcc gaaggtctta caactaatca ctggtagcaa

taaatgcttc aggcccacat gatgctgatt agttctcagt

tttcattcag ttcacaatat aaccaccatt cctgccctcc

ctgccaaggg tcataaatgg tgactgccta acaacaaaat

ttgcagtctc atctcatttt catccagact tctggaactc

aaagattaac ttttgactaa ccctggaata tctcttatct

cacttatagc ttcaggcatg tatttatatg tattcttgat

agcaatacca taatcaatgt gtattcctga tagtaatgct

acaataaatc caaacatttc aactctgtta

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0190] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* opioid growth factor receptor (OGFR), mRNA having NCBI Reference Sequence:

NM_007346.4 (SEQ ID NO: 59):

agcgcgagcc ccgccgccgc cgagcatgga cgaccccgac

tgcgactcca cctgggagga ggacgaggag gatgcggagg

acgcggagga cgaggactgc gaggacggcg aggccgccgg

cgcgagggac gcggacgcag gggacgagga cgaggagtcg

gaggagccgc gggcggcgcg gcccagctcg ttccagtcca

gaatgacagg gtccagaaac tggcgagcca cgagggacat

gtgtaggtat cggcacaact atccggatct ggtggaacga

gactgcaatg gggacacgcc aaacctgagt ttctacagaa

atgagatccg cttcctgccc aacggctgtt tcattgagga

cattcttcag aactggacgg acaactatga cctccttgag

gacaatcact cctacatcca gtggctgttt cctctgcgag

aaccaggagt gaactggcat gccaagcccc tcacgctcag

-continued

ggaggtcgag gtgtttaaaa gctcccagga gatccaggag

cggcttgtcc gggcctacga gctcatgctg ggcttctacg

ggatccggct ggaggaccga ggcacgggca cggtgggccg

agcacagaac taccagaagc gcttccagaa cctgaactgg

cgcagccaca acaacctccg catcacacgc atcctcaagt

cgctgggtga gctgggcctc gagcacttcc aggcgccgct

ggtccgcttc ttcctggagg agacgctggt gcggcgggag

ctgccgggggg tgcggcagag tgccctggac tacttcatgt

tcgccgtgcg ctgccgacac cagcgccgcc agctggtgca

cttcgcctgg gagcacttcc ggccccgctg caagttcgtc

tgggggcccc aagacaagct gcggaggttc aagcccagct

ctctgcccca tccgctcgag ggctccagga aggtggagga

ggaaggaagc cccggggacc ccgaccacga ggccagcacc

cagggtcgga cctgtgggcc agagcatagc aagggtgggg

gcagggtgga cgaggggccc cagccacgga gcgtggagcc

ccaggatgcg ggacccctgg agaggagcca gggggatgag

gcaggggggc acggggaaga taggccggag cccttaagcc

ccaaagagag caagaagagg aagctggagc tgagccggcg

ggagcagccg cccacagagc caggccctca gagtgcctca

gaggtggaga agatcgctct gaatttggag gggtgtgccc

tcagccaggg cagcctcagg acggggaccc aggaagtggg

cggtcaggac cctggggagg cagtgcagcc ctgccgccaa

cccctgggag ccagggtggc cgacaaggtg aggaagcgga

ggaaggtgga tgagggtgct ggggacagtg ctgcggtggc

cagtggtggt gcccagacct tggcccttgc cgggtccct

gccccatcgg ggcaccccaa ggctggacac agtgagaacg

gggttgagga ggacacagaa ggtcgaacgg ggcccaaaga

aggtacccct gggagcccat cggagacccc aggccccagc

ccagcaggac ctgcagggga cgagccagcc gagagcccat

cggagacccc aggcccccgc ccagcaggac ctgcagggga

cgagccagcc gagagcccat cggagacccc aggcccccgc

ccggcaggac ctgcagggga cgagccagcc gagagcccat

cggagacccc aggccccagc ccggcaggac ctacaaggga

tgagccagcc gagagcccat cggagacccc aggcccccgc

ccggcaggac ctgcagggga cgagccagcc gagagcccat

cggagacccc aggcccccgc ccggcaggac ctgcagggga

cgagccagcc gagagcccat cggagacccc aggccccagc

ccggcaggac ctacaaggga tgagccagcc aaggcggggg

aggcagcaga gttgcaggac gcagaggtgg agtcttctgc

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caagtctggg aagccttaag gaaaggagtg cccgtcggcg

tcttggtcct cctgtccctg ctgcaggggc tggggcctcc

ggagctgctg cgggctcccc tcaggctctg cttcgtgacc

cgtgacccat gacccacagt gctggcctcc tgtggggcca

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ccaaggcctg cagaagcctc ctggcctggc tgtgtcttcc

ccacccagct ctcccctgcg cccctgtctt tgtaaattga

cccttctgga gtgggggggcg gcgggcaggg ctgcttttct

tagtctgata ccaagcaagg ccttttctga ataaattcat

ttgactttga

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0191] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* short chain dehydrogenase/reductase family 39U member 1 (SDR39U1), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_020195.3 (SEQ ID NO: 60):

agtcgctatg cgtgtgcttg tgggtggcgg gacaggcttc

attgggacag ccctaaccca gctgctgaat gccagaggcc

acgaagtgac gttggtctcc cgaaagcccg ggcccggccg

gatcacgtgg gatgagctcg ctgcatcggg gctgccgagc

tgcgatgccg ccgtcaacct ggccggagag aacatcctca

accctctccg aagatggaat gaaaccttcc aaaaagaggt

aatcggcagc cgcctagaga ccacccaatt gctggctaaa

gccatcacca aagccccaca acccccaag gcctgggtct

tagtcacagg tgtagcttac taccagccca gtctgactgc

ggagtatgat gaagacagcc caggagggga ctttgacttt

ttctccaacc tcgtaaccaa atgggaagct gcagccaggc

ttcctggaga ttctacacgc caggtggtgg tgcgctcagg

ggttgtgctg ggccgtgggg gtggtgccat gggccacatg

ctgctgccct ttcgcctggg cctgggggggc cccatcggct

caggccacca attcttcccc tggatacaca tcggggacct

ggcaggaatc ctgacccatg cccttgaagc aaaccacgtg

cacggggtcc tgaatggagt ggctccatcc tccgccacta

atgctgagtt tgcccagacc ttgggtgctg ccctgggccg

ccgagccttc atccctctcc ccagcgctgt ggtgcaagct

gtctttgggc gacagcgtgc catcatgctg ctggagggcc

agaaggtgat cccacagcga acactggcca ctggctacca

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tgtctcaagg ccgtaatctc atcaggttgg gacattaatc

ttttcaactc cttgtaagat ttcccagttt ggtttctcta

catgtcctgc agctgcccca cttctccttt acgctgtgta

gagaatgctc tgcagtttag gcaataaaaa taaattgtct

cactaa

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0192] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* regulating synaptic membrane exocytosis 2 (RIMS2), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_001100117.3 (SEQ ID NO: 61):

agttcccctt tcccttgaac cgctcacttc acagcccttc

gcccccggga agaagaaaca tttcccgaag cgcactcctc

agccctcctt ccccacgcgc tcgccctccc ctccccctgc

ttttcttggg ggaggggggc tgtcgccttg gattgaaggc

cattgatttg tatgtatttg tcccagcgct ggaggctgcc

ccagccgccg cgccggtgcc gccgctgcca gtggagttgc

ctccccgctt ccctagggtg gttcggctcc accaaacatg

tcggctcctg tcgggccccg gggccgcctg gctcccatcc

cggcggcctc tcagccgcct ctgcagcccg agatgcctga

cctcagccac ctcacggagg aggagaggaa aatcatcctg

gccgtcatgg ataggcagaa gaaagaagag gagaaggagc

agtccgtgct caaaaaactg catcagcagt ttgaaatgta

taaagagcag gtaaagaaga tgggagaaga atcacagcaa

cagcaagaac agaagggtga tgcgccaacc tgtggtatct

gccacaaaac aaagtttgct gatggatgtg gccataactg

ttcatattgc caaacaaagt tctgtgctcg ttgtggaggt

cgagtgtcat tacgctcaaa caaggttatg tgggtatgta

atttgtgccg aaaacaacaa gaaatcctca ctaaatcagg

agcatggttt tataatagtg gatctaatac accacagcaa

cctgatcaaa aggttcttcg agggctaaga aatgaggagg

cacctcagga gaagaaacca aaactacatg agcagaccca

gttccaagga ccctcaggtg acttatctgt acctgcagtg

gagaaaagtc gatctcatgg gctcacaaga cagcattcta

ttaaaaatgg gtcaggcgtg aagcatcaca ttgccagtga

catagcttca gacaggaaaa gaagcccatc tgtgtccaga

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aatattcaca gtatgctact tcggataccg caatgcctag

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cctcagtttt atgaagactc tgatcattta agttataggg

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atgctgatct ggaagattcc aggatttcta tgctaaggat

ggatcgacca tcaaggcaaa gatctatatc agaacgtaga

gctgccatgg aaaatcagcg atcttattca atggaaagaa

ctcgagaggc tcagggacca agttcttatg cacaaaggac

cacaaaccat agtcctccta cccccaggag gagtccacta

cccatagata gaccagactt gaggcgtact gactcactac

ggaaacagca ccacttagat cctagctctg ctgtaagaaa

aacaaaacgg gaaaaaatgg aaacaatgtt aaggaatgat

tctctcagtt cagaccagtc agagtcagtg agacctccac

caccaaagcc tcataaatca aagaaaggcg gtaaaatgcg

ccagatttcg ttgagcagtt cagaggagga attggcttcc

acgcctgaat atacaagttg tgatgatgtt gagattgaaa

gtgagagtgt aagtgaaaaa ggagacatgg attacaactg

gttggatcat acgtcttggc atagcagtga ggcatcccca

atgtctttgc accctgtaac ctggcaacca tctaaagatg

gagatcgttt aattggtcgc attttattaa ataagcgtct

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ggcttgaagg ttgtaggagg aaagatgact gaatcaggtc

ggctttgtgc atttattact aaagtaaaaa aaggaagttt

agctgatact gtaggacatc ttagaccagg tgatgaagta

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ccgcgaatac ctgatagcac acatgcacaa ctggagtcca

gttctagctc ctttgaatct caaaaaatgg atcgtccttc

tatttctgtt acctctccca tgagtcctgg aatgttgagg

gatgtcccac agttcttatc aggacaactt tcaagccaaa

gccttagtag aagaacaacg ccttttgttc ctagggttca

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gtaaagaaaa cattggaacc caaatggaac caaacattca

tttattctcc agtccaccga agagaatttc gggaacgaat

gctagagatt acccttt ggg atcaagctcg tgttcgagag

gaagaaagtg aattcttagg cgagatttta attgaattag

aaacagcatt attagatgat gagccacatt ggtacaaact

tcagacgcat gatgtctctt cattgccact tccccaccct

tctccatata tgccacgaag acagctccat ggagagagcc

caacacggag gttgcaaagg tcaaagagaa taagtgatag

tgaagtctct gactatgact gtgatgatgg aattggtgta

gtatcagatt atcgacatga tggtcgagat cttcaaagct

caacattatc agtgccagaa caagtaatgt catcaaacca

ctgttcacca tcagggtctc ctcatcgagt agatgttata

ggaaggacta gatcatggtc acccagtgtc cctcctccac

aaagtcggaa tgtggaacag gggcttcgag ggacccgcac

tatgaccgga cattataata caattagccg aatggacaga

catcgtgtca tggatgacca ttattctcca gatagagaca

gggattgtga agcagcagat agacagccat atcacagatc

cagatcaaca gaacaacggc ctctccttga gcggaccacc

acccgctcca gatccactga acgtcctgat acaaacctca

tgaggtcgat gccttcatta atgactggaa gatctgcccc

tccttcacct gccttatcga ggtctcatcc tcgtactggg

tctgtccaga caagcccatc aagtactcca gtcgcaggac

gaaggggccg acagcttcca cagcttccac caaagggaac

gttggataga aaagcaggag gtaaaaaact aaggagcact

gtccaaagaa gtacagaaac aggcctggcc gtggaaatga

ggaactggat gactcgacag gcaagccgag agtctacaga

tggtagcatg aacagctaca gctcagaagg aaatctgatt

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atttcctgga tggccttggc cctgctcagc tagtgggacg

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actgccagca ccgtatgtaa aagtgtatct attagataac

ggagtctgca tagccaaaaa gaaaacaaaa gtggcaagaa

aaacgctgga acccctttac cagcagctat tatctttcga

agagagtcca caaggaaaag ttttacagat catcgtctgg

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gtagatccaa ccttggcccc tctgacaaga agagcttccc

aatcatctct ggaaagttca actggacctt cttactctcg

ttcatagcag ctgtaaaaaa attgttgtca cagcaaccag

cgttacaaaa aaaaaaaaaa aaatcacagg ttgcaaaccc

tggtaacact gcatgcttaa tgttgtgtct tctgagcctg

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cactcgagtt ctggtccaat ctgaagccat ggattaatct

caaagaatca gtcagtttca tgcaacagaa gccctttca

atggcacctt tatattttta tcattccttt ttcttcattt

atctaacccc aaagccctga tatgccacag aaatggagct

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gtcaggaaca atcatcagcc ctcctctggg cgggaatcag

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ccatgggcac gtcaattact aatgctaaga tgtgttggac

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aaaaaaaaga ataaaaatca gccattttca acaatttata

ttatttttaa aaataaattt cactagtgca tggttttaaa

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tgtttattct ttaatcatag tctgtgtttt ggcagacatt

acaaatggaa atactttcta gaagatactt aaaattctct

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tgttaaatat acaaatctta tgaagttcaa tatgtgcaaa

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cctcttttaa actttttctt ctccctgcca gagtgaacct

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gggagtacat taaagtaagt cagcatgtat ttgacgaaga

agatatttga acttttgcag tttattgtac agtgcatggt

aatttttca cctttaaaat tcagtttaca ggaaaattct

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agcaatttct ttagccagtt tccatttact atgtgaatag

aagcactgct aaaaattggg aaccctgaaa cacagggctg

tttattaatt catttttctg tagtaaaatt caatttttca

caaattatat ttctaaagaa atatagtaaa cataaatttg

caacaatttt aaagctccag tttttaggtg actcaaagaa

agtcattatg cctattaata gttatttgat gccatcacca

aaagtctatg tgaaaatctc ctaaagtcaa aacccctgcc

tttggtttta cagacggtta ttaccattgg gtggagctgc

aaggtcaaat ttctcctaag ttcccctatt tagaggaaaa

gtcactggtt attgtaataa accacccatg gttctttatg

tacattttga taacacatta ttatagcttg attttaattt

tttgcattaa ttttttgaaat ccacatacat ctcatttgtt

taaattaagg ccatgcacaa atatttttttt tagttcagtg

ctgaccatta aaaactatca tgcttgatac ggtgcaaaag

ttaaaatgag tatcactaaa aatgccttct ttttatgtgg

tgcaatatga aatacaccaa gactgtgtct tgacattctg

atggacccag gtaaagttgt taaaagaacg aataaaactt

tattaaaata atttagacac ctgtgtacca gcaacaattg

atttaataga cctatagtgt ctatactatc ccttagaata

aaggtttatg attttcctga tactaagatg cagtcacata

atcttttgtg catattccta tacaaattat ttctaatttt

aataagaagg acgtgactac ggaatatttg tacatacttg

tcattatgca gtatttattt aaaagttggt gttttttttt

aattttcaca tctgcacctc gacttgtggt ttagtcatgt

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tccttcaggg cagagaccgt atcttcagta tcaaaaacaa

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a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0193] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 3 (ST8SIA3), mRNA having NCBI Reference Sequence:

NM_015879.3 (SEQ ID NO: 62):

ccttcgccac gccgccgcgc agcccctcca tcttcctgct

cggcaccggg ccccgcgcgc ccctgcctac ggggtcccgc

tgctctccgg ggctcctgcc agccccaacc cccggccccg

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gaatgtgcct gcctcattgc cttgtgttcc aaacacagta

ctgaatgcgt tgtttttaaa taaaccattt cgttttgctt

tgggaaa

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0194] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* cyclin dependent kinase inhibitor 3 (CDKN3), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_005192.4 (SEQ ID NO: 63):
accggtgagt cgccggcgct gcagagggag gcggcactgg

tctcgacgtg gggcggccag cgatgaagcc gcccagttca

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ttgaagatga acagactcca attcatatat catggctatc

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a

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0195] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* T cell immunoglobulin and mucin domain containing 4 (TIMD4), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_138379.3 (SEO ID NO: 64):
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caaccggaac accactccag atgacaacca ttgccgtctt

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agatggatgg aatacccatg tcaatgaaga atgaaatgcc

catctcccaa ctactgatga tcatcgcccc ctccttggga

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tttgtgctct tcgcattgtt tgtggcgttt ctcctgagag

ggaaactcat ggaaacctat tgttcgcaga aacacacaag

gctagactac attggagata gtaaaaatgt cctcaatgac

gtgcagcatg gaagggaaga cgaagacggc ctttttaccc

tctaacaacg cagtagcatg ttagattgag gatgggggca

tgacactcca gtgtcaaaat aagtcttagt agatttcctt

gtttcataaa aaagactcac ttattccatg gatgtcattg

atccaggctt gctttagttt catgaatgaa gggtacttta

gagaccacaa

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0196] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* SYS1 golgi trafficking protein (SYS1), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_033542.4 (SEQ ID NO: 65):

ctttcctacg cagccgctcc tgccgccgtg gtcgctggag

ctttgcctct ctaggccggc agcgcctctc ctccatggtc

ctgtctgtca gcgctgtttt gggagcccgc cggtgaggcc

gggccacgct cagacacttc gatcgtcgag tctgtcactg

ggcatggcgg gtcagttccg cagctacgtg tgggacccgc

tgctgatcct gtcgcagatc gtcctcatgc agaccgtgta

ttacggctcg ctgggcctgt ggctggcgct ggtggacggg

ctagtgcgaa gcagcccctc gctggaccag atgttcgacg

ccgagatcct gggcttttcc acccctccag gccggctctc

catgatgtcc ttcatcctca acgccctcac ctgtgccctg

ggcttgctgt acttcatccg gcgaggaaag cagtgtctgg

atttcactgt cactgtccat ttctttcacc tcctgggctg

ctggttctac agctcccgtt tcccctcggc gctgacctgg

tggctggtcc aagccgtgtg cattgcactc atggctgtca

tcggggagta cctgtgcatg cggacggagc tcaaggagat

acccctcaac tcagccccta aatccaatgt ctagaatcag

gccctttgga catcctgctg acacttgggc cccttaacac

cttgggctgc tcagaccctc cagatgaggt ccagcccaga

tctgagagga accctggaaa tgtgaagtct ctgttggttt

gggagagata gtgagggcct gtcaaagaag gcaggtagca

gtcagcatga cagctgcaag aatgacctct gtctgttgaa

gccttggtat ctgagaggtc aggaagggga cctctttgag

ggtaataaca gaattggaac catgccactc ttgagccaca

atacctgtca ccagcctgtt gttttaagag agaaaaaaaa

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ctgtcttacc cccctgggac agctgttacc tttgcagtgt

tgccgaatca cagcagttac ctttgcagtg ttgccgaatc

acagcagttc tgttggagaa acgcttggtt tccggatcca

gagccacaga aagaaatgta ggtgtgaagt attaggctgc

tgtcagggag aggatggcag atggaggcat caagcacaag

gaaaatgcac aacctgtgcc ctgttataca cacgttcatg

tgcacccaag aacctatgac tttcttccag ttccttctac

caggtcccca tcctgctgcc agctctcaac atagcaggcc

ataggaccca gagaagaatc ccagcgttgc tcaaagtcta

accatcataa agacactgcc tgtcttctag gaatgaccag

gcacccagct cccactggac tccaattttt tttcctgcct

tatttagaat tctttggcgg gaagggtatg atgggttccc

agagacaaga agcccaacct tctggcctgg gctgtgctga

tagtgctgag ggagatagga atttgctgct aagatttttc

tttggggtgg agtttcctct gtgaggggct tgcagctatc

cttcctgtgt atacaaatac agtattttcc atggttctgc

ctgcacttac tttgtaatgc cacggttgag attgagagag

atcagcgcag ccaggcaagg gaactttaaa gaattattag

gccaccttct ccctttcctg gaccccagag tcattcctcc

atttggttaa aatactcagt gcagggaact cttacatcct

gtctccttca cttgcagcgt cccctgctat gcctcaggtg

aaccacataa ttcttgggtt tccgttccta cttgctagtg

atttctgaac atgttcaatg gagcggcaca cagtctagac

ccacttccgc attgaaacct tcactgttcc tctttggttt

cttcagagct ttcccaagag agctgtcagt tttcagctgt

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gctatctctc tgagaagctc atctgacctc ctgactctca

gccctacaga gtagggagtt gatgctgaca ggatgaagat

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agggtgaggc acctcagtaa ctcatggtac cttggccaag

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gctgcagggt ctaggaggta agaccagctg ggatgacctt

ccctgggtta atcaatttcc ctctagacaa cacaaactgc

aggcatgtga ctaactttga aagaacaccc atcatgtggc

tgctgtcacc cttgaccagc cgtggtggtg gttactccat

ctgtggttgg agcgcctctt tgggattcac ttcaaggtct

tgtgcctatt tttctgcata tcttctgtga tgacaaatct

ctgtcccctg agtgttaatt tgatttttag aaatggccaa

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aatgagattt ttatgatttc taaagtaaca ataaaagcag

tttttagagt tgagttccag agagggcagg gcaatggcag

tgacatgttt gtcattttaa taataaataa catctattga

gtgcttaa

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%. 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0197] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* ubiquitin D (UBD), mRNA having NCBI Reference Sequence:

NM_006398.4 (SEQ ID NO: 66):

gtctctggtt tctggcccct tgtctgcaga gatggctccc

aatgcttcct gcctctgtgt gcatgtccgt tccgaggaat

gggatttaat gacctttgat gccaacccat atgacagcgt

gaaaaaaatc aaagaacatg tccggtctaa gaccaaggtt

cctgtgcagg accaggttct tttgctgggc tccaagatct

taaagccacg gagaagcctc tcatcttatg gcattgacaa

agagaagacc atccacctta ccctgaaagt ggtgaagccc

agtgatgagg agctgccctt gtttcttgtg gagtcaggtg

atgaggcaaa gaggcacctc ctccaggtgc gaaggtccag

ctcagtggca caagtgaaag caatgatcga gactaagacg

ggtataatcc ctgagaccca gattgtgact tgcaatggaa

agagactgga agatgggaag atgatggcag attacggcat

cagaaagggc aacttactct tcctggcatg ttattgtatt

ggagggtgac caccctgggc atggggtgtt ggcaggggtc

aaaaagctta tttcttttaa tctcttactc aacgaacaca

tcttctgatg atttcccaaa attaatgaga atgagatgag

tagagtaaga tttgggtggg atgggtagga tgaagtatat

tgcccaactc tatgtttctt tgattctaac acaattaatt

aagtgacatg atttttacta atgtattact gagactagta

aataaatttt taaggcaaaa tagagcattc aaagccagct

tggaatttaa ttctgtcttg ataccttgtt atttatgcaa

aaactcctat ctcctttcct ttatgacaag agagtaagtt

ttaggttggg atcc

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0198] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* mediator complex subunit 17 (MED17), mRNA having NCBI Reference Sequence:

NM_004268.5 (SEQ ID NO: 67):

agttttgctc cgaaagactt accgaggagg gagcttgcgg

tgcgttctgg gaaagttgct gggccagctc ctttctttcc

agtctgagcg ttgcgttcgg tttcccgagg gtcttctgag

gcaccgcggc tgcgggcttc tgagttcccg gctctccgca

gggaagcctc ctcttcgtac ctcgtttttt ggctcgtggg

gggtcctccc accgctggcc gacgcagcca gcatgtccgg

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aagcaggtcc atgaggtggg cctggatggc accgagacgt

acctgccccc gctgtccatg tcgcagaatc tggcgcgtct

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ggccgggcgc cgggtccagc gcagaccagg acgacgagga

aggagtggta aaatttcagc cttccctttg gccttgggac

tcagtgagga acaatttgag aagtgccctg acagagatgt

gtgttctcta tgatgttctc agtattgtta gggataaaaa

atttatgact cttgatcctg tctctcagga tgcacttcct

ccaaaacaga atcctcagac gttgcaattg atatctaaaa

agaagtcact tgctggagca gcacaaatct tattgaaggg

ggcagaaaga ctgactaaat cagttaccga aaaccaagaa

aacaagctac aaagagactt caattctgag cttttgcgat

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tcgatctgga taaaaagata cctgaagatt actgtcctct

tgatgtccaa attcctagtg atttagaggg gtctgcatat

atcaaggttt caatacaaaa acaggctcca gatataggtg

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tcacattgtg gtgaaaaacc agattatctc tcagcccttt

ccgagcttgc agttatctat ttctttgtgc cattcctcaa

atgataagaa atcccaaaaa tttgctactg agaagcaatg

tccggaggac caccttttatg tcctagagca taatttgcat

ctactgatta gagagtttca taaacagacc ttgagttcca

tcatgatgcc tcatccagca agtgcacctt ttggccacaa

gagaatgaga ctttcgggtc ctcaagcttt tgataaaaat

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tggaaggtcg aaattttgtt tataaaatgg agctgcttat

gtctgcactt agcccttgtc tactatgatt ttttccagat

gtttcctaaa gaagtttcca gaaactttga cttgaaatgt

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tatgacaaga tgtaaaataa tatgtttttc atgcagttta

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tttctaaact ttttttttt gagatggtat ctcactctgt

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ccatgttgcc caggctggtt tcgaactcgg ctcaagtgat

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ataaaagccc catttatttg attataactt gattaaattg

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ccccatctga gtagagtggg ataactgaag actttacgtt

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tgttttaacc tgaatttcct ggagtttgaa ggatgtgcta

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ggataacctg attatctcat gttgatcagg aattgtaatt

ggcccttaaa tgctgggatt acaggtatga gccaccatgc

ctggcctcct taggtattgc tgatgaataa aaacaggggc

aactaca

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0199] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* peroxisomal biogenesis factor 13 (PEX13), mRNA having NCBI Reference Sequence:

NM_002618.4 (SEQ ID NO: 68):

agtcaggggt aggagcggga gccgagagga ggcggaggag

atggcgtccc agccgccacc tccccccaaa ccctgggaga

cccgccgaat tccgggagcc ggaccgggac caggaccggg

ccccactttc caatctgctg atttgggtcc tactttaatg

acaagacctg gacaaccagc acttaccaga gtgcccccac

ctattcttcc aaggccatca cagcagacag gaagtagcag

tgtgaacact tttagacctg cttacagttc attttcttct

ggatatggtg cctatggaaa ttcatttttat ggaggctata

gtccttatag ttatggatat aatgggctgg gctacaaccg

cctccgtgta gatgatcttc cacccagtag atttgttcag

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aaagtattgt gcatgcattt gcctctgtca gtatgatgat

ggatgctacc ttttcagctg tctataacag tttcagggct

gtattggatg tagcaaatca ctttttcccga ttgaaaatac

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aagtaattct cgaatagttc agattaaaac atacaggaac

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catatcattt ataatagaaa tcttgaccca gtgcagaaaa

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aacacccagg tattagcctt gaagttgaag agataaggtt

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gtgaccacta ttaaagatgt atagggagaa gagtacagca

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caccaaaaca ttattaatta aataaaatat aagtttacaa

taataaaaca tgtttctttt aatttttctg attatatttt

atgagttcag aaaggaaatg gtaaaagaac tatacatttt

catgttttaa cattttatgt acgtacttga ttctgtctgt

gtcataatta cacatttact tgaacacagc tatcctttat

cttgtgcttt ctttaataga aaaatgaaca gaaactgaat

gcagttaaat ttttatttttt agtaggttgt gaagttactt

ttactggaga aataaaaata tgttaaactt ga

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0200] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* ubiquitin specific peptidase 17 like family member 13 (USP17L13), mRNA having NCBI Reference Sequence:

NM_001256855.1 (SEQ ID NO: 69):

atggaggagg actcactcta cttgggtggt gagtggcagt

tcaaccactt ttcaaaactc acatcttctc ggctcgatgc

agcttttgct gaaatccagc ggacttctct ccctgagaag

tcaccactct catgtgagac ccgtgtcgac ctctgtgatg

atttggttcc tgaggcaaga cagcttgctc ccagggagaa

gcttcctctg agtagcagga gacctgctgc ggtgggggct

gggctccaga atatgggaaa tacctgctac gtgaacgctt

ccttgcagtg cctgacatac acaccgcccc ttgccaacta

catgctgtcc cgggagcact ctcaaacgtg tcatcgtcac

aagggctgca tgctctgtac tatgcaagct cacatcacac

gggccctcca caatcctggc cacgtcatcc agccctcaca

ggcattggct gctggcttcc atagaggcaa gcaggaagat

gcccatgaat ttctcatgtt cactgtggat gccatgaaaa

aggcatgcct tcccgggcac aagcaggtag atcatccctc

taaggacacc accctcatcc accaaatatt tggaggctac

tggagatctc aaatcaagtg tctccactgc cacggcattt

cagacacttt tgacccttac ctggacatcg ccctggatat

ccaggcagct cagagtgtcc agcaagcttt ggaacagttg

gtgaagcccg aagaactcaa tggagagaat gcctatcatt

gtggtgtttg tctccagagg gcgccggcct ccaagacgtt

aactttacac acctctgcca aggtcctcat ccttgtattg

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aagagattct ccgatgtgac aggcaacaag attgccaaga

atgtgcaata tcctgagtgc cttgacatgc agccatacat

gtctcagcag aacacaggac ctcttgtcta tgtcctctat

gctgtgctgg tccacgctgg gtggagttgt cacaacggac

attacttctc ttatgtcaaa gctcaagaag gccaatggta

taaaatggat gatgccgagg tcaccgccgc tagcatcact

tctgtcctga gtcaacaggc ctacgtcctc ttttacatcc

agaagagtga atgggaaaga cacagtgaga gtgtgtcaag

aggcagggaa ccaagagccc ttggcgcaga agacacagac

aggcgagcaa cgcaaggaga gctcaagaga gaccacccct

gcctccaggc ccccgagttg gacgagcact tggtggaaag

agccactcag gaaagcacct tagaccgctg gaaattcctt

caagagcaaa acaaaacgaa gcctgagttc aacgtcagaa

aagtcgaagg taccctgcct cccgacgtac ttgtgattca

tcaatcaaaa tacaagtgtg ggatgaagaa ccatcatcct

gaacagcaaa gctccctgct aaacctctct tcgtcgaccc

cgacacatca ggagtccatg aacactggca cactcgcttc

cctgcgaggg agggccagga gatccaaagg gaagaacaaa

cacagcaaga gggctctgct tgtgtgccag tga

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0201] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* mirror-image polydactyly 1 (MIPOL1), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_001195296.2 (SEQ ID NO: 70):

aggccccacg cgccgccccg ctcctccgcc ggatcgtctg

tgggtgagtc tcgagccagg aggctctgag ccagtggcga

ttggctgacg cggtggctgc gcactcggcc tgagaaactc

ggcaagcgcg cagtgtcgac tccccggtct atgccaggcg

catctcagat accagcattg ccaccggtgg gtagaacact

aagtgggctc ttggagtccc tgattccaga acttgactct

tggatgacat ttctggacct gctctgggcc agagaggaga

ccacttccct taagggaacg aggtctcact atattgccca

gactggtctc gaactcctgg gctcaaacag tccccctgcg

ttggcctccc aaagtgatgg aattacaggt gtgaatcact

gcatctgact atggcaagga tctctgtcac tgagctaatc

caaaagtaaa tgagaaactt agaaaaagat tgccaattcc

aaatcaacat atttagagaa aattggaaaa ggagaagctt

actacagctt tatttgagga ctttttaaag aacgctgggt

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tctatctgtg agctgcaaat cttggagcaa aaaccagaga

cattgccaga gcaaacaaga acagaaatac aaatggagaa

ctggtcaaaa gacataaccc acagttatct tgaacaagaa

actacgggga taaataaaag tacgcagcca gatgagcaac

tgactatgaa ttctgagaaa agtatgcatc ggaaatccac

tgaattagtt aatgaaataa catgtgagaa cacagaatgg

ccagggcaga gatcaacgaa ttttcagatc atcagttctt

atccagatga tgagtctgtt tactgcacta ctgaaaaata

caacgttatg gaacatagac ataatgatat gcattatgaa

tgtatgactc cttgtcaagt tacttcagac tcagataaag

agaagacaat agcatttctt ctaaaagaat tggatattct

cagaacaagc aataaaaagc ttcagcagaa attggctaaa

gaagataaag aacagagaaa actaaagttt aagctggaac

tccaagagaa agaaacagaa gctaaaattg ctgaaaagac

agcagctctg gttgaagaag tgtattttgc gcagaaggaa

cgtgatgaag ctgttatgtc tagactgcaa ttagccattg

aggagagaga tgaagcaatt gcacgagcca agcatatgga

aatgtctcta aaagtgctag aaaatattaa ccctgaagaa

aatgacatga cattacagga attactgaac agaataaaca

atgcagacac agggatagct attcagaaga atggagctat

aattgtggat agaatctaca agaccaagga atgtaaaatg

agaataactg cagaagaaat gagtgcacta atagaagaac

gggatgctgc cttgtctaag tgcaaacggt tagagcagga

gcttcatcat gtgaaagagc agaaccagac ttcagcaaac

aacatgagac atctgactgc tgaaaacaat caagaacgtg

ctctgaaggc aaagttgtta tctatgcaac aagccagaga

aactgcagtt caacagtaca aaaaactgga agaggaaatc

cagacccttc gagtttacta cagtttacac aaatctttat

ctcaagaaga aaatctgaag gatcagttta actatacccct

tagtacatat gaagaagctt taaaaaacag agagaacatt

gtttccatca ctcaacaaca aaatgaggaa ctggctactc

aactgcaaca agctctgaca gagcgagcaa atatggaatt

acaacttcaa catgccagag aggcctccca agtggccaat

gaaaaagttc aaaagttgga aaggctggtg gatgtactga

ggaagaaggt tggaaccggg accatgagga cagtgatctg

attgaaaaaa aacgacagtc tggggaagcg atcacatctg

gtgaccaggc tgcttcattc aacactgtgt aaacaccaaa

gccttaactt agcaaacagt tcttagaagt gggacactcc

aaccacattc caagctgaga taaaatcaaa tcacaaatgt

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ttaaccactt tgctgctgac ttgagttatt tatccaaata

tattaactat agacttttac caatgggtag ctataaggtt

acagcttatt ttgtaactat tttatatctc aatatcttta

atataaatct ttttactgag agatcattat agaaacatgt

taaagttggt taggatcata tcttcacata tggccctttc

tgaatcaaag tgcggcaaag taaatattgt ctaagcttta

atccactgtg ttaggtcaaa acttcaaata catgcatttt

tcaatatagg gtatatttct taactgatga gagaggctta

gacatgagtg tgtagtcttc cttcaatgcg tgtatgtaat

ctttgttagt ataaaagata ttaaatatag gtgccaagaa

ttaaatgtat aatttgttta ataagagatg gatatattaa

aattacattc atcaaggcat gatttttgtt tcactacaaa

taatgcaaac tgttttcaat aaaaagagga gactgttaat

gtgtacttat aaattcacat tgtcagtatt ttttaatatt

gggtctgaat aattatctga attctactta agctataagt

ctctgtcatt tttgcttgaa aattagcatg cctctgtctt

aaaagagacc atcaaaccta ttaagtattc ttattgttta

tctttttttа attgccattt gatttttatt gtggaggagg

aggatctaat atataatatt caatacaatt gtaatgtaga

aatataagaa tttagaaaaa agtaaacttg ccatttcgtt

aaggttacct gctttttatt ttattccaga aataagatag

ttacagcata gcagtcatat gaagttatga atagaactga

gatttttatg taattagtta taggcaaaat actttcatat

ttttagatta gacagacgaa agaccaagag gaaatgactg

tgcctggaac aggatgaaat agacaagtag agatttaatt

agcaaaaatt ttgtagggaa gtaaaatttt ttctaagtct

atacgttttt aattcatctt taagattgag ctaaattatc

taccattgcc tatttacagg ataagtacat tcaggacaat

ttattgtacc attctttcat ataccatagc agattatcca

tttcaatttt tttttactcc acaggaaaat gtaagctact

ttgtcataga tcacaaaaga atcataatgc taacaaactc

tatttcttcc ttattaaatc tgtatccatt aaagtaactt

ttttaactat gagaattaga aaataaggga caacaggggt

taaaaataaa ctgatttaat ttgctctata gtcctaaaga

gaattatatc ctctcataga ccaatgactc tataatagag

aaatatgtaa tgatttggtc atgcatggag tcttgtctct

gggctctatt tgaaacgtgt aacagctccc tatgtgaaga

aacattatct ttaaagtcat ctgggaggtg caggtaagta

aagagaaaca atttttgtca caaagtagtc cattcctgat

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ctcacttaaa ataaatcaca agtaaatttg aattttcggt

ttaatgttga aagcagatga acttttcttg agttattttg

tcttttagaa tacacaaaat atagtataaa gacatttcac

aatttccaaa caaatctttc tacgcttaaa tgatcaaatt

agaaaaacca attcctataa ttaatatgca gaacttttat

agaatatgat attataaagt taaatttgca aaataattct

aacatccact attgttcagt ataggtaatc tcccaaaaat

atcacatcct cttgaaaatg aattgtctac aaaatttcaa

atgcaaagta ttacagccaa atattatctt aattaatttc

ttacacttaa aagtgtccat caacagtgtg tcagatggtc

tttatatatt ttttctgtat gaaggaatag ccttgcctac

tgaagatagg ttctctatgt attcaacaat aatgcaactt

tagaagtatt ccacactgct gagaaatgtt gctttgagtt

tgctttacac atcatcaact ctaaatccta tagtaacatg

agaattcact tcttcttgta aaaataagta atttacagga

aaggcaaaat gctaatacta acatttgtag cacttgatga

tttacaaagt ccttttacat ctgttttttc atttgatcct

atcgacaatc ataataataa taaattatat atataaccca

tataataacg atggtgatga taattttagt attactgtca

ttataattat tattatattc attctacaga tgaggaaaca

gactcagtaa gccttggaat ttgccaagga ctggctagga

cctagaacta agatcttata accacactcc atgcaactat

gagtctctaa atctctctgt aagaaaaaaa tttcaaagta

aagattttac tcttgcaatt tctgttgtga tagtaccatc

tctttcacat actacataca aattccctaa taatcaaaag

attgtacaca ttttttttcaa tgaagtacaa taatgtgaac

tgcatgtgta aacagcatca cattattacc acctctctat

ggtattatag tggcagtatg ctttgcctca gccttcacta

attaggaata ttgtgacaat tcattgctaa taaaacataa

catgagtctc tttgtactgt ttttaatttg gcctgatgct

aaaacctatc agcttagttt tttaacatgg tagtctaaac

ttcaaggctt gctctatctc ctagagcaat ttagagctaa

aaccagtaat aagcaaagtt attggttata agcaaggtat

aagcagttaa agcaaagtta ttaattatta atatatgaga

atttaaaatt ttataaataa gttagaaatt attaatgtat

tttaaatatg gagtaaaata ttttgctaat ttttttcaat

gataaagttg atcctttgta tatttcctta ttcaaataaa

ttcagtcatc ttcttatcag gttgcttatt tatataattt

gtttatttta ttaaaaatct agaatattaa agatttatac

-continued

ttttaatatt gaatatagtt tcgtagaaaa acattttata

tgtactattc ttaaagatca caattatttt taaactttct

attttcaaat acttgtgatt aataaggcat tctatgatga

aatagccatg gcttatatat ttttgtcttt tcacatatga

tgtgtttgga acccaaattt tttactgatt ttattgtgtt

gttggtaact agtatttaca gctaacctat ctattcatat

tttacatata tatatatata tatacatgca cacacaccga

tacatttacc ttttaaaaaa atgatttata agtgaactgt

taggctccag tgatttcagt gttttgttca tyttttattg

gaaatgcacg tggtttctta ggcttttaaa caaatacatg

gaatggttga aagatttatt ttgctcgtgc ttagctaaat

atgtcatctc tagaaaagat gtggtttgtt ttggcactgt

tttaaaaact caaatatttt aaacatttgt taagttggag

cttgcacatt taaaccagca gcatacgttc cagaagagca

tctcaagtta ccaaattttt tgtaatcctt ttactagaaa

aatctttttt gaagagtttt tcttgtgctt gcttcggcag

catatatact gaaattagaa aaagaaaact tttctttttt

attatatatt ttagtgtaag ttaagttaaa cttctaaaag

ttgaattatt taatgtagga cttcataaat agtatttgac

aatgataaat gtgtattttt gagaatcatt aaaatgtata

caatgatatt cctttgcaga agtcttaata tgcataattt

ttaatctaat tgtcttctaa atatagtttt ggtgtatgct

ggtattttag aagccaccaa tttctggact atctgattat

taacaaagat gtattttaat gcacaaactc aaatgtttaa

aatatatatt tactttgtac tcaaataaaa tcccctattg

caaatcctat acatatttca atgcaattct tatacatcga

tcttaatcaa atttataaat gtacaatcct gaagacagtg

tactagatat gcactataaa atatattgca gtaaggaaac

agattaagtt cactgtcaaa ctgtctgact tccttaacaa

atttaataaa gataaatgtc aatatgaaca aatttgttag

gtaccttagg aatctttcaa aactatttag atataaaata

aaattatagt aataaaatat tgaagagaaa tatcatttt

agtgaatatg gttagaaaga acataagaag tgagatcaaa

ttattttaat taaaaaaata ggccaggtgc gatggctcac

gcctgtaatc ccagcatttt gggaggccga ggcgggcgga

tcacaaggtc aggagattga gaccatcctg gctaacacgg

tgaaaccccg tctctactaa aaaaagtaca aaaaagaagt

tagccgggcg tggtggcggg cgcctgtagt cccagctact

tgggaggctg aggcaggaga atggcgtgaa cccggaaggc

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agagcttgca gtgagccgag atcacgccat tgcactccag

cctgggtgac agagtgagac tgtctcaaat aataataata

ataataataa taataataat aataataata gactgactca

aatctaccat aaagcacctc tactcatttt ggaatatgta

cgtggaattt tgcttcaata gctgaaatct aaaaacactc

tttctgttgc atttgattat tcaatcatga taaggtaaat

gtaaacagac tgtgtagcac tctatcacct ggagtgaact

tagaatttac agcttagagt acatgactaa aagaggaatg

gagtggaagt gggcagtagg tgtctttggg gcaaaaattc

tataaactgg tgttatctaa actatcacat tactttgtta

aattattgtt tcatcacgta tgacctttgt gatttctcac

acattttact tctacatatq cacataattg taatttttt

aactttaaaa agtcaattat gtttaagaaa atttttaaaa

taagaatgaa cgtatgtgat atttactgtg a

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0202] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* ribokinase (RBKS), transcript variant 1, mRNA having NCBI Reference Sequence:

NM_022128.3 (SEQ ID NO: 71):

ccccagaggc agtggcaaga ggaggtggcg gcggtggtag

tggtgggctc ctgcatgacc gacctggtca gtcttacttc

tcgtttgcca aaaactggag aaaccatcca tggacataag

ttttttattg gctttggagg gaaaggtgcc aaccagtgtg

tccaagctgc tcggcttgga gcaatgacgt ccatggtgtg

taaggttggc aaagattctt ttggcaatga ttatatagaa

aacttaaaac agaatgatat ttctacagaa tttacatatc

agactaaaga tgctgctaca ggaactgctt ctataattgt

caataatgaa ggccagaata tcattgtcat agtggctgga

gcaaatttac ttttgaatac ggaggatctg agggcagcag

ccaatgtcat tagcagagcc aaagtcatgg tctgccagct

cgaaataact ccagcaactt ctttggaagc cctaacaatg

gcccgcagga gtggagtgaa aaccttgttc aatccagccc

ctgccattgc tgacctggat ccccagttct acaccctctc

agatgtgttc tgctgcaatg aaagtgaggc tgagatttta

actggcctca cggtgggcag cgctgcagat gctggggagg

ctgcattagt gctcttgaaa aggggctgcc aggtggtaat

cattaccttа ggggctgaag gatgtgtggt gctgtcacag

acagaacctg agccaaagca cattcccaca gagaaagtca

aggctgtgga taccacgggt gctggtgaca gctttgtggg

-continued

agctctggcc ttctacctgg cttactatcc aaatctgtcc

ttggaagaca tgctcaacag atccaatttc attgcagcag

tcagtgtcca ggctgcagga acacagtcat cttaccctta

caaaaaagac cttccgctta ctctgttttg attgctatta

gtcccaaaat aaatatacct gggaataaaa tgtacttggg

ggtggctgct cctggctaat gcttattaga aaatgtcctc

gtccccttc tttgcaaata ttagttcttt tacgaagtca

tcctcaagct tcaatttatt tataacgatg attcttttgc

tttccatgca tttgcacaaa acaaccagaa ttaaagattc

cacaaccaag atctgtacaa acataaa

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0203] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* ubiquitin specific peptidase 17 like family member 2 (USP17L2), mRNA having NCBI Reference Sequence:

NM_201402.3 (SEQ ID NO: 72):
gtcatttgaa gactctcttg gaagagatag cgtcttgctg

caacctgcag tcccagcaga aaaaccttgt gatccttgtt

gcgggcgaca tggaggacga ctcactctac ttgggaggtg

agtggcagtt caaccacttt tcaaaactca catcttctcg

gccagatgca gcttttgctg aaatccagcg gacttctctc

cctgagaagt caccactctc atctgaggcc cgtgtcgacc

tctgtgatga tttggctcct gtggcaagac agcttgctcc

caggaagaag cttcctctga gtagcaggag acctgctgcg

gtgggggctg ggctccagaa tatgggaaat acctgctacg

agaacgcttc cctgcagtgc ctgacataca caccgccccc

tgccaactac atgctgtccc gggagcactc tcaaacatgt

cagcgtccca agtgctgcat gctctgtact atgcaagctc

acatcacatg ggccctccac agtcctggtc atgtcatcca

gccctcacag gcattggctg ctggcttcca tagaggcaag

caggaagatg cccatgaatt tctcatgttc actgtggatg

ccatgaaaaa ggcatgcctt cccggccaca agcaggtaga

tcatcactct aaggacacca ccctcatcca ccaaatattt

ggaggctgct ggagatctca aatcaagtgt ctccactgcc

acgggatttc agacactttt gacccttacc tggacatcgc

cctggatatc caggcagctc agagtgtcaa gcaagctttg

gaacagttgg tgaagcccga agaactcaat ggagagaatg

cctatcattg cggtctttgt ctccagaggg cgccggcctc

caagacgtta actttacaca cttctgccaa ggtcctcatc

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ttgccaagaa tgtgcaatat cctgagtgcc ttgacatgca

gccatacatg tctcagcaga acacaggacc tcttgtctat

gtcctctatg ctgtgctggt ccacgctggg tggagttgtc

acgacggaca ttacttctct tatgtcaaag ctcaagaagg

ccagtggtat aaaatggatg atgccaaggt cactgcctgt

agcatcactt ctgtcctgag tcaacaggcc tatgtcctct

tttacatcca gaagagtgaa tgggaaagac acagtgagag

tgtgtcaaga ggcagggaac caagagccct cggcgctgaa

gacacagaca ggcgagcaac gcaaggagag ctcaagagag

accacccctg cctccaggca cccgagttgg acgagcgctt

ggtggaaaga gccactcagg aaagcacctt agaccactgg

aaattccccc aagagcaaaa caaaacgaag cctgagttca

acgtcagaaa agtcgaaggt accctgcctc ccaacgtact

tgtgattcat caatcgaaat acaagtgtgg gatgaaaaac

catcatcctg aacagcaaag ctccctgcta aacctctctt

cgacgacccg gacagatcag gagtccgtga acactggcac

cctcgcttct ctgcaaggga ggaccaggag atccaaaggg

aagaacaaac acagcaagag ggctctgctt gtgtgccagt

gatctcagtg gaagtgccga cccacacgta ggggtgaacg

cacacacaca cacgcacaaa tacacccaca agcgcgcacg

caaacacaca cacacacaca aacacgaaca ccgtcaatcc

tacataaagt aatgaggagt ccaagtttct gtctctacaa

cagggacaac tggatagtga tggctgcatc tcaggatgag

cccacacatg ggaaacatca agttttgggg tcgtgagtct

tccgaacctc tggagagact gtctgtgtgt ttgtgttcat

ggtagatgac attcactgtg tatttctgaa tatgacctac

tgacgtgtag gtttgagtgt gaggttattg caggggactc

ggtttcctat tttctcttgg ggtgtgtttc attcgtcagt

tgttgggcgg cacgagaagg tgaaattttg ctcatgtggc

acatccatgg atcattctcg ccaccttgaa tagtggaaac

tggaatgcat ttagaagata ggaacggtgc tcttctttct

taccctggct caccgttttt acattggttt ctgaatggac

ctcaggcgcc ctgggacttg tgctcttgct ggaacccaca

taacgccgga aacagacaga ccgacttgcc tgtttcacga

tgtccaattc caatgagtcg aaatggaaaa ttttcccact

ggcatgtcag tcatttggaa ataagtcgta ttgataataa

aggaaatcaa acaca

a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0204] In embodiments, the nucleic acid inhibits expression of *Homo sapiens* dystrophin (DMD), transcript variant Dp427m, mRNA having NCBI Reference Sequence:

NM_004006.3 (SEQ ID NO: 73):

atcagttact gtgttgactc actcagtgtt gggatcactc

actttccccc tacaggactc agatctggga ggcaattacc

ttcggagaaa aacgaatagg aaaaactgaa gtgttacttt

ttttaaagct gctgaagttt gttggtttct cattgttttt

aagcctactg gagcaataaa gtttgaagaa cttttaccag

gtttttttta tcgctgcctt gatatacact tttcasaatg

ctttggtggg aagaagtaga ggactgttat gaaagagaag

atgttcaaaa gaaaacattc acaaaatggg taaatgcaca

attttctaag tttgggaagc agcatattga gaacctcttc

agtgacctac aggatgggag gcgcctccta gacctcctcg

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a different transcript variant of the gene, or a sequence with at least 80%, 82%, 85%, 86%, 88%, 90%, 92%, 94%, 95%, 97%, 98% or 99% nucleic acid sequence identity thereto.

[0205] The amino acid sequences for the polypeptides of SEQ ID NOS: 74-91 and the corresponding nucleic acid sequences of SEQ ID NOs: 92-109 that encode the polypeptides of SEQ ID NOS: 74-91 are provided in FIG. **25**.

[0206] The invention will be described by the following non-limiting example.

Example 1

[0207] Most genetic approaches to identify host factors regulating infection have relied upon loss-of-function screens. Knock-out screens are limited in genes they can query, as genes essential for cell survival cannot be investigated. Moreover, existing screens often rely on proxy phenotypes instead of directly measuring viral replication. This leaves a large amount of genetic space unexplored and raises the possibility that entirely new classes of viral co-factors have yet to be discovered. TRPPC overcomes this in at least 3 ways: 1) it is a fitness-based screen dependent on viral replication; 2) TRPPC inherently rank orders host factors, as the abundance of any particular virus reflects the importance of the modulated host gene; and 3) TRPPC can be used for both loss- and gain-of-function screening, exploring new genetic space including essential genes. Furthermore, this system is entirely portable, functioning with any pathogen that can deliver a targeting RNA, amenable to various iterations changing the selective pressure or modes of replication to focus on different aspects of infection, and in principle can also be performed in vivo in transgenic animals expressing the CRISPRa/i machinery.

[0208] TRPPC can be used to identify host factors regulating pathogen replication. The top hits identified by the inventors increase replication of influenza virus, and this information can be used to increase virus yield in commercial settings, and even a modest gain in viral yield would have large impacts on production. Similarly, adenovirus-based vaccines like the adenovirus based COVID19 vaccine are produced in cell culture, and engineering host gene expression to increase yields would have a major impact on this process.

Rank-ordered top hits from influenza virus TRPPC screen in human lung cells:

1.	SLC9C1 (SEQ ID NO: 1)
2.	TICRR (SEQ ID NO: 2)
3.	OR4C6 (SEQ ID NO: 3)
4.	CLEC4C (SEQ ID NO: 4)
5.	NDUFA7 (SEQ ID NO: 5)
6.	OR51A7 (SEQ ID NO: 6)
7.	CLCNKB (SEQ ID NO: 7)
8.	GNG5 (SEQ ID NO: 8)
9.	TYW1 (SEQ ID NO: 9)
10.	RAB42 (SEQ ID NO: 10)
11.	HCN3 (SEQ ID NO: 11)
12.	RASAL1 (SEQ ID NO: 12)

-continued

13.	ULBP1 (SEQ ID NO: 13)
14.	C5orf30 (SEQ ID NO: 14)
15.	PARP15 (SEQ ID NO: 15)
16.	NLGN4X (SEQ ID NO: 16)
17.	CD59 (SEQ ID NO: 17)
18.	CFL2 (SEQ ID NO: 18)
19.	GSDMB (SEQ ID NO: 19)
20.	BRD4 (SEQ ID NO: 20)
21.	IFIT3 (SEQ ID NO: 21)
22.	OGFR (SEQ ID NO: 22)
23.	SDR39U1 (SEQ ID NO: 23)
24.	RIMS2 (SEQ ID NO: 24)
25.	ST8SIA3 (SEQ ID NO: 25)
26.	CDKN3 (SEQ ID NO: 26)
27.	TIMD4 (SEQ ID NO: 27)
28.	SYS1 (SEQ ID NO: 28)
29.	UBD (SEQ ID NO: 29)
30.	MED17 (SEQ ID NO: 30)
31.	PEX13 (SEQ ID NO: 31)
32.	USP17L13 (SEQ ID NO: 32)
33.	MIPOL1 (SEQ ID NO: 33)
34.	RBKS (SEQ ID NO: 34)
35.	USP17L2 (SEQ ID NO: 35)
36.	DMD (SEQ ID NO: 36)

[0209] Additional hits are provided in amino acid sequences of SEQ ID NOs: 74-91 shown in FIG. **25**.

TABLE 1

id	RRA MAGeCK	log10 RRA	p-value	FDR	Rank	log2 fold-change
SLC9C1	4.58E-10	-9.34	2.90E-06	0.001238	1	7.2241
TICRR	9.17E-09	-8.04	2.90E-06	0.001238	2	6.107
TREX1	6.10E-07	-6.21	2.90E-06	0.001238	3	5.4596
OR4C6	7.10E-07	-6.15	2.90E-06	0.001238	4	5.48
CLEC4C	1.22E-06	-5.91	8.71E-06	0.002475	5	4.4016
NDUFA7	1.55E-06	-5.81	8.71E-06	0.002475	6	4.0794
OR51A7	1.83E-06	-5.74	1.45E-05	0.00275	7	5.5662
CLCNKB	1.93E-06	-5.71	1.45E-05	0.00275	8	5.5126

TABLE 1-continued

id	RRA MAGeCK	log10 RRA	p-value	FDR	Rank	log2 fold-change
GNG5	2.49E-06	-5.60	1.45E-05	0.00275	9	4.1712
TYW1	3.75E-06	-5.43	2.03E-05	0.003465	10	3.5509
RAB42	5.37E-06	-5.27	3.19E-05	0.00495	11	4.2745
HCN3	7.41E-06	-5.13	3.77E-05	0.005363	12	3.659
RASAL1	8.19E-06	-5.09	4.94E-05	0.005611	13	3.7478
ULBP1	8.74B-06	-5.06	4.94E-05	0.005611	14	3.8628
C5orf30	9.31E-06	-5.03	4.94E-05	0.005611	15	4.2296
PARP15	1.15E-05	-4.94	6.10E-05	0.006188	16	4.1313
NLGN4X	1.22E-05	-4.91	6.68E-05	0.006188	17	4.0686
CD59	1.29E-05	-4.89	6.68E-05	0.006188	18	4.0867
CFL2	1.48E-05	-4.83	7.26E-05	0.006188	19	2.9664
GSDMB	1.50E-05	-4.82	8.42E-05	0.006664	20	5.4131
BRD4	1.52E-05	-4.82	7.26E-05	0.006188	21	4.1823
IFIT3	1.87E-05	-4.73	9.00E-05	0.006664	22	4.4612
OGFR	2.43E-05	-4.61	9.58E-05	0.006664	23	2.9749
SDR39U1	2.49E-05	-4.60	9.58E-05	0.006664	24	2.7017
RIMS2	2.54E-05	-4.59	0.00010162	0.006664	25	3.1111
ST8SIA3	2.67E-05	-4.57	0.00010162	0.006664	26	1.8644
CDKN3	3.36E-05	-4.47	0.00012485	0.007682	27	2.7467
TIMD4	3.65E-05	-4.44	0.00013066	0.007682	28	2.4562
SYS1	3.79E-05	-4.42	0.00013066	0.007682	29	2.8394
UBD	4.34E-05	-4.36	0.00014808	0.008416	30	4.9229
MED17	4.97E-05	-4.30	0.00017131	0.009422	31	4.8446
PEX13	5.30E-05	-4.28	0.00018292	0.009746	32	2.4674
USP17L13	7.28E-05	-4.14	0.00031068	0.015983	33	3.9451
MIPOL1	7.51E-05	-4.12	0.00032229	0.015983	34	2.4368
RBKS	7.99E-05	-4.10	0.0003281	0.015983	35	2.2546
USP17L2	9.01E-05	-4.05	0.00036294	0.017189	36	3.1472
DMD	9.97E-05	-4.00	0.00038036	0.017527	37	1.8293

[0210] All publications, patents and patent applications are incorporated herein by reference. While in the foregoing specification, this invention has been described in relation to certain preferred embodiments thereof, and many details have been set forth for purposes of illustration, it will be apparent to those skilled in the art that the invention is susceptible to additional embodiments and that certain of the details herein may be varied considerably without departing from the basic principles of the invention.

SEQUENCE LISTING

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source                  1..1177
                        mol_type = protein
                        organism = Homo sapiens
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LVLWHLASVN QLLLKPTQWL LFSAILVSSD PMLTAAAIRD LGLSRSLISL INGESLMTSV  180
ISLITFTSIM DFDQRLQSKR NHTLAEEIVG GICSYIIASF LFGILSSKLI QFWMSTVFGD  240
DVNHISLIFS ILYLIFYICE LVGMSGIFTL AIVGLLLNST SFKAAIEETL LLEFWTFLSR  300
IAFLMVFTFF GLLIPAHTYL YIEFVDIYYS LNIYLTLIVL RFLTLLLISP VLSRVGHEFS  360
WRWIFIMVCS EMKGMPNINM ALLLAYSDLY FGSDKEKSQI LFHGVLVCLI TLVVNRFILP  420
VAVTILGLRD ATSTKYKSVC CTFQHFQELT KSAASALKFD KDLANADWNM IEKAITLENP  480
YMLNEEETTE HQKVKCPHCN KEIDEIFNTE AMELANRRLL SAQIASYQRQ YRNEILSQSA  540
VQVLVGAAES FGEKKGKCMS LDTIKNYSES QKTVTFARKL LLNWVYNTRK EKEGPSKYFF  600
FRICHTIVFT EEFEHVGYLV ILMNIFPFII SWISQLNVIY HSELKHTNYC FLTLYILEAL  660
LKIAAMRKDF FSHAWNIFEL AITLIGILHV ILIEIDTIKY IFNETEVIVF IKVVQFFRIL  720
RIFKLIAPKL LQIIDKRMSH QKTFWYGILK GYVQGEADIM TIIDQITSSK QIKQMLLKQV  780
IRNMEHAIKE LGYLEYDHPE IAVTVKTKEE INVMLNMATE ILKAFGLKGI ISKTEGAGIN  840
KLIMAKKKEV LDSQSIIRPL TVEEVLYHIP WLDKNKDYIN FIQEKAKVVT FDCGNDIFEE  900
GDEPKGIYII ISGMVKLEKS KPGLGIDQMV ESKEKDFPII DTDYMLSGEI IGEINCLTNE  960
PMKYSATCKT VVETCFIPKT HLYDAFEQCS PLIKQKMWLK LGLAITARKI REHLSYEDWN  1020
YNMQLKLSNI YVVDIPMSTK TDIYDENLIY VILIHGAVED CLLRKTYRAP FLIPITCHQI  1080
QSIEDFTKVV IIQTPINMKT FRRNIRKFVP KHKSYLTPGL IGSVGTLEEG IQEERNVKED  1140
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GAHSAATARS PQPCSLLGTK FNCKESPRIN LRKVRKE                          1177

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source                1..1909
                      mol_type = protein
                      organism = Homo sapiens
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RVSDFRELGS RSWEDFEEEL EARLEDRAHL PGPAPRATHT HGALMETLLD YQWDRPEITS  120
PTKPILRSSG RRLLDVESEA KEAEAALGGL VNAVFLLAPC PHSQRELLQF VSGCEAQAQR  180
LPPTPKQVME KLLPKRVREV MVARKITFYW VDTTEWSKLW ESPDHLGYWT VCELLHHGGG  240
TVLPSESFSW DFAQAGEMLL RSGIKLSSEP HLSPWISMLP TDATLNRLLY NSPEYEASFP  300
RMEGMLFLPV EGKEIQETWT VTLEPLAMHQ RHFQKPVRIF LKGSVAQWSL PTSSTLGTDS  360
WMLGSPEEST ATQRLLFQQL VSRLTAEELH LVADVDPGEG RPPITGVISP LSASAMILTV  420
CRTKEAEFQR HVLQTAVADS PRDTASLFSD VVDSILNQTH DSLADTASAA SPVPEWAQQE  480
LGHTTPWSPA VVEKWFPFCN ISGASSDLME SFGLLQAASA NKEESSKTEG ELIHCLAELY  540
QRKSREESTI AHQEDSKKKR GVPRTPVRQK MNTMCRSLKM LNVARLNVKA QKLHPDGSPD  600
VAGEKGIQKI PSGRTVDKLE DRGRTLRSSK PKDFKTEEEL LSYIRENYQK TVATGEIMLY  660
ACARNMISTV KMFLKSKGTK ELEVNCLNQV KSSLLKTSKS LRQNLGKKLD KEDKVRECQL  720
QVFLRLEMCL QCPSINESTD DMEQVVEEVT DLLRMVCLTE DSAYLAEFLE EILRLYIDSI  780
PKTLGNLYNS LGFVIPQKLA GVLPTDFFSD DSMTQENKSP LLSVPFLSSA RRSVSGSPES  840
DELQELRTRS AKKRRKNALI RHKSIAEVSQ NLRQIEIPKV SKRATKKENS HPAPQQPSQP  900
VKDTVQEVTK VRRNLFNQEL LSPSKRSLKR GLPRSHSVSA VDGLEDKLDN FKKNKGYHKL  960
LTKSVAETPV HKQISKRLLH RQIKGRSSDP GPDIGVVEES PEKGDEISLR RSPRIKQLSF  1020
SRTHSASFYS VSQPKSRSVQ RVHSFQQDKS DQRENSPVQS IRSPKSLLFG AMSEMISPSE  1080
KGSARMKKRS RNTLDSEVPA AYQTPKKSHQ KSLSFSKTTP RRISHTPQTP LYTPERLQKS  1140
PAKMTPTKQA AFKESLKDSS SPGHDSPLDS KITPQKRHTQ AGEGTSLETK TPRTPKRQGT  1200
QPPGFLPNCT WPHSVNSSPE SPSCPAPPTS STAQPRRECL TPIRDPLRTP PRAAAFMGTP  1260
QNQTHQQPHV LRAARAEEPA QKLKDKAIKT PKRPGNSTVT SSPPVTPKKL FTSPLCDVSK  1320
KSPFRKSKIE CPSPGELDQK EPQMSPSVAA SLSCPVPSTP PELSQRATLD TVPPPPPSKV  1380
GKRCRKTSDP RRSIVECQPD ASATPGVGTA DSPAAPTDSR DDQKGLSLSP QSPPERRGYP  1440
GPGLRSDWHA SSPLLITSDT EHVTLLSEAE HHGIGDLKSN VLSVEEGEGL RTADAEKSSL  1500
SHPGIPPSPP SCGPGSPLMP SRDVHCTTDG RQCQASAQLD NLPASAWHST DSASPQTYEV  1560
ELEMQASGLP KLRIKKIDPS SSLEAEPLSK EESSLGEESF LPALSMPRAS RSLSKPEPTY  1620
VSPPCPRLSH STPGKSRGQT YICQACTPTH GPSSTPSPFQ TDGVPWTPSP KHSGKTTPDI  1680
IKDWPRRKRA VGCGAGSSSG RGEVGADLPG SLSLLESEGK DHGLELSIHR TPILEDFELE  1740
GVCQLPDQSP PRNSMPKAEE ASSWGQFGLS SRKRVLLAKE EADRGAKRIC DLREDSEVSK  1800
SKEGSPSWSA WQLPSTGDEE VFVSGSTPPP SCAVRSCLSA SALQALTQSP LLFQGKTPSS  1860
QSKDPRDEDV DVLPSTVEDS PFSRAFSRRR PISRTYTRKK LMGTWLEDL              1909

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                      mol_type = protein
                      organism = Homo sp.
SEQUENCE: 3
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LTFLSLLDVM FSSVVAPKVI VDTLSKSTTI SLKGCLTQLF VEHFFGGVGI ILLTVMAYDR  120
YVAICKPLHY TIIMSPRVCC LMVGGAWVGG FMHAMIQLLF MYQIPFCGPN IIDHFICDLF  180
QLLTLACTDT HILGLLVTLN SGMMCVAIFL ILIASYTVIL CSLKSYSSKG RHKALSTCSS  240
HLTVVVLFFV PCIFLYMRPV VTHPIDKAMA VSDSIITPML NPLIYTLRNA EVKSAMKKLW  300
MKWEALAGK                                                         309

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source                1..213
                      mol_type = protein
                      organism = Homo sapiens
SEQUENCE: 4
MVPEEEPQDR EKGLWWFQLK VWSMAVVSIL LLSVCFTVSS VVPHNFMYSK TVKRLSKLRE  60
YQQYHPSLTC VMEGKDIEDW SCCPTPWTSF QSSCYFISTG MQSWTKSQKN CSVMGADLVV  120
INTREEQDFI IQNLKRNSSY FLGLSDPGGR RHWQWVDQTP YNENVTFWHS GEPNNLDERC  180
AIINFRSSEE WGWNDIHCHV PQKSICKMKK IYI                              213

SEQ ID NO: 5          moltype = AA  length = 113
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source                1..113
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MASATRLIQR LRNWASGHDL QGKLQLRYQE ISKRTQPPPK LPVGPSHKLS NNYYCTRDGR  60
RESVPPSIIM SSQKALVSGK PAESSAVAAT EKKAVTPAPP IKRWELSSDQ PYL         113

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                        mol_type = protein
                        organism = Homo sapiens
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YFLAMLAVSD MGLSLSSLPT MLRVFLFNAM GISPNACFAQ EFFIHGFTVM ESSVLLIMSL  120
DRFLAIHNPL RYSSILTSNR VAKMGLILAI RSILLVIPFP FTLRRLKYCQ KNLLSHSYCL  180
HQDTMKLACS DNKTNVIYGF FIALCTMLDL ALIVLSYVLI LKTILSIASL AERLKALNTC  240
VSHICAVLTF YVPIITLAAM HHFAKHKSPL VVILIADMFL LVPPLMNPIV YCVKTRQIWE  300
KILGKLLNVC GR                                                      312

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FEATURE                 Location/Qualifiers
source                  1..687
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                        organism = Homo sapiens
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ALVSCAMDLA VESVVRAHQW LYREIGDSHL LRYLSWTVYP VALVSFSSGF SQSITPSSGG  120
SGIPEVKTML AGVVLEDYLD IKNFGAKVVG LSCTLACGST LFLGKVGPFV HLSVMMAAYL  180
GRVRTTTIGE PENKSKQNEM LVAAAAVGVA TVFAAPFSGV LFSIEVMSSH FSVWDYWRGF  240
FAATCGAFMF RLLAVFNSEQ ETITSLYKTS FRVDVPFDLP EIFFFVALGG LCGILGSAYL  300
FCQRIFFGFI RNNRFSSKLL ATSKPVYSAL ATLVLASITY PPSAGRFLAS RLSMKQHLDS  360
LFDNHSWALM TQNSSPPWPE ELDPQHLWWE WYHPRFTIFG TLAFFLVMKF WMLILATTIP  420
MPAGYFMPIF VYGAAIGRLF GETLSFIFPE GIVAGGITNP IMPGGYALAG AAAFSGAVTH  480
TISTALLAFE VTGQIVHALP VLMAVLAANA IAQSCQPSFY DGTVIVKKLP YLPRILGRNI  540
GSHRVRVEHF MNHSITTLAK DMPLEEVVKV VTSTDVAKYP LVESTESQIL VGIVRRAQLV  600
QALKAEPPSW APGHQQCLQD ILAAGCPTEP VTLKLSPETS LHEAHNLFEL LNLHSLFVTS  660
RGRAVGCVSW VEMKKAISNL TNPPAPK                                      687

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source                  1..732
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LMTNGYVSLQ EKDIFVSGVK IFYGSQTGTA KGFATVLAEA VTSLDLPVAI INLKEYDPDD  120
HLIEEVTSKN VCVFLVATYT DGLPTESAEW FCKWLEEASI DFRFGKTYLK GMRYAVFGLG  180
NSAYASHFNK VGKNVDKWLW MLGAHRVMSR GEGDCDVVKS KHGSIEADFR AWKTKFISQL  240
QALQKGERKK SCGGHCKKGK CESHQHGSEE REEGSHEQDE LHHRDTEEEE PFESSSEEEF  300
GGEDHQSLNS IVDVEDLGKI MDHVKKEKRE KEQQEEKSGL FRNMGRNEDG ERRAMITPAL  360
REALTKQGYQ LIGSHSGVKL CRWTKSMLRG RGGCYKHTFY GIESHRCMET TPSLACANKC  420
VFCWRHHTNP VGTEWRWKMD QPEMILKEAI ENHQNMIKQF KGVPGVKAER FEEGMTVKHC  480
ALSLVGEPIM YPEINRFLKL LHQCKISSFL VTNAQFPAEI RNLEPVTQLY VSVDASTKDS  540
LKKIDRPLFK DFWQRFLDSL KALAVKQQRT VYRLTLVKAW NVDELQAYAQ LVSLGNPDFI  600
EVKGVTYCGE SSASSLTMAH VPWHEEVVQF VHELVDLIPE YEIACEHEHS NCLLIAHRKF  660
KIGGEWWTWI DYNRFQELIQ EYEDSGGSKT FSAKDYMART PHWALFGASE RGFDPKDTRH  720
QRKNKSKAIS GC                                                      732

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KVIFLLVGHK SDLQSTRCVS AQEAEELAAS LGMAFVETSV KNNCNVDLAF DTLADAIQQA  180
LQQGDIKLEE GWGGVRLIHK TQIPRSPSRK QHSGPCQC                          218

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source                  1..774
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ENSPPWIVFN VLSDTFFLLD LVLNFRTGIV VEEGAEILLA PRAIRTRYLR TWFLVDLISS  180
IPVDYIFLVV ELEPRLDAEV YKTARALRIV RFTKILSLLR LLRLSRLIRY IHQWEEIFHM  240
TYDLASAVVR IFNLIGMMLL LCHWDGCLQF LVPMLQDFPP DCWVSINHMV NHSWGRQYSH  300
ALFKAMSHML CIGYGQQAPV GMPDVWLTML SMIVGATCYA MFIGHATALI QSLDSSRRQY  360
QEKYKQVEQY MSFHKLPADT RQRIHEYYEH RYQGKMFDEE SILGELSEPL REEIINFTCR  420
GLVAHMPLFA HADPSFVTAV LTKLRFEVFQ PGDLVVREGS VGRKMYFIQH GLLSVLARGA  480
RDTRLTDGSY FGEICLLTRG RRTASVRADT YCRLYSLSVD HFNAVLEEFP MMRRAFETVA  540
MDRLLRIGKK NSILQRKRSE PSPGSSGGIM EQHLVQHDRD MARGVRGRAP STGAQLSGKP  600
VLWEPLVHAP LQAAAVTSNV AIALTHQRGP LPLSPDSPAT LLARSAWRSA GSPASPLVPV  660
RAGPWASTSR LPAPPARTLH ASLSRAGRSQ VSLLGPPPGG GGRRLGPRGR PLSASQPSLP  720
QRATGDGSPG RKGSGSERLP PSGLLAKPPR TAQPPRPPVP EPATPRGLQL SANM        774

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                       organism = Homo sapiens
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LPLDFHQLAF YVLDEDTVGH DDIIGKISLS REAITADPRG IDSWINLSRV DPDAEVQGEI  120
CLSVQMLEDG QGRCLRCHVL QARDLAPRDI SGTSDPFARV FWGSQSLETS TIKKTRFPHW  180
DEVLELREMP GAPSPLRVEL WDWDMVGKND FLGMVEFSPK TLQQKPPKGW FRLLPFPRAE  240
EDSGGNLGAL RVKVRLIEDR VLPSQCYQPL MELLMESVQG PAEEDTASPL ALLEELTLGD  300
CRQDLATKLV KLFLGRGLAG RFLDYLTRRE VARTMDPNTL FRSNSLASKS MEQFMKLVGM  360
PYLHEVLKPV ISRVFEEKKY MELDPCKMDL GRTRRISFKG ALSEEQMRET SLGLLTGYLG  420
PIVDAIVGSV GRCPPAMRLA FKQLHRRVEE RFPQAEHQQD VKYLAISGFL FLRFFAPAIL  480
TPKLFDLRDQ HADPQTSRSL LLLAKAVQSI GNLGQQLGQG KELWMAPLHP FLLQCVSRVR  540
DFLDRLVDVD GDEEAGVPAR ALFPPSAIVR EGYLLKRKEE PAGLATRFAF KKRYVWLSGE  600
TLSFSKSPEW QMCHSIPVSH IRAVERVDEG AFQLPHVMQV VTQDGTGALH TTYLQCKNVN  660
ELNQWLSALR KASAPNPNKL AACHPGAFRS ARWTCCLQAE RSAAGCSRTH SAVTLGDWSD  720
PLDPDAEAQT VYRQLLLGRD QLRLKLLEDS NMDTTLEADT GACPEVLARQ RAATARLLEV  780
LADLDRAHEE FQQQERGKAA LGPLGP                                       806

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                       organism = Homo sapiens
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FLHYDCVNHK AKAFASLGKK VNVTKTWEEQ TETLRDVVDF LKGQLLDIQV ENLIPIEPLT  120
LQARMSCEHE AHGHGRGSWQ FLFNGQKFLL FDSNNRKWTA LHPGAKKMTE KWEKNRDVTM  180
FFQKISLGDC KMWLEEFLMY WEQMLDPTKP PSLAPGTTQP KAMATTLSPW SLLIIFLCFI  240
LAGR                                                               244

SEQ ID NO: 14          moltype = AA  length = 206
FEATURE                Location/Qualifiers
source                 1..206
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 14
MEVDINGESR STLTTLPFPG AEANSPGKAE AEKPRCSSTP CSPMRRTVSG YQILHMDSNY  60
LVGFTTGEEL LKLAQKCTGG EESKAEAMPS LRSKQLDAGL ARSSRLYKTR SRYYQPYEIP  120
AVNGRRRRRM PSSGDKCTKS LPYEPYKALH GPLPLCLLKG KRAHSKSLDY LNLDKMIKEP  180
ADTEVLQYQL QHLTLRGDRV FARNNT                                       206

SEQ ID NO: 15          moltype = AA  length = 678
FEATURE                Location/Qualifiers
source                 1..678
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 15
MAAPGPLPAA ALSPGAPTPR ELMHGVAGVT SRAGRDREAG SVLPAGNRGA RKASRRSSSR  60
SMSRDNKFSK KDCLSIRNVV ASIQTKEGLN LKLISGDVLY IWADVIVNSV PMNLQLGGGP  120
LSRAFLQKAG PMLQKELDDR RRETEEKVGN IFMTSGCNLD CKAVLHAVAP YWNNGAETSW  180
QIMANIIKKC LTTVEVLSFS SITFPMIGTG SLQFPKAVFA KLILSEVFEY SSSTRPITSP  240
LQEVHFLVYT NDDEGCQAFL DEFTNWSRIN PNKARIPMAG DTQGVVGTVS KPCFTAYEMK  300
IGAITFQVAT GDIATEQVDV IVNSTARTFN RKSGVSRAIL EGAGQAVESE CAVLAAQPHR  360
DFIITPGGCL KCKIIIHVPG GKDVRKTVTS VLEECEQRKY TSVSLPAIGT GNAGKNPITV  420
ADNIIDAIVD FSSQHSTPSL KTVKVVIFQP ELLNIFYDSM KKRDLSASLN FQSTFSMTTC  480
NLPEHWTDMN HQLFCMVQLE PGQSEYNTIK DKFTRTCSSY AIEKIERIQN APLWQSYQVK  540
KRQMDIKNDH KNNERLLFHG TDADSVPYVN QHGFNRSCAG KNAVSYGKGT YFAVDASYSA  600
KDTYSKPDSN GRKHMYVVRV LTGVFTKGRA GLVTPPPKNP HNPTDLFDSV TNNTRSPKLF  660
VVFFDNQAYP EYLITFTA                                                678
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SEQ ID NO: 16          moltype = AA  length = 816
FEATURE                Location/Qualifiers
source                 1..816
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 16
MSRPQGLLWL PLLFTPVCVM LNSNVLLWLT ALAIKFTLID SQAQYPVVNT NYGKIRGLRT  60
PLPNEILGPV EQYLGVPYAS PPTGERRFQP PEPPSSWTGI RNTTQFAAVC PQHLDERSLL  120
HDMLPIWFTA NLDTLMTYVQ DQNEDCLYLN IYVPTEDDIH DQNSKKPVMV YIHGGSYMEG  180
TGNMIDGSIL ASYGNVIVIT INYRLGILGF LSTGDQAAKG NYGLLDQIQA LRWIEENVGA  240
FGGDPKRVTI FGSGAGASCV SLLTLSHYSE GLFQKAIIQS GTALSSWAVN YQPAKYTRIL  300
ADKVGCNMLD TTDMVECLRN KNYKELIQQT ITPATYHIAF GPVIDGDVIP DDPQILMEQG  360
EFLNYDIMLG VNQGEGLKFV DGIVDNEDGV TPNDFDFSVS NFVDNLYGYP EGKDTLRETI  420
KFMYTDWADK ENPETRRKTL VALFTDHQWV APAVATADLH AQYGSPTYFY AFYHHCQSEM  480
KPSWADSAHG DEVPYVFGIP MIGPTELFSC NFSKNDVMLS AVVMTYWTNF AKTGDPNQPV  540
PQDTKFIHTK PNRFEEVAWS KYNPKDQLYL HIGLKPRVRD HYRATKVAFW LELVPHLHNL  600
NEIFQYVSTT TKVPPPDMTS FPYGTRRSPA KIWPTTKRPA ITPANNPKHS KDPHKTGPED  660
TTVLIETKRD YSTELSVTIA VGASLLFLNI LAFAALYYKK DKRRHETHRR PSPQRNTTND  720
IAHIQNEEIM SLQMKQLEHD HECESLQAHD TLRLTCPPDY TLTLRRSPDD IPLMTPNTIT  780
MIPNTLTGMQ PLHTFNTFSG GQNSTNLPHG HSTTRV                            816

SEQ ID NO: 17          moltype = AA  length = 128
FEATURE                Location/Qualifiers
source                 1..128
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 17
MGIQGGSVLF GLLLVLAVFC HSGHSLQCYN CPNPTADCKT AVNCSSDFDA CLITKAGLQV  60
YNKCWKFEHC NFNDVTTRLR ENELTYYCCK KDLCNFNEQL ENGGTSLSEK TVLLLVTPFL  120
AAAWSLHP                                                           128

SEQ ID NO: 18          moltype = AA  length = 166
FEATURE                Location/Qualifiers
source                 1..166
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 18
MASGVTVNDE VIKVFNDMKV RKSSTQEEIK KRKKAVLFCL SDDKRQIIVE EAKQILVGDI  60
GDTVEDPYTS FVKLLPLNDC RYALYDATYE TKESKKEDLV FIFWAPESAP LKSKMIYASS  120
KDAIKKKFTG IKHEWQVNGL DDIKDRSTLG EKLGGNVVVS LEGKPL                 166

SEQ ID NO: 19          moltype = AA  length = 403
FEATURE                Location/Qualifiers
source                 1..403
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 19
MFSVFEEITR IVVKEMDAGG DMIAVRSLVD ADRFRCFHLV GEKRTFFGCR HYTTGLTLMD  60
ILDTDGDKWL DELDSGLQGQ KAEFQILDNV DSTGELIVRL PKEITISGSF QGFHHQKIKI  120
SENRISQQYL ATLENRKLKR ELPFSFRSIN TRENLYLVTE TLETVKEETL KSDRQYKFWS  180
QISQGHLSYK HKGQREVTIP PNRVLSYRVK QLVFPNKETM KKDGASSCLG KSLGSEDSRN  240
MKEKLEDMES VLKDLTEEKR KDVLNSLAKC LGKEDIRQDL EQRVSEVLIS GELHMEDPDK  300
PLLSSLFNAA GVLVEARAKA ILDFLDALLE LSEEQQFVAE ALEKGTLPLL KDQVKSVMEQ  360
NWDELASSPP DMDYDPEARI LCALYVVVSI LLELAEGPTS VSS                    403

SEQ ID NO: 20          moltype = AA  length = 1362
FEATURE                Location/Qualifiers
source                 1..1362
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 20
MSAESGPGTR LRNLPVMGDG LETSQMSTTQ AQAQPQPANA ASTNPPPPET SNPNKPKRQT  60
NQLQYLLRVV LKTLWKHQFA WPFQQPVDAV KLNLPDYYKI IKTPMDMGTI KKRLENNYYW  120
NAQECIQDFN TMFTNCYIYN KPGDDIVLMA EALEKLFLQK INELPTEETE IMIVQAKGRG  180
RGRKETGTAK PGVSTVPNTT QASTPPQTQT PQPNPPPVQA TPHPFPAVTP DLIVQTPVMT  240
VVPPQPLQTP PPVPPQPQPP PAPAPQPVQS HPPIIAATPQ PVKTKKGVKR KADTTTPTTI  300
DPIHEPPSLP PEPKTTKLGQ RRESSRPVKP PKKDVPDSQQ HPAPEKSSKV SEQLKCCSGI  360
LKEMFAKKHA AYAWPFYKPV DVEALGLHDY CDIIKHPMDM STIKSKLEAR EYRDAQEFGA  420
DVRLMFSNCY KYNPPDHEVV AMARKLQDVF EMRFAKMPDE PEEPVVAVSS PAVPPPTKVV  480
APPSSSDSSS DSSSDSDSST DDSEEERAQR LAELQEQLKA VHEQLAALSQ PQQNKPKKKE  540
KDKKEKKKEK HKRKEEVEEN KKSKAKEPPP KKTKKNNSSN SNVSKKEPAP MKSKPPPTYE  600
SEEEDKCKPM SYEEKRQLSL DINKLPGEKL GRVVHIIQSR EPSLKNSNPD EIEIDFETLK  660
PSTLRELERY VTSCLRKKRK PQAEKVDVIA GSSKMKGFSS SESESSSESS SSDSEDSETE  720
MAPKSKKKGH PGREQKKHHH HHHQQMQQAP APVPQQPPPP PQQPPPPPPP QQQQQPPPPP  780
PPPSMPQQAA PAMKSSPPPF IATQVPVLEP QLPGSVFDPI GHFTQPILHL PQPELPPHLP  840
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QPPEHSTPPH LNQHAVVSPP ALHNALPQQP SRPSNRAAAL PPKPARPPAV SPALTQTPLL  900
PQPPMAQPPQ VLLEDEEPPA PPLTSMQMQL YLQQLQKVQP PTPLLPSVKV QSQPPPPLPP  960
PPHPSVQQQL QQQPPPPPPP QPQPPPQQQH QPPPRPVHLQ PMQFSTHIQQ PPPPQGQQPP 1020
HPPPGQQPPP PQPAKPQQVI QHHHSPRHHK SDPYSTGHLR EAPSPLMIHS PQMSQFQSLT 1080
HQSPPQQNVQ PKKQELRAAS VVQPQPLVVV KEEKIHSPII RSEPFSPSLR PEPPKHPESI 1140
KAPVHLPQRP EMKPVDVGRP VIRPPEQNAP PPGAPDKDKQ KQEPKTPVAP KKDLKIKNMG 1200
SWASLVQKHP TTPSSTAKSS SDSFEQFRRA AREKEEREKA LKAQAEHAEK EKERLRQERM 1260
RSREDEDALE QARRAHEEAR RRQEQQQQQR QEQQQQQQQQ AAAVAAAATP QAQSSQPQSM 1320
LDQQRELARK REQERRRREA MAATIDMNFQ SDLLSIFEEN LF                     1362

SEQ ID NO: 21          moltype = AA  length = 490
FEATURE                Location/Qualifiers
source                 1..490
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 21
MSEVTKNSLE KILPQLKCHF TWNLFKEDSV SRDLEDRVCN QIEFLNTEFK ATMYNLLAYI  60
KHLDGNNEAA LECLRQAEEL IQQEHADQAE IRSLVTWGNY AWVYYHLGRL SDAQIYVDKV 120
KQTCKKFSNP YSIEYSELDC EEGWTQLKCG RNERAKVCFE KALEEKPNNP EFSSGLAIAM 180
YHLDNHPEKQ FSTDVLKQAI ELSPDNQYVK VLLGLKLQKM NKEAEGEQFV EEALEKSPCQ 240
TDVLRSAAKF YRRKGDLDKA IELFQRVLES TPNNGYLYHQ IGCCYKAKVR QMQNTGESEA 300
SGNKEMIEAL KQYAMDYSNK ALEKGLNPLN AYSDLAEFLE TECYQTPFNK EVPDAEKQQS 360
HQRYCNLQKY NGKSEDTAVQ HGLEGLSISK KSTDKEEIKD QPQNVSENLL PQNAPNYWYL 420
QGLIHKQNGD LLQAAKCYEK ELGRLLRDAP SGIGSIFLSA SELEDGSEEM GQGAVSSSPR 480
ELLSNSEQLN                                                        490

SEQ ID NO: 22          moltype = AA  length = 677
FEATURE                Location/Qualifiers
source                 1..677
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 22
MDDPDCDSTW EEDEEDAEDA EDEDCEDGEA AGARDADAGD EDEESEEPRA ARPSSFQSRM  60
TGSRNWRATR DMCRYRHNYP DLVERDCNGD TPNLSFYRNE IRFLPNGCFI EDILQNWTDN 120
YDLLEDNHSY IQWLFPLREP GVNWHAKPLT LREVEVFKSS QEIQERLVRA YELMLGFYGI 180
RLEDRGTGTV GRAQNYQKRF QNLNWRSHNN LRITRILKSL GELGLEHFQA PLVRFFLEET 240
LVRRELPGVR QSALDYFMFA VRCRHQRRQL VHFAWEHFRP RCKFVWGPQD KLRRFKPSSL 300
PHPLEGSRKV EEEGSPGDPD HEASTQGRTC GPEHSKGGGR VDEGPQPRSV EPQDAGPLER 360
SQGDEAGGHG EDRPEPLSPK ESKKRKLELS RREQPPTEPG PQSASEVEKI ALNLEGCALS 420
QGSLRTGTQE VGGQDPGEAV QPCRQPLGAR VADKVRKRRK VDEGAGDSAA VASGGAQTLA 480
LAGSPAPSGH PKAGHSENGV EEDTEGRTGP KEGTPGSPSE TPGPSPAGPA GDEPAESPSE 540
TPGPRPAGPA GDEPAESPSE TPGPRPAGPA GDEPAESPSE TPGPSPAGPT RDEPAESPSE 600
TPGPRPAGPA GDEPAESPSE TPGPRPAGPA GDEPAESPSE TPGPSPAGPT RDEPAKAGEA 660
AELQDAEVES SAKSGKP                                               677

SEQ ID NO: 23          moltype = AA  length = 293
FEATURE                Location/Qualifiers
source                 1..293
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 23
MRVLVGGGTG FIGTALTQLL NARGHEVTLV SRKPGPGRIT WDELAASGLP SCDAAVNLAG  60
ENILNPLRRW NETFQKEVIG SRLETTQLLA KAITKAPQPP KAWVLVTGVA YYQPSLTAEY 120
DEDSPGGDFD FFSNLVTKWE AAARLPGDST RQVVVRSGVV LGRGGGAMGH MLLPFRLGLG 180
GPIGSGHQFF PWIHIGDLAG ILTHALEANH VHGVLNGVAP SSATNAEFAQ TLGAALGRRA 240
FIPLPSAVVQ AVFGRQRAIM LLEGQKVIPQ RTLATGYQYS FPELGAALKE IVA       293

SEQ ID NO: 24          moltype = AA  length = 1349
FEATURE                Location/Qualifiers
source                 1..1349
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 24
MSAPVGPRGR LAPIPAASQP PLQPEMPDLS HLTEEERKII LAVMDRQKKE EEKEQSVLKK  60
LHQQFEMYKE QVKKMGEESQ QQQEQKGDAP TCGICHKTKF ADGCGHNCSY CQTKFCARCG 120
GRVSLRSNKV MWVCNLCRKQ QEILTKSGAW FYNSGSNTPQ QPDQKVLRGL RNEEAPQEKK 180
PKLHEQTQFQ GPSGDLSVPA VEKSRSHGLT RQHSIKNGSG VKHHIASDIA SDRKRSPSVS 240
RDQNRRYDQR EEREEYSQYA TSDTAMPRSP SDYADRRSQH EPQFYEDSDH LSYRDSNRRS 300
HRHSKEYIVD DEDVESRDEY ERQRREEEYQ SRYRSDPNLA RYPVKPQPYE EQMRIHAEVS 360
RARHERRHSD VSLANADLED SRISMLRMDR PSRQRSISER RAAMENQRSY SMERTREAQG 420
PSSYAQRTTN HSPPTPRRSP LPIDRPDLRR TDSLRKQHHL DPSSAVRKTK REKMETMLRN 480
DSLSSDQSES VRPPPPKPHK SKKGGKMRQI SLSSSEEELA STPEYTSCDD VEIESESVSE 540
KGDMDYNWLD HTSWHSSEAS PMSLHPVTWQ PSKDGDRLIG RILLNKRLKD GSVPRDSGAM 600
LGLKVVGGKM TESGRLCAFI TKVKKGSLAD TVGHLRPGDE VLEWNGRLLQ GATFEEVYNI 660
ILESKPEPQV ELVVSRPIGD IPRIPDSTHA QLESSSSSFE SQKMDRPSIS VTSPMSPGML 720
RDVPQFLSGQ LSSQSLSRRT TPFVPRVQIK LWFDKVGHQL IVTILGAKDL PSREDGRPRN 780
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PYVKIYFLPD RSDKNKRRTK TVKKTLEPKW NQTFIYSPVH RREFRERMLE ITLWDQARVR  840
EEESEFLGEI LIELETALLD DEPHWYKLQT HDVSSLPLPH PSPYMPRRQL HGESPTRRLQ  900
RSKRISDSEV SDYDCDDGIG VVSDYRHDGR DLQSSTLSVP EQVMSSNHCS PSGSPHRVDV  960
IGRTRSWSPS VPPPQSRNVE QGLRGTRTMT GHYNTISRMD RHRVMDDHYS PDRDRDCEAA 1020
DRQPYHRSRS TEQRPLLERT TTRSRSTERP DTNLMRSMPS LMTGRSAPPS PALSRSHPRT 1080
GSVQTSPSST PVAGRRGRQL PQLPPKGTLD RKAGGKKLRS TVQRSTETGL AVEMRNWMTR 1140
QASRESTDGS MNSYSSEGNL IFPGVRLASD SQFSDFLDGL GPAQLVGRQT LATPAMGDIQ 1200
VGMMDKKGQL EVEIIRARGL VVKPGSKTLP APYVKVYLLD NGVCIAKKKT KVARKTLEPL 1260
YQQLLSFEES PQGKVLQIIV WGDYGRMDHK SFMGVAQILL DELELSNMVI GWFKLFPPSS 1320
LVDPTLAPLT RRASQSSLES STGPSYSRS                                   1349

SEQ ID NO: 25          moltype = AA  length = 380
FEATURE                Location/Qualifiers
source                 1..380
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 25
MRNCKMARVA SVLGLVMLSV ALLILSLISY VSLKKENIFT TPKYASPGAP RMYMFHAGFR  60
SQFALKFLDP SFVPITNSLT QELQEKPSKW KFNRTAFLHQ RQEILQHVDV IKNFSLTKNS 120
VRIGQLMHYD YSSHKYVFSI SNNFRSLLPD VSPIMNKHYN ICAVVGNSGI LTGSQCGQEI 180
DKSDFVFRCN FAPTEAFQRD VGRKTNLTTF NPSILEKYYN NLLTIQDRNN FFLSLKKLDG 240
AILWIPAFFF HTSATVTRTL VDFFVEHRGQ LKVQLAWPGN IMQHVNRYWK NKHLSPKRLS 300
TGILMYTLAS AICEEIHLYG FWPFGFDPNT REDLPYHYYD KKGTKFTTKW QESHQLPAEF 360
QLLYRMHGEG LTKLTLSHCA                                             380

SEQ ID NO: 26          moltype = AA  length = 212
FEATURE                Location/Qualifiers
source                 1..212
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 26
MKPPSSIQTS EFDSSDEEPI EDEQTPIHIS WLSLSRVNCS QFLGLCALPG CKFKDVRRNV  60
QKDTEELKSC GIQDIFVFCT RGELSKYRVP NLLDLYQQCG IITHHHPIAD GGTPDIASCC 120
EIMEELTTCL KNYRKTLIHC YGGLGRSCLV AACLLLYLSD TISPEQAIDS LRDLRGSGAI 180
QTIKQYNYLH EFRDKLAAHL SSRDSQSRSV SR                               212

SEQ ID NO: 27          moltype = AA  length = 378
FEATURE                Location/Qualifiers
source                 1..378
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 27
MSKEPLILWL MIEFWWLYLT PVTSETVVTE VLGHRVTLPC LYSSWSHNSN SMCWGKDQCP  60
YSGCKEALIR TDGMRVTSRK SAKYRLQGTI PRGDVSLTIL NPSESDSGVY CCRIEVPGWF 120
NDVKINVRLN LQRASTTTHR TATTTTRRTT TTSPTTTRQM TTTPAALPTT VVTTPDLTTG 180
TPLQMTTIAV FTTANTCLSL TPSTLPEEAT GLLTPEPSKE GPILTAESET VLPSDSWSSV 240
ESTSADTVLL TSKESKVWDL PSTSHVSMWK TSDSVSSPQP GASDTAVPEQ NKTTKTGQMD 300
GIPMSMKNEM PISQLLMIIA PSLGFVLFAL FVAFLLRGKL METYCSQKHT RLDYIGDSKN 360
VLNDVQHGRE DEDGLFTL                                               378

SEQ ID NO: 28          moltype = AA  length = 156
FEATURE                Location/Qualifiers
source                 1..156
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 28
MAGQFRSYVW DPLLILSQIV LMQTVYYGSL GLWLALVDGL VRSSPSLDQM FDAEILGFST  60
PPGRLSMMSF ILNALTCALG LLYFIRRGKQ CLDFTVTVHF FHLLGCWFYS SRFPSALTWW 120
LVQAVCIALM AVIGEYLCMR TELKEIPLNS APKSNV                           156

SEQ ID NO: 29          moltype = AA  length = 165
FEATURE                Location/Qualifiers
source                 1..165
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 29
MAPNASCLCV HVRSEEWDLM TFDANPYDSV KKIKEHVRSK TKVPVQDQVL LLGSKILKPR  60
RSLSSYGIDK EKTIHLTLKV VKPSDEELPL FLVESGDEAK RHLLQVRRSS SVAQVKAMIE 120
TKTGIIPETQ IVTCNGKRLE DGKMMADYGI RKGNLLFLAC YCIGG                 165

SEQ ID NO: 30          moltype = AA  length = 651
FEATURE                Location/Qualifiers
source                 1..651
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 30
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MSGVRAVRIS IESACEKQVH EVGLDGTETY LPPLSMSQNL ARLAQRIDFS QGSGSEEEEA  60
AGTEGDAQEW PGAGSSADQD DEEGVVKFQP SLWPWDSVRN NLRSALTEMC VLYDVLSIVR  120
DKKFMTLDPV SQDALPPKQN PQTLQLISKK KSLAGAAQIL LKGAERLTKS VTENQENKLQ  180
RDFNSELLRL RQHWKLRKVG DKILGDLSYR SAGSLFPHHG TFEVIKNTDL DLDKKIPEDY  240
CPLDVQIPSD LEGSAYIKVS IQKQAPDIGD LGTVNLFKRP LPKSKPGSPH WQTKLEAAQN  300
VLLCKEIFAQ LSREAVQIKS QVPHIVVKNQ IISQPFPSLQ LSISLCHSSN DKKSQKFATE  360
KQCPEDHLYV LEHNLHLLIR EFHKQTLSSI MMPHPASAPF GHKRMRLSGP QAFDKNEINS  420
LQSSEGLLEK IIKQAKHIFL RSRAAATIDS LASRIEDPQI QAHWSNINDV YESSVKVLIT  480
SQGYEQICKS IQLQLNIGVE QIRVVHRDGR VITLSYQEQE LQDFLLSQMS QHQVHAVQQL  540
AKVMGWQVLS FSNHVGLGPI ESIGNASAIT VASPSGDYAI SVRNGPESGS KIMVQFPRNQ  600
CKDLPKSDVL QDNKWSHLRG PFKEVQWNKM EGRNFVYKME LLMSALSPCL L           651

SEQ ID NO: 31          moltype = AA  length = 403
FEATURE                Location/Qualifiers
source                 1..403
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 31
MASQPPPPPK PWETRRIPGA GPGPGPGPTF QSADLGPTLM TRPGQPALTR VPPPILPRPS  60
QQTGSSSVNT FRPAYSSFSS GYGAYGNSFY GGYSPYSYGY NGLGYNRLRV DDLPPSRFVQ  120
QAEESSRGAF QSIESIVHAF ASVSMMMDAT FSAVYNSFRA VLDVANHFSR LKIHFTKVFS  180
AFALVRTIRY LYRRLQRMLG LRRGSENEDL WAESEGTVAC LGAEDRAATS AKSWPIFLFF  240
AVILGGPYLI WKLLSTHSDE VTDSINWASG EDDHVVARAE YDFAAVSEEE ISFRAGDMLN  300
LALKEQQPKV RGWLLASLDG QTTGLIPANY VKILGKRKGR KTVESSKVSK QQQSFTNPTL  360
TKGATVADSL DEQEAAFESV FVETNKVPVA PDSIGKDGEK QDL                    403

SEQ ID NO: 32          moltype = AA  length = 530
FEATURE                Location/Qualifiers
source                 1..530
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 32
MEEDSLYLGG EWQFNHFSKL TSSRLDAAFA EIQRTSLPEK SPLSCETRVD LCDDLVPEAR  60
QLAPREKLPL SSRRPAAVGA GLQNMGNTCY VNASLQCLTY TPPLANYMLS REHSQTCHRH  120
KGCMLCTMQA HITRALHNPG HVIQPSQALA AGFHRGKQED AHEFLMFTVD AMKKACLPGH  180
KQVDHPSKDT TLIHQIFGGY WRSQIKCLHC HGISDTFDPY LDIALDIQAA QSVQQALEQL  240
VKPEELNGEN AYHCGVCLQR APASKTLTLH TSAKVLILVL KRFSDVTGNK IAKNVQYPEC  300
LDMQPYMSQQ NTGPLVYVLY AVLVHAGWSC HNGHYFSYVK AQEGQWYKMD DAEVTAASIT  360
SVLSQQAYVL FYIQKSEWER HSESVSRGRE PRALGAEDTD RRATQGELKR DHPCLQAPEL  420
DEHLVERATQ ESTLDRWKFL QEQNKTKPEF NVRKVEGTLP PDVLVIHQSK YKCGMKNHHP  480
EQQSSLLNLS SSTPTHQESM NTGTLASLRG RARRSKGKNK HSKRALLVCQ              530

SEQ ID NO: 33          moltype = AA  length = 442
FEATURE                Location/Qualifiers
source                 1..442
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 33
MENWSKDITH SYLEQETTGI NKSTQPDEQL TMNSEKSMHR KSTELVNEIT CENTEWPGQR  60
STNFQIISSY PDDESVYCTT EKYNVMEHRH NDMHYECMTP CQVTSDSDKE KTIAFLLKEL  120
DILRTSNKKL QQKLAKEDKE QRKLKFKLEL QEKETEAKIA EKTAALVEEV YFAQKERDEA  180
VMSRLQLAIE ERDEAIARAK HMEMSLKVLE NINPEENDMT LQELLNRINN ADTGIAIQKN  240
GAIIVDRIYK TKECKMRITA EEMSALIEER DAALSKCKRL EQELHHVKEQ NQTSANNMRH  300
LTAENNQERA LKAKLLSMQQ ARETAVQQYK KLEEEIQTLR VYYSLHKSLS QEENLKDQFN  360
YTLSTYEEAL KNRENIVSIT QQQNEELATQ LQQALTERAN MELQLQHARE ASQVANEKVQ  420
KLERLVDVLR KKVGTGTMRT VI                                           442

SEQ ID NO: 34          moltype = AA  length = 322
FEATURE                Location/Qualifiers
source                 1..322
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 34
MAASGEPQRQ WQEEVAAVVV VGSCMTDLVS LTSRLPKTGE TIHGHKFFIG FGGKGANQCV  60
QAARLGAMTS MVCKVGKDSF GNDYIENLKQ NDISTEFTYQ TKDAATGTAS IIVNNEGQNI  120
IVIVAGANLL LNTEDLRAAA NVISRAKVMV CQLEITPATS LEALTMARRS GVKTLFNPAP  180
AIADLDPQFY TLSDVFCCNE SEAEILTGLT VGSAADAGEA ALVLLKRGCQ VVIITLGAEG  240
CVVLSQTEPE PKHIPTEKVK AVDTTGAGDS FVGALAFYLA YYPNLSLEDM LNRSNFIAAV  300
SVQAAGTQSS YPYKKDLPLT LF                                           322

SEQ ID NO: 35          moltype = AA  length = 530
FEATURE                Location/Qualifiers
source                 1..530
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 35
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mol_type = other DNA
organism = Homo sapiens

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mol_type = other DNA
organism = Homo sapiens

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FEATURE                Location/Qualifiers
source                 1..81
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 74
MLRQIIGQAK KHPSLIPLFV FIGTGATGAT LYLLRLALFN PDVCWDRNNP EPWNKLGPND  60
QYKFYSVNVD YSKLKKERPD F                                            81

SEQ ID NO: 75          moltype = AA  length = 212
FEATURE                Location/Qualifiers
source                 1..212
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 75
MEISMPPPQI YVEKTLAIIK PDIVDKEEEI QDIILRSGFT IVQRRKLRLS PEQCSNFYVE  60
KYGKMFFPNL TAYMSSGPLV AMILARHKAI SYWLELLGPN NSLVAKETHP DSLRAIYGTD  120
DLRNALHGSN DFAAAEREIR FMFPEVIVEP IPIGQAAKDY LNLHIMPTLL EGLTELCKQK  180
PADPLIWLAD WLLKNNPNKP KLCHHPIVEE PY                                 212

SEQ ID NO: 76          moltype = AA  length = 412
FEATURE                Location/Qualifiers
source                 1..412
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 76
MGLHLRPYRV GLLPDGLLFL LLLLMLLADP ALPAGRHPPV VLVPGDLGNQ LEAKLDKPTV  60
VHYLCSKKTE SYFTIWLNLE LLLPVIIDCW IDNIRLVYNK TSRATQFPDG VDVRVPGFGK  120
TFSLEFLDPS KSSVGSYFHT MVESLVGWGY TRGEDVRGAP YDWRRAPNEN GPYFLALREM  180
IEEMYQLYGG PVVLVAHSMG NMYTLYFLQR QPQAWKDKYI RAFVSLGAPW GGVAKTLRVL  240
ASGDNNRIPV IGPLKIREQQ RSAVSTSWLL PYNYTWSPEK VFVQTPTINY TLRDYRKFFQ  300
DIGFEDGWLM RQDTEGLVEA TMPPGVQLHC LYGTGVPTPD SFYYESFPDR DPKICFGDGD  360
GTVNLKSALQ CQAWQSRQEH QVLLQELPGS EHIEMLANAT TLAYLKRVLL GP          412

SEQ ID NO: 77          moltype = AA  length = 67
FEATURE                Location/Qualifiers
source                 1..67
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 77
MEEWDVPQMK KEVESLKYQL AFQREMASKT IPELLKWIED GIPKDPFLNP DLMKNNPWVE  60
KGKCTIL                                                            67

SEQ ID NO: 78          moltype = AA  length = 299
FEATURE                Location/Qualifiers
source                 1..299
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 78
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MLRLFYFSAI IASVILNFVG IIMNLFITVV NCKTWVKSHR ISSSDRILFS LGITRFLMLG  60
LFLVNTIYFV SSNTERSVYL SAFFVLCFMF LDSSSVWFVT LLNILYCVKI TNFQHSVFLL  120
LKRNISPKIP RLLLACVLIS AFTTCLYITL SQASPFPELV TTRNNTSFNI SEGILSLVVS  180
LVLSSSLQFI INVTSASLLI HSLRRHIQKM QKNATGFWNP QTEAHVGAMK LMVYFLILYI  240
PYSVATLVQY LPFYAGMDMG TKSICLIFAT LYSPGHSVLI IITHPKLKTT AKKILCFKK   299

SEQ ID NO: 79          moltype = AA  length = 462
FEATURE                Location/Qualifiers
source                 1..462
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 79
MARVLGAPVA LGLWSLCWSL AIATPLPPTS AHGNVAEGET KPDPDVTERC SDGWSFDATT  60
LDDNGTMLFF KGEFVWKSHK WDRELISERW KNFPSPVDAA FRQGHNSVFL IKGDKVWVYP  120
PEKKEKGYPK LLQDEFPGIP SPLDAAVECH RGECQAEGVL FFQGDREWFW DLATGTMKER  180
SWPAVGNCSS ALRWLGRYYC FQGNQFLRFD PVRGEVPPRY PRDVRDYFMP CPGRGHGHRN  240
GTGHGNSTHH GPEYMRCSPH LVLSALTSDN HGATYAFSGT HYWRLDTSRD GWHSWPIAHQ  300
WPQGPSAVDA AFSWEEKLYL VQGTQVYVFL TKGGYTLVSG YPKRLEKEVG TPHGIILDSV  360
DAAFICPGSS RLHIMAGRRL WWLDLKSGAQ ATWTELPWPH EKVDGALCME KSLGPNSCSA  420
NGPGLYLIHG PNLYCYSDVE KLNAAKALPQ PQNVTSLLGC TH                      462

SEQ ID NO: 80          moltype = AA  length = 263
FEATURE                Location/Qualifiers
source                 1..263
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 80
MMPKHCFLGF LISFFLTGVA GTQSTHESLK PQRVQFQSRN FHNILQWQPG RALTGNSSVY  60
FVQYKIMFSC SMKSSHQKPS GCWQHISCNF PGCRTLAKYG QRQWKNKEDC WGTQELSCDL  120
TSETSDIQEP YYGRVRAASA GSYSEWSMTP RFTPWWETKI DPPVMNITQV NGSLLVILHA  180
PNLPYRYQKE KNVSIEDYYE LLYRVFIINN SLEKEQKVYE GAHRAVEIEA LTPHSSYCVV  240
AEIYQPMLDR RSQRSEERCV EIP                                          263

SEQ ID NO: 81          moltype = AA  length = 483
FEATURE                Location/Qualifiers
source                 1..483
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 81
MTKMDIRGAV DAAVPTNIIA AKAAEVRANK VNWQSYLQGQ MISAEDCEFI QRFEMKRSPE  60
EKQEMLQTEG SQCAKTFINL MTHICKEQTV QYILTMVDDM LQENHQRVSI FFDYARCSKN  120
TAWPYFLPML NRQDPFTVHM AARIIAKLAA WGKELMEGSD LNYYFNWIKT QLSSQKLRGS  180
GVAVETGTVS SSDSSQYVQC VAGCLQLMLR VNEYRFAWVE ADGVNCIMGV LSNKCGFQLQ  240
YQMIFSIWLL AFSPQMCEHL RRYNIIPVLS DILQESVKEK VTRIILAAFR NFLEKSTERE  300
TRQEYALAMI QCKVLKQLEN LEQQKYDDED ISEDIKFLLE KLGESVQDLS SFDEYSSELK  360
SGRLEWSPVH KSEKFWRENA VRLNEKNYEL LKILTKLLEV SDDPQVLAVA AHDVGEYVRH  420
YPRGKRVIEQ LGGKQLVMNH MHHEDQQVRY NALLAVQKLM VHNWEYLGKQ LQSEQPQTAA  480
ARS                                                                483

SEQ ID NO: 82          moltype = AA  length = 636
FEATURE                Location/Qualifiers
source                 1..636
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 82
MKKLQGAHLR KPVTPDLLMT PSDQGDVDLD VDFAAHRGNW TGKLDFLLSC IGYCVGLGNV  60
WRFPYRAYTN GGGAFLVPYF LMLAICGIPL FFLELSLGQF SSLGPLAVWK ISPLFKGAGA  120
AMLLIVGLVA IYYNMIIAYV LFYLFASLTS DLPWEHCGNW WNTELCLEHR VSKDGNGALP  180
LNLTCTVSPS EEYWSRYVLH IQGSQGIGSP GEIRWNLCLC LLLAWVIVFL CILKGVKSSG  240
KVVYFTATFP YLILLMLLVR GVTLPGAWKG IQFYLTPQFH HLLSSKVWIE AALQIFYSLG  300
VGFGGLLTFA SYNTFHQNIY RDTFIVTLGN AITSILAGFA IFSVLGYMSQ ELGVPVDQVA  360
KAGPGLAFVV YPQAMTMLPL SPFWSFLFFF MLLTLGLDSQ FAFLETIVTA VTDEFPYYLR  420
PKKAVFSGLI CVAMYLMGLI LTTDGGMYWL VLLDDYSASF GLMVVVITTC LAVTRVYGIQ  480
RFCRDIHMML GFKPGLYFRA CWLFLSPATL LALMVYSIVK YQPSEYGSYR FPPWAELLGI  540
LMGLLSCLMI PAGMLVAVLR EEGSLWERLQ QASRPAMDWG PSLEENRTGM YVATLAGSQS  600
PKPLMVHMRK YGGITSFENT AIEVDREIAE EEESMM                             636

SEQ ID NO: 83          moltype = AA  length = 1896
FEATURE                Location/Qualifiers
source                 1..1896
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 83
MKASSGDQGS PPCFLRFPRP VRVVSGAEAE LKCVVLGEPP PVVVWEKGGQ QLAASERLSF  60
PADGAEHGLL LTAALPTDAG VYVCRARNAA GEAYAAAAVT VLEPPASDPE LQPAERPLPS  120
PGSGEGAPVF LTGPRSQWVL RGAEVVLTCR AGGLPEPTLY WEKDGMALDE VWDSSHFALQ  180
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PGRAEDGPGA SLALRILAAR LPDSGVYVCH ARNAHGHAQA GALLQVHQPP ESPPADPDEA  240
PAPVVEPLKC APKTFWVNEG KHAKFRCYVM GKPEPEIEWH WEGRPLLPDR RRLMYRDRDG  300
GFVLKVLYCQ AKDRGLYVCA ARNSAGQTLS AVQLHVKEPR LRFTRPLQDV EGREHGIAVL  360
ECKVPNSRIP TAWFREDQRL LPCRKYEQIE EGTVRRLIIH RLKADDDGIY LCEMRGRVRT  420
VANVTVKGPI LKRLPRKLDV LEGENAVLLV ETLEAGVEGR WSRDGEELPV ICQSSSGHMH  480
ALVLPGVTRE DAGEVTFSLG NSRTTTLLRV KCVKHSPPGP PILAEMFKGH KNTVLLTWKP  540
PEPAPETPFI YRLERQEVGS EDWIQCFSIE KAGAVEVPGD CVPSEGDYRF RICTVSGHGR  600
SPHVVFHGSA HLVPTARLVA GLEDVQVYDG EDAVFSLDLS TIIQGTWFLN GEELKSNEPE  660
GQVEPGALRY RIEQKGLQHR LILHAVKHQD SGALVGFSCP GVQDSAALTI QESPVHILSP  720
QDRVSLTFTT SERVVLTCEL SRVDFPATWY KDGQKVEESE LLVVKMDGRK HRLILPEAKV  780
QDSGEFECRT EGVSAFFGVT VQDPPVHIVD PREHVFVHAI TSECVMLACE VDREDAPVRW  840
YKDGQEVEES DFVVLENEGP HRRLVLPATQ PSDGGEFQCV AGDECAYFTV TITDVSSWIV  900
YPSGKVYVAA VRLERVVLTC ELCRPWAEVR WTKDGEEVVE SPALLLQKED TVRRLVLPAV  960
QLEDSGEYLC EIDDESASFT VTVTEPPVRI IYPRDEVTLI AVTLECVVLM CELSREDAPV  1020
RWYKDGLEVE ESEALVLERD GPRCRLVLPA AQPEDGGEFV CDAGDDSAFF TVTVTAPPER  1080
IVHPAARSLD LHFGAPGRVE LRCEVAPAGS QVRWYKDGLE VEASDALQLG AEGPTRTLTL  1140
PHAQPEDAGE YVCETRHEAI TFNVILAEPP VQFLALETTP SPLCVAPGEP VVLSCELSRA  1200
GAPVVWSHNG RPVQEGEGLE LHAEGPRRVL CIQAAGPAHA GLYTCQSGAA PGAPSLSFTV  1260
QVAEPPVRVV APEAAQTRVR STPGGDLELV VHLSGPGGPV RWYKDGERLA SQGRVQLEQA  1320
GARQVLRVQG ARSGDAGEYL CDAPQDSRIF LVSVEEPLLV KLVSELTPLT VHEGDDATFR  1380
CEVSPPDADV TWLRNGAVVT PGPQVEMAQN GSSRILTLRG CQLGDAGTVT LRAGSTATSA  1440
RLHVRETELL FLRRLQDVRA EEGQDVCLEV ETGRVGAAGA VRWVRGGQPL PHDSRLSMAQ  1500
DGHIHRLFIH GVILADQGTY GCESHHDRTL ARLSVRPRQL RVLRPLEDVT ISEGGSATFQ  1560
LELSQEGVTG EWARGGVQLY PGPKCHIHSD GHRHRLVLNG LGLADSGCVS FTADSLRCAA  1620
RLIVREVPVT IVRGPHDLEV TEGDTATFEC ELSQALADVT WEKDGNALTP SPRLRLQALG  1680
TRRLLQLRRC GPSDAGTYSC AVGTARAGPV RLTVRERTVA VLSELRSVSA REGDGATFEC  1740
TVSEVETTGR WELGGRPLRP GARVRIRQEG KKHILVLSEL RAEDAGEVRF QAGPAQSLAL  1800
LEVEALPLQM CRHPPREKTV LVGRRAVLEV TVSRSGGHVC WLREGAELCP GDKYEMRSHG  1860
PTHSLVIHDV RPEDQGTYCC QAGQDSTHTR LLVEGN                            1896

SEQ ID NO: 84          moltype = AA  length = 275
FEATURE                Location/Qualifiers
source                 1..275
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 84
MQLQVFWTGL EYTCRLLGIT TAAVLIGVGT ETFLQGQFKS LAFYLLFTGA AVSICEGAYF  60
VAQLLAICFQ CQPGSLADRV REKAHWLGCF QKFLAYLLLS VACFLHPVLV WHVTIPGSML  120
IITGLAYFLL SKRKKRKAAP EVLASPEQYT DPSSSAVSTT GSGDTEQTYT FHGALKEGPS  180
SLFIHMKSIL KGTKKPSALQ PPNTLMELSL EPADSLAKKK QVHFEDNLVR IVPSLAEGLD  240
DGDSEPEETT SDTTPIIPPP QAPLFLSSLT ATGLF                             275

SEQ ID NO: 85          moltype = AA  length = 480
FEATURE                Location/Qualifiers
source                 1..480
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 85
MEVAPEQPRW MAHPAVLNAQ HPDSHHPGLA HNYMEPAQLL PPDEVDVFFN HLDSQGNPYY  60
ANPAHARARV SYSPAHARLT GGQMCRPHLL HSPGLPWLDG GKAALSAAAA HHHNPWTVSP  120
FSKTPLHPSA AGGPGGPLSV YPGAGGGSGG GSGSSVASLT PTAAHSGSHL FGFPPTPPKE  180
VSPDPSTTGA ASPASSSAGG SAARGEDKDG VKYQVSLTES MKMESGSPLR PGLATMGTQP  240
ATHHPIPTYP SYVPAAAHDY SSGLFHPGGF LGGPASSFTP KQRSKARSCS EGRECVNCGA  300
TATPLWRRDG TGHYLCNACG LYHKMNGQNR PLIKPKRRLS AARRAGTCCA NCQTTTTTLW  360
RRNANGDPVC NACGLYYKLH NVNRPLTMKK EGIQTRNRKM SNKSKKSKKG AECFEELSKC  420
MQEKSSPFSA AALAGHMAPV GHLPPFSHSG HILPTPTPIH PSSSLSFGHP HPSSMVTAMG  480

SEQ ID NO: 86          moltype = AA  length = 530
FEATURE                Location/Qualifiers
source                 1..530
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 86
MEDDSLYLGG EWQFNHFSKL TSSRPDAAFA EIQRTSLPEK SPLSCETRVD LCDDLAPVAR  60
QLAPREKPPL SSRRPAAVGA GLQNMGNTCY VNASLQCLTY KPPLANYMLF REHSQTCHRH  120
KGCMLCTMQA HITRALHIPG HVIQPSQALA AGFHRGKQED AHEFLMFTVD AMRKACLPGH  180
KQVDRHSKDT TLIHQIFGGY WRSQIKCLHC HGISDTFDPY LDIALDIQAA QSVQQALEQL  240
VKPEELNGEN AYHCGVCLQR APASKTLTLH NSAKVLILVL KRFPDVTGNK IAKNVQYPEC  300
LDMQPYMSQQ NTGPLVYVLY AVLVHAGWSC HNGHYSSYVK AQEGQWYKMD DAEVTASSIT  360
SVLSQQAYVL FYIQKSEWER HSESVSRGRE PRALGVEDTD RRATQGELKR DHPCLQAPEL  420
DEHLVERATQ ESTLDHWKFL QEQNKTKPEF NVRRVEGTVP PDVLVIHQSK YKCRMKNHHP  480
EQQSSLLNLS STTPTDQESM NTGTLASLRG RTRRSKGKNK HSKRALLVCQ              530

SEQ ID NO: 87          moltype = AA  length = 530
FEATURE                Location/Qualifiers
source                 1..530
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                     mol_type = protein
                     organism = Homo sapiens
SEQUENCE: 87
MEDDSLYLGG DWQFNHFSKL TSSRLDAAFA EIQRTSLSEK SPLSSETRFD LCDDLAPVAR  60
QLAPREKLPL SSRRPAAVGA GLQKIGNTFY VNVSLQCLTY TLPLSNYMLS REDSQTCHLH  120
KCCMFCTMQA HITWALHSPG HVIQPSQVLA AGFHRGEQED AHEFLMFTVD AMKKACLPGH  180
KQLDHHSKDT TLIHQIFGAY WRSQIKYLHC HGVSDTFDPY LDIALDIQAA QSVKQALEQL  240
VKPKELNGEN AYHCGLCLQK APASKTLTLP TSAKVLILVL KRFSDVTGNK LAKNVQYPKC  300
RDMQPYMSQQ NTGPLVYVLY AVLVHAGWSC HNGHYFSYVK AQEGQWYKMD DAEVTASGIT  360
SVLSQQAYVL FYIQKSEWER HSESVSRGRE PRALGAEDTD RPATQGELKR DHPCLQVPEL  420
DEHLVERATQ ESTLDHWKFP QEQNKTKPEF NVRKVEGTLP PNVLVIHQSK YKCGMKNHHP  480
EQQSSLLNLS STKPTDQESM NTGTLASLQG STRRSKGNNK HSKRSLLVCQ              530

SEQ ID NO: 88          moltype = AA  length = 384
FEATURE                Location/Qualifiers
source                 1..384
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 88
MEGLGRSCLW LRRELSPPRP RLLLLDCRSR ELYESARIGG ALSVALPALL LRRLRRGSLS  60
VRALLPGPPL QPPPPAPVLL YDQGGGRRRR GEAEAEAEEW EAESVLGTLL QKLREEGYLA  120
YYLQGGFSRF QAECPHLCET SLAGRAGSSM APVPGPVPVV GLGSLCLGSD CSDAESEADR  180
DSMSCGLDSE GATPPPVGLR ASFPVQILPN LYLGSARDSA NLESLAKLGI RYILNVTPNL  240
PNFFEKNGDF HYKQIPISDH WSQNLSRFFP EAIEFIDEAL SQNCGVLVHC LAGVSRSVTV  300
TVAYLMQKLH LSLNDAYDLV KRKKSNISPN FNFMGQLLDF ERSLRLEERH SQEQGSGGQA  360
SAASNPPSFF TTPTSDGAFE LAPT                                          384

SEQ ID NO: 89          moltype = AA  length = 237
FEATURE                Location/Qualifiers
source                 1..237
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 89
MALPPSPLAM EYVNDFDLMK FEVKREPSEG RPGPPTASLG STPYSSVPPS PTFSEPGMVG  60
ATEGTRPGLE ELYWLATLQQ QLGAGEALGL SPEEAMELLQ GQGPVPVDGP HGYYPGSPEE  120
TGAQHVQLAE RFSDAALVSM SVRELNRQLR GCGRDEALRL KQRRRTLKNR GYAQACRSKR  180
LQQRRGLEAE RARLAAQLDA LRAEVARLAR ERDLYKARCD RLTSSGPGSG DPSHLFL     237

SEQ ID NO: 90          moltype = AA  length = 1399
FEATURE                Location/Qualifiers
source                 1..1399
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 90
MSGLGDSSSD PANPDSHKRK GSPCDTLASS TEKRRREQEN KYLEELAELL SANISDIDSL  60
SVKPDKCKIL KKTVDQIQLM KRMEQEKSTT DDDVQKSDIS SSSQGVIEKE SLGPLLLEAL  120
DGFFFVVNCE GRIVFVSENV TSYLGYNQEE LMNTSVYSIL HVGDHAEFVK NLLPKSLVNG  180
VPWPQEATRR NSHTFNCRML IHPPDEPGTE NQEACQRYEV MQCFTVSQPK SIQEDGEDFQ  240
SCLICIARRL PRPPAITGVE SFMTKQDTTG KIISIDTSSL RAAGRTGWED LVRKCIYAFF  300
QPQGREPSYA RQLFQEVMTR GTASSPSYRF ILNDGTMLSA HTKCKLCYPQ SPDMQPFIMG  360
IHIIDREHSG LSPQDDTNSG MSIPRVNPSV NPSISPAHGV ARSSTLPPSN SNMVSTRINR  420
QQSSDLHSSS HSNSSNSQGS FGCSPGSQIV ANVALNQGQA SSQSSNPSLN LNNSPMEGTG  480
ISLAQFMSPR RQVTSGLATR PRMPNNSFPP NISTLSSPVG MTSSACNNNN RSYSNIPVTS  540
LQGMNEGPNN SVGFSASSPV LRQMSSQNSP SRLNIQPAKA ESKDNKEIAS ILNEMIQSDN  600
SSSDGKPLDS GLLHNNDRLS DGDSKYSQTS HKLVQLLTTT AEQQLRHADI DTSCKDVLSC  660
TGTSNSASAN SSGGSCPSSH SSLTERHKIL HRLLQEGSPS DITTLSVEPD KKDSASTSVS  720
VTGQVQGNSS IKLELDASKK KESKDHQLLR YLLDKDEKDL RSTPNLSLDD VKVKVEKKEQ  780
MDPCNTNPTP MTKPTPEEIK LEAQSQFTAD LDQFDQLLPT LEKAAQLPGL CETDRMDGAV  840
TSVTIKSEIL PASLQSATAR PTSRLNRLPE LELEAIDNQF GQPGTGDQIP WTNNTVTAIN  900
QSKSEDQCIS SQLDELLCPP TTVEGRNDEK ALLEQLVSFL SGKDETELAE LDRALGIDKL  960
VQGGGLDVLS ERFPPQQATP PLIMEERPNL YSQPYSSPSP TANLPSPFQG MVRQKPSLGT  1020
MPVQVTPPRG AFSPGMGMQP RQTLNRPPAA PNQLRLQLQQ RLQGQQQLIH QNRQAILNQF  1080
AATAPVGINM RSGMQQQITP QPPLNAQMLA QRQRELYSQQ HRQRQLIQQQ RAMLMRQQSF  1140
GNNLPPSSGL PVQMGNPRLP QGAPQQFPYP PNYGTNPGTP PASTSPFSQL AANPEASLAN  1200
RNSMVSRGMT GNIGGQFGTG INPQMQQNVF QYPGAGMVPQ GEANFAPSLS PGSSMVPMPI  1260
PPPQSSLLQQ TPPASGYQSP DMKAWQQGAI GNNNVFSQAV QNQPTPAQPG VYNNMSITVS  1320
MAGGNTNVQN MNPMMAQMQM SSLQMPGMNT VCPEQINDPA LRHTGLYCNQ LSSTDLLKTE  1380
ADGTQDKKTE EFFSVVTTD                                                1399

SEQ ID NO: 91          moltype = AA  length = 319
FEATURE                Location/Qualifiers
source                 1..319
                       mol_type = protein
                       organism = Homo sapiens
SEQUENCE: 91
MDPQNQHGSG SSLVVIQQPS LDSRQRLDYE REIQPTAILS LDQIKAIRGS NEYTEGPSVV  60
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KRPAPRTAPR QEKHERTHEI IPINVNNNYE HRHTSHLGHA VLPSNARGPI LSRSTSTGSA  120
ASSGSNSSAS SEQGLLGRSP PTRPVPGHRS ERAIRTQPKQ LIVDDLKGSL KEDLTQHKFI  180
CEQCGKCKCG ECTAPRTLPS CLACNRQCLC SAESMVEYGT CMCLVKGIFY HCSNDDEGDS  240
YSDNPCSCSQ SHCCSRYLCM GAMSLFLPCL LCYPPAKGCL KLCRRCYDWI HRPGCRCKNS  300
NTVYCKLESC PSRGQGKPS                                               319

SEQ ID NO: 92          moltype = DNA  length = 1593
FEATURE                Location/Qualifiers
source                 1..1593
                       mol_type = other DNA
                       organism = Homo sapiens
SEQUENCE: 92
atggaggacg actcactcta cttgggaggt gagtggcagt tcaaccactt ttcaaaactc  60
acatcttctc ggccagatgc agcttttgct gaaatccagc gtacttctct ccctgagaag  120
tcaccactct catgtgagac ccgtgtcgac ctctgtgatg atttggctcc tgtggcaaga  180
cagcttgctc ccagggagaa gcctcctctg agtagcagga gacctgctgc ggtgggggct  240
gggctccaga atatgggaaa tacctgctac gtgaacgctt ccctgcagtg cctgacatac  300
aaaccgccac ttgccaacta catgctgttc cgggagcact ctcaaacgtg tcatcgtcac  360
aagggctgca tgctctgtac tatgcaagct cacatcacaa gggccctcca cattcctggc  420
catgtcatcc agccctcaca ggcattggct gctggcttcc atagaggcaa gcaggaagat  480
gcccatgaat ttctcatgtt cactgtggat gccatgagaa aggcatgcct tcccgggcac  540
aagcaggtag atcgtcactc taaggacacc accctcatcc accaaatatt tggaggctac  600
tggagatctc aaatcaagtg tctccactgc cacggcattt cagacacttt tgacccttac  660
ctggacatcg ccctggatat ccaggcagct cagagtgtcc agcaagcttt ggaacagttg  720
gtgaagcccg aagaactcaa tggagagaat gcctatcatt gtggtgtttg tctccagagg  780
gcgccggcct ccaagacgtt aactttacac aactctgcca aggtcctcat ccttgtattg  840
aagagattcc ccgatgtcac aggcaacaaa attgccaaga atgtgcaata tcctgagtgc  900
cttgacatgc agccatacat gtctcagcag aacacaggac ctctcgtcta tgtcctctat  960
gctgtgctgg tccacgctgg gtggagttgt cacaacggac attactcctc ttatgtcaaa  1020
gctcaagaag gccagtggta taaaatggat gatgccgagg tcaccgcctc tagcatcact  1080
tctgtcctga gtcaacaggc ctacgtcctc ttttacatcc agaagagtga atgggaaaga  1140
cacagtgaga gtgtgtcaag aggcagggaa ccaagagccc ttggcgtaga agacacagac  1200
aggcgagcaa cgcaaggaga gctcaagaga gaccacccct gcctccaggc ccccgagttg  1260
gacgagcact tggtggaaag agccactcag gaaagcacct tagaccactg gaaattcctt  1320
caagagcaaa acaaaacgaa gcctgagttc aacgtcagaa gagtcgaagg tacggtgcct  1380
cccgacgtac ttgtgattca tcaatcaaaa tacaagtgtc ggatgaagaa ccatcatcct  1440
gaacagcaaa gctccctgct aaacctctct tcgacgaccc cgacagatca ggagtccatg  1500
aacactggca cactcgcttc cctacgaggg aggaccagga gatccaaagg gaagaacaaa  1560
cacagcaaga gggctctgct tgtgtgccag tga                                1593

SEQ ID NO: 93          moltype = DNA  length = 2657
FEATURE                Location/Qualifiers
source                 1..2657
                       mol_type = other DNA
                       organism = Homo sapiens
SEQUENCE: 93
agcttcccgg ctgctttgtt tacctaatca agcctgggca atggcgggct cccctccccc  60
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What is claimed is:

1. A nucleic acid vector comprising a heterologous promoter operably linked to an open reading frame encoding a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91.

2. The vector of claim **1**, wherein the promoter is a viral promoter.

3. The vector of claim **1**, wherein the polypeptide has at least 90% or 95% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or the portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91.

4. The vector of claim **1**, which is a viral vector or a plasmid.

5. A host cell having the vector of claim **1**, or wherein the genome of the host cell is augmented with a nucleic acid encoding a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91, or comprising a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91.

6. The host cell of claim **1**, which is an eukaryotic cell or a prokaryotic cell.

7. The host cell of claim **5**, wherein the vector or nucleic acid is maintained extrachromosomally.

8. The host cell of 6 which is an insect cell, a plant cell, or a mammalian cell.

9. A method to increase influenza virus yield in cells, comprising: contacting influenza virus and cells comprising the vector of any one of claim **1** or contacting the cells with a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91; and collecting progeny influenza virus.

10. The method of claim **9**, wherein the cells are human, canine, or non-human primate cells.

11. The method of claim **9**, wherein the cells are Vero cells, MDCK cells, 293T or PER.C6® cells, or MvLu1 cells.

12. The method of claim **9**, wherein the cell is contacted with the vector or the polypeptide before contacting the cell with the influenza virus.

13. The method of claim **9**, wherein the cell is contacted with the vector or the polypeptide after contacting the cell with the influenza virus.

14. The method of claim **9**, wherein the yield of influenza virus is increased at least two-fold relative to the corresponding yield in cells not having the vector or the polypeptide.

15. A method to detect influenza virus in a sample, comprising: contacting cells having the vector of claim **1** or contacting the cells with a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91 and a biological sample; and determining whether the sample comprises influenza virus.

16. The method of claim **15**, wherein the cells are human, canine or non-human primate cells.

17. The method of claim **15**, wherein the cells are Vero cells, MDCK cells, 293T or PER.C6® cells, or MvLu1 cells.

18. The method of claim **15**, wherein the sample is a physiological sample.

19. The method of claim **18**, wherein the sample is a nasal sample.

20. A method to decrease influenza virus replication in a mammal, comprising: administering to the mammal a composition comprising the vector of claim **1** or a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91.

21. A method to screen for compounds that alter the activity of a pathogen, comprising: contacting cells with a sample having a pathogen, wherein the cells express a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91, or wherein the cells comprise an isolated polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91; and determining whether the polypeptide alters the activity of the pathogen.

22. The method of claim **21**, wherein the pathogen is a virus.

23. The method of claim **21**, wherein the cells are mammalian cells.

24. The method of claim **23**, wherein the cells are canine, non-human primate, or human cells.

25. The method of claim **23**, wherein the cells are MDCK cells.

26. A method to inhibit expression of pro-viral genes in a mammal, comprising administering to the mammal an effective amount a composition that specifically inhibits the expression of an amino acid sequence any one of SEQ ID Nos. 1-36 or 74-91.

27. The method of claim **26**, wherein the composition comprises RNA.

28. The method of claim **27**, wherein the RNA triggers RNA interference (RNAi).

29. The method of claim **28**, wherein the RNA comprises a small interfering RNA (siRNA).

30. The method of claim **26**, wherein the mammal is infected with influenza virus.

31. The method of claim **30**, wherein the composition prevents or inhibits influenza virus replication.

32. A method to screen for inhibitory compounds, comprising combining cells expressing a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91 or isolated nucleic acid that encodes a polypeptide having at least 80% amino acid sequence identity to one of SEQ ID Nos. 1-36 or 74-91 or a portion thereof with the activity of SEQ ID Nos. 1-36 or 74-91 and one or more test compounds; and determining whether the one or more test compounds inhibit expression of the polypeptide or inhibit transcription or translation of the isolated nucleic acid.

33. A method to prevent, inhibit, or treat influenza virus infection in an avian or a mammal, comprising administering to the avian or mammal an effective amount of RNA that triggers RNA interference (RNAi) specific an amino acid sequence of any one of SEQ ID Nos. 1-36 or 74-91 or an antibody or fragment thereof specific for one of SEQ ID Nos. 1-36 or 74-91.

34. The method of claim **33**, wherein the mammal is a human.

35. The method of claim **33**, wherein the RNA comprises a small interfering RNA (siRNA).

36. The method of claim **33**, wherein the composition is administered locally, systemically, or intranasally.

37. The method of claim **33**, wherein the composition comprises liposomes or nanoparticles comprising the RNAi.

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