

A GENETIC PHARMACOPEIA FOR COMPREHENSIVE FUNCTIONAL PROFILING OF HUMAN CANCERS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application claims the benefit of U.S. Provisional Patent Application Serial No. 62/865,047, filed June 21, 2019, which is incorporated herein by reference in its entirety.

SEQUENCE LISTING

[0002] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. Said ASCII copy, created on June 18, 2020, is named 56322-701_601_SL.txt and is 732,058 bytes in size.

BACKGROUND OF THE INVENTION

[0003] Human cancers are extraordinarily heterogeneous, differing in DNA sequence, epigenomic landscape, RNA expression, and protein levels, resulting in vast combinatorial complexity in cell behavior. Despite impressive advances in our armamentarium of molecularly targeted anti-cancer therapies, the extreme molecular complexity underlying cancer cell behavior has led to dramatic shortfalls in our ability to predict which patients will benefit from any particular therapy. The lack of an effective means of predicting patient response directly leads to cycles of futile therapy, at enormous opportunity cost to patients and economic cost to both patients and healthcare payers.

SUMMARY

[0004] The presently disclosed methods seek to provide a rational and personalized selection of therapeutics by determining which molecularly targeted therapy would be effective for a particular patient's disease. In one aspect, the methods comprise determining the functional susceptibility of a patient's cancer cells to a library of perturbagens which model the action of a library of known oncology drugs. Representative perturbagens include components of a gene editing or silencing system capable of knocking out, or knocking down, the genes encoding for the protein targets of the known oncology drugs. For instance, the perturbagens may include gene modulatory reagents such as guide RNA sequences for CRISPR-based gene editing, or RNAi for gene silencing. Accordingly, an exemplary method of functional susceptibility profiling comprises modifying a patient's cancer cells with a library of gene modulatory reagents capable of knocking down, or knocking out, the function of the genes encoding for protein targets of a library of known oncology drugs. In some methods the functionality of all such genes is knocked down or knocked out such that the susceptibility of a patient's cancer to all available molecularly targeted therapies may be interrogated. The modified cancer cells may be screened by next-generation sequencing to determine the effect of the individual genetic perturbations on the viability of the patient's cancer cells. Oncology drugs associated with the perturbagens that reduce viability of the cancer cells may be selected as a putative therapeutic, allowing for personalized selection of a cancer therapeutic.

[0005] In one aspect, provided herein is a method of treating cancer in a subject in need thereof, the method comprising administering to the subject a therapeutic molecule selected from a library of therapeutic molecules; wherein the therapeutic molecule has been selected by a method comprising: modifying cancer cells from the subject to knock down or knock out the function of a plurality of genes, each gene in the plurality of genes encoding for a protein target of a therapeutic molecule in the library of therapeutic molecules, whereby the therapeutic molecule has been selected if knocking down or knocking out the function of the gene that encodes for the protein target of the selected therapeutic molecule impairs cancer cell viability. In some embodiments, the library of therapeutic molecules comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 therapeutic agents of Table 2. In some embodiments, the library of therapeutic molecules comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 therapeutic agents of Table 3. In some embodiments, one or more of the plurality of genes encode for a protein of Table 5B. In some embodiments, one or more of the plurality of genes encode for a protein of Table 5A. In some embodiments, one or more of the plurality of genes encode for a protein of Table 5C. In some embodiments, one or more of the plurality of genes encode for a protein of Table 5D. In some embodiments, one or more of the plurality of genes encode for a protein of Table 4. In some embodiments, one or more of the plurality of genes encode for a protein of Table 3.

[0006] In another aspect, provided herein is a method of treating cancer in a subject in need thereof, the method comprising administering to the subject a therapeutic molecule selected from a library of therapeutic molecules; wherein the cancer of the subject has been determined to be susceptible to the selected therapeutic molecule by a method comprising: (a) contacting a sample of cancer cells from the subject with a library of gene modulatory reagents to generate a plurality of modified cancer cells, wherein each modified cancer cell harbors one or more of the gene modulatory reagents, and each gene modulatory reagent is capable of knocking down or knocking out the function of a gene that encodes a protein target of a therapeutic molecule in the library of therapeutic molecules, and (b) sequencing the plurality of modified cancer cells, wherein a gene modulatory reagent that impairs cell viability will have fewer sequence reads than a gene modulatory reagent that does not impair cell viability, and the gene that is knocked down or knocked out by the gene modulatory reagent that impairs cell viability encodes for the protein targeted by the selected therapeutic molecule. In some embodiments, prior to sequencing, one or more of the plurality of modified cancer cells have been propagated. In some embodiments, propagation comprises maintenance of the modified cancer cells in a 2D *in vitro* culture. In some embodiments, propagation comprises maintenance of the modified cancer cells in a 3D *in vitro* culture. In some embodiments, propagation comprises maintenance of the modified cancer cells *in vivo*. In some embodiments, propagation occurs within an animal model. In some embodiments, the animal is a rodent. In some embodiments, the cancer cells are primary cancer cells.

[0007] In some embodiments, contacting comprises introducing the one or more gene modulatory reagents into each cancer cell by a viral or non-viral delivery method. In some embodiments, one or more of the gene modulatory reagents in the library are encoded on a viral vector. In some embodiments, the viral vector comprises a lentiviral vector, adenoviral vector, or adeno-associated viral vector. In some

embodiments, the non-viral delivery method comprises transposase-mediated transposition.

[0008] In some embodiments, the library comprises from about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, from about 50 to about 2,000, from about 100 to about 2,000, or from about 500 to about 2,000 different gene modulatory reagents. In some embodiments, one or more gene modulatory reagents from the library of gene modulatory reagents comprises a nucleic acid sequence homologous to at least about 15 contiguous nucleotides of a gene encoding a protein of Tables 3-5D. In some embodiments, one or more gene modulatory reagents from the library of gene modulatory reagents comprises a nucleic acid sequence homologous to at least about 15 contiguous nucleotides of a gene encoding a protein of Table 5B. In some embodiments, one or more gene modulatory reagents from the library of gene modulatory reagents comprises a nucleic acid sequence homologous to at least about 15 contiguous nucleotides of a gene encoding a protein of Table 5C. In some embodiments, one or more gene modulatory reagents from the library of gene modulatory reagents comprises a nucleic acid sequence homologous to at least about 15 contiguous nucleotides of a gene encoding a protein of Table 5D. In some embodiments, the homology is at least about 90% sequence homology. In some embodiments, the homology is at least about 90% sequence identity. In some embodiments, the library of therapeutic molecules comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 therapeutic agents of Table 2. In some embodiments, the library of therapeutic molecules comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 therapeutic agents of Table 3.

[0009] In some embodiments, the cancer comprises at least one cancer chosen from the group comprising acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), adrenocortical carcinoma, AIDS-related cancers, Kaposi sarcoma, AIDS-related lymphoma, primary CNS lymphoma, anal cancer, appendix cancer, astrocytomas, atypical teratoid/rhabdoid tumor, central nervous system cancers, basal cell carcinoma of the skin, bile duct cancer, bladder cancer, bone cancer, brain tumors, breast cancer, bronchial tumors, Burkitt lymphoma, carcinoid tumor, cardiac tumors, central nervous system cancers, embryonal tumors, germ cell tumor, primary CNS lymphoma, cervical cancer, cholangiocarcinoma, chordoma, chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), chronic myeloproliferative neoplasms, colorectal cancer, craniopharyngioma, cutaneous t-cell lymphoma, ductal carcinoma in situ (DCIS), embryonal tumors, central nervous system cancer, endometrial cancer, ependymoma, esophageal cancer, esthesioneuroblastoma, Ewing sarcoma, extracranial germ cell tumor, extragonadal germ cell tumor, eye cancer, intraocular melanoma, retinoblastoma, fallopian tube cancer, fibrous histiocytoma of bone, osteosarcoma, gallbladder cancer, gastric cancer, gastrointestinal carcinoid tumor, gastrointestinal stromal tumors (GIST), testicular cancer, gestational trophoblastic disease, hairy cell leukemia, head and neck cancer, heart tumors, hepatocellular cancer, Hodgkin lymphoma, hypopharyngeal cancer, intraocular melanoma, islet cell tumors, pancreatic neuroendocrine tumors, kidney cancer, Langerhans cell histiocytosis, laryngeal cancer, leukemia, lip and oral cavity cancer, liver cancer, lung cancer (non-small cell and small cell), lymphoma, male breast cancer, malignant fibrous histiocytoma of bone and osteosarcoma, melanoma, intraocular melanoma,

Merkel cell carcinoma, mesothelioma, metastatic cancer, metastatic squamous neck cancer with occult primary, midline tract carcinoma with NUT gene changes, mouth cancer, multiple endocrine neoplasia syndromes, multiple myeloma/plasma cell neoplasms, mycosis fungoides, myelodysplastic syndromes, myelodysplastic/myeloproliferative neoplasms, myelogenous leukemia, chronic (CML), myeloid leukemia, acute (AML), nasal cavity and paranasal sinus cancer, nasopharyngeal cancer, neuroblastoma, non-Hodgkin lymphoma, non-small cell lung cancer, oral cancer, oropharyngeal cancer, ovarian cancer, pancreatic cancer, pancreatic neuroendocrine tumors (islet cell tumors), papillomatosis, paraganglioma, paranasal sinus and nasal cavity cancer, parathyroid cancer, penile cancer, pharyngeal cancer, pheochromocytoma, pituitary tumor, plasma cell neoplasm/multiple myeloma, pleuropulmonary blastoma, primary central nervous system (CNS) lymphoma, primary peritoneal cancer, prostate cancer, rectal cancer, recurrent cancer, renal cell cancer, retinoblastoma, rhabdomyosarcoma, salivary gland cancer, sarcoma, rhabdomyosarcoma, vascular tumors, osteosarcoma, soft tissue sarcoma, uterine sarcoma, Sézary syndrome, skin cancer, small intestine cancer, squamous cell carcinoma of the skin, squamous neck cancer with occult primary, stomach cancer, T-cell lymphoma, testicular cancer, throat cancer, nasopharyngeal cancer, oropharyngeal cancer, hypopharyngeal cancer, thymoma and thymic carcinoma, thyroid cancer, transitional cell cancer of the renal pelvis and ureter, ureter and renal pelvis, urethral cancer, uterine cancer, endometrial, uterine sarcoma, vaginal cancer, vascular tumors, vulvar cancer, Wilms tumor, and other childhood kidney tumors.

[0010] In some embodiments, one or more of the gene modulatory reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 1-2789, 2980-3071. In some embodiments, one or more of the gene modulatory reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 1526-2789. In some embodiments, one or more of the gene modulatory reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 2980-3071. In some embodiments, the at least about 90% homology is at least about 90% identity. In some embodiments, one or more of the gene modulatory reagents comprise a guide RNA (gRNA) sequence comprising homology to at least a portion of the gene that encodes a protein target of a therapeutic molecule in the library of therapeutic molecules. In some embodiments, the gRNA comprises homology to about 10 to about 50 contiguous nucleotides of the gene. In some embodiments, the homology is at least about 90% sequence homology. In some embodiments, the homology is at least about 90% sequence identity. In some embodiments, the sample of cancer cells is contacted with an endonuclease. In some embodiments, the endonuclease comprises a Cas9 or Cas12a endonuclease. In some embodiments, the Cas9 or Cas12a endonuclease is selected from *S. pyogenes* Cas9 (SpCas9), SpCas9 D1135E variant, SpCas9 VRER variant, SpCas9 EQR variant, xCas9, SpCas9-NG, *S. aureus* Cas9 (SaCas9), *Acidaminococcus* sp. (AsCpf1), *Lachnospiraceae bacterium* (LbCpf1), AsCpf1 RR variant, LbCpf1 RR variant, AsCpf1 RVR variant, *C. jejuni* Cas9 (CjCas9), *N. meningitidis* (NmCas9), *S. thermophilus* (StCas9), *T. denticola* (TdCas9), and Mad7. In some embodiments, the endonuclease does not comprise a Cas9 or Cas12a endonuclease. In some embodiments, the gRNA is positioned within a

vector. In some embodiments, the vector further comprises genetic elements of a virus. In some embodiments, the virus comprises an adenovirus, retrovirus, adeno-associated virus (AAV), pox virus, parvovirus, baculovirus, measles virus, herpes simplex virus (HSV), Moloney Murine Leukemia Virus (MoMLV, MMLV, MuLV, or MLV), Murine Stem cell Virus (MSCV), or human immunodeficiency virus (HIV), or a combination thereof. In some embodiments, the vector further comprises an auxiliary nucleic acid sequence. In some embodiments, the auxiliary nucleic acid sequence comprises a sequence encoding a marker, an antibiotic resistance cassette, and surface epitope expression cassette. In some embodiments, the marker is a fluorescent marker. In some embodiments, the auxiliary nucleic acid allows for the selection of cancer cells that have been modified to harbor the one or more gene modulatory reagents.

[0011] In some embodiments, one or more of the gene modulatory reagents comprise a short hairpin RNA (shRNA) sequence comprising homology to at least a portion of the gene that encodes a protein target of a therapeutic molecule in the library of therapeutic molecules. In some embodiments, the shRNA comprises homology to about 10 to about 50 contiguous nucleotides of the gene. In some embodiments, the homology is at least about 90% sequence homology. In some embodiments, the homology is at least about 90% sequence identity. In some embodiments, the shRNA is positioned within a vector. In some embodiments, the vector further comprises genetic elements of a virus. In some embodiments, the virus comprises an adenovirus, retrovirus, adeno-associated virus (AAV), pox virus, parvovirus, baculovirus, measles virus, herpes simplex virus (HSV), Moloney Murine Leukemia Virus (MoMLV, MMLV, MuLV, or MLV), Murine Stem cell Virus (MSCV), or human immunodeficiency virus (HIV), or a combination thereof. In some embodiments, the vector further comprises an auxiliary nucleic acid sequence. In some embodiments, the auxiliary nucleic acid sequence comprises a sequence encoding a marker, an antibiotic resistance cassette, or surface epitope expression cassette. In some embodiments, the marker is a fluorescent marker. In some embodiments, the auxiliary nucleic acid allows for the selection of cancer cells that have been modified to harbor the one or more gene modulatory reagents.

[0012] In another aspect, provided herein is a method of generating a plurality of modified cancer cells from a subject having cancer, the method comprising delivering a library of gene modulatory reagents to a sample of cancer cells from the subject to generate the plurality of modified cancer cells; wherein each modified cancer cell harbors one or more of the gene modulatory reagents, and each gene modulatory reagent is capable of knocking down or knocking out the function of a gene that encodes a protein target from a library of protein targets. In some embodiments, one or more of the gene modulatory reagents comprises a guide RNA (gRNA) sequence comprising homology to at least a portion of the gene whose function is knocked down or knocked out in the modified cancer cell. In some embodiments, the gRNA comprises homology to about 10 to about 50 contiguous nucleotides of the gene. In some embodiments, the homology is at least about 90% sequence homology. In some embodiments, the homology is at least about 90% sequence identity. In some embodiments, one or more of the gene modulatory reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 1-2789, 2980-3071. In some embodiments, one or more of the gene modulatory

reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 1526-2789. In some embodiments, one or more of the gene modulatory reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 2980-3071. In some embodiments, the homology is at least about 90% identity. In some embodiments, the sample of cancer cells is contacted with an endonuclease. In some embodiments, the endonuclease comprises a Cas9 or Cas12a endonuclease. In some embodiments, the Cas9 or Cas12a endonuclease is selected from *S. pyogenes* Cas9 (SpCas9), SpCas9 D1135E variant, SpCas9 VRER variant, SpCas9 EQR variant, xCas9, SpCas9-NG, *S. aureus* Cas9 (SaCas9), *Acidaminococcus* sp. (AsCpf1), *Lachnospiraceae bacterium* (LbCpf1), AsCpf1 RR variant, LbCpf1 RR variant, AsCpf1 RVR variant, *C. jejuni* Cas9 (CjCas9), *N. meningitidis* (NmCas9), *S. thermophilus* (StCas9), *T. denticola* (TdCas9), and Mad7. In some embodiments, the endonuclease does not comprise a Cas9 or Cas12a endonuclease. In some embodiments, the gRNA is positioned within a vector. In some embodiments, the vector further comprises genetic elements of a virus. In some embodiments, the virus comprises an adenovirus, retrovirus, adeno-associated virus (AAV), pox virus, parvovirus, baculovirus, measles virus, herpes simplex virus (HSV), Moloney Murine Leukemia Virus (MoMLV, MMLV, MuLV, or MLV), Murine Stem cell Virus (MSCV), or human immunodeficiency virus (HIV), or a combination thereof. In some embodiments, the vector further comprises an auxiliary nucleic acid sequence. In some embodiments, the auxiliary nucleic acid sequence comprises a sequence encoding a marker, an antibiotic resistance cassette, or surface epitope expression cassette. In some embodiments, the marker is a fluorescent marker. In some embodiments, the auxiliary nucleic acid allows for the selection of cancer cells that have been modified to harbor the one or more gene modulatory reagents.

[0013] In some embodiments, one or more of the gene modulatory reagents comprise a short hairpin RNA (shRNA) sequence comprising homology to at least a portion of the gene whose function is knocked down or knocked out in the modified cancer cell. In some embodiments, the shRNA comprises homology to about 10 to about 50 contiguous nucleotides of the gene. In some embodiments, the homology is at least about 90% sequence homology. In some embodiments, the homology is at least about 90% sequence identity. In some embodiments, the shRNA is positioned within a vector. In some embodiments, the vector further comprises genetic elements of a virus. In some embodiments, the virus comprises an adenovirus, retrovirus, adeno-associated virus (AAV), pox virus, parvovirus, baculovirus, measles virus, herpes simplex virus (HSV), Moloney Murine Leukemia Virus (MoMLV, MMLV, MuLV, or MLV), Murine Stem cell Virus (MSCV), or human immunodeficiency virus (HIV), or a combination thereof. In some embodiments, the vector further comprises an auxiliary nucleic acid sequence. In some embodiments, the auxiliary nucleic acid sequence comprises a sequence encoding a marker, an antibiotic resistance cassette, or surface epitope expression cassette. In some embodiments, the marker is a fluorescent marker. In some embodiments, the auxiliary nucleic acid allows for the selection of cancer cells that have been modified to harbor the one or more gene modulatory reagents.

[0014] In some embodiments, delivery comprises transposase-mediated transposition. In some

embodiments, the sample of cancer cells comprises primary cancer cells. In some embodiments, the sample of cancer cells comprises about 10^5 to about 10^8 cells. In some embodiments, the library comprises from about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, from about 50 to about 2,000, from about 100 to about 2,000, or from about 500 to about 2,000 different gene modulatory reagents. In some embodiments, at least about 90% of the gene modulatory reagents are present in the library in a quantity within about 10% of the average gene modulatory reagent quantity. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5B. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5A. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5C. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5D. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 4. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 3. In some embodiments, the sample of cancer cells has been processed to preserve cell viability.

[0015] In some embodiments, the method further comprises preparing the sample of cancer cells to preserve cell viability prior to and/or after delivery of the library of gene modulatory reagents. In some embodiments, the method further comprises propagating the modified cancer cells. In some embodiments, propagation comprises maintenance of the modified cancer cells in a 2D *in vitro* culture. In some embodiments, propagation comprises maintenance of the modified cancer cells in a 3D *in vitro* culture. In some embodiments, propagation comprises maintenance of the modified cancer cells *in vivo*. In some embodiments, propagation occurs within an animal model. In some embodiments, the animal model is a rodent.

[0016] In another aspect, provided herein is a compilation comprising a plurality of modified cancer cells, wherein each modified cancer cell harbors one or more gene modulatory reagents, and each gene modulatory reagent is capable of knocking down or knocking out the function of a gene that encodes a protein target from a library of protein targets. In some embodiments, at least one of the one or more gene modulatory reagents comprises a sequence selected from SEQ ID NOS: 1-2789, 2980-3071. In some embodiments, at least one of the one or more gene modulatory reagents comprises a sequence selected from SEQ ID NOS: 1526-2789. In some embodiments, at least one of the one or more gene modulatory reagents comprises a sequence selected from SEQ ID NOS: 2980-3071. In some embodiments, at least one of the one or more of gene modulatory reagents comprises a sequence at least about 90% homologous to a sequence selected from SEQ ID NOS: 1-2789, 2980-3071. In some embodiments, at least one of the one or more of gene modulatory reagents comprises a sequence at least about 90% homologous to a sequence selected from SEQ ID NOS: 1526-2789. In some embodiments, at least one of the one or more

of gene modulatory reagents comprises a sequence at least about 90% homologous to a sequence selected from SEQ ID NOS: 2980-3071. In some embodiments, the homology is 90% identity.

[0017] In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5B. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5A. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5C. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5D. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 4. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 3. In some embodiments, one or more of the gene modulatory reagents comprise a guide RNA (gRNA) sequence comprising homology to at least a portion of the gene whose function is knocked down or knocked out in the modified cancer cell. In some embodiments, the gRNA comprises homology to about 10 to about 50 contiguous nucleotides of the gene. In some embodiments, the homology is at least about 90% sequence homology. In some embodiments, the homology is at least about 90% sequence identity.

[0018] In some embodiments, the compilation comprises an endonuclease. In some embodiments, the endonuclease comprises a Cas9 or Cas12a endonuclease. In some embodiments, the Cas9 or Cas12a endonuclease is selected from *S. pyogenes* Cas9 (SpCas9), SpCas9 D1135E variant, SpCas9 VRER variant, SpCas9 EQR variant, xCas9, SpCas9-NG, *S. aureus* Cas9 (SaCas9), *Acidaminococcus* sp. (AsCpf1), *Lachnospiraceae bacterium* (LbCpf1), AsCpf1 RR variant, LbCpf1 RR variant, AsCpf1 RVR variant, *C. jejuni* Cas9 (CjCas9), *N. meningitidis* (NmCas9), *S. thermophilus* (StCas9), *T. denticola* (TdCas9), and Mad7. In some embodiments, the endonuclease does not comprise a Cas9 or Cas12a endonuclease.

[0019] In some embodiments, the gRNA is positioned within a vector. In some embodiments, the vector further comprises genetic elements of a virus. In some embodiments, the virus comprises an adenovirus, retrovirus, adeno-associated virus (AAV), pox virus, parvovirus, baculovirus, measles virus, herpes simplex virus (HSV), Moloney Murine Leukemia Virus (MoMLV, MMLV, MuLV, or MLV), Murine Stem cell Virus (MSCV), or human immunodeficiency virus (HIV), or a combination thereof. In some embodiments, the vector further comprises an auxiliary nucleic acid sequence. In some embodiments, the auxiliary nucleic acid sequence comprises a sequence encoding a marker, an antibiotic resistance cassette, or surface epitope expression cassette. In some embodiments, the marker is a fluorescent marker. In some embodiments, the auxiliary nucleic acid allows for the selection of the modified cancer cells.

[0020] In some embodiments, one or more of the gene modulatory reagents comprise a short hairpin RNA (shRNA) sequence comprising homology to at least a portion of the gene whose function is knocked down or knocked out in the modified cancer cell. In some embodiments, the shRNA comprises homology

to about 10 to about 50 contiguous nucleotides of the gene. In some embodiments, the homology is at least about 90% sequence homology. In some embodiments, the homology is at least about 90% sequence identity. In some embodiments, the shRNA is positioned within a vector. In some embodiments, the vector further comprises genetic elements of a virus. In some embodiments, the virus comprises an adenovirus, retrovirus, adeno-associated virus (AAV), pox virus, parvovirus, baculovirus, measles virus, herpes simplex virus (HSV), Moloney Murine Leukemia Virus (MoMLV, MMLV, MuLV, or MLV), Murine Stem cell Virus (MSCV), or human immunodeficiency virus (HIV), or a combination thereof. In some embodiments, the vector further comprises an auxiliary nucleic acid sequence. In some embodiments, the auxiliary nucleic acid sequence comprises a sequence encoding a marker, an antibiotic resistance cassette, or surface epitope expression cassette. In some embodiments, the marker is a fluorescent marker. In some embodiments, the auxiliary nucleic acid allows for the selection of the modified cancer cells. In some embodiments, delivering comprising transposase-mediated transposition.

[0021] In some embodiments, the modified cancer cells are modified primary cancer cells. In some embodiments, the compilation comprises from about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, from about 50 to about 2,000, from about 100 to about 2,000, or from about 500 to about 2,000 different gene modulatory reagents. In some embodiments, the compilation comprises from about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, from about 50 to about 2,000, from about 100 to about 2,000, or from about 500 to about 2,000 different populations of modified cancer cells.

[0022] In another aspect, provided herein is a method of evaluating the functional effect of genetically modifying cancer cells from a subject, the method comprising: sequencing a plurality of modified cancer cells, wherein each modified cancer cell harbors one or more gene modulatory reagents, each gene modulatory reagent capable of knocking down or knocking out the function of a gene that encodes a protein target in a library of protein targets; and wherein a gene modulatory reagent that impairs cell viability will have fewer sequence reads than a gene modulatory reagent that does not impair cell viability. In some embodiments, the method comprises determining which gene modulatory reagents have fewer than a threshold number of sequence reads. In some embodiments, the threshold number of sequence reads is an expected number of sequence reads if the gene modulatory reagent did not impair cell viability. In some embodiments, the threshold number of sequence reads is an average number of sequence reads for each gene modulatory reagent in the plurality of modified cancer cells.

[0023] In some embodiments, the method comprises correlating each gene modulatory reagent that has fewer than the threshold number of sequence reads to its corresponding protein target in the library of protein targets. In some embodiments, the method comprises correlating the corresponding protein target to a therapeutic molecule. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5B. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5A. In some embodiments, the library of protein targets

comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5C. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5D. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 4. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 3.

[0024] In some embodiments, one or more of the gene modulatory reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 1-2789, 2980-3071. In some embodiments, one or more of the gene modulatory reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 1526-2789. In some embodiments, one or more of the gene modulatory reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 2980-3071. In some embodiments, the at least about 90% homology is at least about 90% identity.

[0025] In another aspect, provided herein is a library comprising a plurality of gene modulatory reagents, each gene modulatory reagent capable of knocking down or knocking out the function of a gene that encodes a protein target from a library of protein targets. In some embodiments, the plurality of gene modulatory reagents is capable of knocking down or knocking out the function of at least about 50% of the genes that encode for the protein targets in the library. In some embodiments, the at least about 50% is at least about 60%. In some embodiments, the at least about 60% is at least about 70%. In some embodiments, the at least about 70% is at least about 80%. In some embodiments, the at least about 80% is at least about 90%. In some embodiments, the library of protein targets comprises all known proteins targeted by known drugs capable of treating a particular disease or condition. In some embodiments, the disease or condition is cancer. In some embodiments, the cancer comprises at least one cancer from the group comprising acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), adrenocortical carcinoma, AIDS-related cancers, Kaposi sarcoma, AIDS-related lymphoma, primary CNS lymphoma, anal cancer, appendix cancer, astrocytomas, atypical teratoid/rhabdoid tumor, central nervous system cancers, basal cell carcinoma of the skin, bile duct cancer, bladder cancer, bone cancer, brain tumors, breast cancer, bronchial tumors, Burkitt lymphoma, carcinoid tumor, cardiac tumors, central nervous system cancers, embryonal tumors, germ cell tumor, primary CNS lymphoma, cervical cancer, cholangiocarcinoma, chordoma, chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), chronic myeloproliferative neoplasms, colorectal cancer, craniopharyngioma, cutaneous t-cell lymphoma, ductal carcinoma in situ (DCIS), embryonal tumors, central nervous system cancer, endometrial cancer, ependymoma, esophageal cancer, esthesioneuroblastoma, Ewing sarcoma, extracranial germ cell tumor, extragonadal germ cell tumor, eye cancer, intraocular melanoma, retinoblastoma, fallopian tube cancer, fibrous histiocytoma of bone, osteosarcoma, gallbladder cancer, gastric cancer, gastrointestinal carcinoid tumor, gastrointestinal stromal tumors (GIST), testicular cancer, gestational trophoblastic disease, hairy cell leukemia, head and neck cancer, heart tumors, hepatocellular

cancer, Hodgkin lymphoma, hypopharyngeal cancer, intraocular melanoma, islet cell tumors, pancreatic neuroendocrine tumors, kidney cancer, Langerhans cell histiocytosis, laryngeal cancer, leukemia, lip and oral cavity cancer, liver cancer, lung cancer (non-small cell and small cell), lymphoma, male breast cancer, malignant fibrous histiocytoma of bone and osteosarcoma, melanoma, intraocular melanoma, Merkel cell carcinoma, mesothelioma, metastatic cancer, metastatic squamous neck cancer with occult primary, midline tract carcinoma with NUT gene changes, mouth cancer, multiple endocrine neoplasia syndromes, multiple myeloma/plasma cell neoplasms, mycosis fungoides, myelodysplastic syndromes, myelodysplastic/myeloproliferative neoplasms, myelogenous leukemia, chronic (CML), myeloid leukemia, acute (AML), nasal cavity and paranasal sinus cancer, nasopharyngeal cancer, neuroblastoma, non-Hodgkin lymphoma, non-small cell lung cancer, oral cancer, oropharyngeal cancer, ovarian cancer, pancreatic cancer, pancreatic neuroendocrine tumors (islet cell tumors), papillomatosis, paraganglioma, paranasal sinus and nasal cavity cancer, parathyroid cancer, penile cancer, pharyngeal cancer, pheochromocytoma, pituitary tumor, plasma cell neoplasm/multiple myeloma, pleuropulmonary blastoma, primary central nervous system (CNS) lymphoma, primary peritoneal cancer, prostate cancer, rectal cancer, recurrent cancer, renal cell cancer, retinoblastoma, rhabdomyosarcoma, salivary gland cancer, sarcoma, rhabdomyosarcoma, vascular tumors, osteosarcoma, soft tissue sarcoma, uterine sarcoma, Sézary syndrome, skin cancer, small intestine cancer, squamous cell carcinoma of the skin, squamous neck cancer with occult primary, stomach cancer, T-cell lymphoma, testicular cancer, throat cancer, nasopharyngeal cancer, oropharyngeal cancer, hypopharyngeal cancer, thymoma and thymic carcinoma, thyroid cancer, transitional cell cancer of the renal pelvis and ureter, ureter and renal pelvis, urethral cancer, uterine cancer, endometrial, uterine sarcoma, vaginal cancer, vascular tumors, vulvar cancer, Wilms tumor, and other childhood kidney tumors.

[0026] In some embodiments, the known drugs comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 drugs of Table 2. In some embodiments, the known drugs comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 drugs of Table 3. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5B. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5A. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5C. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5D. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 4. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 3. In some embodiments, one or more of the plurality of gene modulatory reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 1-2789, 2980-3071. In some embodiments, one or more of the plurality of gene modulatory reagents each comprise a guide RNA (gRNA) sequence

comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 1526-2789. In some embodiments, one or more of the plurality of gene modulatory reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 2980-3071. In some embodiments, the at least about 90% homology is at least about 90% identity.

[0027] In some embodiments, the plurality of gene modulatory reagents is capable of knocking down or knocking out the function of about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, about 50 to about 2,000, or about 100 to about 2,000 genes. In some embodiments, the library comprises about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, about 50 to about 2,000, or about 100 to about 2,000 gene modulatory reagents.

[0028] In some embodiments, at least one of the gene modulatory reagents is capable of knocking out the function of a gene. In some embodiments, at least one of the gene modulatory reagents comprise a gRNA sequence having homology to at least a portion of the gene whose function is knocked out by the gene modulatory reagent. In some embodiments, at least one of the gene modulatory reagents is capable of knocking down the function of a gene. In some embodiments, at least one of the gene modulatory reagents comprise a shRNA sequence having homology to at least a portion of the gene whose function is knocked down by the gene modulatory reagent. In some embodiments, the homology is at least about 90% sequence homology. In some embodiments, the homology is at least about 90% sequence identity. In some embodiments, the at least a portion is at least about 15 contiguous nucleotides.

[0029] In some embodiments, at least one of the gene modulatory reagents is positioned within a vector. In some embodiments, the vector comprises an adapter sequence. In some embodiments, the adapter sequence comprises a type IIS restriction enzyme cleavage sites. In some embodiments, the vector further comprises genetic elements of a virus. In some embodiments, the virus comprises an adenovirus, retrovirus, adeno-associated virus (AAV), pox virus, parvovirus, baculovirus, measles virus, herpes simplex virus (HSV), Moloney Murine Leukemia Virus (MoMLV, MMLV, MuLV, or MLV), Murine Stem cell Virus (MSCV), or human immunodeficiency virus (HIV), or a combination thereof. In some embodiments, the vector further comprises a sequence encoding a marker, an antibiotic resistance cassette, or surface epitope expression cassette. In some embodiments, the marker is a fluorescent marker.

BRIEF DESCRIPTION OF THE DRAWINGS

[0030] FIG. 1 is a clinical workflow of a cancer functional susceptibility profiling method described herein.

[0031] FIG. 2 is a schematic of a CRISPR-based platform for personalized functional genomics.

[0032] FIG. 3 is a schematic for identifying cancer therapeutic vulnerabilities in the gene space via CRISPR.

[0033] FIG. 4 is a table of the characteristics of a targeted oncology CRISPR library.

[0034] FIG. 5 shows distribution of gRNA representation in pooled plasmid DNA (left) and

transduced cells (right).

[0035] FIG. 6A shows a 3D collagen scaffold containing infected primary tumor cells.

[0036] FIG. 6B shows re-isolated cells demonstrating the outgrowth of the small tumor-derived tumoroids/organoids.

[0037] FIG. 7 shows expression of B2M, demonstrating loss of B2M protein expression at the precise frequency expected based on the relative abundance of B2M-targeting gRNAs in a gRNA library.

[0038] FIG. 8 is a volcano plot of CRISPR library screening in A549 lung carcinoma cells. Core selected genes are shown in dark circles (TOP2A, TUBB, RPL3, TUBG1, PSMB5). Negative control genes are shown in gray circles.

[0039] FIG. 9 is a volcano plot of CRISPR library screening in primary PDX-derived human melanoma tumor cells. The known melanoma driver gene BRAF is identified as a therapeutic vulnerability. Negative control genes are shown in gray circles.

DETAILED DESCRIPTION OF THE INVENTION

[0040] Most previous efforts in personalized cancer sensitivity testing have focused on treatment of tumor cells with proposed therapeutic small molecules *in vitro*. However, numerous studies have demonstrated that key differences exist between the behavior of cancer cells *in vitro* and their corresponding behavior *in vivo*, including the response of cancer cells to inhibition of various molecular pathways. Indeed, one of the most clinically successful approaches to date for chemosensitivity testing utilizes engraftment of primary patient-derived cancer cells into mice, followed by *in vivo* treatment of the animals with drugs. This approach is effective but extraordinarily slow (6-12 months), expensive (cost of goods related to compounds and animals; hands-on time for dosing, analysis), and non-comprehensive (i.e. only a few drugs can be tested). As a result, the approach is intrinsically non-scalable.

[0041] Over 300 molecularly targeted therapies are either approved or under study for the treatment of cancer. Each of these drugs (usually a low molecular weight compound, or in some cases an antibody) binds to and, in nearly all cases, inactivates the function of a particular protein target. While it is conceptually appealing to test each of these drugs on an individual patient's cancer cells in order to find effective therapies, this has proven over several decades to be an inherently limited and suboptimal process for a number of reasons: (1) The number of cells required to perform the test limits the number of therapies (drugs) which can be tested. (2) Testing can only be performed *in vitro*, which differs significantly from the *in vivo* context in which clinical therapy is performed. (3) Accurate testing depends on knowledge of *in vitro* drug stability and cellular exposure, which are usually not known. As a result, the data gathered from compound testing *in vitro* does not reflect achievable *in vivo* tissue exposure. (4) High cost of goods associated with maintaining validated and updated stocks of all drugs. (5) Testing cannot be performed in a pooled or multiplexed format, raising costs and limiting throughput. These processes are therefore in principle unable to be scaled to commercial levels. (6) Testing cannot be used to identify new targets, i.e. those for which drugs are not already available.

[0042] The presently described methods work by pivoting the currently available suite of anti-cancer

therapies from ‘drug space’ to ‘gene space’. Specifically, the methods depend on the critical insight that each protein target of an existing therapy can also be inhibited indirectly via mutagenesis of the gene encoding that protein target, *e.g.* via gene editing. Thus, the ‘drug pharmacopeia’ can instead be represented by a ‘genetic pharmacopeia’. The genetic pharmacopeia can represent an entire targeted therapy landscape (*e.g.*, for the oncology landscape, over 300 therapeutic molecules are represented), in a genetic format. This may be achieved by designing inhibitory genetic elements, for instance sgRNAs (CRISPR) or shRNAs (RNAi) corresponding to the gene or mRNA respectively of the protein target of each potential therapeutic. Accordingly, the genetic pharmacopeia allows for a genetic determination of the functional susceptibility of cancer cells to known oncology drugs, mitigating the shortcomings described above and as shown in Table 1.

Table 1. Mitigating the shortcomings of existing methods with a genetic pharmacopeia.

Shortcoming of existing solutions	Mitigation via Genetic Pharmacopeia
The number of cells required to perform the test limits the number of therapies (drugs) which can be tested	Genetic platform allows pooled screening with highly parallel, NGS-based readout of target modulation
Testing can only be performed <i>in vitro</i> , which differs significantly from the <i>in vivo</i> context in which clinical therapy is performed	Testing can be performed <i>in vivo</i> , as well as in complex <i>in vitro</i> environments mimicking the <i>in vivo</i> context (<i>e.g.</i> 3D matrices, engineered niches)
Accurate testing depends on knowledge of <i>in vitro</i> drug stability and cellular exposure, which are usually not known. As a result, the data gathered from compound testing <i>in vitro</i> does not reflect achievable <i>in vivo</i> tissue exposure	No knowledge needed of pharmacokinetic or chemical properties of existing drug entities
High cost of goods associated with maintaining validated and updated stocks of all drugs	No pharmacologic stocks are required. Required consumable reagents are widely available at commodity pricing
Testing cannot be performed in a pooled or multiplexed format, raising costs and limiting throughput	Tests are performed in a pooled, highly multiplexed format
Testing cannot be used to identify new targets, <i>i.e.</i> those for which drugs are not already available	Genetic pools can be designed to support novel drug discovery, <i>i.e.</i> for protein targets for which no current inhibitor is available, in primary patient-derived cells

[0043] In the same way that a chemical pharmacopeia reduces the vast potential drug space (*i.e.* all LMW chemical structures) to a size that is useful for the selection of therapies in actual practice, a genetic pharmacopeia reduces the complexity of the human genome to a scale suitable for practical use in personalized diagnostics. The limited availability of patient-derived cells, which are usually derived from scant biopsy or resection specimens, and the limited ability to propagate these cells in culture mandates this reduction in complexity, and makes the use of a genetic pharmacopeia indispensable for diagnostics applications. The use of larger (*e.g.* whole genome) libraries for personalized medicine is simply not feasible, which until now has precluded the use of these technologies for precision medicine.

[0044] In one aspect, provided herein are methods of determining the susceptibility of a disease or condition to a library of therapeutic agents represented by a library of perturbagens which model the action of those therapeutic agents. A clinical workflow of a functional susceptibility profiling method for

a patient with cancer is shown in **FIG. 1**. In an initial step **101**, a sample of primary, patient-derived cancer cells is obtained from the patient. In a subsequent step **102**, the cancer cells are contacted with a library of gene modulatory reagents which model the function of a library of cancer drugs having known protein targets by editing (*e.g.*, CRISPR-based methods) and/or silencing (*e.g.*, siRNA) the genes encoding for those protein targets. The resulting modified cancer cells are propagated by *in vitro* 2D culture, *in vitro* 2.5D/3D culture, or *in vivo*. This step may involve use of improved 3D *in vitro* models of *in vivo* growth, methods for suppression of stromal cell outgrowth, co-culture with autologous or allogenic immune cells (*e.g.* T cells), or improved methods for xenograft development *in vivo*, or any combination thereof. To evaluate the effect of each gene perturbation, in a subsequent step **103**, the propagated modified cancer cells are tested, *e.g.*, by next generation sequencing (NGS), to obtain a readout regarding which gene modulatory reagents affect the viability of the patient's cancer cells. This step may involve use of developed internal references to calibrate dropout analysis and correct for sample-to-sample variation. A clinical panel **104** is generated identifying the effective gene modulatory reagents and/or corresponding cancer drugs. A clinician, such as an oncologist, or a group of clinicians, such as a tumor board, evaluate the clinical panel **104** and make a clinical decision **106** regarding a course of treatment for the patient. To assist with the clinical decision **106**, the unmodified tumor itself may be subjected to DNA sequencing **105**.

[0045] In another aspect, the methods described herein facilitate the generation of a discovery panel **107**, which may include newly discovered drug targets, *e.g.*, to assist with drug development; newly discovered use(s) of a known drug (drug repurposing); and/or the functional correlation to the discoveries based on whole exome sequencing. These discoveries may be partnered with Biopharmaceutical companies **108** to assist with expansion of drug indications for known drugs; function-based clinical trials of known drugs; development of drugs against newly discovered targets; and/or improvement of sequence-based analyses via deorphanization of variants of unknown significance (VUS).

[0046] The method described in **FIG. 1** may further comprise designing the library of gene modulatory reagents used in the functional analysis step **102**. The design may involve defining the full targeted pharmacologic landscape by generating a list of all targeted drugs (drug library) for cancer. As an example, the drug library comprises at least one of the cancer drugs of Table 2, *e.g.*, at least about 5, 10, 20, 50, 100, 150, 200, 250, 300, 400, 500, 1000, or 1500 of the drugs listed in Table 2. As another example, the drug library comprises at least one of the cancer drugs of Table 3. In some cases, the drug library comprises a plurality of cancer drugs of Table 3, *e.g.*, at least about 5, 10, 20, 50, 100, 150, 200, 250, 300, 400, 500, 1000, or 1500 of the drugs listed in Table 3. The drug library may comprise all of the targeted drugs for a particular type of cancer. As used herein, "all targeted drugs" may refer to at least about 90%, 95%, or 100% of all FDA-approved drugs for a particular indication, *e.g.*, cancer in general or a particular type of cancer. All targeted drugs may also include investigational drugs, such as drugs undergoing regulatory review, but have not yet been approved, and drugs used in clinical trials or pre-clinical testing.

[0047] The method described in **FIG. 1** may further comprise determining the protein and associated

gene targets of the drugs in a drug library, such as the drug library comprising one or more cancer drugs of Tables 2-3, *e.g.*, a drug of Table 2. This requires that a target is known or proposed for each drug included in the analysis. In the case of non-specific inhibitors, such as multi-kinase inhibitors, the targets may include multiple gene targets. As a non-limiting example, the library comprises at least one of the targets of Tables 4-6B, 6D. In some cases, the library comprises a plurality of targets of Tables 4-6B, 6D, *e.g.*, at least about 5, 10, 20, 50, 100, 150, 200, 250, or 300 of the targets listed in Tables 4-6B, 6D.

[0048] The library of gene modulatory reagents used in the functional analysis shown in **FIG. 1** may be designed by selecting reagents that target the genes of the target library, *e.g.*, the reagents target the genes encoding for one or more targets of Tables 4-6B, 6D, *e.g.*, a target from Table 6D. Reagents may be selected that have been validated for efficacy in inhibiting the target, thus providing a more “compact” library. In an exemplary embodiment, the library comprises at least one nucleic acid comprising a sequence selected from SEQ ID NOS: 1-2789, 2980-3071. In some cases, the library comprises a plurality of nucleic acid sequences selected from SEQ ID NOS: 1-2789, 2980-3071. In an exemplary embodiment, the library comprises at least one nucleic acid comprising a sequence selected from SEQ ID NOS: 1526-2789. In some cases, the library comprises a plurality of nucleic acid sequences selected from SEQ ID NOS: 1526-2789. In an exemplary embodiment, the library comprises at least one nucleic acid comprising a sequence selected from SEQ ID NOS: 2980-3071. In some cases, the library comprises a plurality of nucleic acid sequences selected from SEQ ID NOS: 2980-3071. In some CRISPR-based methods, the library comprises a control gRNA sequence, *e.g.*, a non-cutting control sequence that does not have a target in the human genome and/or a cutting sequence that targets a non-genetic region of the human genome. For example, the library may comprise one or more of the sequences of SEQ ID NOS: 2790-2971 (Table 6C). The library of reagents may be constructed in a format compatible with use in cells, *e.g.*, primary (directly patient-derived) cancer cells. This step may involve the use of novel viral vector systems, the use of non-viral methods for reagent delivery to the cells, or the use of novel gene editing agents (*e.g.*, non-Cas9 CRISPR nucleases), or any combination thereof.

[0049] Accordingly, an exemplary method of the present disclosure may comprise one or more of the following steps: (1) Defining the full targeted pharmacologic landscape by generating a list of all targeted drugs for a disease or condition (drug library). (2) Determining the protein targets of these drugs, and the genes encoding those protein targets (genetic pharmacopeia). (3) Designing a library of gene modulatory reagents to target the genes encoding these proteins. (4) Constructing the library as well as any needed gene silencing/editing agents in a format compatible with use in cells, *e.g.*, primary cancer cells. (5) Delivering the library and any needed gene silencing/editing agents into cells, *e.g.*, primary, patient-derived cancer cells. (6) Propagating the edited cells. (7) Obtaining a readout of the effect of each perturbation, *e.g.*, by next generation sequencing (NGS)-based methods. (8) Interpreting the resulting barcode distributions to determine the effect of individual perturbations on the viability of the patient’s diseased cells. Although the methods have been exemplified with regard to personalized cancer treatment, these methods are also suitable for treatment of non-cancer based diseases or conditions.

[0050] A non-limiting exemplary generic flowchart for the identification of patient-specific tumor

therapeutic vulnerabilities utilizing function genomics described herein is shown in FIG. 2. Patient-derived samples (201), either obtained directly from the patient or after passage in mice (PDX), are dissociated (202) and infected with a gRNA library corresponding to the desired therapeutic drug collection (203). Cells are viably maintained in vitro, for instance using 3D and/or organoid approaches, allowing gRNA which target essential tumor regulators to be gradually depleted from the population (“drop-out”) (204). Next-generation sequencing is performed to identify depleted barcodes corresponding to genes depleted from the population and encoding for patient-specific drug targets (205). Oncology drugs corresponding to the patient-specific drug targets are validated in vivo (206). As represented by the schematic in FIG. 3, this approach leverages the insight that the effect of each clinically used targeted oncology drug (302) can be modeled by CRISPR-mediated mutation of the corresponding gene encoding the drug target (301).

[0051] In the present description, certain specific details are set forth in order to provide a thorough understanding of various embodiments. However, one skilled in the art will understand that the embodiments provided may be practiced without these details. Unless the context requires otherwise, throughout the description and claims which follow, the word “comprise” and variations thereof, such as, “comprises” and “comprising,” are to be construed in an open, inclusive sense, that is, as “including, but not limited to.” As used in this description and the appended claims, the singular forms “a,” “an,” and “the” include plural referents unless the context clearly dictates otherwise. It should also be noted that the term “or” includes “and/or” unless the context clearly dictates otherwise. Further, headings provided herein are for convenience only and do not interpret the scope or meaning of the claimed embodiments.

[0052] The terms “homologous,” “homology,” or “percent homology” when used herein to describe to an amino acid sequence or a nucleic acid sequence, relative to a reference sequence, can be determined using the formula described by Karlin and Altschul (Proc. Natl. Acad. Sci. USA 87: 2264-2268, 1990, modified as in Proc. Natl. Acad. Sci. USA 90:5873-5877, 1993). Such a formula is incorporated into the basic local alignment search tool (BLAST) programs of Altschul et al. (J Mol Biol. 1990 Oct 5;215(3):403-10; Nucleic Acids Res. 1997 Sep 1;25(17):3389-402). Percent homology of sequences can be determined using the most recent version of BLAST, as of the filing date of this application. Percent identity of sequences can be determined using the most recent version of BLAST, as of the filing date of this application.

Targeted Pharmacologic Landscape

[0053] In one aspect, provided herein is a pharmacologic landscape comprising a library of therapeutic agents having known protein targets, referred to as a drug library. The drug library may include low molecular weight drugs (*e.g.*, having a molecule weight less than about 1 kDa) and biologic drugs (*e.g.*, proteins such as antibodies). The drug library may comprise drugs suitable for a patient’s particular disease or condition, such as cancer or an autoimmune disease. In various embodiments, the drug library includes FDA-approved therapeutic agents and as such may be expanded as new drugs are developed. The drug library may include all or nearly all of the targeted drugs treating a particular class of disease, *e.g.*, the drug library includes at least about 50%, at least about 60%, at least about 70%, at least

about 80%, at least about 90%, or 100% of known FDA-approved drugs for a particular disease class having a known protein target. Also provided herein are focused libraries for investigational therapies (*e.g.*, those in Phase I-III clinical testing), and libraries of a particular target classes of interest (*e.g.*, G-protein coupled receptors, kinases, etc.).

[0054] *Drug Library for Cancer*

[0055] In certain embodiments, a drug library is designed comprising two or more therapies shown to be efficacious for, and/or have received FDA approval for, treating cancer. In some embodiments, the drug library comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 110, at least 120, at least 130, at least 140, at least 150, at least 160, at least 170, at least 180, at least 190, at least 200, at least 210, at least 220, at least 230, at least 240, at least 250, at least 260, at least 270, at least 280, at least 290, or at least 300 therapeutic agents. In some embodiments, the drug library comprises up to about 100, up to about 200, up to about 300, up to about 400, up to about 500, or up to about 1000 therapeutic agents. One or more of the therapeutic agents may be selected from Table 2. One or more of the therapeutic agents may be selected from Table 3.

[0056] In certain embodiments, a drug library is designed comprising two or more cancer therapeutics specific for a certain type of cancer. As non-limiting examples, the drug library comprises two or more cancer therapeutics shown to be efficacious for, and/or have received FDA approved for, melanoma, thyroid, colorectal, endometrial, lung, pancreatic, breast, genitourinary, gastrointestinal, ovarian, or head and neck cancer, or any cancer listed herein or known in the art. In some embodiments, the cancer-specific drug library comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, or at least 10 therapeutic agents. In some embodiments, the cancer-specific drug library comprises up to about 10, 20, 30, 40, 50, 60, 70, 80, 90, or 100 therapeutic agents. One or more of the therapeutic agents may be selected from Table 2. One or more of the therapeutic agents may be selected from Table 3.

[0057] In certain embodiments, the drug library comprises at least one cancer therapeutic agent chosen from Table 2. The drug library may include at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 120, at least 140, at least 160, at least 180, at least 200, at least 250, at least 300, at least 350, at least 400, at least 450, at least 500, at least 600, at least 700, at least 800, or at least 900 therapeutic agents chosen from Table 2. The drug library may comprise the at least one cancer therapeutic agent chosen from Table 2, and one or more additional FDA-approved therapeutic agent(s) for cancer. The drug library may comprise at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or 100% of known FDA-approved molecularly targeted cancer drugs. The drug library may comprise the at least one

cancer therapeutic agent chosen from Table 2, and one or more additional therapeutic agent(s) for cancer that is undergoing FDA-approval and/or is the subject of any current or completed clinical trial.

[0058] In certain embodiments, the drug library comprises at least one cancer therapeutic agent chosen from Table 3. The drug library may include at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 60, at least 70, at least 80, at least 90, at least 100, at least 120, at least 140, at least 160, at least 180, at least 200, at least 250, at least 300, at least 350, at least 400, at least 450, at least 500, at least 600, at least 700, at least 800, or at least 900 therapeutic agents chosen from Table 3. The drug library may comprise the at least one cancer therapeutic agent chosen from Table 3, and one or more additional FDA-approved therapeutic agent(s) for cancer. The drug library may comprise at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or 100% of known FDA-approved molecularly targeted cancer drugs. The drug library may comprise the at least one cancer therapeutic agent chosen from Table 3, and one or more additional therapeutic agent(s) for cancer that is undergoing FDA-approval and/or is the subject of any current or completed clinical trial.

[0059] Gene Target Libraries

[0060] Further provided herein is a library of genetic targets comprising the genes encoding the proteins targeted by the therapeutic agents in the drug library. For therapeutic agents that are non-specific inhibitors, such as multi-kinase inhibitors, the targets may include multiple gene targets. The number of targeted genes must be significantly smaller than the “whole genome,” generating a compact library amenable to both *in vitro* and *in vivo* analysis. Non-limiting examples of targeted genes are shown in Table 4. Non-limiting examples of targeted genes for oncology are shown in Tables 5A-6B, 6D. The targeted genes described herein may comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 110, at least 120, at least 130, at least 140, at least 150, at least 160, at least 170, at least 180, at least 190, at least 200, at least 210, at least 220, at least 230, at least 240, at least 250, at least 260, at least 270, at least 280, at least 290, or at least 300 genes from Table 5A. The targeted genes described herein may comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 110, at least 120, at least 130, at least 140, at least 150, at least 160, at least 170, at least 180, at least 190, at least 200, at least 210, at least 220, at least 230, at least 240, at least 250, at least 260, at least 270, at least 280, at least 290, or at least 300 genes from Table 5B. The targeted genes described herein may comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at

least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 110, at least 120, at least 130, at least 140, at least 150, at least 160, at least 170, at least 180, at least 190, at least 200, at least 210, at least 220, at least 230, at least 240, at least 250, at least 260, at least 270, at least 280, at least 290, or at least 300 genes from Table 5C. The targeted genes described herein may comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, or all of the genes from Table 5D. The targeted genes described herein may comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 110, at least 120, at least 130, at least 140, at least 150, at least 160, at least 170, at least 180, at least 190, at least 200, at least 210, at least 220, at least 230, at least 240, at least 250, at least 260, at least 270, at least 280, at least 290, or at least 300 genes from Table 6A. The targeted genes described herein may comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, at least 95, at least 100, at least 110, at least 120, at least 130, at least 140, at least 150, at least 160, at least 170, at least 180, at least 190, at least 200, at least 210, at least 220, at least 230, at least 240, at least 250, at least 260, at least 270, at least 280, at least 290, or at least 300 genes from Table 6B. The targeted genes described herein may comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, or all of the genes from Table 6D. In some embodiments, the library comprises one or more genes to validate successful gene editing. A non-limiting example utilized in experiments described herein is the B2M gene.

[0061] A non-limiting exemplary gene target library was constructed as further described in the examples and characterized in FIG. 4 as targeting 316 unique genes. The genes targeted by the library include those listed in Table 5C. Accordingly, provided herein is a library targeting one or more of the genes of Table 5C, e.g., at least about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 20, 25, 30, 35, 40, 45, 50, 60, 70, 80, 90, 100, 120, 140, 160, 180, 200, 220, 240, 260, 280, 300, 310, or all of the genes of Table 5C.

[0062] Another non-limiting exemplary gene target library was constructed that targets 23 unique genes, as further described in the examples. The genes targeted by the library include those listed in Table

5D and B2M. Accordingly, provided herein is a library targeting one or more of the genes of Table 5D, e.g., at least about 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, or all of the genes of Table 5D. In some cases the gene target library comprises a gene for validation purposes, such as B2M.

Genetic Pharmacopeia

[0063] In one aspect, provided herein is a library of genetic elements which represent a collection of existing drugs for a particular disease or condition. These genetic elements are capable of modifying a patient's cells to mimic the effect of the existing drugs on the patient, allowing for personalized comprehensive functional profiling. The profiling may be performed in a pooled screening format to allow for screening of the effects of the modifications in parallel. Such highly parallel functional genomics methodology is utilized in preclinical biology, but has not been applicable to personalized therapeutic sensitivity profiling. Additionally, this approach enables comprehensive assessment of the impact of therapeutic manipulations in an *in vivo* testing paradigm, of critical importance for the reasons previously indicated herein.

[0064] Accordingly, disclosed herein are methods for the design, construction, and use of a genetic pharmacopeia comprising a plurality of gene modulatory reagents capable of modifying a patient's cells to knock out, or knock down, function of genes encoding for protein targets of a collection of existing drugs. In some embodiments, a genetic pharmacopeia is designed using publicly available tools, e.g., publicly available methods and reagents for gene editing or gene silencing. In some embodiments, a subset of these reagents will work poorly, most will be acceptable, and a minority will demonstrate exceptional performance. Pre-selection of reagents that have been validated to work well will be advantageous both with regard to efficiency of delivery and production of a more "compact" library, both of which reduce the number of patient-derived cells needed and increase the quality of data produced. In some embodiments, the design includes selection of the most efficacious or advantageous modulatory mechanism (e.g., CRISPR, RNAi). For CRISPR-based methods, the design comprises selection of the most advantageous RNA-guided endonuclease (e.g., Cas9 vs. Cas12a vs. Cas13a). The design may also include selection of the most efficacious guide or seed sequences. The design may also include multiple gene modulatory reagents expressed from a single vector as a single or multiple transcriptional units. For instance, multiplexed gRNAs may be constructed for use with a Cas12 based nuclease (e.g., Cpf1) to generate a highly compact library. The design may also include elements in the library that allow for the identification, selection, or enrichment of transduced cells (e.g., fluorescent markers, antibiotic resistance cassettes, surface epitope expression cassettes).

[0065] The genetic pharmacopeia may be constructed in a format that is compatible with use in patient derived cells, e.g., primary cancer cells. In some embodiments, a viral delivery method is chosen for introduction of the gene modulatory reagent (e.g., guide or seed sequence). Non-limiting examples of viruses include lentivirus, adenovirus, adeno-associated virus, and other viruses disclosed herein. In some embodiments, a non-viral delivery method is selected. As a non-limiting example, the delivery method is transposase-mediated transposition. The library may be constructed using a combination of gene synthesis

and pooled molecular cloning techniques. The library may be subject to quality control analysis to ensure full and approximately equal representation of the desired sequences. In some embodiments of a viral delivery method, pooled high-titer virus is prepared. In other embodiments, the virus is delivered in an array to facilitate an arrayed screening format.

[0066] *Library of Gene Modulatory Reagents*

[0067] In one aspect, provided herein are libraries comprising a plurality of gene modulatory reagents, each gene modulatory reagent capable of knocking down or knocking out the function of a gene that encodes a protein target from a library of protein targets. The plurality of gene modulatory reagents may be capable of knocking down or knocking out the function of at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, or at least about 95% of the genes that encode for the protein targets in the library. In some cases, the library of protein targets comprises all known proteins targeted by known drugs capable of treating a particular disease or condition. An exemplary disease or condition is cancer, *e.g.*, a cancer disclosed herein or otherwise known in the art.

[0068] In some embodiments, the library of gene modulatory reagents is capable of knocking down or knocking out the function of one or more genes encoding protein targets selected from Table 5B. In some cases, the protein targets comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5B. In some embodiments, the library of gene modulatory reagents is capable of knocking down or knocking out the function of one or more genes encoding protein targets selected from Table 5A. In some cases, the protein targets comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5A. In some embodiments, the library of gene modulatory reagents is capable of knocking down or knocking out the function of one or more genes encoding protein targets selected from Table 5C. In some cases, the protein targets comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5C. In some embodiments, the library of gene modulatory reagents is capable of knocking down or knocking out the function of one or more genes encoding protein targets selected from Table 5D. In some cases, the protein targets comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5D. In some cases, the library of gene modulatory reagents is capable of knocking down or knocking out the function of one or more genes encoding for protein targets of one or more known drugs selected from Table 2-3. In some cases, the one or more known drugs comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 drugs of Table 2-3. In some cases, the library of gene modulatory reagents is capable of knocking down or knocking out the function of one or more genes encoding for protein targets of one or more known drugs selected from Table 2. In some cases, the one or more known drugs comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 drugs of Table 2. The plurality of gene modulatory reagents may be capable of knocking down or knocking out the function of about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, about 50 to about 2,000, or about 100 to about 2,000 genes. The library may comprise about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about

500, from about 50 to about 200, about 50 to about 2,000, or about 100 to about 2,000 gene modulatory reagents.

[0069] At least one of the gene modulatory reagents may be capable of knocking out the function of a gene. For instance, the at least one gene modulatory reagent is part of a CRISPR-based gene editing system. In some cases, one or more of the plurality of gene modulatory reagents each comprise a gRNA sequence comprising at least about 90% homology or identity to a sequence selected from SEQ ID NOS: 1-2789, 2980-3071. In some cases, one or more of the plurality of gene modulatory reagents each comprise a gRNA sequence comprising at least about 90% homology or identity to a sequence selected from SEQ ID NOS: 1526-2789. In some cases, one or more of the plurality of gene modulatory reagents each comprise a gRNA sequence comprising at least about 90% homology or identity to a sequence selected from SEQ ID NOS: 2980-3071. In some cases, at least one of the gene modulatory reagents comprise a gRNA sequence having homology to at least a portion of the gene whose function is knocked out by the gene modulatory reagent. In some embodiments, the gene modulatory reagents comprise one or more control sequences. As a non-limiting example, the sequence is a gRNA control that does not have a target in the human genome. As another non-limiting example, the sequence is a gRNA control that targets a non-genetic region of the human genome. For instance, the library may comprise one or more of the sequences of SEQ ID NOS: 2790-2971 (Table 6C). The inclusion of targeting (*e.g.*, CTRL-hg38 of Table 6C) and non-targeting (*e.g.*, CTRL-non sequences of Table 6C) control gRNAs enables an estimate of the impact of dsDNA breaks in innocuous genome locations. In some embodiments, the gene modulatory reagents comprise a gRNA that targets a gene for validation of successful gene editing. For instance, as described in the examples and FIG. 7, gRNAs may be included that target the cell surface marker B2M at 6.25% of all gRNAs in the focused library (SEQ ID NOS: 2960-3071 and 2890-2905), enabling the validation of successful CRISPR editing in the population by flow cytometry.

[0070] At least one of the gene modulatory reagents may be capable of knocking down the function of a gene. For instance, the at least one gene modulatory reagent comprises an shRNA sequence having homology to at least a portion of the gene whose function is knocked down by the gene modulatory reagent. The homology may be at least about 90% sequence homology or identity. The at least a portion may be at least about 15 contiguous nucleotides.

[0071] Non-limiting exemplary libraries of gene modulatory reagents were prepared and characterized (FIG. 4). One library was constructed for CRISPR-based gene editing, targeting 316 unique genes, with 4 guide RNAs per target. The guide RNAs utilized are listed in Table 6B. The library also included the control guide RNAs of Table 6C. Another library of gene modulatory reagents was constructed for CRISPR-based gene editing, targeting 23 unique genes, with 4 guide RNAs per target. The guide RNAs utilized in the later library are listed in Table 6D. The library also included guide RNAs of Table 6C having SEQ ID NOS: 2890-2905 and 2960-2979. This later library has a smaller size, which enables screening to be performed with smaller cell numbers, such as with primary cancer cells.

[0072] In some embodiments, a library of gene modulatory reagents comprises one or more gene modulatory reagents that target a gene of Table 5D. In some embodiments, the library comprises one or

more gene modulatory reagents that target at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, or all of the gene targets of Table 5D. In some embodiments, the library comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 11, at least 12, at least 13, at least 14, at least 15, at least 16, at least 17, at least 18, at least 19, at least 20, at least 21, at least 22, at least 23, at least 24, at least 25, at least 30, at least 35, at least 40, at least 45, at least 50, at least 55, at least 60, at least 65, at least 70, at least 75, at least 80, at least 85, at least 90, or all of the gRNA of Table 6D.

[0073] In some embodiments, one or more of the gene modulatory reagents is designed to knock out or knock down the function of a positive control gene, such as a core essential gene for the cell. Such reagents may serve as a positive control for library functionality. In some embodiments, one or more of the gene modulatory reagents is designed to knock out or knock down the function of a non-targeting gene and/or a targeting and non-genic gene. Such gene modulatory reagents may serve as negative controls. Non-limiting control gene modulatory reagents are provided in Table 6C.

[0074] In some embodiments, one or more of the gene modulatory reagents is positioned within a vector. The vector may comprise an adapter sequence. The adapter sequence may comprise a type IIS restriction enzyme cleavage site, which may allow for GoldenGate assembly cloning. The adapter sequence may comprise homology arms compatible with a destination vector allowing for cloning by overhang homology based methods, such as Gibson assembly. The vector may also comprise genetic elements of a virus. Non-limiting examples of viruses include adenovirus, retrovirus, adeno-associated virus (AAV), pox virus, parvovirus, baculovirus, measles virus, herpes simplex virus (HSV), Moloney Murine Leukemia Virus (MoMLV, MMLV, MuLV, or MLV), Murine Stem cell Virus (MSCV), and human immunodeficiency virus (HIV). The vector may also comprise a sequence encoding a marker, an antibiotic resistance cassette, or surface epitope expression cassette, or a combination thereof. The marker may be a fluorescent marker.

[0075] CRISPR

[0076] In one aspect, provided is a library comprising a plurality of gene modulatory reagents, wherein each modulatory reagent comprises a guide RNA (gRNA) homologous to a target gene. The target gene may encode for a protein targeted by a known therapeutic agent (*e.g.*, a therapeutic agent from Tables 2-3). Non-limiting examples of target genes are listed in Tables 4-6B, 6D. In some embodiments, one or more of the gRNAs comprise a sequence at least about 85%, 90%, 95%, or 100% homologous to at least about 10, 15, or 20 contiguous nucleobases of a target gene. In some embodiments, one or more of the gRNAs comprise a sequence at least about 85%, 90%, 95%, or 100% homologous to at least about 10, 15, or 20 contiguous nucleobases of a target gene chosen from Tables 4-6B, 6D. In some embodiments, the library comprises one or a plurality of sequences selected from SEQ ID NOS: 1-2789, 2980-3071. In some embodiments, the library comprises one or a plurality of sequences having at least about 85%, 90%, 95%, or 100% homology to a sequence selected from SEQ ID NOS: 1-2789, 2980-3071. In some embodiments, the library comprises one or a plurality of sequences selected from SEQ ID NOS: 1526-

2789. In some embodiments, the library comprises one or a plurality of sequences having at least about 85%, 90%, 95%, or 100% homology to a sequence selected from SEQ ID NOS: 1526-2789. In some embodiments, the library comprises one or a plurality of sequences selected from SEQ ID NOS: 2790-2959. In some embodiments, the library comprises one or a plurality of sequences having at least about 85%, 90%, 95%, or 100% homology to a sequence selected from SEQ ID NOS: 2790-2959. In some embodiments, the library comprises one or a plurality of sequences selected from SEQ ID NOS: 1526-2790. In some embodiments, the library comprises one or a plurality of sequences having at least about 85%, 90%, 95%, or 100% homology to a sequence selected from SEQ ID NOS: 1526-2790. In some embodiments, the library comprises one or a plurality of sequences selected from SEQ ID NOS: 2980-3071. In some embodiments, the library comprises one or a plurality of sequences having at least about 85%, 90%, 95%, or 100% homology to a sequence selected from SEQ ID NOS: 2980-3071. The library may comprise from about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, from about 50 to about 2,000, from about 100 to about 2,000, from about 200 to about 2,000, or from about 500 to about 2,000 different gRNA sequences. In some embodiments, one or more of the gRNA sequences is encoded on a vector.

[0077] In some embodiments, the library further comprises an RNA-guided endonuclease such as Cas9, Cas12, Cas12a (or Cpf1 or Mad7), Cas12b (or C2c1 or Cpf2), Cas12c (C2c3), Cas12d (or CasY), Cas12e (or CasX), Cas13, Cas13a (or C2c2), Cas13b (or C2c6), Cas13c (or C2c7), Cas13d (or Casrx), Cas14, Cas14a, Cas14b, Cas14c, Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas5e (CasD), Cas6, Cas6e, Cas6f, Cas7, Cas8a, Cas8a1, Cas8a2, Cas8b, Cas8c, Csn1, Csx12, Cas10, Cas10d, Cas1O, Cas1Od, CasF, CasG, CasH, Csy1, Csy2, Csy3, Cse1 (CasA), Cse2 (CasB), Cse3 (CasE), Cse4 (CasC), Cse1, Cse2, Cas5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Csb1, Csb2, Csb3, Csx17, Csx14, Csx1O, Csx16, CsaX, Csx3, Csx1, Csx15, Csf1, Csf2, Csf3, Csf4, or Cul966, or derivative thereof, variant thereof, fragment thereof, or any combination thereof. In some embodiments, the endonuclease is of the Cas9 or Cas12a family, which may include, but is not limited to, *S. pyogenes* Cas9 (SpCas9), SpCas9 D1135E variant, SpCas9 VRER variant, SpCas9 EQR variant, xCas9, SpCas9-NG, *S. aureus* Cas9 (SaCas9), *Acidaminococcus sp.* (AsCpf1), *Lachnospiraceae bacterium* (LbCpf1), AsCpf1 RR variant, LbCpf1 RR variant, AsCpf1 RVR variant, *C. jejuni* Cas9 (CjCas9), *N. meningitidis* (NmCas9), *S. thermophilus* (StCas9), *T. denticola* (TdCas9), and Mad7. Additionally, other RNA-guided endonucleases that are suitable for the library disclosed herein include zinc finger nucleases (ZFN), transcription activator-like effector nucleases (TALEN), meganucleases, RNA-binding proteins (RBP), recombinases, flippases, transposases, Argonaute (Ago) proteins (*e.g.*, prokaryotic Argonaute (pAgo), archaeal Argonaute (aAgo), and eukaryotic Argonaute (eAgo)), and any functional fragment thereof, and any combination thereof.

[0078] In some cases, the gRNA and/or endonuclease is encoded on a vector. In some cases, a vector comprising gRNA and/or endonuclease comprises one or more features of a viral genome. As a non-limiting example, the viral vector includes retroviral vector, adenoviral vector, adeno-associated viral

vector (AAV), pox vectors, parvoviral vectors, baculovirus vectors, measles viral vectors, or herpes simplex virus vector (HSV). In some instances, the retroviral vector includes gamma-retroviral vector, such as a vector derived from the Moloney Murine Leukemia Virus (MoMLV, MMLV, MuLV, or MLV) or the Murine Stem cell Virus (MSCV) genome. In some instances, the retroviral vector comprises lentiviral vectors such as those derived from the human immunodeficiency virus (HIV) genome. In some instances, AAV vector comprises AAV1, AAV2, AAV4, AAV5, AAV6, AAV7, AAV8, or AAV9 serotype. In some instances, the viral vector is a chimeric viral vector, comprising viral portions from two or more viruses. In additional instances, the viral vector is a recombinant viral vector.

[0079] In some embodiments, the vector comprises a marker for selection, *e.g.*, an antibiotic resistance cassette or surface epitope expression cassette. In some embodiments, the gene modulatory reagent and endonuclease are encoded by separate vectors. As a non-limiting example, the endonuclease is delivered via adenovirus, while the gRNA is delivered by lentivirus. In some embodiments, the endonuclease coding sequence may be split between two vectors. For instance, this method may be employed when constructing large endonucleases such as Cas9. In some embodiments, the gene modulatory reagent is encoded by a viral vector and the endonuclease is provided as a ribonuclear protein complex transfected into target cells, for instance using lipid or electroporation techniques.

[0080] RNAi

[0081] In one aspect, provided is a library comprising a plurality of gene modulatory reagents, wherein one or more of the modulatory reagents comprise a short hairpin RNA (shRNA) complementary to a target mRNA of a protein targeted by a known therapeutic agent (*e.g.*, a therapeutic agent chosen from Tables 2-3). Non-limiting examples of target proteins include those encoded by the genes listed in Tables 4-6B, 6D. In some embodiments, one or more of the shRNA each comprise a sequence at least about 85%, 90%, 95%, or 100% complementary to at least about 10, 15, or 20 contiguous nucleobases of a target mRNA. In some embodiments, one or more of the shRNA each comprise a sequence at least about 85%, 90%, 95%, or 100% complementary to at least about 10, 15, or 20 contiguous nucleobases of a target mRNA encoding for a protein selected from Tables 4-6B, 6D. The library may comprise from about 10 to about 2,000, from about 50 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, from about 50 to about 2,000, from about 100 to about 2,000, or from about 500 to about 2,000 different shRNA sequences.

Genetic Modification and Cell Propagation

[0082] In some aspects of the disclosure, a library comprising a plurality of gene modulatory reagents is delivered to a sample of cells from a subject having a disease or condition to generate a plurality of modified cells. In exemplary embodiments, the subject has cancer and the sample of cells comprise primary cancer cells. For some embodiments involving cancer cells, tumor samples are processed in a manner that preserves cancer cell viability, while maximizing cellular yield. Non-limiting examples of delivery methods include viral methods (*e.g.*, lentivirus, adenovirus, or adeno-associated virus) as well as non-viral methods (*e.g.*, transposase-mediated transposition employing transposons such

as piggybac or sleeping beauty, or integrases such as phi31). In some embodiments, delivery of viral particles to the cells is performed in a manner that ensures equal and adequate representation of clones, while minimizing multiplicity of infection. In particular, the number of times each clone is presented within the population (“representation”) may be a crucial factor which determines the power of the eventual analysis to sensitively and specifically detect changes in barcode abundance following *in vitro* or in *in vivo* propagation.

[0083] *Methods of Genetic Modification*

[0084] An exemplary method for generating a plurality of modified cancer cells from a subject comprises: delivering a library of gene modulatory reagents to a sample of cancer cells from the subject to generate the plurality of modified cancer cells, wherein each modified cancer cell harbors one or more of the gene modulatory reagents, and each gene modulatory reagent is capable of knocking down or knocking out the function of a gene that encodes a protein target from a library of protein targets.

[0085] In some embodiments, the method for generating the plurality of modified cancer cells comprises a CRISPR/endonuclease-based gene editing system. For instance, one or more of the gene modulatory reagents comprises a gRNA sequence comprising homology to at least a portion of the gene whose function is knocked out in the modified cancer cell. The gRNA may comprise homology to about 10 to about 50 contiguous nucleotides of the gene. The homology may be at least about 90% sequence homology or identity. In some embodiments, one or more of the gene modulatory reagents each comprise a gRNA sequence comprising at least about 90% homology or identity to a sequence selected from SEQ ID NOS: 1-2789, 2980-3071. In some embodiments, one or more of the gene modulatory reagents each comprise a gRNA sequence comprising at least about 90% homology or identity to a sequence selected from SEQ ID NOS: 1526-2789. In some embodiments, one or more of the gene modulatory reagents each comprise a gRNA sequence comprising at least about 90% homology or identity to a sequence selected from SEQ ID NOS: 2790-2959. In some embodiments, one or more of the gene modulatory reagents each comprise a gRNA sequence comprising at least about 90% homology or identity to a sequence selected from SEQ ID NOS: 2980-3071. The gRNA may be positioned within a vector, *e.g.*, for viral delivery as discussed herein.

[0086] The method for generating modified cancer cells may further comprise contacting the cancer cells with an endonuclease. The endonuclease may comprise a Cas9 or Cas12a endonuclease. Non-limiting examples of Cas9 or Cas12a endonucleases include *S. pyogenes* Cas9 (SpCas9), SpCas9 D1135E variant, SpCas9 VRER variant, SpCas9 EQR variant, xCas9, SpCas9-NG, *S. aureus* Cas9 (SaCas9), *Acidaminococcus sp.* (AsCpf1), *Lachnospiraceae bacterium* (LbCpf1), AsCpf1 RR variant, LbCpf1 RR variant, AsCpf1 RVR variant, *C. jejuni* Cas9 (CjCas9), *N. meningitidis* (NmCas9), *S. thermophilus* (StCas9), *T. denticola* (TdCas9), and Mad7. In some cases, the endonuclease does not comprise a Cas9 or Cas12a endonuclease.

[0087] In some embodiments, the method for generating the plurality of modified cancer cells comprises an RNA interference (RNAi) gene silencing system. For instance, each gene modulatory reagent comprises a shRNA sequence targeting mRNA encoding for a protein target from the library of

protein targets. The shRNA may have homology to about 10 to about 50 contiguous nucleotides of the gene. The homology may be at least about 90% sequence homology or identity. The shRNA may be positioned within a vector, *e.g.*, for viral delivery as discussed herein.

[0088] In some embodiments, the library of gene modulatory reagents comprises from about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, from about 50 to about 2,000, from about 100 to about 2,000, or from about 500 to about 2,000 different gene modulatory reagents. In some cases, at least about 90% of the gene modulatory reagents are present in the library in a quantity within about 10% of the average gene modulatory reagent quantity.

[0089] In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5B. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5A. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5C. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5D.

[0090] In some embodiments, the sample of cancer cells comprises primary cancer cells. The sample of cancer cells may comprise about 10^5 to about 10^8 cells. The sample of cancer cells may have been processed to preserve cell viability. The method may thus further comprise preparing the sample of cancer cells to preserve cell viability prior to and/or after delivery of the library of gene modulatory reagents. The method may also further comprise propagating the modified cancer cells. Propagation may comprise maintenance of the modified cancer cells in a 2D *in vitro* culture. Propagation may comprise maintenance of the modified cancer cells in a 3D *in vitro* culture. Propagation may comprise maintenance of the modified cancer cells *in vivo*. In some cases, propagation occurs within an animal model, *e.g.*, in a rodent.

[0091] CRISPR Gene Editing

[0092] In some embodiments, a sample of cells is modified using a CRISPR-based gene editing method. The gene editing method may comprise contacting the sample of cells with a plurality of gRNA sequences, wherein one or more of the gRNAs have sequence homology to a target gene encoding a protein targeted by a therapeutic agent. Non-limiting examples of target genes are provided in Tables 4-6B, 6D. Non-limiting examples of therapeutic agents are provided in Tables 2-3. In some embodiments, the sample of cells is contacted with at least one or a plurality of gRNA sequences chosen from SEQ ID NOS: 1-2789, 2980-3071. In some embodiments, the sample of cells is contacted with at least one or a plurality of gRNA sequences, each having at least about 85% homology to a sequence chosen from SEQ ID NOS: 1-2789, 2980-3071. In some embodiments, the sample of cells is contacted with at least one or a plurality of gRNA sequences chosen from SEQ ID NOS: 2980-3071. In some embodiments, the sample of cells is contacted with at least one or a plurality of gRNA sequences, each having at least about 85% homology to a sequence chosen from SEQ ID NOS: 2980-3071. In some embodiments, the sample of cells is contacted with at least one or a plurality of gRNA sequences chosen from SEQ ID NOS: 1526-

2789. In some embodiments, the sample of cells is contacted with at least one or a plurality of gRNA sequences, each having at least about 85% homology to a sequence chosen from SEQ ID NOS: 1526-2789. In some embodiments, the sample of cells is contacted with at least one or a plurality of gRNA sequences chosen from SEQ ID NOS: 1526-2959. In some embodiments, the sample of cells is contacted with at least one or a plurality of gRNA sequences, each having at least about 85% homology to a sequence chosen from SEQ ID NOS: 1526-2959. In some embodiments, the sample of cells is contacted with at least one or a plurality of gRNA sequences chosen from SEQ ID NOS: 2790-2959. In some embodiments, the sample of cells is contacted with at least one or a plurality of gRNA sequences, each having at least about 85% homology to a sequence chosen from SEQ ID NOS: 2790-2959. The sample of cells is also contacted with an RNA-guided endonuclease, *e.g.*, Cas9, Cas12, Cas12a (or Cpf1 or Mad7), Cas12b (or C2c1 or Cpf2), Cas12c (C2c3), Cas12d (or CasY), Cas12e (or CasX), Cas13, Cas13a (or C2c2), Cas13b (or C2c6), Cas13c (or C2c7), Cas13d (or Casrx), Cas14, Cas14a, Cas14b, Cas14c, Cas1, Cas1B, Cas2, Cas3, Cas4, Cas5, Cas5e (CasD), Cas6, Cas6e, Cas6f, Cas7, Cas8a, Cas8a1, Cas8a2, Cas8b, Cas8c, Csn1, Csx12, Cas10, Cas10d, Cas1O, Cas1Od, CasF, CasG, CasH, Csy1, Csy2, Csy3, Cse1 (CasA), Cse2 (CasB), Cse3 (CasE), Cse4 (CasC), Csc1, Csc2, Csa5, Csn2, Csm2, Csm3, Csm4, Csm5, Csm6, Cmr1, Cmr3, Cmr4, Cmr5, Cmr6, Csb1, Csb2, Csb3, Csx17, Csx14, Csx1O, Csx16, CsaX, Csx3, Csx1, Csx15, Csf1, Csf2, Csf3, Csf4, Cul966, zinc finger nucleases (ZFN), transcription activator-like effector nucleases (TALEN), meganucleases, RNA-binding proteins (RBP), recombinases, flippases, transposases, Argonaute (Ago) proteins (*e.g.*, prokaryotic Argonaute (pAgo), archaeal Argonaute (aAgo), or eukaryotic Argonaute (eAgo)), or derivative thereof, variant thereof, fragment thereof, or combination thereof.

[0093] RNAi

[0094] In some embodiments, a sample of cells is modified using an RNAi method. In some embodiments, the sample of cells is contacted with a plurality of shRNA sequences, each shRNA sequence complementary to a target mRNA of a protein targeted by a therapeutic agent. Non-limiting examples of target proteins include those encoded by the genes listed in Tables 4-6B, 6D. Non-limiting examples of therapeutic agents are provided in Tables 2-3.

[0095] Compilation of Modified Cancer Cells

[0096] Further provided herein are compilations of modified cancer cells. An exemplary compilation comprises a plurality of modified cancer cells, wherein each modified cancer cell harbors one or more gene modulatory reagents, and each gene modulatory reagent is capable of knocking down or knocking out the function of a gene that encodes a protein target from a library of protein targets. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5B. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5C. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5D. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5A. In some embodiments, the library of protein targets comprises at least 1, at

least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 3. In some embodiments, the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 4. In some embodiments, the modified cancer cells are modified primary cancer cells. The modified cancer cells may comprise from about 10 to about 2,000, from about 50 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, from about 100 to about 2,000, or from about 500 to about 2,000 different populations of modified cancer cells.

[0097] The modified cancer cells may comprise from about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, from about 50 to about 2,000, from about 100 to about 2,000, or from about 500 to about 2,000 different gene modulatory reagents. At least one of the one or more gene modulatory reagents may comprise a sequence selected from SEQ ID NOS: 1-2789, 2980-3071. At least one of the one or more of gene modulatory reagents may comprise a sequence at least about 90% homologous or identical to a sequence selected from SEQ ID NOS: 1-2789, 2980-3071. At least one of the one or more gene modulatory reagents may comprise a sequence selected from SEQ ID NOS: 2980-3071. At least one of the one or more of gene modulatory reagents may comprise a sequence at least about 90% homologous or identical to a sequence selected from SEQ ID NOS: 2980-3071. At least one of the one or more gene modulatory reagents may comprise a sequence selected from SEQ ID NOS: 1526-2789. At least one of the one or more of gene modulatory reagents may comprise a sequence at least about 90% homologous or identical to a sequence selected from SEQ ID NOS: 1526-2789. At least one of the one or more gene modulatory reagents may comprise a sequence selected from SEQ ID NOS: 1526-2959. At least one of the one or more of gene modulatory reagents may comprise a sequence at least about 90% homologous or identical to a sequence selected from SEQ ID NOS: 1526-2959. At least one of the one or more gene modulatory reagents may comprise a sequence selected from SEQ ID NOS: 2790-2959. At least one of the one or more of gene modulatory reagents may comprise a sequence at least about 90% homologous or identical to a sequence selected from SEQ ID NOS: 2790-2959.

[0098] The modified cancer cells may have been modified by gene editing using a CRISPR-based method. As such, the gene modulatory reagents harbored by the modified cancer cells may comprise a gRNA sequence comprising homology to at least a portion of the gene whose function is knocked down or knocked out in the modified cancer cell. In some cases, the gRNA comprises homology to about 10 to about 50 contiguous nucleotides of the gene. The homology may be at least about 90% sequence homology or identity. The shRNA may be positioned within a vector, *e.g.*, for viral delivery as discussed herein.

[0099] The modified cancer cells may also comprise an endonuclease, for instance, where the cells are modified using a gene editing system such as CRISPR. The endonuclease may comprise a Cas9 or Cas12a endonuclease. Non-limiting examples of Cas9 or Cas12a endonuclease include *S. pyogenes* Cas9 (SpCas9), SpCas9 D1135E variant, SpCas9 VRER variant, SpCas9 EQR variant, xCas9, SpCas9-NG, *S. aureus* Cas9 (SaCas9), *Acidaminococcus* sp. (AsCpf1), *Lachnospiraceae* bacterium (LbCpf1), AsCpf1

RR variant, LbCpf1 RR variant, AsCpf1 RVR variant, *C. jejuni* Cas9 (CjCas9), *N. meningitidis* (NmCas9), *S. thermophilus* (StCas9), *T. denticola* (TdCas9), and Mad7. The endonuclease may not comprise a Cas9 or Cas12a endonuclease.

[00100] The modified cancer cells may have been modified by gene silencing using shRNA gene modulatory reagents. Therefore, one or more of the gene modulatory reagents may comprise an shRNA sequence comprising homology to at least a portion of the gene whose function is knocked down in the modified cancer cell. The shRNA may comprise homology to about 10 to about 50 contiguous nucleotides of the gene. The homology may be at least about 90% sequence homology or identity. The shRNA may be positioned within a vector, *e.g.*, for viral delivery as discussed herein.

[00101] Cell propagation

[00102] In one aspect, provided herein are methods of propagating the plurality of genetically modified cells. For example, the genetically modified cells are modified using a CRISPR gene editing system or RNAi as described herein. The cells may be modified from primary cancer cells. In some embodiments, the plurality of modified cells is propagated in 2D format *in vitro*, 3D format *in vitro*, or *in vivo*. Non-limiting examples of the 3D *in vitro* format could include propagating cells embedded in sponge matrices (*e.g.*, collagen-based), scaffolds, extracellular matrix (ECM) conditions such as basement membrane extract or Matrigel, in suspension, in organoid culture, or in microfluidic platforms. Exemplary materials constituting 3D *in vitro* format for cell propagation include collagen, gelatin, elastin, fibronectin, laminin, vitronectin, poly-lysine, poly-L-ornithine, silicone, polysaccharide polymers such as alginate, agar, dextran, carrageenan, chitosan, pectin, cellulose, gellan gum, xanthan gum, pullulan, glycosaminoglycan and any fragmented or derivative forms, hyaluronic acid, heparan, heparin, dermatan, chondroitin, or any hydrogel or biocompatible polymer. For *in vitro* approaches with cancer cells, the cancer cells are maintained under conditions that both support bulk cell survival while allowing selective pressure from induced mutations. For *in vivo* approaches, a propagation technique is selected which maximizes engraftment efficiency and survival. In some embodiments, *in vivo* cell propagation can include patient derived xenograft via either heterotopic implantation or orthotopic implantation. Additionally, for *in vivo* approaches, modified cancer cells may be implanted orthotopically (*e.g.*, within the pancreas, for a pancreatic-origin tumor) or ectopically (*e.g.*, subcutaneously, for a pancreatic origin tumor).

Screening Methods

[00103] In one aspect, provided are methods of evaluating a sample of cells for the presence, absence, and/or quantity of a nucleic acid sequence from the genetic pharmacopeia. The power of the genetic pharmacopeia becomes evident in the ability to read out effects on cell growth directly via ‘barcode’ counting of modified cells (*e.g.*, transduced cancer cells). Cells harboring a gRNA or shRNA impairing cell viability will be less represented in the overall population (*i.e.* will ‘dropout’); this manifests as less frequent appearance of the gRNA/shRNA sequence itself within the overall population of guide/shRNA sequences. The method may employ next-generation sequencing (NGS), which is well-established, cost effective, commercial scale, robust, highly quantitative, and highly amenable to multiplexed analysis.

[00104] Sequencing can be performed with any appropriate sequencing technology, including but not limited to, single-molecule real-time (SMRT) sequencing, Polony sequencing, sequencing by ligation, reversible terminator sequencing, proton detection sequencing, ion semiconductor sequencing, nanopore sequencing, electronic sequencing, pyrosequencing, Maxam-Gilbert sequencing, chain termination (*e.g.*, Sanger) sequencing, +S sequencing, or sequencing by synthesis. Sequencing methods also include next-generation sequencing, *e.g.*, modern sequencing technologies such as Illumina sequencing (*e.g.*, Solexa), Roche 454 sequencing, Ion torrent sequencing, and SOLiD sequencing. In some cases, next-generation sequencing involves high-throughput sequencing methods. Additional sequencing methods available to one of skill in the art may also be employed.

[00105] The resulting barcode distributions are interpreted to determine the effect of individual perturbations on the viability of a subject's cells. In some implementations, raw sequencing read counts are interpreted and remapped back into 'drug space'. For instance, in the hypothetical case described above, if a particular gRNA was found to be less prevalent than expected within the population, this would suggest that the protein encoded by the gene target of the gRNA is required for the survival or proliferation of the patient's cancer cells. As such, the drug targeting that protein (identified in step 1 above) is suggested to be a potentially higher value therapeutic for the patient.

[00106] An exemplary method of evaluating the functional effect of genetically modifying cancer cells from a subject comprises: sequencing a plurality of modified cancer cells, wherein each modified cancer cell harbors one or more gene modulatory reagents, each gene modulatory reagent capable of knocking down or knocking out the function of a gene that encodes a protein target in a library of protein targets; and wherein a gene modulatory reagent that impairs cell viability will have fewer sequence reads than a gene modulatory reagent that does not impair cell viability. The method may further comprise determining which gene modulatory reagents have fewer than a threshold number of sequence reads. The threshold number of sequence reads may be an expected number of sequence reads if the gene modulatory reagent did not impair cell viability. In some cases the threshold number of sequence reads is an average number of sequence reads for each gene modulatory reagent in the plurality of modified cancer cells. In some embodiments, the method further comprises correlating each gene modulatory reagent that has fewer than the threshold number of sequence reads to its corresponding protein target in the library of protein targets. The method may then also comprise correlating the corresponding protein target to a therapeutic molecule. The library of protein targets may comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5B. The library of protein targets may comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5C. The library of protein targets may comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5D. The library of protein targets may comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 5A. The library of protein targets may comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 3. The library of protein targets may comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Table 4. At least one of the one or more

of the gene modulatory reagents may comprise a gRNA sequence comprising at least about 90% homology or identity to a sequence selected from SEQ ID NOS: 1-2789, 2980-3071. At least one of the one or more of the gene modulatory reagents may comprise a gRNA sequence comprising at least about 90% homology or identity to a sequence selected from SEQ ID NOS: 2980-3071. At least one of the one or more of the gene modulatory reagents may comprise a gRNA sequence comprising at least about 90% homology or identity to a sequence selected from SEQ ID NOS: 1526-2789.

Methods of Treatment

[00107] Further provided herein are methods of treating a subject having a disease or condition, wherein the subject has been determined to be susceptible to a therapeutic agent using a method described herein. In some cases, the disease or condition is cancer. Non-limiting examples of cancer include acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), adrenocortical carcinoma, AIDS-related cancers, Kaposi sarcoma, AIDS-related lymphoma, primary CNS lymphoma, anal cancer, appendix cancer, astrocytomas, atypical teratoid/rhabdoid tumor, central nervous system cancers, basal cell carcinoma of the skin, bile duct cancer, bladder cancer, bone cancer, brain tumors, breast cancer, bronchial tumors, Burkitt lymphoma, carcinoid tumor, cardiac tumors, central nervous system cancers, embryonal tumors, germ cell tumor, primary CNS lymphoma, cervical cancer, cholangiocarcinoma, chordoma, chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), chronic myeloproliferative neoplasms, colorectal cancer, craniopharyngioma, cutaneous t-cell lymphoma, ductal carcinoma in situ (DCIS), embryonal tumors, central nervous system cancer, endometrial cancer, ependymoma, esophageal cancer, esthesioneuroblastoma, Ewing sarcoma, extracranial germ cell tumor, extragonadal germ cell tumor, eye cancer, intraocular melanoma, retinoblastoma, fallopian tube cancer, fibrous histiocytoma of bone, osteosarcoma, gallbladder cancer, gastric cancer, gastrointestinal carcinoid tumor, gastrointestinal stromal tumors (GIST), testicular cancer, gestational trophoblastic disease, hairy cell leukemia, head and neck cancer, heart tumors, hepatocellular cancer, Hodgkin lymphoma, hypopharyngeal cancer, intraocular melanoma, islet cell tumors, pancreatic neuroendocrine tumors, kidney cancer, Langerhans cell histiocytosis, laryngeal cancer, leukemia, lip and oral cavity cancer, liver cancer, lung cancer (non-small cell and small cell), lymphoma, male breast cancer, malignant fibrous histiocytoma of bone and osteosarcoma, melanoma, intraocular melanoma, Merkel cell carcinoma, mesothelioma, metastatic cancer, metastatic squamous neck cancer with occult primary, midline tract carcinoma with NUT gene changes, mouth cancer, multiple endocrine neoplasia syndromes, multiple myeloma/plasma cell neoplasms, mycosis fungoides, myelodysplastic syndromes, myelodysplastic/myeloproliferative neoplasms, myelogenous leukemia, chronic (CML), myeloid leukemia, acute (AML), nasal cavity and paranasal sinus cancer, nasopharyngeal cancer, neuroblastoma, non-Hodgkin lymphoma, non-small cell lung cancer, oral cancer, oropharyngeal cancer, ovarian cancer, pancreatic cancer, pancreatic neuroendocrine tumors (islet cell tumors), papillomatosis, paraganglioma, paranasal sinus and nasal cavity cancer, parathyroid cancer, penile cancer, pharyngeal cancer, pheochromocytoma, pituitary tumor, plasma cell neoplasm/multiple myeloma, pleuropulmonary blastoma, primary central nervous system (CNS) lymphoma, primary peritoneal cancer, prostate cancer, rectal

cancer, recurrent cancer, renal cell cancer, retinoblastoma, rhabdomyosarcoma, salivary gland cancer, sarcoma, rhabdomyosarcoma, vascular tumors, osteosarcoma, soft tissue sarcoma, uterine sarcoma, Sézary syndrome, skin cancer, small intestine cancer, squamous cell carcinoma of the skin, squamous neck cancer with occult primary, stomach cancer, T-cell lymphoma, testicular cancer, throat cancer, nasopharyngeal cancer, oropharyngeal cancer, hypopharyngeal cancer, thymoma and thymic carcinoma, thyroid cancer, transitional cell cancer of the renal pelvis and ureter, ureter and renal pelvis, urethral cancer, uterine cancer, endometrial, uterine sarcoma, vaginal cancer, vascular tumors, vulvar cancer, and Wilms tumor and other childhood kidney tumors. In some embodiments, the therapeutic agent is selected from Table 2A. In some embodiments, the therapeutic agent is selected from Table 2B. In some embodiments, the therapeutic agent is selected from Table 3.

[00108] A non-limiting example of a method for treating cancer in a subject comprises: administering to the subject a therapeutic molecule selected from a library of therapeutic molecules, wherein the therapeutic molecule has been selected by a method comprising: modifying cancer cells from the subject to knock down or knock out the function of a plurality of genes, each gene in the plurality of genes encoding for a protein target of a therapeutic molecule in the library of therapeutic molecules, whereby the therapeutic molecule has been selected if knocking down or knocking out the function of the gene that encodes for the protein target of the selected therapeutic molecule impairs cancer cell viability. The library of therapeutic molecules may comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 therapeutic agents of Table 2. The library of therapeutic molecules may comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 therapeutic agents of Table 3. The one or more of the plurality of genes may encode for a protein of Table 5B. The one or more of the plurality of genes may encode for a protein of Table 5A. The one or more of the plurality of genes may encode for a protein of Table 5C. The one or more of the plurality of genes may encode for a protein of Table 5D. The one or more of the plurality of genes may encode for a protein of Table 3. The one or more of the plurality of genes may encode for a protein of Table 4.

[00109] Another exemplary method for treating cancer comprises: administering to the subject a therapeutic molecule selected from a library of therapeutic molecules; wherein the cancer of the subject has been determined to be susceptible to the selected therapeutic molecule by a method comprising: (a) contacting a sample of cancer cells from the subject with a library of gene modulatory reagents to generate a plurality of modified cancer cells, wherein each modified cancer cell harbors one or more of the gene modulatory reagents, and each gene modulatory reagent is capable of knocking down or knocking out the function of a gene that encodes a protein target of a therapeutic molecule in the library of therapeutic molecules, and (b) sequencing the plurality of modified cancer cells, wherein a gene modulatory reagent that impairs cell viability will have fewer sequence reads than a gene modulatory reagent that does not impair cell viability, and the gene that is knocked down or knocked out by the gene modulatory reagent that impairs cell viability encodes for the protein targeted by the selected therapeutic molecule. In some cases, prior to sequencing, the plurality of modified cancer cells has been propagated. Propagation may comprise maintenance of the modified cancer cells in a 2D in vitro culture. Propagation

may comprise maintenance of the modified cancer cells in a 3D in vitro culture. Propagation may comprise maintenance of the modified cancer cells in vivo. Propagation may occur within an animal model, *e.g.*, where the animal is a rodent.

[00110] In some embodiments, the cancer cells contacted with the library of gene modulatory reagents are primary cancer cells. Contacting may comprise introducing the one or more gene modulatory reagents into each cancer cell by a viral or non-viral delivery method. Each of the gene modulatory reagents in the library may be encoded on a viral vector. In non-limiting embodiments, the viral vector comprises a lentiviral vector, adenoviral vector, or adeno-associated viral vector. An exemplary non-viral delivery method comprises transposase-mediated transposition.

[00111] In some embodiments, the library of therapeutic molecules comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 therapeutic agents of Table 2. In some embodiments, the library of therapeutic molecules comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 therapeutic agents of Table 3. In some embodiments, the library of gene modulatory reagents comprises from about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, from about 50 to about 2,000, from about 100 to about 2,000, or from about 500 to about 2,000 different gene modulatory reagents. In some embodiments, one or more gene modulatory reagents from the library of gene modulatory reagents comprises a nucleic acid sequence homologous to at least about 15 contiguous nucleotides of a gene encoding a protein of Table 5B. In some embodiments, one or more gene modulatory reagents from the library of gene modulatory reagents comprises a nucleic acid sequence homologous to at least about 15 contiguous nucleotides of a gene encoding a protein of Table 5C. In some embodiments, one or more gene modulatory reagents from the library of gene modulatory reagents comprises a nucleic acid sequence homologous to at least about 15 contiguous nucleotides of a gene encoding a protein of Table 5A. In some embodiments, one or more gene modulatory reagents from the library of gene modulatory reagents comprises a nucleic acid sequence homologous to at least about 15 contiguous nucleotides of a gene encoding a protein of Table 5D. In some embodiments, one or more gene modulatory reagents from the library of gene modulatory reagents comprises a nucleic acid sequence homologous to at least about 15 contiguous nucleotides of a gene encoding a protein of Table 3. In some embodiments, one or more gene modulatory reagents from the library of gene modulatory reagents comprises a nucleic acid sequence homologous to at least about 15 contiguous nucleotides of a gene encoding a protein of Table 4. The homology may be least about 90% sequence homology or identity.

[00112] In some cases, one or more of the gene modulatory reagents each comprise a gRNA sequence comprising at least about 90% homology or identity to a sequence selected from SEQ ID NOS: 1-1525. In some cases, one or more of the gene modulatory reagents each comprise a gRNA sequence comprising at least about 90% homology or identity to a sequence selected from SEQ ID NOS: 1-2789, 2980-3071. In some cases, one or more of the gene modulatory reagents each comprise a gRNA sequence comprising at least about 90% homology or identity to a sequence selected from SEQ ID NOS: 2980-3071. In some cases, one or more of the gene modulatory reagents each comprise a gRNA sequence comprising at least

about 90% homology or identity to a sequence selected from SEQ ID NOS: 1526-2789. In some cases, one or more of the gene modulatory reagents each comprise a gRNA sequence comprising at least about 90% homology or identity to a sequence selected from SEQ ID NOS: 2790-2959. In some embodiments, each gene modulatory reagent comprises a gRNA sequence comprising homology to at least a portion of the gene that encodes a protein target of a therapeutic molecule in the library of therapeutic molecules. The gRNA may comprise homology to about 10 to about 50 contiguous nucleotides of the gene. The homology may be at least about 90% sequence homology or identity. The gRNA may be positioned within a vector, *e.g.*, for viral delivery as discussed herein.

[00113] The method of determining susceptibility to the selected therapeutic molecule may further comprise contacting the cells with an endonuclease. In some embodiments, the endonuclease comprises a Cas9 or Cas12a endonuclease. Non-limiting examples of Cas9 or Cas12a endonucleases include *S. pyogenes* Cas9 (SpCas9), SpCas9 D1135E variant, SpCas9 VRER variant, SpCas9 EQR variant, xCas9, SpCas9-NG, *S. aureus* Cas9 (SaCas9), *Acidaminococcus sp.* (AsCpf1), *Lachnospiraceae bacterium* (LbCpf1), AsCpf1 RR variant, LbCpf1 RR variant, AsCpf1 RVR variant, *C. jejuni* Cas9 (CjCas9), *N. meningitidis* (NmCas9), *S. thermophilus* (StCas9), *T. denticola* (TdCas9), and Mad7. In some embodiments, the endonuclease does not comprise a Cas9 or Cas12a endonuclease.

[00114] In some embodiments, the gene modulatory reagents comprise a shRNA sequence comprising homology to at least a portion of the gene that encodes a protein target of a therapeutic molecule in the library of therapeutic molecules. The shRNA may comprise homology to about 10 to about 50 contiguous nucleotides of the gene. The homology may be at least about 90% sequence homology or identity. The shRNA may be positioned within a vector, *e.g.*, for viral delivery as discussed herein.

[00115] Further Embodiments

[00116] (1) A method of treating cancer in a subject in need thereof, the method comprising administering to the subject a therapeutic molecule selected from a library of therapeutic molecules; wherein the therapeutic molecule has been selected by a method comprising: modifying cancer cells from the subject to knock down or knock out the function of a plurality of genes, each gene in the plurality of genes encoding for a protein target of a therapeutic molecule in the library of therapeutic molecules, whereby the therapeutic molecule has been selected if knocking down or knocking out the function of the gene that encodes for the protein target of the selected therapeutic molecule impairs cancer cell viability.

[00117] (2) The method of embodiment 1, wherein the library of therapeutic molecules comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 therapeutic agents of Tables 2-3.

[00118] (3) The method of embodiment 1 or embodiment 2, wherein one or more of the plurality of genes encode for a protein of Table 3-5D.

[00119] (4) A method of treating cancer in a subject in need thereof, the method comprising administering to the subject a therapeutic molecule selected from a library of therapeutic molecules; wherein the cancer of the subject has been determined to be susceptible to the selected therapeutic molecule by a method comprising:

(a) contacting a sample of cancer cells from the subject with a library of gene modulatory reagents to generate a plurality of modified cancer cells, wherein each modified cancer cell harbors one or more of the gene modulatory reagents, and each gene modulatory reagent is capable of knocking down or knocking out the function of a gene that encodes a protein target of a therapeutic molecule in the library of therapeutic molecules, and

(b) sequencing the plurality of modified cancer cells, wherein a gene modulatory reagent that impairs cell viability will have fewer sequence reads than a gene modulatory reagent that does not impair cell viability, and the gene that is knocked down or knocked out by the gene modulatory reagent that impairs cell viability encodes for the protein targeted by the selected therapeutic molecule.

[00120] (5) The method of embodiment 4, wherein prior to sequencing, one or more of the plurality of modified cancer cells have been propagated.

[00121] (6) The method of embodiment 5, wherein propagation comprises maintenance of the modified cancer cells in a 2D *in vitro* culture.

[00122] (7) The method of embodiment 5, wherein propagation comprises maintenance of the modified cancer cells in a 3D *in vitro* culture.

[00123] (8) The method of embodiment 5, wherein propagation comprises maintenance of the modified cancer cells *in vivo*.

[00124] (9) The method of embodiment 8, wherein propagation occurs within an animal model.

[00125] (10) The method of embodiment 9, wherein the animal is a rodent.

[00126] (11) The method of any one of embodiments 4-10, wherein the cancer cells are primary cancer cells.

[00127] (12) The method of any one of embodiments 4-11, wherein contacting comprises introducing the one or more gene modulatory reagents into each cancer cell by a viral or non-viral delivery method.

[00128] (13) The method of embodiment 12, wherein one or more of the gene modulatory reagents in the library are encoded on a viral vector.

[00129] (14) The method of embodiment 13, wherein the viral vector comprises a lentiviral vector, adenoviral vector, or adeno-associated viral vector.

[00130] (15) The method of embodiment 12, wherein the non-viral delivery method comprises transposase-mediated transposition.

[00131] (16) The method of any one of embodiments 4-15, wherein the library comprises from about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, from about 50 to about 2,000, from about 100 to about 2,000, or from about 500 to about 2,000 different gene modulatory reagents.

[00132] (17) The method of any one of embodiments 4-16, wherein one or more gene modulatory reagents from the library of gene modulatory reagents comprises a nucleic acid sequence homologous to at least about 15 contiguous nucleotides of a gene encoding a protein of Tables 3-5D.

[00133] (18) The method of embodiment 17, wherein the homology is at least about 90% sequence homology.

[00134] (19) The method of embodiment 18, wherein the homology is at least about 90% sequence identity.

[00135] (20) The method of any one of embodiments 4-19, wherein the library of therapeutic molecules comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 therapeutic agents of Tables 2-3.

[00136] (21) The method of any one of embodiments 4-20, wherein the cancer comprises at least one cancer chosen from the group comprising acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), adrenocortical carcinoma, AIDS-related cancers, Kaposi sarcoma, AIDS-related lymphoma, primary CNS lymphoma, anal cancer, appendix cancer, astrocytomas, atypical teratoid/rhabdoid tumor, central nervous system cancers, basal cell carcinoma of the skin, bile duct cancer, bladder cancer, bone cancer, brain tumors, breast cancer, bronchial tumors, Burkitt lymphoma, carcinoid tumor, cardiac tumors, central nervous system cancers, embryonal tumors, germ cell tumor, primary CNS lymphoma, cervical cancer, cholangiocarcinoma, chordoma, chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), chronic myeloproliferative neoplasms, colorectal cancer, craniopharyngioma, cutaneous t-cell lymphoma, ductal carcinoma in situ (DCIS), embryonal tumors, central nervous system cancer, endometrial cancer, ependymoma, esophageal cancer, esthesioneuroblastoma, Ewing sarcoma, extracranial germ cell tumor, extragonadal germ cell tumor, eye cancer, intraocular melanoma, retinoblastoma, fallopian tube cancer, fibrous histiocytoma of bone, osteosarcoma, gallbladder cancer, gastric cancer, gastrointestinal carcinoid tumor, gastrointestinal stromal tumors (GIST), testicular cancer, gestational trophoblastic disease, hairy cell leukemia, head and neck cancer, heart tumors, hepatocellular cancer, Hodgkin lymphoma, hypopharyngeal cancer, intraocular melanoma, islet cell tumors, pancreatic neuroendocrine tumors, kidney cancer, Langerhans cell histiocytosis, laryngeal cancer, leukemia, lip and oral cavity cancer, liver cancer, lung cancer (non-small cell and small cell), lymphoma, male breast cancer, malignant fibrous histiocytoma of bone and osteosarcoma, melanoma, intraocular melanoma, Merkel cell carcinoma, mesothelioma, metastatic cancer, metastatic squamous neck cancer with occult primary, midline tract carcinoma with NUT gene changes, mouth cancer, multiple endocrine neoplasia syndromes, multiple myeloma/plasma cell neoplasms, mycosis fungoides, myelodysplastic syndromes, myelodysplastic/myeloproliferative neoplasms, myelogenous leukemia, chronic (CML), myeloid leukemia, acute (AML), nasal cavity and paranasal sinus cancer, nasopharyngeal cancer, neuroblastoma, non-Hodgkin lymphoma, non-small cell lung cancer, oral cancer, oropharyngeal cancer, ovarian cancer, pancreatic cancer, pancreatic neuroendocrine tumors (islet cell tumors), papillomatosis, paraganglioma, paranasal sinus and nasal cavity cancer, parathyroid cancer, penile cancer, pharyngeal cancer, pheochromocytoma, pituitary tumor, plasma cell neoplasm/multiple myeloma, pleuropulmonary blastoma, primary central nervous system (CNS) lymphoma, primary peritoneal cancer, prostate cancer, rectal cancer, recurrent cancer, renal cell cancer, retinoblastoma, rhabdomyosarcoma, salivary gland cancer, sarcoma, rhabdomyosarcoma, vascular tumors, osteosarcoma, soft tissue sarcoma, uterine sarcoma, Sézary syndrome, skin cancer, small intestine cancer, squamous cell carcinoma of the skin, squamous neck cancer with occult primary, stomach cancer, T-cell lymphoma, testicular cancer, throat cancer,

nasopharyngeal cancer, oropharyngeal cancer, hypopharyngeal cancer, thymoma and thymic carcinoma, thyroid cancer, transitional cell cancer of the renal pelvis and ureter, ureter and renal pelvis, urethral cancer, uterine cancer, endometrial, uterine sarcoma, vaginal cancer, vascular tumors, vulvar cancer, Wilms tumor, and other childhood kidney tumors.

[00137] (22) The method of any one of embodiments 4-21, wherein one or more of the gene modulatory reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 1-1525, SEQ ID NOS: 1-2789, SEQ ID NOS: 1526-2789, and/or SEQ ID NOS: 2980-3071.

[00138] (23) The method of embodiment 22, wherein the at least about 90% homology is at least about 90% identity.

[00139] (24) The method of any one of embodiments 4-23, wherein one or more of the gene modulatory reagents comprise a guide RNA (gRNA) sequence comprising homology to at least a portion of the gene that encodes a protein target of a therapeutic molecule in the library of therapeutic molecules.

[00140] (25) The method of embodiment 24, wherein the gRNA comprises homology to about 10 to about 50 contiguous nucleotides of the gene.

[00141] (26) The method of embodiment 24 or embodiment 25, wherein the homology is at least about 90% sequence homology.

[00142] (27) The method of embodiment 26, wherein the homology is at least about 90% sequence identity.

[00143] (28) The method of any one of embodiments 4-27, wherein the sample of cancer cells is contacted with an endonuclease.

[00144] (29) The method of embodiment 28, wherein the endonuclease comprises a Cas9 or Cas12a endonuclease.

[00145] (30) The method of embodiment 29, wherein the Cas9 or Cas12a endonuclease is selected from *S. pyogenes* Cas9 (SpCas9), SpCas9 D1135E variant, SpCas9 VRER variant, SpCas9 EQR variant, xCas9, SpCas9-NG, *S. aureus* Cas9 (SaCas9), *Acidaminococcus sp.* (AsCpf1), *Lachnospiraceae bacterium* (LbCpf1), AsCpf1 RR variant, LbCpf1 RR variant, AsCpf1 RVR variant, *C. jejuni* Cas9 (CjCas9), *N. meningitidis* (NmCas9), *S. thermophilus* (StCas9), *T. denticola* (TdCas9), and Mad7.

[00146] (31) The method of embodiment 28, wherein the endonuclease does not comprise a Cas9 or Cas12a endonuclease.

[00147] (32) The method of any one of embodiments 24-31, wherein the gRNA is positioned within a vector.

[00148] (33) The method of embodiment 32, wherein the vector further comprises genetic elements of a virus.

[00149] (34) The method of embodiment 33, wherein the virus comprises an adenovirus, retrovirus, adeno-associated virus (AAV), pox virus, parvovirus, baculovirus, measles virus, herpes simplex virus (HSV), Moloney Murine Leukemia Virus (MoMLV, MMLV, MuLV, or MLV), Murine Stem cell Virus (MSCV), or human immunodeficiency virus (HIV), or a combination thereof.

- [00150] (35) The method of any one of embodiments 32-34, wherein the vector further comprises an auxiliary nucleic acid sequence.
- [00151] (36) The method of embodiment 35, wherein the auxiliary nucleic acid sequence comprises a sequence encoding a marker, an antibiotic resistance cassette, and surface epitope expression cassette.
- [00152] (37) The method of embodiment 36, wherein the marker is a fluorescent marker.
- [00153] (38) The method of any one of embodiments 35-37, wherein the auxiliary nucleic acid allows for the selection of cancer cells that have been modified to harbor the one or more gene modulatory reagents.
- [00154] (39) The method of any one of embodiments 4-23, wherein one or more of the gene modulatory reagents comprise a short hairpin RNA (shRNA) sequence comprising homology to at least a portion of the gene that encodes a protein target of a therapeutic molecule in the library of therapeutic molecules.
- [00155] (40) The method of embodiment 39, wherein the shRNA comprises homology to about 10 to about 50 contiguous nucleotides of the gene.
- [00156] (41) The method of embodiment 39 or embodiment 40, wherein the homology is at least about 90% sequence homology.
- [00157] (42) The method of embodiment 41, wherein the homology is at least about 90% sequence identity.
- [00158] (43) The method of any one of embodiments 39-42, wherein the shRNA is positioned within a vector.
- [00159] (44) The method of embodiment 43, wherein the vector further comprises genetic elements of a virus.
- [00160] (45) The method of embodiment 44, wherein the virus comprises an adenovirus, retrovirus, adeno-associated virus (AAV), pox virus, parvovirus, baculovirus, measles virus, herpes simplex virus (HSV), Moloney Murine Leukemia Virus (MoMLV, MMLV, MuLV, or MLV), Murine Stem cell Virus (MSCV), or human immunodeficiency virus (HIV), or a combination thereof.
- [00161] (46) The method of any one of embodiments 43-45, wherein the vector further comprises an auxiliary nucleic acid sequence.
- [00162] (47) The method of embodiment 46, wherein the auxiliary nucleic acid sequence comprises a sequence encoding a marker, an antibiotic resistance cassette, or surface epitope expression cassette.
- [00163] (48) The method of embodiment 47, wherein the marker is a fluorescent marker.
- [00164] (49) The method of any one of embodiments 46-48, wherein the auxiliary nucleic acid allows for the selection of cancer cells that have been modified to harbor the one or more gene modulatory reagents.
- [00165] (50) A method of generating a plurality of modified cancer cells from a subject having cancer, the method comprising delivering a library of gene modulatory reagents to a sample of cancer cells from the subject to generate the plurality of modified cancer cells; wherein each modified cancer cell harbors one or more of the gene modulatory reagents, and each gene modulatory reagent is capable of knocking down or knocking out the function of a gene that encodes a protein target from a library of protein targets.

- [00166] (51) The method of embodiment 50, wherein one or more of the gene modulatory reagents comprises a guide RNA (gRNA) sequence comprising homology to at least a portion of the gene whose function is knocked down or knocked out in the modified cancer cell.
- [00167] (52) The method of embodiment 51, wherein the gRNA comprises homology to about 10 to about 50 contiguous nucleotides of the gene.
- [00168] (53) The method of embodiment 51 or embodiment 52, wherein the homology is at least about 90% sequence homology.
- [00169] (54) The method of embodiment 53, wherein the homology is at least about 90% sequence identity.
- [00170] (55) The method of embodiment 50, wherein one or more of the gene modulatory reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 1-1525, SEQ ID NOS: 1-2789, SEQ ID NOS: 1526-2789, and/or SEQ ID NOS: 2980-3071.
- [00171] (56) The method of embodiment 55, wherein the homology is at least about 90% identity.
- [00172] (57) The method of any one of embodiments 50-56, wherein the sample of cancer cells is contacted with an endonuclease.
- [00173] (58) The method of embodiment 57, wherein the endonuclease comprises a Cas9 or Cas12a endonuclease.
- [00174] (59) The method of embodiment 58, wherein the Cas9 or Cas12a endonuclease is selected from *S. pyogenes* Cas9 (SpCas9), SpCas9 D1135E variant, SpCas9 VRER variant, SpCas9 EQR variant, xCas9, SpCas9-NG, *S. aureus* Cas9 (SaCas9), *Acidaminococcus* sp. (AsCpf1), *Lachnospiraceae* bacterium (LbCpf1), AsCpf1 RR variant, LbCpf1 RR variant, AsCpf1 RVR variant, *C. jejuni* Cas9 (CjCas9), *N. meningitidis* (NmCas9), *S. thermophilus* (StCas9), *T. denticola* (TdCas9), and Mad7.
- [00175] (60) The method of embodiment 57, wherein the endonuclease does not comprise a Cas9 or Cas12a endonuclease.
- [00176] (61) The method of any one of embodiments 51-56, wherein the gRNA is positioned within a vector.
- [00177] (62) The method of embodiment 61, wherein the vector further comprises genetic elements of a virus.
- [00178] (63) The method of embodiment 62, wherein the virus comprises an adenovirus, retrovirus, adeno-associated virus (AAV), pox virus, parvovirus, baculovirus, measles virus, herpes simplex virus (HSV), Moloney Murine Leukemia Virus (MoMLV, MMLV, MuLV, or MLV), Murine Stem cell Virus (MSCV), or human immunodeficiency virus (HIV), or a combination thereof.
- [00179] (64) The method of any one of embodiments 61-63, wherein the vector further comprises an auxiliary nucleic acid sequence.
- [00180] (65) The method of embodiment 64, wherein the auxiliary nucleic acid sequence comprises a sequence encoding a marker, an antibiotic resistance cassette, or surface epitope expression cassette.
- [00181] (66) The method of embodiment 65, wherein the marker is a fluorescent marker.

[00182] (67) The method of any one of embodiments 64-66, wherein the auxiliary nucleic acid allows for the selection of cancer cells that have been modified to harbor the one or more gene modulatory reagents.

[00183] (68) The method of embodiment 50, wherein one or more of the gene modulatory reagents comprise a short hairpin RNA (shRNA) sequence comprising homology to at least a portion of the gene whose function is knocked down or knocked out in the modified cancer cell.

[00184] (69) The method of embodiment 68, wherein the shRNA comprises homology to about 10 to about 50 contiguous nucleotides of the gene.

[00185] (70) The method of embodiment 68 or embodiment 69, wherein the homology is at least about 90% sequence homology.

[00186] (71) The method of embodiment 70, wherein the homology is at least about 90% sequence identity.

[00187] (72) The method of any one of embodiments 68-71, wherein the shRNA is positioned within a vector.

[00188] (73) The method of embodiment 72, wherein the vector further comprises genetic elements of a virus.

[00189] (74) The method of embodiment 73, wherein the virus comprises an adenovirus, retrovirus, adeno-associated virus (AAV), pox virus, parvovirus, baculovirus, measles virus, herpes simplex virus (HSV), Moloney Murine Leukemia Virus (MoMLV, MMLV, MuLV, or MLV), Murine Stem cell Virus (MSCV), or human immunodeficiency virus (HIV), or a combination thereof.

[00190] (75) The method of any one of embodiments 72-74, wherein the vector further comprises an auxiliary nucleic acid sequence.

[00191] (76) The method of embodiment 75, wherein the auxiliary nucleic acid sequence comprises a sequence encoding a marker, an antibiotic resistance cassette, or surface epitope expression cassette.

[00192] (77) The method of embodiment 76, wherein the marker is a fluorescent marker.

[00193] (78) The method of any one of embodiments 75-77, wherein the auxiliary nucleic acid allows for the selection of cancer cells that have been modified to harbor the one or more gene modulatory reagents.

[00194] (79) The method of embodiment 50, wherein delivering comprising transposase-mediated transposition.

[00195] (80) The method of any one of embodiments 50-79, wherein the sample of cancer cells comprises primary cancer cells.

[00196] (81) The method of any one of embodiments 50-80, wherein the sample of cancer cells comprises about 10^5 to about 10^8 cells.

[00197] (82) The method of any one of embodiments 50-81, wherein the library comprises from about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, from about 50 to about 2,000, from about 100 to about 2,000, or from about 500 to about 2,000 different gene modulatory reagents.

[00198] (83) The method of any one of embodiments 50-82, wherein at least about 90% of the gene modulatory reagents are present in the library in a quantity within about 10% of the average gene modulatory reagent quantity.

[00199] (84) The method of any one of embodiments 50-83, wherein the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Tables 3-5D.

[00200] (85) The method of any one of embodiments 50-84, wherein the sample of cancer cells has been processed to preserve cell viability.

[00201] (86) The method of any one of embodiments 50-85, further comprising preparing the sample of cancer cells to preserve cell viability prior to and/or after delivery of the library of gene modulatory reagents.

[00202] (87) The method of any one of embodiments 50-86, further comprising propagating the modified cancer cells.

[00203] (88) The method of embodiment 87, wherein propagation comprises maintenance of the modified cancer cells in a 2D *in vitro* culture.

[00204] (89) The method of embodiment 87, wherein propagation comprises maintenance of the modified cancer cells in a 3D *in vitro* culture.

[00205] (90) The method of embodiment 87, wherein propagation comprises maintenance of the modified cancer cells *in vivo*.

[00206] (91) The method of embodiment 90, wherein propagation occurs within an animal model.

[00207] (92) The method of embodiment 91, wherein the animal model is a rodent.

[00208] (93) A compilation comprising a plurality of modified cancer cells, wherein each modified cancer cell harbors one or more gene modulatory reagents, and each gene modulatory reagent is capable of knocking down or knocking out the function of a gene that encodes a protein target from a library of protein targets.

[00209] (94) The compilation of embodiment 93, wherein at least one of the one or more gene modulatory reagents comprises a sequence selected from SEQ ID NOS: 1-1525, SEQ ID NOS: 1-2789, SEQ ID NOS: 1526-2789, and/or SEQ ID NOS: 2980-3071.

[00210] (95) The compilation of embodiment 93, wherein at least one of the one or more of gene modulatory reagents comprises a sequence at least about 90% homologous to a sequence selected from SEQ ID NOS: 1-1525, SEQ ID NOS: 1-2789, SEQ ID NOS: 1526-2789, and/or SEQ ID NOS: 2980-3071.

[00211] (96) The compilation of embodiment 95, wherein the homology is 90% identity.

[00212] (97) The compilation of any of embodiments 93-96, wherein the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Tables 3-5D.

[00213] (98) The compilation of any of embodiments 93-97, wherein one or more of the gene modulatory reagents comprise a guide RNA (gRNA) sequence comprising homology to at least a portion of the gene whose function is knocked down or knocked out in the modified cancer cell.

[00214] (99) The compilation of embodiment 98, wherein the gRNA comprises homology to about 10 to about 50 contiguous nucleotides of the gene.

[00215] (100) The compilation of embodiment 98 or embodiment 99, wherein the homology is at least about 90% sequence homology.

[00216] (101) The compilation of embodiment 100, wherein the homology is at least about 90% sequence identity.

[00217] (102) The compilation of any one of embodiments 93-101, further comprising an endonuclease.

[00218] (103) The compilation of embodiment 102, wherein the endonuclease comprises a Cas9 or Cas12a endonuclease.

[00219] (104) The method of embodiment 103, wherein the Cas9 or Cas12a endonuclease is selected from *S. pyogenes* Cas9 (SpCas9), SpCas9 D1135E variant, SpCas9 VRER variant, SpCas9 EQR variant, xCas9, SpCas9-NG, *S. aureus* Cas9 (SaCas9), *Acidaminococcus* sp. (AsCpf1), *Lachnospiraceae* bacterium (LbCpf1), AsCpf1 RR variant, LbCpf1 RR variant, AsCpf1 RVR variant, *C. jejuni* Cas9 (CjCas9), *N. meningitidis* (NmCas9), *S. thermophilus* (StCas9), *T. denticola* (TdCas9), and Mad7.

[00220] (105) The compilation of embodiment 102, wherein the endonuclease does not comprise a Cas9 or Cas12a endonuclease.

[00221] (106) The compilation of any one of embodiments 98-105, wherein the gRNA is positioned within a vector.

[00222] (107) The compilation of embodiment 106, wherein the vector further comprises genetic elements of a virus.

[00223] (108) The compilation of embodiment 107, wherein the virus comprises an adenovirus, retrovirus, adeno-associated virus (AAV), pox virus, parvovirus, baculovirus, measles virus, herpes simplex virus (HSV), Moloney Murine Leukemia Virus (MoMLV, MMLV, MuLV, or MLV), Murine Stem cell Virus (MSCV), or human immunodeficiency virus (HIV), or a combination thereof.

[00224] (109) The compilation of any one of embodiments 106-108, wherein the vector further comprises an auxiliary nucleic acid sequence.

[00225] (110) The compilation of embodiment 109, wherein the auxiliary nucleic acid sequence comprises a sequence encoding a marker, an antibiotic resistance cassette, or surface epitope expression cassette.

[00226] (111) The compilation of embodiment 110, wherein the marker is a fluorescent marker.

[00227] (112) The compilation of any one of embodiments 109-111, wherein the auxiliary nucleic acid allows for the selection of the modified cancer cells.

[00228] (113) The compilation of embodiment 93, wherein one or more of the gene modulatory reagents comprise a short hairpin RNA (shRNA) sequence comprising homology to at least a portion of the gene whose function is knocked down or knocked out in the modified cancer cell.

[00229] (114) The compilation of embodiment 113, wherein the shRNA comprises homology to about 10 to about 50 contiguous nucleotides of the gene.

[00230] (115) The compilation of embodiment 113 or embodiment 114, wherein the homology is at least about 90% sequence homology.

[00231] (116) The compilation of embodiment 115, wherein the homology is at least about 90% sequence identity.

[00232] (117) The compilation of any one of embodiments 113-116, wherein the shRNA is positioned within a vector.

[00233] (118) The compilation of embodiment 117, wherein the vector further comprises genetic elements of a virus.

[00234] (119) The compilation of embodiment 118, wherein the virus comprises an adenovirus, retrovirus, adeno-associated virus (AAV), pox virus, parvovirus, baculovirus, measles virus, herpes simplex virus (HSV), Moloney Murine Leukemia Virus (MoMLV, MMLV, MuLV, or MLV), Murine Stem cell Virus (MSCV), or human immunodeficiency virus (HIV), or a combination thereof.

[00235] (120) The compilation of any one of embodiments 117-119, wherein the vector further comprises an auxiliary nucleic acid sequence.

[00236] (121) The compilation of embodiment 120, wherein the auxiliary nucleic acid sequence comprises a sequence encoding a marker, an antibiotic resistance cassette, or surface epitope expression cassette.

[00237] (122) The compilation of embodiment 121, wherein the marker is a fluorescent marker.

[00238] (123) The compilation of any one of embodiments 120-122, wherein the auxiliary nucleic acid allows for the selection of the modified cancer cells.

[00239] (124) The compilation of any one of embodiments 93-105, wherein delivering comprising transposase-mediated transposition.

[00240] (125) The compilation of any one of embodiments 93-124, wherein the modified cancer cells are modified primary cancer cells.

[00241] (126) The compilation of any one of embodiments 93-125, comprising from about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, from about 50 to about 2,000, from about 100 to about 2,000, or from about 500 to about 2,000 different gene modulatory reagents.

[00242] (127) The compilation of any one of embodiments 93-126, comprising from about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, from about 50 to about 2,000, from about 100 to about 2,000, or from about 500 to about 2,000 different populations of modified cancer cells.

[00243] (128) A method of evaluating the functional effect of genetically modifying cancer cells from a subject, the method comprising: sequencing a plurality of modified cancer cells, wherein each modified cancer cell harbors one or more gene modulatory reagents, each gene modulatory reagent capable of knocking down or knocking out the function of a gene that encodes a protein target in a library of protein

targets; and wherein a gene modulatory reagent that impairs cell viability will have fewer sequence reads than a gene modulatory reagent that does not impair cell viability.

[00244] (129) The method of embodiment 128, further comprising determining which gene modulatory reagents have fewer than a threshold number of sequence reads.

[00245] (130) The method of embodiment 129, wherein the threshold number of sequence reads is an expected number of sequence reads if the gene modulatory reagent did not impair cell viability.

[00246] (131) The method of embodiment 129, wherein the threshold number of sequence reads is an average number of sequence reads for each gene modulatory reagent in the plurality of modified cancer cells.

[00247] (132) The method of any one of embodiments 128-131, further comprising correlating each gene modulatory reagent that has fewer than the threshold number of sequence reads to its corresponding protein target in the library of protein targets.

[00248] (133) The method of embodiment 132, further comprising correlating the corresponding protein target to a therapeutic molecule.

[00249] (134) The method of any one of embodiments 128-133, wherein the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Tables 3-5D.

[00250] (135) The method of any one of embodiments 128-134, wherein one or more of the gene modulatory reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 1-1525, SEQ ID NOS: 1-2789, SEQ ID NOS: 1526-2789, and/or SEQ ID NOS: 2980-3071.

[00251] (136) The method of embodiment 135, wherein the at least about 90% homology is at least about 90% identity.

[00252] (137) A library comprising a plurality of gene modulatory reagents, each gene modulatory reagent capable of knocking down or knocking out the function of a gene that encodes a protein target from a library of protein targets.

[00253] (138) The library of embodiment 137, wherein the plurality of gene modulatory reagents is capable of knocking down or knocking out the function of at least about 50% of the genes that encode for the protein targets in the library.

[00254] (139) The library of embodiment 138, wherein the at least about 50% is at least about 60%.

[00255] (140) The library of embodiment 139, wherein the at least about 60% is at least about 70%.

[00256] (141) The library of embodiment 140, wherein the at least about 70% is at least about 80%.

[00257] (142) The library of embodiment 141, wherein the at least about 80% is at least about 90%.

[00258] (143) The library of any one of embodiments 137-142, wherein the library of protein targets comprises all known proteins targeted by known drugs capable of treating a particular disease or condition.

[00259] (144) The library of embodiment 143, wherein the disease or condition is cancer.

[00260] (145) The library of embodiment 144, wherein the cancer comprises at least one cancer from the group comprising acute lymphoblastic leukemia (ALL), acute myeloid leukemia (AML), adrenocortical carcinoma, AIDS-related cancers, Kaposi sarcoma, AIDS-related lymphoma, primary CNS lymphoma, anal cancer, appendix cancer, astrocytomas, atypical teratoid/rhabdoid tumor, central nervous system cancers, basal cell carcinoma of the skin, bile duct cancer, bladder cancer, bone cancer, brain tumors, breast cancer, bronchial tumors, Burkitt lymphoma, carcinoid tumor, cardiac tumors, central nervous system cancers, embryonal tumors, germ cell tumor, primary CNS lymphoma, cervical cancer, cholangiocarcinoma, chordoma, chronic lymphocytic leukemia (CLL), chronic myelogenous leukemia (CML), chronic myeloproliferative neoplasms, colorectal cancer, craniopharyngioma, cutaneous t-cell lymphoma, ductal carcinoma in situ (DCIS), embryonal tumors, central nervous system cancer, endometrial cancer, ependymoma, esophageal cancer, esthesioneuroblastoma, Ewing sarcoma, extracranial germ cell tumor, extragonadal germ cell tumor, eye cancer, intraocular melanoma, retinoblastoma, fallopian tube cancer, fibrous histiocytoma of bone, osteosarcoma, gallbladder cancer, gastric cancer, gastrointestinal carcinoid tumor, gastrointestinal stromal tumors (GIST), testicular cancer, gestational trophoblastic disease, hairy cell leukemia, head and neck cancer, heart tumors, hepatocellular cancer, Hodgkin lymphoma, hypopharyngeal cancer, intraocular melanoma, islet cell tumors, pancreatic neuroendocrine tumors, kidney cancer, Langerhans cell histiocytosis, laryngeal cancer, leukemia, lip and oral cavity cancer, liver cancer, lung cancer (non-small cell and small cell), lymphoma, male breast cancer, malignant fibrous histiocytoma of bone and osteosarcoma, melanoma, intraocular melanoma, Merkel cell carcinoma, mesothelioma, metastatic cancer, metastatic squamous neck cancer with occult primary, midline tract carcinoma with NUT gene changes, mouth cancer, multiple endocrine neoplasia syndromes, multiple myeloma/plasma cell neoplasms, mycosis fungoides, myelodysplastic syndromes, myelodysplastic/myeloproliferative neoplasms, myelogenous leukemia, chronic (CML), myeloid leukemia, acute (AML), nasal cavity and paranasal sinus cancer, nasopharyngeal cancer, neuroblastoma, non-Hodgkin lymphoma, non-small cell lung cancer, oral cancer, oropharyngeal cancer, ovarian cancer, pancreatic cancer, pancreatic neuroendocrine tumors (islet cell tumors), papillomatosis, paraganglioma, paranasal sinus and nasal cavity cancer, parathyroid cancer, penile cancer, pharyngeal cancer, pheochromocytoma, pituitary tumor, plasma cell neoplasm/multiple myeloma, pleuropulmonary blastoma, primary central nervous system (CNS) lymphoma, primary peritoneal cancer, prostate cancer, rectal cancer, recurrent cancer, renal cell cancer, retinoblastoma, rhabdomyosarcoma, salivary gland cancer, sarcoma, rhabdomyosarcoma, vascular tumors, osteosarcoma, soft tissue sarcoma, uterine sarcoma, Sézary syndrome, skin cancer, small intestine cancer, squamous cell carcinoma of the skin, squamous neck cancer with occult primary, stomach cancer, T-cell lymphoma, testicular cancer, throat cancer, nasopharyngeal cancer, oropharyngeal cancer, hypopharyngeal cancer, thymoma and thymic carcinoma, thyroid cancer, transitional cell cancer of the renal pelvis and ureter, ureter and renal pelvis, urethral cancer, uterine cancer, endometrial, uterine sarcoma, vaginal cancer, vascular tumors, vulvar cancer, Wilms tumor, and other childhood kidney tumors.

[00261] (146) The library of any one of embodiments 143-145, wherein the known drugs comprise at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 drugs of Tables 2-3.

[00262] (147) The library of any one of embodiments 137-146, wherein the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Tables 3-5D.

[00263] (148) The library of any one of embodiments 137-147, wherein one or more of the plurality of gene modulatory reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 1-1525, SEQ ID NOS: 1-2789, SEQ ID NOS: 1526-2789, or SEQ ID NOS: 2980-3071.

[00264] (149) The library of embodiment 148, wherein the at least about 90% homology is at least about 90% identity.

[00265] (150) The library of any one of embodiments 137-149, wherein the plurality of gene modulatory reagents is capable of knocking down or knocking out the function of about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, about 50 to about 2,000, or about 100 to about 2,000 genes.

[00266] (151) The library of any one of embodiments 137-150, wherein the library comprises about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, about 50 to about 2,000, or about 100 to about 2,000 gene modulatory reagents.

[00267] (152) The library of any one of embodiments 137-151, wherein at least one of the gene modulatory reagents is capable of knocking out the function of a gene.

[00268] (153) The library of embodiment 152, wherein at least one of the gene modulatory reagents comprise a gRNA sequence having homology to at least a portion of the gene whose function is knocked out by the gene modulatory reagent.

[00269] (154) The library of any one of embodiments 137-147, wherein at least one of the gene modulatory reagents is capable of knocking down the function of a gene.

[00270] (155) The library of embodiment 154, wherein at least one of the gene modulatory reagents comprise a shRNA sequence having homology to at least a portion of the gene whose function is knocked down by the gene modulatory reagent.

[00271] (156) The library of embodiment 153 or embodiment 155, wherein the homology is at least about 90% sequence homology.

[00272] (157) The library of embodiment 156, wherein the homology is at least about 90% sequence identity.

[00273] (158) The library of embodiment 155 or embodiment 156, wherein the at least a portion is at least about 15 contiguous nucleotides.

[00274] (159) The library of any one of embodiments 137-158, wherein at least one of the gene modulatory reagents is positioned within a vector.

[00275] (160) The library of embodiment 159, wherein the vector comprises an adapter sequence.

[00276] (161) The library of embodiment 160, wherein the adapter sequence comprises a type IIS restriction enzyme cleavage sites.

[00277] (162) The library of any one of embodiments 159-161, wherein the vector further comprises genetic elements of a virus.

[00278] (163) The library of embodiment 162, wherein the virus comprises an adenovirus, retrovirus, adeno-associated virus (AAV), pox virus, parvovirus, baculovirus, measles virus, herpes simplex virus (HSV), Moloney Murine Leukemia Virus (MoMLV, MMLV, MuLV, or MLV), Murine Stem cell Virus (MSCV), or human immunodeficiency virus (HIV), or a combination thereof.

[00279] (164) The library of any one of embodiments 159-163, wherein the vector further comprises a sequence encoding a marker, an antibiotic resistance cassette, or surface epitope expression cassette.

[00280] (165) The library of embodiment 164, wherein the marker is a fluorescent marker.

Tables

[00281] Tables 2-3 provide exemplary therapeutic agents, one or more of which may be a member of a drug library described herein.

Table 2. Exemplary cancer therapeutic agents.

681640	copanlisib hydrochloride	KW 2449	REGN1400
(5Z)-7-oxozeaenol	copper Cu 64-DOTA-trastuzumab	KW-6002	REGN421
17-AAG	CP-358774	KX01	regorafenib
4EGI-1	CPI-444	KX2-391	relugolix
5-fluorouracil	crenolanib	L-685458	remetinostat
6-bromoindirubin-3'-oxime	crizotinib	lanreotide	reparixin
7-ethyl-10-hydroxycamptothecin	CS 7017, RS5444	lanreotide acetate	Repligen 136
Abarelix	CT 99021	lapatinib	resminostat
Abemaciclib	CT53518	lapatinib ditosylate	retaspimycin
Abexinostat	CT99021	larotrectinib sulfate	revatio
Abiraterone	CX-4945	LB-100	RG-108
abiraterone acetate	cycloquinoline 11	LBH-589	RG7204
Abitrexate	cyclopamine	LBW242	Ribavirin
ABT-199	CYT-387	LE-135	ribociclib
ABT-263	dabrafenib	lenalidomide	ricolinostat
ABT-737	dabrafenib mesylate	lenvatinib	ridaforolimus (deforolimus)
ABT-869	dacomitinib	lenvatinib mesylate	rigosertib
ABT-888	dactolisib	leptomycin b	rilotumumab
AC220	dalantercept	lestaurtinib	rimiducid
AC55649	dalotuzumab	letrozole	RITA
acalabrutinib	danusertib	leucovorin	rituximab
ado-trastuzumab emtansine	daraprim	leuprolide	rituximab and hyaluronidase human

Adriamycin	daratumumab	leuprolide acetate	rituximab/hyaluronidase human
adriamycin PFS	dasatinib	leurocristine	RO-3306
Adrucil	daunorubicin	LFM-A13/DDE-28	RO4929097, R4733
AEB071	daunorubicin hydrochloride	LGK974	RO5126766, CH5126766
AEE788, NVP-AEE788	daunoxome	linifanib	RO5185426
AEW541	Debio 0932	linsitinib	RO5212054, PLX3603
Afatinib	Debio 1347, CH5183284	liposomal daunorubicin	rociletinib
afatinib dimaleate	decadron	liposomal doxorubicin	romidepsin
Aflibercept	decitabine	LJM716	roniciclib
Afuresertib	defactinib	lomeguatrib	rosomidnar
AG013736	degarelix	loprox	rucaparib
AG014699	denileukin diftitox	lorlatinib	Rucaparib
AG-014699	denintuzumab mafodotin	LOXO-101	rucaparib camsylate
AHPN	denosumab	lucitanib	ruxolitinib
AKT inhibitor VIII	depatuxizumab	luminespib	ruxolitinib phosphate
aldesleukin	depatuxizumab mafodotin	lupron	S3I-201
alectinib	dexamethasone	luspatercept	SAHA
alemtuzumab	dezapelisib	lutetium Lu 177-dotatate	salermide
alisertib	dinaciclib	LY-2157299	sapanisertib
alitretinoin	dinutuximab	LY2510924	SAR125844
all-trans retinoic acid	DMOT4039A	LY2874455	SAR245409
alpelisib	docetaxel	LY317615	SAR302503
alvocidib	dociparstat sodium	LY450139	SAR3419
AM-580	doramapimod	manumycin a	SAR405838, MI-773
amatuximab	dovitinib	margetuximab	SAR650984
AMG 208	doxil	marinopyrrole a	saracatinib
AMG 337	doxorubicin	maritoclax	SB 216763
AMG 595	doxorubicin hydrochloride	masitinib	SB-225002
AMG 780	DPD	masivet	SB-431542
AMG-706	duligotuzumab	MDX-1105, BMS-936559	SB-505124
AMG900	durvalumab	MEDI-3617	SB-525334
AMN107	dusigitumab	mercaptopurine	SB-743921
amonafide	duvelisib	Merck60	SC144
amuvatinib	E7080	methotrexate	SCH 530348
anastrozole	efudex	methyltestosterone	SCH727965
anti-mesothelin iCasp9M28z CAR-transduced autologous T lymphocytes	EGF816	Metyrapone	SCH772984
AP26113	EHT 1864	Metyrapone	SCH-79797

apalutamide	EHT 5372	MGCD-265	seliciclib
apatinib	elesclomol	MH2075	selinexor
apatorsen	ellence	midostaurin	selumetinib
apicidin	elocalcitol	mipsagargin	semagacestat
apitolisib	elotuzumab	mirin	SEN0014196
APO866	emactuzumab	mirvetuximab soravtansine	serdemetan
arimidex	embelin	Mitotane	seribantumab
armala	EMD 1214063, MSC2156119J	mitoxantrone	SF1126
aromasin	emibetuzumab	MK-0457	SGC0946
ARQ 736	enasidenib	MK-0752	SGX-523
ARQ-197	enasidenib mesylate	MK-1775	sildenafil
ASP3026	encorafenib	MK-2206	silmitasertib
AT101	ENMD-0276	MK-2461	siltuximab
AT13148	ENMD-2076	MK5108	sipuleucel-T
AT13387	enobosarm	MK-8353, SCH900353	sirolimus
AT-406	ensituximab	ML204	sitagliptin
AT7867	entinostat	MLN2238	sitravatinib
AT9283	entolimod	MLN-2480	SJ-172550
atezolizumab	entospletinib	MLN-4924	skepinone-L
ATRA	entrectinib	MLN518	SKI-606
AV 203	enzalutamide	MLN8237	SL 0101-1
AV-951	enzastaurin	MLN9708	SL 0101-1
avelumab	epacadostat	MM_V_GSK_2d1	SM-406
avicin D	epidaza	MM-111	SN-38
AVL-292	epirubicin	MM-151	SNS-032
acicabtagene ciloleucel	epitinib	mocetinostat	SNS-314
axitinib	Eplerenone	modotuximab	SNX-2112
AZ191	EPZ004777 analog	mogamulizumab-kpkc	SNX-5422
AZ628	EPZ-5676	momelotinib	sonidegib
AZ960	EPZ-6438, E7438	motesanib	sophoretin, quercetin
azacitidine	erdafitinib	motolimod	sorafenib
AZD0530	eribulin mesylate	moxetumomab pasudotox- tdfk	sorafenib tosylate
AZD1152-HQPA	erlotinib	MRK 003	sotatercept
AZD1208	erlotinib hydrochloride	MRK-560	sotrastaurin
AZD1480	estramustine	MST-312	SP600125
AZD1775, MK1775	estramustine phosphate	mubritinib	Spironolactone
AZD2014	estybon	muparfostat	Spironolactone
AZD2171	etimoxir	N9-isopropylolomoucine	SRT-1720
AZD-2281	etirinotecan pegol	naquotinib	stelazine
AZD4547	Etomidate	navicixizumab	STI571
AZD5069	etoposide	navitoclax	streptozocin

AZD5363	etoposide/etoposide phosphate	navoximod	SU11248
AZD6244	eulexin, apimid	necitumumab	SU11274
AZD6482	everolimus	nelarabine	sulfatinib
AZD7451	evista, keoxifene	neratinib	sunitinib
AZD7762	EX-527	neratinib maleate	sunitinib malate
AZD8055	EXEL-2880	nesvacumab	sutent
AZD8186	exemestane	N-hexanoyl-D-sphingosine	SZ4TA2
AZD8330	fareston	niclocide	tagraxofusp-erzs
AZD8931	faslodex	niclosamide	TAK-733
bafetinib	faz053	nilandron, anandron	TAK901
barasertib	fedratinib	nilotinib	taladegib
bax channel blocker	femara	nilutamide	talazoparib
BAY 1187982	ficlatuzumab	nimotuzumab	tamoxifen
BAY1125976	figitumumab	nintedanib	tamoxifen citrate
BAY1143572	filanesib	niraparib	tandutinib
BAY-43-9006	ingolimod	niraparib tosylate monohydrate	tanespimycin
BAY-73-4506	firmagon	nirogacestat	tanespymicin
Bazedoxifene	FK866	nivolumab	tarextumab
BCL-LZH-4	flavopiridol	NMS-1286937	targretin
belimumab	fluorouracil	novantrone	TAS-119
belinostat	fluoxymesterone	novonex	taselisib
bevacizumab	flutamide	NSC23766	tasocitinib
bexarotene	foretinib	NSC303580	taxol
bextra	fostamatinib	NSC652287	taxotere
BEZ235	fruquintinib	NSC718781	telatinib
BGB-283	FTY720	NSC74859	telisotuzumab
BGJ398, NVP-BGJ398	fulvestrant	NU-7441	temsirolimus
BGT226, NVP-BGT226	futuximab	nutlin-3	teniposide
BI 836845	galeterone	Nutlin-3a	TEW-7197
BI 847325	galunisertib	NVP-ADW742	TG100-115
BI-2536	gandotinib	NVP-BEZ235	TG-101348
BIBF 1120	ganetespib	NVP-BGJ-398	TGX-221
BIBR-1532	ganitumab	NVP-BSK805	thalidomide
BIBW2992	GANT-61	NVP-BYL-719	theliatinib
bicalutamide	GDC-0449	NVP-LDE225	THM-I-91
BIIB022	GDC-0623	NVP-TAE684	tipifarnib
BIND-014	GDC-0879	O-6-benzylguanine	tipifarnib-P1
binimetinib	GDC-0941	obatoclox	tipifarnib-P2
BIO	gedatolisib	obatoclox mesylate	tisagenlecleucel
birabresib	gefitinib	obinutuzumab	tisagenlecleucel-T
BIRB-796	geldanamycin	oblimerson	tivantinib
birinapant	gemcitabine	ofatumumab	tivozanib

BIX-01294	gemtuzumab ozogamicin	olaparib	TL-32711
blinatumomab	genasense	olaratumab	tocilizumab
BLZ945	gilenya	olmutinib	tofacitinib
BMN-673	gilteritinib	omacetaxine mepesuccinate	tofacitinib citrate
BMS-195614	glasdegib	omipalisib	toposar, etopophos
BMS-270394	glasdegib maleate	ON-01910	topotecan
BMS-345541	glesatinib	onalespib	topotecan hydrochloride
BMS-354825	glycooptimized trastuzumab-GEX	onartuzumab	toremifene
BMS-387032	GMX-1778	Oncovin	tosedostat
BMS-536924	GNF4877	Onivyde	tositumomab
BMS-582664	goserelin	OPB-31121	tositumomab and iodine i 131 tositumomab
BMS-599626, AC480	gossypol	orantinib	tovetumab
BMS-690514, EVRI	GSK089	OSI-027	tozasertib
BMS-708163	GSK1059615	OSI-774	trametinib
BMS-754807	GSK1070916	OSI-906	trastuzumab
BMS-777607	GSK1120212 (Trametinib)	OSI-930	trastuzumab emtansine
BMS-907351	GSK1210151A	osimertinib	trebananib
BMS-911543	GSK1363089	ostarine	trelstar
bortezomib	GSK2118436 (Dabrafenib)	paclitaxel	tretinoin
bosutinib	GSK2256098	pacritinib	trifluoperazine
BRD0667	GSK-2636771	palbociclib	triptorelin
BRD3547	GSK269962A	pandacostat	TSR-011
BRD4658	GSK2879552	panitumumab	tubastatinA
BRD4770	GSK3326595	panobinostat	tucatinib
BRD6430	GSK461364	patidegib	tucidinostat
BRD6929	GSK525762A	patritumab	TW-37
BRD9047	GSK-626616	pazopanib	tyverb
BRD9876	GU 17	pazopanib hydrochloride	ublituximab
BRD-K11533227	guadecitabine	PCI-32765	ulocuplumab
BRD-K29313308	GW 441756	PD 153035	umbralisibtosylate
BRD-K51490254	GW 5074	PD0325901	UNC0321
BRD-K55478147	GW2016	PD-0332991	UNC0638
BRD-K61166597	GW572016	PD-173074	UNC0642
BRD-K69840642	GW786034	PD318088	uprosertib
BRD-K81491172	GW-843682X	peginterferon alfa-2b	valdecocix
BRD-K85133207	HGS1036, FP-1039, GSK3052230	pelitinib	valodex
BRD-K88742110	HKI-272	pembrolizumab	valrubicin
brentuximab vedotin	HLI-373	pemetrexed disodium	valstar

briciclib	HMN-214	pentostatin	vandetanib
briciclib sodium	hycamptin	pertuzumab	vanucizumab
brigatinib	hycamptin	pevonedistat	vargatef
brilanestrant	hydroxydaunorubicin	PF-01367338	vatalanib
brivanib	hydroxyurea	PF-02341066	veliparib
brontictuzumab	I-BET	PF-03814735	vemurafenib
buparlisib	I-BET151	PF-04217903	vemurarinib
BVD-523	ibritumomab tiuxetan	PF-184	venetoclax
BX-795	ibrutinib	PF-2341066	VER-155008
BXL-628	IC-87114	PF-4691502	vesanoid
BYL719	icotinib	PF-4708671	viagra
BYL-719	idamycin	PF477736	vinblastine sulfate
C6-ceramide	idarubicin	PF-562271	vincristine
cabazitaxel	idasanutlin	PF-573228	vincristine sulfate
cabozantinib	idelalisib	PHA665752	vinorelbine tartrate
CAL-101	ilorasertib	PHA-793887	vintafolide
camptosar	imatinib	PI-103	vismodegib
camptothecin	imatinib mesylate	pictilisib	VM-26
canakinumab	imgatuzumab	pifithrin-mu	volasertib
canertinib	imiquimod	PIK-93	volitinib
capecitabine	INCB018424	pilaralisib	vorapaxar
carfilzomib	INCB028060, INC280	PIM447	vorinostat
casodex	INCB052793	pimasertib	voxtalisib
CAY10618	INCB-18424	pluripotin	VS-4718
CBB-1007	Indisulam	PLX3397, PLX108-01	vumon
CC-223	indoximod	PLX-4032	VX-680
CCI-779	inebilizumab	PLX4720	VX-803
CD-1530	Infinity compound 1	PLX-4720	WH-4-025
CD-437	iniparib	PLX7486	WZ4002
CDK9 inhibitor 14	INK-1117	pomalidomide	WZ8040
cediranib	inotuzumab ozogamicin	ponatinib	X-396
cemiplimab-rwlc	interferon alfa-2b, recombinant	ponatinib hydrochloride	X-82
cenisertib	iobenguane I 131	porfimer	XAV 939
CEP-701	ipafricept	poziotinib	XL019
ceritinib	ipatasertib	pralatrexate	XL184
cerubidine	ipilimumab	prexasertib	XL228
cetuximab	irinotecan	prochlorperazine	XL281, BMS-908662
CF102	irinotecan liposome	prochlorperazine dimaleate	XL647, KD019
CGP60474	irinotecan trihydrochloride	PRT062070	XL765
Ch-55	isoliquritigenin	PSMA ADC	XL820
Chembridge cat# 7667791	ISOX	purmorphamine	XL880

CHIR-265	istiratumab	PWT33597	XL888
CHIR-99021	istradefylline	PX-12	XMT-1522
CHR-2797	istubal	PX-866	Xtandi
CHS-828	itacitinib	PXD-101	YK 4-279
CI-1033	IV-2	pyrimethamine	YM155
CI-1040	ivosidenib	quizartinib	YM-155
CI-994	ixabepilone	QW-BI-011	zactima
ciclopirox olamine	ixazomib citrate	R-406	zarnestra
Cimetidine	jakavi	R428	ZD-1839
citarinostat	JNJ-26854165	rabusertib	ZD6474
cixutumumab	JNK Inhibitor VIII	radium 223 dichloride	zebularine
clofarabine	JQ1	RAF265	zibotentan
clolar	JTP-74057	ralimetinib	ziv-aflibercept
cMet CAR-mRNA Electroporated autologous T lymphocytes	JW74	raloxifene	ZM-447439
cobimetinib	Ketoconazole	ramucirumab	zoladex
cometriq	Ki8751	rapamune	ZSTK474
compazine	KU-0059436	rapamycin	ZW25
compound 7d-cis	KU-0060648	rebastinib tosylate	zytiga
copanlisib	KU-0063794	refametinib	

Table 3. Exemplary cancer therapeutic agents with associated targets.

Target Gene Symbol	Drug Names (Development, Generic or Trade Name)
ABL1	nilotinib (e.g., Tassigna®, AMN107); ponatinib (e.g., Iclusig®); cenisertib; AT9283; dasatinib (e.g., BMS-354825, Sprycel®); bafetinib; bosutinib (e.g., Bosulif®, SKI-606); imatinib (e.g., Gleevec®); XL228saracatinib (AZD0530); regorafenib (e.g., Stivarga®); KW 2449; imatinib mesylate (e.g., STI571)
ABL2	dasatinib (e.g., BMS-354825, Sprycel®)
ACPP (ACP3)	sipuleucel-T
ADA	pentostatin
ADORA2A	CPI-444; istradefylline (e.g., KW-6002)
ADORA3	CF102
AGXT	O-6-benzylguanine
AKT1	cenisertib; AT13148; AZD5363; BAY1125976; ipatasertib; afuresertib; uprosertib; MK-2206; AT7867; gefitinib (e.g., ZD-1839; Iressa®); AKT inhibitor VIII
AKT2	cenisertib; AT13148; AZD5363; BAY1125976; ipatasertib; afuresertib; uprosertib; MK-2206; AT7867; AKT inhibitor VIII
AKT3	cenisertib; AT13148; AZD5363; BAY1125976; ipatasertib; afuresertib; uprosertib; MK-2206; AT7867; AKT inhibitor VIII
ALK	dalantercept; brigatinib (e.g., Alunbrig®); gilteritinib (e.g., Xospata®); ASP3026; alectinib (e.g., Alecensa®); ceritinib (e.g., Zykadia®); crizotinib (e.g., Xalkori®); lorlatinib (e.g., Lorbrena®); entrectinib; TSR-011; X-396 (ensartinib); AP26113; NVP-TAE684; PF-2341066

ANGPT1	AMG 780; trebananib
ANGPT2	AMG 780; MEDI-3617; nesvacumab; vanucizumab; trebananib
ANPEP	tosedostat; CHR-2797
APH1A	MK0752; MRK 003; RO4929097; semagacestat; LY450139; L-685458; BMS-708163
APH1B	MK0752; MRK 003; BMS-708163
AR	enobosarm (Ostarine®); nilutamide (e.g., Nilandron®, Anandron®); bicalutamide (e.g., Casodex®); flutamide (e.g., Eulexin®, Apimid); enzalutamide (e.g., Xtandi®); galeterone; fluoxymesterone; methyltestosterone
ARAF	AZ628; MLN-2480
ATR	VX-803
AURKA	cenisertib; AT9283; ENMD-2076; MK5108; alisertib; PF-03814735; TAK901; TAS-119; ilorasertib; AMG900; BI 847325; danusertib; SNS-314; SNS 314; MLN8237; KW 2449; tozasertib; VX-680; MK-0457
AURKB	cenisertib; AT9283; barasertib; GSK1070916; PF-03814735; ilorasertib; AMG900; BI 847325; danusertib; SNS-314; SNS 314; tozasertib; azd1152-HQPA; SL 0101-1; VX-680; MK-0457; BX-795; ZM-447439
AURKC	GSK1070916; SNS 314; tozasertib; VX-680; MK-0457; BX-795
AXL	gilteritinib; glesatinib; sitravatinib; R428
B4GALNT1	dinutuximab (e.g., Unituxin®)
BAX	Bax channel blocker; BRD3547; gossypol
BCL2	navitoclax; AT101; venetoclax (e.g., Venclexta®); obatoclax; oblimerson (e.g., Genasense®); rosomidnar; docetaxel (e.g., Taxotere®); gossypol; TW-37; ABT-737; ABT-199; Infinity compound 1; ABT-263; obatoclax mesylate
BCL2L1	navitoclax; BCL-LZH-4; obatoclax; TW-37; SZ4TA2; ABT-737; ABT-263; obatoclax mesylate
BCL2L2	navitoclax; ABT-737; ABT-263
BIRC5	YM155
BLK	dasatinib (e.g., BMS-354825, Sprycel®)
BMX	dasatinib (e.g., BMS-354825, Sprycel®)
BRAF	ARQ 736; BGB-283; (dabrafenib, e.g., Tafinlar®); vemurafenib (e.g., Zelboraf®); RAF265; RO5212054; PLX3603; sorafenib (e.g., Nexavar®, BAY-43-9006); regorafenib (e.g., Stivarga®); encorafenib; MLN2480; RO5126766; CH5126766; XL281, BMS-908662; AZ628; sorafenib tosylate; dabrafenib mesylate (e.g., GSK2118436); PLX-4720; MLN-2480; PLX-4032; RG7204; RO5185426; GDC-0879; CHIR-265
BRD2	birabresib; GSK525762A; I-BET; GSK1210151A; I-BET151; JQ1
BRD3	birabresib; GSK525762A; I-BET; GSK1210151A; I-BET151; JQ1
BRD4	birabresib; GSK525762A; I-BET; GSK1210151A; I-BET151; JQ1
BTK	acalabrutinib; cenisertib; AVL-292; ibrutinib (e.g., Imbruvica®, PCI-32765) dasatinib (e.g., Sprycel® BMS-354825); LFM-A13/DDE-28
CCND1	briciclib; briciclib sodium
CCND2	briciclib; briciclib sodium
CCND3	briciclib; briciclib sodium
CD19	inebilizumab; blinatumomab (e.g., Blincyto®); SAR3419; denintuzumab mafodotin; tisagenlecleucel-T
CD274	MDX-1105, BMS-936559; durvalumab; (e.g., Imfinzi®); atezolizumab (e.g., Tecentriq®); avelumab (e.g., Bavencio); FAZ053
CD38	daratumumab (e.g., Darzalex®), HuMax-CD38; SAR650984
CDK1	alvocidib; roniciclib; dinaciclib; CGP60474; RO-3306; SCH727965; PHA-793887; flavopiridol; N9-isopropylolomoucine
CDK2	alvocidib; roniciclib; dinaciclib; seliciclib; CGP60474; SCH727965; SNS-032; BMS-387032; PHA-793887; flavopiridol
CDK4	alvocidib; roniciclib; ribociclib (e.g., Kisqali®); abemaciclib; palbociclib (e.g., Ibrance®); PHA-793887; flavopiridol; PD-0332991

CDK5	alvociclib; dinaciclib; CGP60474; SCH727965; PHA-793887; N9-isopropylolomoucine
CDK6	alvociclib; ribociclib (e.g., Kisqali®); abemaciclib; palbociclib (e.g., Ibrance®); flavopiridol; PD-0332991
CDK7	alvociclib; roniciclib; seliciclib; CGP60474; SNS-032; BMS-387032; PHA-793887
CDK9	alvociclib; roniciclib; dinaciclib; seliciclib; BAY1143572; CGP60474; SCH727965; CDK9 inhibitor 14; SNS-032; BMS-387032; PHA-793887
CHD1	epirubicin
CHEK1	prexasertib; 681640; AZD7762; PF477736
CHEK2	rabusertib; AZD7762; PF477736
CPT1A	etimoxir
CRBN	thalidomide; lenalidomide; pomalidomide
CRTC1	AZD8055; sapanisertib; OSI-027; NVP-BEZ235
CRTC2	AZD8055; sapanisertib; OSI-027; NVP-BEZ235
CSF1R	PLX3397, PLX108-01; PLX7486; emactuzumab; BLZ945; sunitinib malate (e.g., Sutent®; SU11248); linifanib; ABT-869; pazopanib
CSNK2A1	silmitasertib; CX-4945
CSNK2A2	silmitasertib; CX-4945
CXCR1	reparixin
CXCR2	AZD5069; reparixin; SB-225002
CXCR4	ulocuplumab; LY2510924; dociparstat sodium
CYP17A1	abiraterone acetate (e.g., Zytiga®)
CYP19A1	letrozole (e.g., Femara®); exemestane (e.g., Aromasin®); anastrozole (e.g., Arimidex®)
CYP11B1	Metirapone; Mitotane; Ketoconazole; Spironolactone; Cimetidine
CYP11B2	Eplerenone; Etomidate; Metirapone; Spironolactone
DDR2	regorafenib (e.g., Sitravatinib®)
DHFR	methotrexate; pemetrexed disodium; pralatrexate; abiraterone
DHH	glasdegib; vismodegib (e.g., Erivedge®)
DHX9	YK 4-279
DNMT1	guadecitabine; azacitidine; decitabine; zebularine; RG-108
DOT1L	EPZ-5676; EPZ004777 analog; SGC0946
DPP4	sitagliptin
DRD2	prochlorperazine; prochlorperazine dimaleate (e.g., Compazine®); trifluoperazine (e.g., Stelazine®)
DYRK1A	EHT 5372; GNF4877; AZ191
DYRK1B	EHT 5372; GNF4877; AZ191
DYRK2	GSK-626616
DYRK3	GSK-626616
DYRK4	GSK-626616
EDNRA	Zibotentan
EGFR	AEE788, NVP-AEE788; brigatinib (e.g., Alunbrig®); naquotinib; vandetanib (e.g., Zactima®, Caprelsa®); osimertinib (e.g., Tagrisso®); BGB-283; afatinib (e.g., Gilotrif™, Tomtovok®, BIBW2992); icotinib; canertinib; rociletinib; EGF816; olmutinib; epitinib; theliatinib; erlotinib (e.g., Tarceva®); XL647, KD019; gefitinib (e.g., Iressa®); AZD8931; BMS-599626, AC480; modotuximab; depatuxizumab; panitumumab (e.g., Vectibix®); nimotuzumab; necitumumab (e.g., Portrazza™); cetuximab (e.g., Erbitux®); duligotuzumab; MM-151; imgatuzumab; futuximab; depatuxizumab mafodotin; AMG 595; aldesleukin (e.g., Proleukin®); lapatinib (e.g., Tykerb®); osimertinib (e.g., Tagrisso®); AP26113; dacomitinib; erlotinib hydrochloride; lapatinib ditosylate; cyanoquinoline 11; GW572016; GW2016; Tyverb; PD 153035; CI-1033; ZD-1839; CP-358774; OSI-774; NSC718781; WZ4002; WZ8040; neratinib; HKI-272
EHMT1	UNC0638; UNC0642

EHMT2	BIX-01294; QW-BI-011; BRD4770; UNC0321; UNC0638; UNC0642
EIF4E	4EGI-1; Ribavirin
EPHA2	regorafenib; dasatinib (e.g., BMS-354825, Sprycel®); vandetanib
EPHB4	sitravatinib; XL647, KD019; vandetanib
ERBB2	tucatinib; BMS-690514, EVRI; AEE788, NVP-AEE788; afatinib (e.g., Gilotrif™, Tomtovok®, BIBW2992); canertinib; lapatinib (e.g., Tykerb®); neratinib (e.g., Nerlynx®); mubritinib; XL647, KD019; glycooptimized trastuzumab-GEX; margetuximab; MM-111; pertuzumab (e.g., Perjeta®, Omnitarg®); trastuzumab (e.g., Herceptin®); ado trastuzumab emtansine (e.g., Kadcyla®); XMT-1522; ZW25; copper Cu 64-DOTA-trastuzumab; aldesleukin (e.g., Proleukin®); dacomitinib; lapatinib ditosylate; GW572016; GW2016; Tyverb; CI-1033; erlotinib (e.g., Tarceva®); CP-358774; OSI-774; NSC718781; HKI-272; AZD8931; vandetanib
ERBB3	afatinib (e.g., Gilotrif™); AV 203; LJM716; duligotuzumab; MM-111; seribantumab; istratumab; REGN1400; patritumab; dacomitinib; AZD8931; vandetanib
ERBB4	pelitinib; poziotinib; dacomitinib; afatinib; (e.g., Gilotrif™); vandetanib
ESR1	fulvestrant (e.g., Faslodex®); tamoxifen; tamoxifen citrate (e.g., Nolvadex®, Istubal, Valodex, Soltamox™); raloxifene (e.g., Evista®, Keoxifene); toremifene (e.g., Fareston®); brilanestrant; galeterone; fluoxymesterone; estramustine
ESR2	fulvestrant (e.g., Faslodex®); tamoxifen; tamoxifen citrate (e.g., Nolvadex®, Istubal, Valodex, Soltamox™); raloxifene (e.g., Evista®, Keoxifene); toremifene (e.g., Fareston®); brilanestrant; galeterone; estramustine; estramustine phosphate
EZH2	EPZ-6438, E7438; MM_V_GSK_2d1; QW-BI-011; BRD4770
F2R	SCH-79797; vorapaxar; SCH-530348
FCGR1A	porfimer
FGF1	muparfostat; pazopanib hydrochloride
FGF2	muparfostat
FGFR1	masitinib; ponatinib (e.g., Iclusig®); AZD4547; BGJ398, NVP-BGJ398; nintedanib (e.g., Vargatef®, BIBF 1120); Debio 1347, CH5183284; lucitanib; sulfatinib; LY2874455; dovitinib; XL228; erdafitinib; orantinib; HGS1036, FP-1039, GSK3052230; sorafenib tosylate; regorafenib; PD-173074; lenvatinib; pazopanib
FGFR2	masitinib; ponatinib (e.g., Iclusig®); AZD4547; BGJ398, NVP-BGJ398; nintedanib (e.g., Vargatef®, BIBF 1120); Debio 1347, CH5183284; lucitanib; sulfatinib; LY2874455; dovitinib; XL228; erdafitinib; BAY 1187982; regorafenib; Ki8751
FGFR3	masitinib; ponatinib (e.g., Iclusig®); AZD4547; BGJ398, NVP-BGJ398; nintedanib (e.g., Vargatef®, BIBF 1120); Debio 1347, CH5183284; lucitanib; sulfatinib; LY2874455; dovitinib; XL228; erdafitinib; ENMD-2076; NVP-BGJ-398; pazopanib hydrochloride; masivet; PD-173074; pazopanib
FGFR4	erdafitinib; NVP-BGJ-398; nintedanib
FGR	dasatinib (e.g., BMS-354825, Sprycel®)
FKBP1A	Rimiducid
FLT1	ilorasertib; axitinib (e.g., Inlyta®); motesanib; regorafenib (e.g., Stivarga®, BAY-73-4506); nintedanib (e.g., Vargatef®, BIBF 1120); lucitanib; pazopanib (e.g., Votrient®, GW786034, Armala™); fruquintinib; tivozanib; glesatinib; sitravatinib; sorafenib tosylate; sunitinib malate; pazopanib hydrochloride; sunitinib (e.g., Sutent®, SU11248); MGCD-265; cediranib; AZD2171; linifanib; ABT-869
FLT3	quizartinib; ponatinib (e.g., Iclusig®); cenisertib; gilteritinib; sorafenib (e.g., Nexavar®, BAY-43-9006); lestaurtinib; crenolanib; ENMD-0276; tandutinib; amuvatinib; midostaurin (e.g., Rydapt®); PLX3397, PLX108-01; sunitinib malate (e.g., Sutent®, SU11248); cabozantinib (e.g., Cabometyx® (tablet), Cometriq® (capsule)); tozasertib; AZD1152-HQPA; sorafenib tosylate; KW 2449; XL184; BMS-907351; MLN518; CT53518; AC220; linifanib; ABT-869; CEP-701
FLT4	ilorasertib; axitinib (e.g., Inlyta®); motesanib; regorafenib (e.g., Stivarga®, BAY-73-4506); nintedanib (e.g., Vargatef®, BIBF 1120); lucitanib; pazopanib (e.g., Votrient®, GW786034, Armala); fruquintinib; tivozanib; glesatinib; sitravatinib; telatinib; sorafenib tosylate; sunitinib malate (e.g., Sutent®, SU11248); pazopanib hydrochloride; sorafenib (e.g., BAY-43-9006, Nexavar®); AG013736; lenvatinib; E7080; MGCD-265; cediranib; AZD2171

FNTA	tipifarnib; Zarnestra; tipifarnib-P2; tipifarnib-P1; manumycin A
FOLH1	PSMA ADC; mipsagargin; BIND-014
FOLR1	mirvetuximab soravtansine; vintafolide
FOLR2	vintafolide
FOLR3	vintafolide
FRK	regorafenib; dasatinib (e.g., BMS-354825, Sprycel®)
FYN	dasatinib (e.g., BMS-354825, Sprycel®)
FZD8	ipafricept
GART	pemetrexed disodium
GNRH1	Degarelix (e.g., Firmagon®); leuprolide (e.g., Lupron®); triptorelin (e.g., Trelstar®); goserelin (e.g., Zoladex®); relugolix
GNRHR	goserelin; leuprolide acetate; abarelix; degarelix
GSK3A	CT 99021; CHIR-99021; CT99021; SB 216763
GSK3B	CT 99021; BIO; 6-bromoindirubin-3'-oxime; 6BIO; CHIR-99021; CT99021; JW74; BRD-K81491172; SB 216763
HCK	dasatinib (e.g., BMS-354825, Sprycel®); bosutinib
HDAC1	resminostat; citarinostat; abexinostat; romidepsin (e.g., Istodax®); tucidinostat; Epidaza®; panobinostat (e.g., Farydak®, Faridak); mocetinostat; vorinostat (e.g., Zolinza®); entinostat; belinostat (e.g., Beleodaq®); remetinostat; THM-I-91; LBH-589; Merck60; BRD6929; BRD-K11533227; PXD-101; pandacostat; CI-994; BRD-K61166597; apicidin; SAHA; BRD-K85133207
HDAC10	vorinostat (e.g., Zolinza®)
HDAC11	vorinostat (e.g., Zolinza®)
HDAC2	resminostat; citarinostat; abexinostat; romidepsin (e.g., Istodax®); tucidinostat; Epidaza®; panobinostat (e.g., Farydak®, Faridak); mocetinostat; vorinostat (e.g., Zolinza®); entinostat; belinostat (e.g., Beleodaq®); remetinostat; romidepsin; THM-I-91; LBH-589; Merck60; BRD6929; BRD-K11533227; PXD-101; pandacostat; CI-994; BRD-K61166597; apicidin; SAHA
HDAC3	resminostat; citarinostat; abexinostat; romidepsin (e.g., Istodax®); tucidinostat; Epidaza®; panobinostat (e.g., Farydak®, Faridak); mocetinostat; vorinostat (e.g., Zolinza®); entinostat; belinostat (e.g., Beleodaq®); remetinostat; THM-I-91; LBH-589; PXD-101; BRD-K29313308; pandacostat; Repligen 136; CI-994; apicidin; SAHA
HDAC4	vorinostat (e.g., Zolinza®); belinostat; panobinostat; romidepsin
HDAC5	vorinostat (e.g., Zolinza®); belinostat; panobinostat; romidepsin
HDAC6	resminostat; citarinostat; abexinostat; romidepsin (e.g., Istodax®); tucidinostat; Epidaza®; panobinostat (e.g., Farydak®, Faridak); mocetinostat; vorinostat (e.g., Zolinza®); entinostat; belinostat (e.g., Beleodaq®); remetinostat; ricolinostat; tubastatin A; THM-I-91; LBH-589; PXD-101; pandacostat; BRD-K51490254; CI-994; BRD-K55478147; apicidin; ISOX; BRD-K69840642; SAHA
HDAC7	vorinostat (e.g., Zolinza®); belinostat; panobinostat; romidepsi
HDAC8	vorinostat (e.g., Zolinza®); panobinostat; THM-I-91; LBH-589; belinostat; PXD-101; pandacostat; BRD-K51490254; CI-994; apicidin; entinostat; SAHA; BRD-K88742110; romidepsin
HDAC9	vorinostat (e.g., Zolinza®); belinostat; panobinostat; romidepsin
HPRT1	mercaptopurine
HPSE	muparfostat
HSP90AA1	tanespimycin; onalespib; luminespib; Debio 0932; retaspimycin; SNX-5422; ganetespib; XL888; geldanamycin; AT13387; SNX-2112; tanespymicin; 17-AAG
HSPA1A	elesclomol; VER-155008; pifithrin-mu; NSC303580
HSPA1B	elesclomol; VER-155008; pifithrin-mu; NSC303580
HSPB1	apatorsen
IDH1	ivosidenib; ML204; MH2075
IDH2	enasidenib (e.g., Idhifa®)

IDO1	epacadostat; navoximod; indoximod
IFNAR1	interferon alfa-2b, recombinant; peginterferon alfa-2b
IFNAR2	interferon alfa-2b, recombinant; peginterferon alfa-2b
IGF1R	BMS-536924; BMS-754807; linsitinib; XL228; ganitumab; BI 836845; BIIB022; figitumumab; cixutumumab; dusigitumab; dalotuzumab; istiratumab; AEW541; NVP-ADW742; OSI-906
IHH	glasdegib; vismodegib (e.g., Erivedge®)
IKBKB	PF-184; BMS-345541
IL1B	canakinumab (e.g., Ilaris®)
IL2RA	aldesleukin; denileukin diftitox
IL2RB	aldesleukin; denileukin diftitox
IL2RG	aldesleukin; denileukin diftitox
IL6	Siltuximab (e.g., Sylvant®)
IL6R	Tocilizumab (e.g., Actemra®)
IL6ST	Bazedoxifene; SC144
INHA	sotatercept
INHBA	sotatercept
INHBB	sotatercept
INHBC	sotatercept
INHBE	sotatercept
ITK	pazopanib hydrochloride; pazopanib
JAK1	PRT062070; itacitinib; INCB052793; AZD1480; momelotinib; ruxolitinib (e.g., Jakafi®, Jakavi, INCB018424); ruxolitinib phosphate; BIO; 6-bromoindirubin-3'-oxime (6BIO); CYT-387; INCB-18424
JAK2	AZD1480; momelotinib; ruxolitinib (e.g., Jakafi®, INCB018424, Jakavi); AT9283; BMS-911543; lestaurtinib; fedratinib; pacritinib; XL019; gandotinib; AZD1152-HQPA; AZ960; ruxolitinib phosphate; NVP-BSK805; BIO; 6-bromoindirubin-3'-oxime (6BIO); TG-101348; SAR302503; CYT-387; CEP-701; INCB-18424
JAK3	tofacitinib citrate (e.g., Xeljanz®); PRT062070; tasocitinib; BIO; 6-bromoindirubin-3'-oxime (6BIO)
KDM1A	GSK2879552; CBB-1007
KDR	linifanib; ENMD-2076; foretinib; sulfatinib; vatalanib; orantinib; X-82; XL647, KD019; ilorasertib; axitinib (e.g., Inlyta®); motesanib; regorafenib (e.g., Stivarga®, BAY-73-4506); nintedanib (e.g., Vargatef®, BIBF 1120); lucitanib; pazopanib (e.g., Votrient®, armala, GW786034); fruquintinib; tivozanib; glesatinib; sitravatinib; AEE788, NVP-AEE788; ponatinib (e.g., Iclusig®); cediranib; vandetanib (e.g., Zactima™, Caprelsa®, ZD6474); sorafenib (e.g., Nexavar®, BAY-43-9006); brivanib; BMS-690514, EVRI; rebastinib tosylate; lenvatinib (e.g., Lenvima®); midostaurin (e.g., Rydapt®); RAF265; sunitinib (e.g., Sutent®, SU11248); cabozantinib (e.g., Cabometyx® (tablet), Cometriq® (capsule)); XL820; apatinib; telatinib; ramucirumab (e.g., Cyramza®); sorafenib tosylate; sunitinib malate; pazopanib hydrochloride; thalidomide; XL880; EXEL-2880; GSK1363089; GSK089; OSI-930; BMS-582664; AG013736; E7080; Ki8751; XL184; BMS-907351; AV-951; BRD4658; MGCD-265; AZD2171; CHIR-265; ABT-869
KIF11	filanesib; SB-743921
KIT	masitinib; axitinib (e.g., Inlyta®); motesanib; cenisertib; telatinib; regorafenib (e.g., Stivarga®, BAY-73-4506); dasatinib (e.g., BMS-354825, Sprycel®); pazopanib (e.g., Votrient®, GW786034, armala); sitravatinib; tandutinib; amuvatinib; midostaurin (e.g., Rydapt®); PLX3397, PLX108-01; imatinib (e.g., Gleevec®); sunitinib malate (e.g., Sutent®, SU11248); cabozantinib (e.g., Cabometyx® (tablet), Cometriq® (capsule)); XL820; sorafenib (e.g., Nexavar®); midostaurin; sorafenib tosylate; pazopanib hydrochloride; sorafenib (e.g., BAY-43-9006, Nexavar®); Ki8751; cabozantinib (e.g., Cometriq®); XL184; BMS-907351; Masivet; nilotinib (e.g., AMN107, Tasigna®); MLN518; CT53518; AMG-706; imatinib; lenvatinib; ponatinib
KRAS	BGB-283

LAP3	tosedostat; CHR-2797
LCK	dasatinib (e.g., BMS-354825, Sprycel®); pazopanib
LDLR	porfimer
LHCGR	goserelin
LIMK1	dabrafenib
LYN	bafetinib; cenisertib; dasatinib (e.g., BMS-354825, Sprycel®); bosutinib; ponatinib
MAP1A	estramustine
MAP2	estramustine
MAP2K1	pimasertib; selumetinib; AZD8330; refametinib; BI 847325; CI-1040; GDC-0623; cobimetinib (e.g., Cotellic®); trametinib (e.g., Mekinist®; GSK1120212); binimetinib; PD0325901, RO5126766, CH5126766; TAK-733; PD318088; GSK1120212; JTP-74057; AZD6244
MAP2K2	pimasertib; selumetinib; AZD8330; refametinib; BI 847325; CI-1040; GDC-0623; cobimetinib (e.g., Cotellic®); trametinib (e.g., Mekinist®); binimetinib; PD0325901; RO5126766, CH5126766; TAK-733; PD318088; GSK1120212; JTP-74057; AZD6244; GSK1120212
MAP3K7	(5Z)-7-Oxozeaenol
MAP3K8	cyanquinoline 11
MAPK1	BVD-523; ralimetinib; MK-8353, SCH900353; N-hexanoyl-D-sphingosine; C6-ceramide; SCH772984
MAPK11	regorafenib
MAPK14	BIRB-796; doramapimod; skepinone-L; BIRB 0796
MAPK3	pluripotin; SCH772984
MAPK8	SP600125; BIRB 0796; JNK Inhibitor VIII
MAPK9	SP600125
MCL1	navitoclax; obatoclax; marinopyrrole a; maritoclax; obatoclax mesylate
MDM2	SAR405838, MI-773; idasanutlin; nutlin-3; RITA; NSC652287; HLI-373; DPD; JNJ-26854165; serdemetan; SJ-172550; Nutlin-3a
MET	sitravatinib; AMG 208; AMG 337; tivantinib; BMS-777607; EMD 1214063, MSC2156119J; foretinib; volitinib; INCB028060, INC280; glesatinib; MK-2461; amuvatinib; crizotinib (e.g., Xalkori®); PF-04217903; SAR125844; cabozantinib (e.g., Cabometyx® (tablet), Cometriq® (capsule)); rilotumumab; ficlatuzumab; telisotuzumab; emibetuzumab; onartuzumab; cMet CAR-mRNA Electroporated autologous T lymphocytes; MGCD-265; PHA665752; SU11274; XL880; EXEL-2880; GSK1363089; GSK089; SGX-523; OSI-930; ARQ-197; XL184; BMS-907351; PF-2341066; PF-02341066
MGMT	Lomeguatrib
MRE11	Mirin
MS4A1	obinutuzumab (e.g., Gazyvaro®, Gazyva®); rituximab (e.g., Rituxan®, Mabthera®); ibritumomab tiuxetan (e.g., Zevalin®); ublituximab; ofatumumab (e.g., Arzerra®, HuMax-CD20); rituximab/hyaluronidase human (e.g., Rituxan Hycela); rituximab (e.g., Rituxan®, Mabthera); tositumomab (e.g., Bexxar®); tositumomab and Iodine I 131 tositumomab; ofatumumab; obinutuzumab
MSLN	DMOT4039A; anti-mesothelin iCasp9M28z CAR-transduced autologous T lymphocytes; amatuximab
MST1R	Glesatinib
MTOR	ridaforolimus (deforolimus); sirolimus (e.g., Rapamune®); AZD2014; AZD8055; dactolisib; BGT226, NVP-BGT226; CC-223; temsirolimus (e.g., Torisel®); apitolisib; sapanisertib; OSI-027; PF-4691502; PI-103; gedatolisib; PWT33597; everolimus (e.g., Afinitor®); SF1126; voxalisib; BEZ235; GSK1059615; CCI-779; NVP-BEZ235; KU-0063794; XL765; SAR245409; rapamycin
MUC5AC	ensituximab
NAE1	pevonedistat; MLN-4924
NAMPT	GMX-1778; CHS-828; APO866; FK866; BRD0667; CAY10618

NBN	Rucaparib ; AG014699 ; PF-01367338 ; AG-014699
NCSTN	MK-0752; RO4929097; semagacestat; LY450139; L-685458
NEK11	dabrafenib
NOTCH1	brontictuzumab; MK0752; tarextumab; nirogacestat; REGN421; RO4929097, R4733
NOTCH2	MK0752; tarextumab; nirogacestat; REGN421; RO4929097, R4733
NOTCH3	MK0752; tarextumab; nirogacestat; REGN421; RO4929097, R4733
NOTCH4	MK0752; tarextumab; nirogacestat; REGN421; RO4929097, R4733
NPEPPS	tosedostat; CHR-2797
NR3C1	fluoxymersterone; avicin D; dexamethasone (e.g., Decadron®)
NRAS	BGB-283
NTRK1	AZD7451; LOXO-101; sitravatinib; PLX7486; entrectinib; TSR-011; lestaurtinib; regorafenib; CEP-701; GW 441756
NTRK2	AZD7451; LOXO-101; sitravatinib; PLX7486; entrectinib; TSR-011
NTRK3	AZD7451; LOXO-101; sitravatinib; PLX7486; entrectinib; TSR-011
PARP1	veliparib; rucaparib (e.g., Rubraca®); olaparib (e.g., Lynparza®); talazoparib; iniparib; niraparib (e.g., Zejula®); rucaparib camsylate; AZD-2281; KU-0059436; NVP-LDE225; BRD6430; ABT-888; BMN-673
PARP2	veliparib; rucaparib (e.g., Rubraca®); olaparib (e.g., Lynparza®); talazoparib; iniparib; niraparib (e.g., Zejula®); rucaparib camsylate; AZD-2281; KU-0059436; NVP-LDE225; BRD6430; ABT-888; BMN-673
PARP3	veliparib; rucaparib (e.g., Rubraca®); olaparib (e.g., Lynparza®); talazoparib; iniparib; niraparib (e.g., Zejula®); rucaparib camsylate
PDE5A	Sildenafil (e.g., Viagra®, Revatio®)
PDGFRA	ilorasertib; motesanib; nintedanib (e.g., Vargatef®, BIBF 1120); pazopanib (e.g., Votrient®); sitravatinib; tandutinib; imatinib (e.g., Gleevec®); X-82; crenolanib; amuvatinib; midostaurin (e.g., Rydapt®); olaratumab (e.g., Lartruvo®); tovetumab; sorafenib (e.g., Nexavar®); sunitinib malate; pazopanib hydrochloride; regorafenib; Ki8751; masitinib (e.g., Masivet®); AMG-706; axitinib
PDGFRB	ilorasertib; motesanib; nintedanib (e.g., Vargatef®, BIBF 1120); pazopanib (e.g., Votrient®, GW786034, armala); sitravatinib; tandutinib; imatinib (e.g., Gleevec®); X-82; linifanib; axitinib (e.g., Inlyta®); sorafenib (e.g., Nexavar®); telatinib; regorafenib (e.g., Stivarga®, BAY-43-9006); sunitinib (e.g., Sutent®, SU11248); orantinib; XL820; midostaurin; sorafenib tosylate; sunitinib malate; pazopanib hydrochloride; dasatinib (e.g., BMS-354825, Sprycel®); masitinib (e.g., Masivet®); MLN518; CT53518; ABT-869; AMG-706
PGF	ziv-aflibercept (e.g., Zaltrap®)
PIGF	ziv-aflibercept (e.g., Zaltrap®)
PIK3CA	copanlisib; dactolisib; BGT226; NVP-BGT226; buparlisib; alpelisib; pictilisib; apitolisib; omipalisib; GSK2636771; PF-4691502; PI-103; gedatolisib; PWT33597; PX-866; SF1126; pilaralisib; voxalisib; sophoretin; quercetin; taselisib; INK-1117; BEZ235; GDC0941; NVP-BYL-719; GSK1059615; NVP-BEZ235; BYL-719; XL765; SAR245409
PIK3CB	AZD8186; BEZ235; GDC0941; TGX-221; GSK1059615; NVP-BEZ235; GSK-2636771; AZD6482; PI-103; XL765; SAR245409
PIK3CD	Idelalisib (e.g., Zydelig®); dezapelisib; umbralisib tosylate; duvelisib; GDC0941; GSK1059615; BEZ235; NVP-BEZ235; CAL-101; TG100-115; PI-103; XL765; SAR245409; IC-87114
PIK3CG	AZD8186; duvelisib; GDC0941; GSK1059615; BEZ235; NVP-BEZ235; PIK-93; ZSTK474; TG100-115; PI-103; XL765; SAR245409
PIM1	AZD1208; PIM447
PIM2	AZD1208; PIM447
PIM3	AZD1208; PIM447; SL 0101-1
PLK1	volasertib; BI 2536; GSK461364; NMS-1286937; rigosertib (e.g., Estybon®, ON-01910); LFM-A13/DDE-28; Novonex; HMN-214; GW-843682X
PLK2	BI-2536; LFM-A13/DDE-28

PLK3	BI-2536; LFM-A13/DDE-28; GW-843682X
POLA1	clofarabine (e.g., Clolar®); nelarabine
PORCN	LGK974
PPARG	CS 7017, RS5444
PPP2CA	LB-100; N-hexanoyl-D-sphingosine; C6-ceramide
PRKCA	sophoretin, quercetin; enzastaurin; midostaurin (e.g., Rydapt®)
PRKCB	sophoretin, quercetin; enzastaurin; sotrastaurin; AEB071; LY317615
PRKCE	sophoretin, quercetin; enzastaurin
PRKCG	sophoretin, quercetin; enzastaurin
PRKCI	Gossypol
PRKDC	KU-0060648; PI-103; NU-7441
PRLR	Fluoxymesterone
PSEN1	MK-0752; RO4929097; semagacestat; LY450139; L-685458
PRMT5	GSK3326595
PSEN1	MRK-560
PSENN	MK0752; MRK 003; RO4929097; semagacestat; LY450139; L-685458; BMS-708163
PSMB1	bortezomib (e.g., Velcade®); carfilzomib
PSMB10	Carfilzomib
PSMB2	bortezomib; carfilzomib
PSMB5	bortezomib (e.g., Velcade®); carfilzomib; MLN2238; MLN9708
PSMB8	Carfilzomib
PSMB9	Carfilzomib
PSMD1	Bortezomib
PSMD2	Bortezomib
PTCH1	vismodegib (e.g., Erivedge®)
PTGS2	valdecoxib (e.g., Bextra®)
PTK2	masitinib; GSK2256098; VS-4718; defactinib; PF-573228; PF-562271
PTK6	Vandetanib
RAC1	NSC23766; EHT 1864
RAD50	Mirin
RAF1	sorafenib (e.g., Nexavar®); regorafenib (e.g., Stivarga®, BAY-73-4506); encorafenib; MLN2480; RO5126766; CH5126766; XL281, BMS-908662; RAF265; AZ628; GW 5074; sorafenib tosylate; dabrafenib
RARA	alitretinoin; AM-580; BMS-195614; ATRA; all-trans retinoic acid; tretinoin (e.g., Vesanoïd®); Ch-55
RARB	alitretinoin; LE-135; AM-580; BMS-195614; ATRA; all-trans retinoic acid; tretinoin (e.g., Vesanoïd®); Ch-55; AC55649
RARG	alitretinoin; BMS-270394; AM-580; CD-1530; CD-437; AHPN; BMS-195614; ATRA; all-trans retinoic acid; tretinoin (e.g., Vesanoïd®); Ch-55
RBM39	Indisulam
RET	motesanib; vandetanib (e.g., Zactima™, Caprelsa®); sorafenib (e.g., Nexavar®); regorafenib (e.g., Stivarga®, BAY-73-4506); sitravatinib; amuvatinib; sunitinib (e.g., Sutent®, SU11248); cabozantinib (e.g., Cabometyx® (tablet), Cometriq® (capsule)); AZD1152-HQPA; lestaurtinib; sorafenib tosylate; AMG-706; CEP-701; lenvatinib
RICTOR	OSI-027
ROCK1	GSK269962A
ROCK2	GSK269962A
ROS1	crizotinib (e.g., Xalkori®); lorlatinib; entrectinib
RPL3	omacetaxine mepesuccinate

RPS6KB1	AT13148; PF-4708671
RPTOR	OSI-027
RRM1	gemcitabine; Hydroxyurea; ciclopirox olamine (e.g., Loprox®); clofarabine (e.g., Clolar®)
RXRA	alitretinoin; bexarotene; targretin
RXRB	alitretinoin; bexarotene; targretin
RXRG	alitretinoin; bexarotene; targretin
S1PR1	fingolimod (e.g., FTY720, Gilenya®)
SH2B3	pazopanib hydrochloride
SHH	glasdegib; vismodegib (e.g., Erivedge)
SIK1	dabrafenib
SIRT1	salermide; isoliquiritigenin; GU 17; SRT-1720; EX-527; SEN0014196
SLAMF7	elotuzumab (e.g., Empliciti®)
SLC2A2	streptozocin
SMO	vismodegib (e.g., Erivedge®); patidegib; sonidegib (e.g., Odomzo®); taladegib; Cyclopamine; Vismodegib; GANT-61; purmorphamine; GDC-0449
SRC	saracatinib; ilarasertib; dasatinib (e.g., BMS-354825, Sprycel®); KX2-391; XL228; WH-4-025; AZD0530; KX01; bosutinib (e.g., SKI-606, Bosulif®); vandetanib
SSTR2	lanreotide
SSTR5	lanreotide
STAT3	OPB-31121; pyrimethamine (e.g., Daraprim®); niclosamide (e.g., Niclocide®); S3I-201; NSC74859
SYK	entospletinib; PRT062070; fostamatinib; R-406
TBK1	mometinib; BX-795
TEK	glesatinib; cabozantinib (e.g., Cabometyx® (tablet), Cometriq® (capsule)); vandetanib; regorafenib; XL184; BMS-907351; MGCD-265
TERT	BIBR-1532; MST-312
TGFB1	luspatercept
TGFB1	galunisertib; TEW-7197; SB-525334; SB-431542; LY-2157299; SB-505124
TLR5	Entolimod
TLR7	Imiquimod
TLR8	motolimod; imiquimod
TNF	thalidomide; lenalidomide
TNFRSF8	brentuximab vedotin (e.g., Adcetris®)
TNFSF11	denosumab (e.g., Xgeva)
TNFSF13B	belimumab (e.g., Benlysta)
TNKS	Chembridge cat# 7667791; XAV 939
TOP1	etirinotecan pegol; irinotecan (e.g., Camptosar®); irinotecan liposome (e.g., Onivyde®); camptothecin; irinotecan; topotecan hydrochloride; SN-38; 7-ethyl-10-hydroxycamptothecin; topotecan (e.g., Hycamtin®); irinotecan trihydrochloride
TOP1MT	irinotecan; topotecan hydrochloride
TOP2A	mitoxantrone (e.g., Novantrone®); daunorubicin (e.g., Cerubidine®); liposomal daunorubicin (e.g., DaunoXome®); doxorubicin (e.g., Adriamycin PFS®); liposomal doxorubicin (e.g., Doxil®); epirubicin (e.g., Ellence®); idarubicin (e.g., Idamycin®); valrubicin (e.g., Valstar); etoposide/etoposide phosphate (e.g., Toposar, Etopophos®); teniposide (e.g., Vumon®, VM-26); amonafide; hydroxydaunorubicin
TOP2B	mitoxantrone (e.g., Novantrone®); daunorubicin (e.g., Cerubidine®); liposomal daunorubicin (e.g., DaunoXome®); doxorubicin (e.g., Adriamycin PFS®); liposomal doxorubicin (e.g., Doxil®); epirubicin (e.g., Ellence®); idarubicin (e.g., Idamycin®); valrubicin (e.g., Valstar); etoposide/etoposide phosphate (e.g., Toposar, Etopophos®); teniposide (e.g., Vumon®, VM-26); amonafide
TUBA1A	vinblastine sulfate (e.g., Oncovin®)

TUBA4A	vincristine sulfate (e.g., Oncovin®); paclitaxel (e.g., Taxol®); docetaxel (e.g., Taxotere®); cabazitaxel; eribulin mesylate
TUBB	vincristine sulfate (e.g., Oncovin®); vinblastine sulfate; vinorelbine tartrate
TUBB1	paclitaxel (e.g., Taxol®); docetaxel (e.g., Taxotere®); cabazitaxel; eribulin mesylate; vincristine (e.g., Oncovin®); leurocristine
TUBB3	Ixabepilone
TUBD1	vinblastine sulfate
TUBE1	vinblastine sulfate
TUBG1	vinblastine sulfate
TXN	PX-12; IV-2
TYK2	INCB-18424
TYMS	leucovorin; gemcitabine; capecitabine; pemetrexed disodium; pralatrexate; fluorouracil (e.g., Adrucil®, Efudex®)
VDR	BXL-628; elocalcitol
VEGFA	bevacizumab (e.g., Avastin®); navicixizumab; vanucizumab; muparfostat; ziv-aflibercept (e.g., Zaltrap®); vandetanib
VEGFB	ziv-aflibercept (e.g., Zaltrap®); muparfostat; bevacizumab (e.g., Avastin®)
WEE1	AZD1775, MK1775; 681640; MK-1775; BRD9876
XIAP	birinapant; embelin; LBW242; SM-406; AT-406; TL-32711
XPO1	selinexor; leptomycin B; compound 7d-cis; BRD9047
YES1	dasatinib (e.g., BMS-354825, Sprycel®)

[00282] Tables 4-5C provide exemplary protein targets of known therapeutic agents, one or more of which may be useful in a target library described herein.

Table 4. Gene targets of therapeutic agents.

<i>Gene Symbol</i>	<i>Ensembl ID</i>	<i>Gene Name</i>	<i>Chr</i>	<i>Position</i>
ABAT	ENSG00000183044	4-aminobutyrate aminotransferase	16	8674596-8784575
ABCA1	ENSG00000165029	ATP binding cassette subfamily A member 1	9	104781006-104928155
ABCC1	ENSG00000103222	ATP binding cassette subfamily C member 1	16	15949577-16143074
ABCC2	ENSG00000023839	ATP binding cassette subfamily C member 2	10	99782640-99852594
ABCC8	ENSG00000006071	ATP binding cassette subfamily C member 8	11	17392498-17476879
ABL1	ENSG00000097007	ABL proto-oncogene 1, non-receptor tyrosine kinase	9	130713016-130887675
ABL2	ENSG00000143322	ABL proto-oncogene 2, non-receptor tyrosine kinase	1	179099330-179229684
ACAA1	ENSG00000060971	Acetyl-CoA acyltransferase 1	3	38103129-38137242
ACE	ENSG00000159640	Angiotensin I converting enzyme	17	63477061-63498380
ACE2	ENSG00000130234	Angiotensin I converting enzyme 2	X	15561033-15602148
ACHE	ENSG00000087085	Acetylcholinesterase (Cartwright blood group)	7	100889994-100896974
ACP3	ENSG00000014257	Acid phosphatase 3	3	132317369-132368298
ADA	ENSG00000196839	Adenosine deaminase	20	44619522-44652233

ADH1A	ENSG00000187758	Alcohol dehydrogenase 1A (class I), alpha polypeptide	4	99276369-99291003
ADH1B	ENSG00000196616	Alcohol dehydrogenase 1B (class I), beta polypeptide	4	99304971-99352760
ADH1C	ENSG00000248144	Alcohol dehydrogenase 1C (class I), gamma polypeptide	4	99336497-99352746
ADK	ENSG00000156110	Adenosine kinase	10	74151202-74709963
ADORA1	ENSG00000163485	Adenosine A1 receptor	1	203090654-203167405
ADORA2A	ENSG00000128271	Adenosine A2a receptor	22	24417879-24442357
ADORA2B	ENSG00000170425	Adenosine A2b receptor	17	15944917-15975746
ADORA3	ENSG00000282608	Adenosine A3 receptor	1	111499429-111503633
ADRA1A	ENSG00000120907	Adrenoceptor alpha 1A	8	26748150-26867278
ADRA1B	ENSG00000170214	Adrenoceptor alpha 1B	5	159865080-159973012
ADRA1D	ENSG00000171873	Adrenoceptor alpha 1D	20	4220630-4249287
ADRA2A	ENSG00000150594	Adrenoceptor alpha 2A	10	111077029-111080907
ADRA2C	ENSG00000184160	Adrenoceptor alpha 2C	4	3766348-3768526
ADRB1	ENSG00000043591	Adrenoceptor beta 1	10	114043866-114046904
ADRB2	ENSG00000169252	Adrenoceptor beta 2	5	148825245-148828687
ADRB3	ENSG00000188778	Adrenoceptor beta 3	8	37962990-37966599
AGTR1	ENSG00000144891	Angiotensin II receptor type 1	3	148697784-148743008
AGXT	ENSG00000172482	Alanine--glyoxylate and serine--pyruvate aminotransferase	2	240868824-240880502
AKR1C2	ENSG00000151632	Aldo-keto reductase family 1 member C2	10	4987400-5018031
AKR1D1	ENSG00000122787	Aldo-keto reductase family 1 member D1	7	138002324-138118305
AKT1	ENSG00000142208	AKT serine/threonine kinase 1	14	104769349-104795751
AKT2	ENSG00000105221	AKT serine/threonine kinase 2	19	40230317-40285536
AKT3	ENSG00000117020	AKT serine/threonine kinase 3	1	243488233-243851079
ALAD	ENSG00000148218	Aminolevulinate dehydratase	9	113386312-113401290
ALDH2	ENSG00000111275	Aldehyde dehydrogenase 2 family member	12	111766887-111817532
ALK	ENSG00000171094	ALK receptor tyrosine kinase	2	29192774-29921586
ALOX5	ENSG00000012779	Arachidonate 5-lipoxygenase	10	45374176-45446119
ALPG	ENSG00000163286	Alkaline phosphatase, germ cell	2	232406844-232410714
AMY2A	ENSG00000243480	Amylase alpha 2A	1	103616811-103625780
ANGPT1	ENSG00000154188	Angiopietin 1	8	107249482-107498055

ANGPT2	ENSG00000091879	Angiopoietin 2	8	6499632-6563409
ANO1	ENSG00000131620	Anoctamin 1	11	70078302-70189528
ANPEP	ENSG00000166825	Alanyl aminopeptidase, membrane	15	89784895-89815401
ANXA1	ENSG00000135046	Annexin A1	9	73151865-73170393
AOC3	ENSG00000131471	Amine oxidase copper containing 3	17	42851184-42858130
APEX1	ENSG00000100823	Apurinic/apurimidinic endodeoxyribonuclease 1	14	20455191-20457772
APH1A	ENSG00000117362	Aph-1 homolog A, gamma-secretase subunit	1	150265399-150269580
APH1B	ENSG00000138613	Aph-1 homolog B, gamma-secretase subunit	15	63276018-63309126
APP	ENSG00000142192	Amyloid beta precursor protein	21	25880550-26171128
AR	ENSG00000169083	Androgen receptor	X	67544021-67730619
ARAF	ENSG00000078061	A-Raf proto-oncogene, serine/threonine kinase	X	47561100-47571920
ASIC1	ENSG00000110881	Acid sensing ion channel subunit 1	12	50057548-50083611
ATIC	ENSG00000138363	5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase/IMP cyclohydrolase	2	215311956-215349773
ATP1A1	ENSG00000163399	ATPase Na ⁺ /K ⁺ transporting subunit alpha 1	1	116372668-116410261
ATP2C1	ENSG00000017260	ATPase secretory pathway Ca ²⁺ transporting 1	3	130850595-131016712
ATP4A	ENSG00000105675	ATPase H ⁺ /K ⁺ transporting subunit alpha	19	35550031-35563658
ATP6V1B2	ENSG00000147416	ATPase H ⁺ transporting V1 subunit B2	8	20197381-20226819
ATR	ENSG00000175054	ATR serine/threonine kinase	3	142449007-142578733
AURKA	ENSG00000087586	Aurora kinase A	20	56369389-56392337
AURKB	ENSG00000178999	Aurora kinase B	17	8204733-8210600
AURKC	ENSG00000105146	Aurora kinase C	19	57230802-57235548
AVPR1A	ENSG00000166148	Arginine vasopressin receptor 1A	12	63142759-63151201
AVPR1B	ENSG00000198049	Arginine vasopressin receptor 1B	1	206106936-206117699
AVPR2	ENSG00000126895	Arginine vasopressin receptor 2	X	153902531-153907166
AXL	ENSG00000167601	AXL receptor tyrosine kinase	19	41219223-41261766
B4GALNT1	ENSG00000135454	Beta-1,4-N-acetyl-galactosaminyltransferase 1	12	57623409-57633239
BAX	ENSG00000087088	BCL2 associated X, apoptosis regulator	19	48954815-48961798
BCHE	ENSG00000114200	Butyrylcholinesterase	3	165772904-165837462
BCL2	ENSG00000171791	BCL2 apoptosis regulator	18	63123346-63320128
BCL2L1	ENSG00000171552	BCL2 like 1	20	31664452-31723989

BCL2L2	ENSG00000129473	BCL2 like 2	14	23298790- 23311751
BCR	ENSG00000186716	BCR activator of RhoGEF and GTPase	22	23179704- 23318037
BDKRB2	ENSG00000168398	Bradykinin receptor B2	14	96204679- 96244166
BGLAP	ENSG00000242252	Bone gamma-carboxyglutamate protein	1	156242184- 156243317
BIRC5	ENSG00000089685	Baculoviral IAP repeat containing 5	17	78214186- 78225636
BLK	ENSG00000136573	BLK proto-oncogene, Src family tyrosine kinase	8	11486894- 11564599
BLVRB	ENSG00000090013	Biliverdin reductase B	19	40447765- 40465764
BMX	ENSG00000102010	BMX non-receptor tyrosine kinase	X	15464246- 15556529
BRAF	ENSG00000157764	B-Raf proto-oncogene, serine/threonine kinase	7	140719327- 140924928
BRD2	ENSG00000204256	Bromodomain containing 2	6	32968594- 32981505
BRD3	ENSG00000169925	Bromodomain containing 3	9	134030305- 134068535
BRD4	ENSG00000141867	Bromodomain containing 4	19	15235519- 15332545
BTK	ENSG0000010671	Bruton tyrosine kinase	X	101349447- 101390796
C1R	ENSG00000159403	Complement C1r	12	7080214- 7092540
C1S	ENSG00000182326	Complement C1s	12	6988259- 7071032
C3	ENSG00000125730	Complement C3	19	6677704- 6730562
C4A	ENSG00000244731	Complement C4A (Rodgers blood group)	6	31982057- 32002681
C4B	ENSG00000224389	Complement C4B (Chido blood group)	6	32014795- 32035418
C5	ENSG00000106804	Complement C5	9	120952335- 121050275
CA1	ENSG00000133742	Carbonic anhydrase 1	8	85327608- 85379014
CA14	ENSG00000118298	Carbonic anhydrase 14	1	150257251- 150265078
CA2	ENSG00000104267	Carbonic anhydrase 2	8	85463968- 85481493
CA3	ENSG00000164879	Carbonic anhydrase 3	8	85373436- 85449040
CA4	ENSG00000167434	Carbonic anhydrase 4	17	60149942- 60170899
CA7	ENSG00000168748	Carbonic anhydrase 7	16	66844414- 66854153
CACNA1A	ENSG00000141837	Calcium voltage-gated channel subunit alpha1 A	19	13206442- 13633025
CACNA1B	ENSG00000148408	Calcium voltage-gated channel subunit alpha1 B	9	137877782- 138124624
CACNA1C	ENSG00000151067	Calcium voltage-gated channel subunit alpha1 C	12	1970786- 2697950
CACNA1D	ENSG00000157388	Calcium voltage-gated channel subunit alpha1 D	3	53328963- 53813733
CACNA1F	ENSG00000102001	Calcium voltage-gated channel subunit alpha1 F	X	49205063- 49233371

CACNA1G	ENSG00000006283	Calcium voltage-gated channel subunit alpha1 G	17	50560715-50627474
CACNA1H	ENSG00000196557	Calcium voltage-gated channel subunit alpha1 H	16	1153106-1221771
CACNA1I	ENSG00000100346	Calcium voltage-gated channel subunit alpha1 I	22	39570753-39689735
CACNA1S	ENSG00000081248	Calcium voltage-gated channel subunit alpha1 S	1	201039512-201112451
CACNA2D1	ENSG00000153956	Calcium voltage-gated channel auxiliary subunit alpha2delta 1	7	81946444-82443777
CACNA2D2	ENSG00000007402	Calcium voltage-gated channel auxiliary subunit alpha2delta 2	3	50362799-50504244
CACNB1	ENSG00000067191	Calcium voltage-gated channel auxiliary subunit beta 1	17	39173453-39197703
CACNB2	ENSG00000165995	Calcium voltage-gated channel auxiliary subunit beta 2	10	18140424-18543557
CACNB3	ENSG00000167535	Calcium voltage-gated channel auxiliary subunit beta 3	12	48813794-48828941
CACNB4	ENSG00000182389	Calcium voltage-gated channel auxiliary subunit beta 4	2	151832768-152099475
CACNG1	ENSG00000108878	Calcium voltage-gated channel auxiliary subunit gamma 1	17	67044554-67056797
CALY	ENSG00000130643	Calcyon neuron specific vesicular protein	10	133324072-133336935
CAMLG	ENSG00000164615	Calcium modulating ligand	5	134738548-134752157
CARTPT	ENSG00000164326	CART prepropeptide	5	71719275-71721048
CASR	ENSG00000036828	Calcium sensing receptor	3	122183668-122291629
CAT	ENSG00000121691	Catalase	11	34438934-34472060
CCKAR	ENSG00000163394	Cholecystokinin A receptor	4	26481396-26490484
CCKBR	ENSG00000110148	Cholecystokinin B receptor	11	6259806-6272127
CCL2	ENSG00000108691	C-C motif chemokine ligand 2	17	34255218-34257203
CCND1	ENSG00000110092	Cyclin D1	11	69641156-69654474
CCND2	ENSG00000118971	Cyclin D2	12	4273762-4305353
CCND3	ENSG00000112576	Cyclin D3	6	41934934-42050357
CCR5	ENSG00000160791	C-C motif chemokine receptor 5 (gene/pseudogene)	3	46370854-46376206
CD19	ENSG00000177455	CD19 molecule	16	28931965-28939342
CD2	ENSG00000116824	CD2 molecule	1	116754430-116769229
CD247	ENSG00000198821	CD247 molecule	1	167430640-167518610
CD274	ENSG00000120217	CD274 molecule	9	5450503-5470566
CD33	ENSG00000105383	CD33 molecule	19	51225064-51243860
CD38	ENSG00000004468	CD38 molecule	4	15778275-15853232
CD3D	ENSG00000167286	CD3d molecule	11	118338954-118342744

CD3E	ENSG00000198851	CD3e molecule	11	118304730-118316175
CD3G	ENSG00000160654	CD3g molecule	11	118344344-118355161
CD4	ENSG00000010610	CD4 molecule	12	6786858-6820799
CD44	ENSG00000026508	CD44 molecule (Indian blood group)	11	35138870-35232402
CD52	ENSG00000169442	CD52 molecule	1	26317958-26320523
CD80	ENSG00000121594	CD80 molecule	3	119524293-119559614
CD86	ENSG00000114013	CD86 molecule	3	122055362-122121139
CDK1	ENSG00000170312	Cyclin dependent kinase 1	10	60778331-60794852
CDK2	ENSG00000123374	Cyclin dependent kinase 2	12	55966781-55972789
CDK4	ENSG00000135446	Cyclin dependent kinase 4	12	57747727-57756013
CDK5	ENSG00000164885	Cyclin dependent kinase 5	7	151053815-151057897
CDK6	ENSG00000105810	Cyclin dependent kinase 6	7	92604921-92836573
CDK7	ENSG00000134058	Cyclin dependent kinase 7	5	69234795-69277430
CDK9	ENSG00000136807	Cyclin dependent kinase 9	9	127785679-127790792
CES1	ENSG00000198848	Carboxylesterase 1	16	55802851-55833337
CFTR	ENSG00000001626	CF transmembrane conductance regulator	7	117287120-117715971
CHD1	ENSG00000153922	Chromodomain helicase DNA binding protein 1	5	98853985-98928957
CHEK1	ENSG00000149554	Checkpoint kinase 1	11	125625665-125676255
CHEK2	ENSG00000183765	Checkpoint kinase 2	22	28687743-28742422
CHRM1	ENSG00000168539	Cholinergic receptor muscarinic 1	11	62908679-62921807
CHRM2	ENSG00000181072	Cholinergic receptor muscarinic 2	7	136868669-137020255
CHRM3	ENSG00000133019	Cholinergic receptor muscarinic 3	1	239386565-239915452
CHRM4	ENSG00000180720	Cholinergic receptor muscarinic 4	11	46385098-46386608
CHRM5	ENSG00000184984	Cholinergic receptor muscarinic 5	15	33968497-34067458
CHRNA10	ENSG00000129749	Cholinergic receptor nicotinic alpha 10 subunit	11	3665587-3671384
CHRNA2	ENSG00000120903	Cholinergic receptor nicotinic alpha 2 subunit	8	27459756-27479883
CHRNA3	ENSG00000080644	Cholinergic receptor nicotinic alpha 3 subunit	15	78593052-78621295
CHRNA4	ENSG00000101204	Cholinergic receptor nicotinic alpha 4 subunit	20	63343223-63378401
CHRNA7	ENSG00000175344	Cholinergic receptor nicotinic alpha 7 subunit	15	31923438-32173018
CHRNB2	ENSG00000160716	Cholinergic receptor nicotinic beta 2 subunit	1	154567778-154580013

CHRNA4	ENSG00000117971	Cholinergic receptor nicotinic beta 4 subunit	15	78624111-78727754
CKB	ENSG00000166165	Creatine kinase B	14	103519667-103522833
CKM	ENSG00000104879	Creatine kinase, M-type	19	45306413-45322875
CKMT1A	ENSG00000223572	Creatine kinase, mitochondrial 1A	15	43692886-43699222
CKMT1B	ENSG00000237289	Creatine kinase, mitochondrial 1B	15	43593054-43604901
CKMT2	ENSG00000131730	Creatine kinase, mitochondrial 2	5	81233320-81266398
CLCN2	ENSG00000114859	Chloride voltage-gated channel 2	3	184346185-184361650
CNR1	ENSG00000118432	Cannabinoid receptor 1	6	88139864-88166359
CNR2	ENSG00000188822	Cannabinoid receptor 2	1	23870515-23913362
COMT	ENSG00000093010	Catechol-O-methyltransferase	22	19941733-19969975
CPS1	ENSG00000021826	Carbamoyl-phosphate synthase 1	2	210477682-210679107
CPT1A	ENSG00000110090	Carnitine palmitoyltransferase 1A	11	68754620-68844410
CPT2	ENSG00000157184	Carnitine palmitoyltransferase 2	1	53196792-53214197
CRBN	ENSG00000113851	Cereblon	3	3144628-3179727
CRHR1	ENSG00000120088	Corticotropin releasing hormone receptor 1	17	45784280-45835828
CRTC1	ENSG00000105662	CREB regulated transcription coactivator 1	19	18683678-18782333
CRTC2	ENSG00000160741	CREB regulated transcription coactivator 2	1	153947669-153958615
CSF1R	ENSG00000182578	Colony stimulating factor 1 receptor	5	150053291-150113372
CSF2RA	ENSG00000198223	Colony stimulating factor 2 receptor subunit alpha	X	1268800-1310381
CSF2RB	ENSG00000100368	Colony stimulating factor 2 receptor subunit beta	22	36913628-36940439
CSF3R	ENSG00000119535	Colony stimulating factor 3 receptor	1	36466043-36483278
CSNK2A1	ENSG00000101266	Casein kinase 2 alpha 1	20	472498-543835
CSNK2A2	ENSG00000070770	Casein kinase 2 alpha 2	16	58157907-58198106
CTLA4	ENSG00000163599	Cytotoxic T-lymphocyte associated protein 4	2	203867771-203873965
CXCR1	ENSG00000163464	C-X-C motif chemokine receptor 1	2	218162841-218166962
CXCR2	ENSG00000180871	C-X-C motif chemokine receptor 2	2	218125289-218137251
CXCR4	ENSG00000121966	C-X-C motif chemokine receptor 4	2	136114349-136118149
CYP11A1	ENSG00000140459	Cytochrome P450 family 11 subfamily A member 1	15	74337759-74367646
CYP11B1	ENSG00000160882	Cytochrome P450 family 11 subfamily B member 1	8	142872356-142879846
CYP11B2	ENSG00000179142	Cytochrome P450 family 11 subfamily B member 2	8	142910558-142917862

CYP17A1	ENSG00000148795	Cytochrome P450 family 17 subfamily A member 1	10	102830531-102837472
CYP19A1	ENSG00000137869	Cytochrome P450 family 19 subfamily A member 1	15	51208057-51338601
CYP51A1	ENSG00000001630	Cytochrome P450 family 51 subfamily A member 1	7	92112153-92134803
CYSLTR1	ENSG00000173198	Cysteinyl leukotriene receptor 1	X	78271468-78327691
CYSLTR2	ENSG00000152207	Cysteinyl leukotriene receptor 2	13	48653711-48711226
DBH	ENSG00000123454	Dopamine beta-hydroxylase	9	133636363-133659329
DCK	ENSG00000156136	Deoxycytidine kinase	4	70992538-71030914
DDC	ENSG00000132437	Dopa decarboxylase	7	50458436-50565405
DDR2	ENSG00000162733	Discoidin domain receptor tyrosine kinase 2	1	162631373-162787405
DHFR	ENSG00000228716	Dihydrofolate reductase	5	80626226-80654983
DHH	ENSG00000139549	Desert hedgehog signaling molecule	12	49086656-49094801
DHODH	ENSG00000102967	Dihydroorotate dehydrogenase (quinone)	16	72008588-72027664
DHX9	ENSG00000135829	DEXH-box helicase 9	1	182839347-182887982
DNMT1	ENSG00000130816	DNA methyltransferase 1	19	10133345-10231286
DOT1L	ENSG00000104885	DOT1 like histone lysine methyltransferase	19	2163933-2232578
DPEP1	ENSG00000015413	Dipeptidase 1	16	89613308-89638456
DPP4	ENSG00000197635	Dipeptidyl peptidase 4	2	161992245-162074215
DRD1	ENSG00000184845	Dopamine receptor D1	5	175440036-175444182
DRD2	ENSG00000149295	Dopamine receptor D2	11	113409605-113475691
DRD3	ENSG00000151577	Dopamine receptor D3	3	114127580-114199407
DRD4	ENSG00000069696	Dopamine receptor D4	11	637269-640706
DRD5	ENSG00000169676	Dopamine receptor D5	4	9781634-9784009
DYRK1A	ENSG00000157540	Dual specificity tyrosine phosphorylation regulated kinase 1A	21	37365573-37526358
DYRK1B	ENSG00000105204	Dual specificity tyrosine phosphorylation regulated kinase 1B	19	39825350-39834201
DYRK2	ENSG00000127334	Dual specificity tyrosine phosphorylation regulated kinase 2	12	67648338-67665406
DYRK3	ENSG00000143479	Dual specificity tyrosine phosphorylation regulated kinase 3	1	206635536-206684419
DYRK4	ENSG00000010219	Dual specificity tyrosine phosphorylation regulated kinase 4	12	4562204-4615302
EDNRA	ENSG00000151617	Endothelin receptor type A	4	147480917-147544954
EDNRB	ENSG00000136160	Endothelin receptor type B	13	77895481-77975529
EGF	ENSG00000138798	Epidermal growth factor	4	109912883-110013766

EGFR	ENSG00000146648	Epidermal growth factor receptor	7	55019021-55211628
EHMT1	ENSG00000181090	Euchromatic histone lysine methyltransferase 1	9	137618992-137870016
EHMT2	ENSG00000204371	Euchromatic histone lysine methyltransferase 2	6	31879759-31897687
EIF4E	ENSG00000151247	Eukaryotic translation initiation factor 4E	4	98871684-98930637
ELANE	ENSG00000197561	Elastase, neutrophil expressed	19	851014-856247
EPHA2	ENSG00000142627	EPH receptor A2	1	16124337-16156069
EPHB4	ENSG00000196411	EPH receptor B4	7	100802565-100827523
EPOR	ENSG00000187266	Erythropoietin receptor	19	11377207-11384342
ERBB2	ENSG00000141736	Erb-b2 receptor tyrosine kinase 2	17	39687914-39730426
ERBB3	ENSG00000065361	Erb-b2 receptor tyrosine kinase 3	12	56076799-56103505
ERBB4	ENSG00000178568	Erb-b2 receptor tyrosine kinase 4	2	211375717-212538841
ESR1	ENSG00000091831	Estrogen receptor 1	6	151656691-152129619
ESR2	ENSG00000140009	Estrogen receptor 2	14	64084232-64338112
ESRRG	ENSG00000196482	Estrogen related receptor gamma	1	216503246-217137755
EZH2	ENSG00000106462	Enhancer of zeste 2 polycomb repressive complex 2 subunit	7	148807383-148884321
F10	ENSG00000126218	Coagulation factor X	13	113122799-113149529
F11	ENSG00000088926	Coagulation factor XI	4	186266189-186289681
F12	ENSG00000131187	Coagulation factor XII	5	177402140-177409576
F2	ENSG00000180210	Coagulation factor II, thrombin	11	46719196-46739506
F2R	ENSG00000181104	Coagulation factor II thrombin receptor	5	76716126-76735770
F3	ENSG00000117525	Coagulation factor III, tissue factor	1	94529173-94541759
F5	ENSG00000198734	Coagulation factor V	1	169511951-169586588
F7	ENSG00000057593	Coagulation factor VII	13	113105788-113120685
F8	ENSG00000185010	Coagulation factor VIII	X	154835788-155026940
F9	ENSG00000101981	Coagulation factor IX	X	139530739-139563459
FADS1	ENSG00000149485	Fatty acid desaturase 1	11	61799627-61829318
FADS2	ENSG00000134824	Fatty acid desaturase 2	11	61792980-61867354
FASN	ENSG00000169710	Fatty acid synthase	17	82078338-82098294
FCER1A	ENSG00000179639	Fc fragment of IgE receptor Ia	1	159289714-159308224
FCER1G	ENSG00000158869	Fc fragment of IgE receptor Ig	1	161215234-161220699

FCGR1A	ENSG00000150337	Fc fragment of IgG receptor Ia	1	149782671- 149792518
FCGR1B	ENSG00000198019	Fc fragment of IgG receptor Ib	1	121087345- 121097161
FCGR2A	ENSG00000143226	Fc fragment of IgG receptor IIa	1	161505430- 161524013
FCGR2B	ENSG00000072694	Fc fragment of IgG receptor IIb	1	161663147- 161678654
FCGR3A	ENSG00000203747	Fc fragment of IgG receptor IIIa	1	161541759- 161550737
FCGR3B	ENSG00000162747	Fc fragment of IgG receptor IIIb	1	161623196- 161631963
FDPS	ENSG00000160752	Farnesyl diphosphate synthase	1	155308748- 155320666
FFAR1	ENSG00000126266	Free fatty acid receptor 1	19	35351552- 35353862
FGA	ENSG00000171560	Fibrinogen alpha chain	4	154583128- 154590745
FGF1	ENSG00000113578	Fibroblast growth factor 1	5	142592178- 142698070
FGF2	ENSG00000138685	Fibroblast growth factor 2	4	122826708- 122898236
FGFR1	ENSG00000077782	Fibroblast growth factor receptor 1	8	38400215- 38468834
FGFR2	ENSG00000066468	Fibroblast growth factor receptor 2	10	121478332- 121598458
FGFR3	ENSG00000068078	Fibroblast growth factor receptor 3	4	1793293- 1808872
FGFR4	ENSG00000160867	Fibroblast growth factor receptor 4	5	177086905- 177098144
FGR	ENSG00000000938	FGR proto-oncogene, Src family tyrosine kinase	1	27612064- 27635185
FKBP1A	ENSG00000088832	FKBP prolyl isomerase 1A	20	1368978- 1393172
FLT1	ENSG00000102755	Fms related receptor tyrosine kinase 1	13	28300346- 28495145
FLT3	ENSG00000122025	Fms related receptor tyrosine kinase 3	13	28003274- 28100592
FLT4	ENSG00000037280	Fms related receptor tyrosine kinase 4	5	180601506- 180649624
FN1	ENSG00000115414	Fibronectin 1	2	215360440- 215436073
FNTA	ENSG00000168522	Farnesyltransferase, CAAX box, alpha	8	43034194- 43085788
FOLH1	ENSG00000086205	Folate hydrolase 1	11	49145092- 49208638
FOLR1	ENSG00000110195	Folate receptor alpha	11	72189558- 72196323
FOLR2	ENSG00000165457	Folate receptor beta	11	72216601- 72221950
FOLR3	ENSG00000110203	Folate receptor gamma	11	72114869- 72139892
FRK	ENSG00000111816	Fyn related Src family tyrosine kinase	6	115931149- 116060891
FSHR	ENSG00000170820	Follicle stimulating hormone receptor	2	48962157- 49154527
FTH1	ENSG00000167996	Ferritin heavy chain 1	11	61959718- 61967634
FTL	ENSG00000087086	Ferritin light chain	19	48965309- 48966879

FXD2	ENSG00000137731	FXD domain containing ion transport regulator 2	11	117800844-117828698
FYN	ENSG0000010810	FYN proto-oncogene, Src family tyrosine kinase	6	111660332-111873452
FZD8	ENSG00000177283	Frizzled class receptor 8	10	35638249-35642278
GAA	ENSG00000171298	Glucosidase alpha, acid	17	80101556-80119881
GABBR1	ENSG00000204681	Gamma-aminobutyric acid type B receptor subunit 1	6	29555629-29633976
GABBR2	ENSG00000136928	Gamma-aminobutyric acid type B receptor subunit 2	9	98288109-98708935
GABRA1	ENSG00000022355	Gamma-aminobutyric acid type A receptor subunit alpha1	5	161847063-161899981
GABRA2	ENSG00000151834	Gamma-aminobutyric acid type A receptor subunit alpha2	4	46248427-46475230
GABRA3	ENSG00000011677	Gamma-aminobutyric acid type A receptor subunit alpha3	X	152166234-152451315
GABRA4	ENSG00000109158	Gamma-aminobutyric acid type A receptor subunit alpha4	4	46918900-46993581
GABRA5	ENSG00000186297	Gamma-aminobutyric acid type A receptor subunit alpha5	15	26866911-26949208
GABRA6	ENSG00000145863	Gamma-aminobutyric acid type A receptor subunit alpha6	5	161547063-161702593
GABRB1	ENSG00000163288	Gamma-aminobutyric acid type A receptor subunit beta1	4	46993723-47426447
GABRB2	ENSG00000145864	Gamma-aminobutyric acid type A receptor subunit beta2	5	161288429-161549044
GABRB3	ENSG00000166206	Gamma-aminobutyric acid type A receptor subunit beta3	15	26543546-26939539
GABRD	ENSG00000187730	Gamma-aminobutyric acid type A receptor subunit delta	1	2019329-2030758
GABRE	ENSG00000102287	Gamma-aminobutyric acid type A receptor subunit epsilon	X	151953124-151974680
GABRG1	ENSG00000163285	Gamma-aminobutyric acid type A receptor subunit gamma1	4	46035769-46124054
GABRG2	ENSG00000113327	Gamma-aminobutyric acid type A receptor subunit gamma2	5	162000057-162162977
GABRG3	ENSG00000182256	Gamma-aminobutyric acid type A receptor subunit gamma3	15	26971181-27541984
GABRP	ENSG00000094755	Gamma-aminobutyric acid type A receptor subunit pi	5	170763350-170814047
GABRQ	ENSG00000268089	Gamma-aminobutyric acid type A receptor subunit theta	X	152637895-152657542
GABRR1	ENSG00000146276	Gamma-aminobutyric acid type A receptor subunit rho1	6	89177504-89231278
GABRR2	ENSG00000111886	Gamma-aminobutyric acid type A receptor subunit rho2	6	89254464-89315299
GABRR3	ENSG00000183185	Gamma-aminobutyric acid type A receptor subunit rho3 (gene/pseudogene)	3	97986673-98035304
GAMT	ENSG00000130005	Guanidinoacetate N-methyltransferase	19	1397026-1401570
GANAB	ENSG00000089597	Glucosidase II alpha subunit	11	62624826-62646726
GANC	ENSG00000214013	Glucosidase alpha, neutral C	15	42273233-42356935
GART	ENSG00000159131	Phosphoribosylglycinamide formyltransferase, phosphoribosylglycinamide synthetase, phosphoribosylaminoimidazole synthetase	21	33503931-33543491
GCGR	ENSG00000215644	Glucagon receptor	17	81804132-81814008

GGCX	ENSG00000115486	Gamma-glutamyl carboxylase	2	85544720- 85561547
GGPS1	ENSG00000152904	Geranylgeranyl diphosphate synthase 1	1	235327350- 235344532
GHR	ENSG00000112964	Growth hormone receptor	5	42423439- 42721878
GHRHR	ENSG00000106128	Growth hormone releasing hormone receptor	7	30938669- 30993254
GLP1R	ENSG00000112164	Glucagon like peptide 1 receptor	6	39048781- 39091303
GLP2R	ENSG00000065325	Glucagon like peptide 2 receptor	17	9822206- 9892099
GLRA1	ENSG00000145888	Glycine receptor alpha 1	5	151822513- 151924851
GLRA2	ENSG00000101958	Glycine receptor alpha 2	X	14529298- 14731812
GLRA3	ENSG00000145451	Glycine receptor alpha 3	4	174636920- 174829247
GLRB	ENSG00000109738	Glycine receptor beta	4	157076125- 157172090
GNRH1	ENSG00000147437	Gonadotropin releasing hormone 1	8	25419258- 25424654
GNRHR	ENSG00000109163	Gonadotropin releasing hormone receptor	4	67737118- 67754388
GRIA1	ENSG00000155511	Glutamate ionotropic receptor AMPA type subunit 1	5	153489615- 153813869
GRIK1	ENSG00000171189	Glutamate ionotropic receptor kainate type subunit 1	21	29536933- 29940033
GRIN1	ENSG00000176884	Glutamate ionotropic receptor NMDA type subunit 1	9	137139154- 137168756
GRIN2A	ENSG00000183454	Glutamate ionotropic receptor NMDA type subunit 2A	16	9753404- 10182754
GRIN2B	ENSG00000273079	Glutamate ionotropic receptor NMDA type subunit 2B	12	13437942- 13981957
GRIN2C	ENSG00000161509	Glutamate ionotropic receptor NMDA type subunit 2C	17	74842023- 74861504
GRIN2D	ENSG00000105464	Glutamate ionotropic receptor NMDA type subunit 2D	19	48394875- 48444931
GRIN3A	ENSG00000198785	Glutamate ionotropic receptor NMDA type subunit 3A	9	101569352- 101738647
GRIN3B	ENSG00000116032	Glutamate ionotropic receptor NMDA type subunit 3B	19	1000419- 1009732
GRM5	ENSG00000168959	Glutamate metabotropic receptor 5	11	88504576- 89065945
GSK3A	ENSG00000105723	Glycogen synthase kinase 3 alpha	19	42230190- 42242625
GSK3B	ENSG00000082701	Glycogen synthase kinase 3 beta	3	119821321- 120094447
GSR	ENSG00000104687	Glutathione-disulfide reductase	8	30678066- 30727846
GSS	ENSG00000100983	Glutathione synthetase	20	34928432- 34956027
GUCY1A2	ENSG00000152402	Guanylate cyclase 1 soluble subunit alpha 2	11	106674019- 107018476
GUCY2C	ENSG00000070019	Guanylate cyclase 2C	12	14612632- 14696599
HBA1	ENSG00000206172	Hemoglobin subunit alpha 1	16	176680-177522
HBA2	ENSG00000188536	Hemoglobin subunit alpha 2	16	172876-173710
HBB	ENSG00000244734	Hemoglobin subunit beta	11	5225464- 5229395

HCAR2	ENSG00000182782	Hydroxycarboxylic acid receptor 2	12	122701293- 122703357
HCAR3	ENSG00000255398	Hydroxycarboxylic acid receptor 3	12	122714756- 122716811
HCK	ENSG00000101336	HCK proto-oncogene, Src family tyrosine kinase	20	32052188- 32101856
HCRTR1	ENSG00000121764	Hypocretin receptor 1	1	31617686- 31632518
HCRTR2	ENSG00000137252	Hypocretin receptor 2	6	55106460- 55282620
HDAC1	ENSG00000116478	Histone deacetylase 1	1	32292083- 32333635
HDAC10	ENSG00000100429	Histone deacetylase 10	22	50245183- 50251405
HDAC11	ENSG00000163517	Histone deacetylase 11	3	13479724- 13506424
HDAC2	ENSG00000196591	Histone deacetylase 2	6	113933028- 114011308
HDAC3	ENSG00000171720	Histone deacetylase 3	5	141620876- 141636849
HDAC4	ENSG00000068024	Histone deacetylase 4	2	239048168- 239401654
HDAC5	ENSG00000108840	Histone deacetylase 5	17	44076746- 44123702
HDAC6	ENSG00000094631	Histone deacetylase 6	X	48801377- 48824982
HDAC7	ENSG00000061273	Histone deacetylase 7	12	47782722- 47833132
HDAC8	ENSG00000147099	Histone deacetylase 8	X	72329516- 72573101
HDAC9	ENSG00000048052	Histone deacetylase 9	7	18086949- 19002416
HMGCR	ENSG00000113161	3-hydroxy-3-methylglutaryl-CoA reductase	5	75336329- 75362101
HMMR	ENSG00000072571	Hyaluronan mediated motility receptor	5	163460203- 163491941
HPD	ENSG00000158104	4-hydroxyphenylpyruvate dioxygenase	12	121839527- 121863596
HPRT1	ENSG00000165704	Hypoxanthine phosphoribosyltransferase 1	X	134460165- 134520513
HPSE	ENSG00000173083	Heparanase	4	83292461- 83335153
HRH1	ENSG00000196639	Histamine receptor H1	3	11137093- 11263557
HRH2	ENSG00000113749	Histamine receptor H2	5	175658030- 175710756
HRH3	ENSG00000101180	Histamine receptor H3	20	62214960- 62220278
HSD3B1	ENSG00000203857	Hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1	1	119507198- 119515054
HSD3B2	ENSG00000203859	Hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2	1	119414931- 119423035
HSP90AA1	ENSG00000080824	Heat shock protein 90 alpha family class A member 1	14	102080742- 102139699
HSPA1A	ENSG00000204389	Heat shock protein family A (Hsp70) member 1A	6	31815543- 31817946
HSPA1B	ENSG00000204388	Heat shock protein family A (Hsp70) member 1B	6	31827738- 31830254
HSPB1	ENSG00000106211	Heat shock protein family B (small) member 1	7	76302673- 76304295

HTR1A	ENSG00000178394	5-hydroxytryptamine receptor 1A	5	63957874-63962507
HTR1B	ENSG00000135312	5-hydroxytryptamine receptor 1B	6	77460924-77463491
HTR1D	ENSG00000179546	5-hydroxytryptamine receptor 1D	1	23191895-23194729
HTR1E	ENSG00000168830	5-hydroxytryptamine receptor 1E	6	86937528-87016679
HTR1F	ENSG00000179097	5-hydroxytryptamine receptor 1F	3	87990696-87993835
HTR2A	ENSG00000102468	5-hydroxytryptamine receptor 2A	13	46831550-46897076
HTR2B	ENSG00000135914	5-hydroxytryptamine receptor 2B	2	231108230-231125042
HTR2C	ENSG00000147246	5-hydroxytryptamine receptor 2C	X	114584078-114910061
HTR3A	ENSG00000166736	5-hydroxytryptamine receptor 3A	11	113974881-113990313
HTR3B	ENSG00000149305	5-hydroxytryptamine receptor 3B	11	113904677-113949078
HTR3C	ENSG00000178084	5-hydroxytryptamine receptor 3C	3	184053047-184060673
HTR3D	ENSG00000186090	5-hydroxytryptamine receptor 3D	3	184031544-184039369
HTR3E	ENSG00000186038	5-hydroxytryptamine receptor 3E	3	184097064-184106995
HTR4	ENSG00000164270	5-hydroxytryptamine receptor 4	5	148451032-148677235
HTR6	ENSG00000158748	5-hydroxytryptamine receptor 6	1	19664875-19680966
HTR7	ENSG00000148680	5-hydroxytryptamine receptor 7	10	90740823-90858039
ICAM1	ENSG00000090339	Intercellular adhesion molecule 1	19	10271093-10286615
IDE	ENSG00000119912	Insulin degrading enzyme	10	92451684-92574093
IDH1	ENSG00000138413	Isocitrate dehydrogenase (NADP(+)) 1	2	208236227-208266074
IDH2	ENSG00000182054	Isocitrate dehydrogenase (NADP(+)) 2	15	90083045-90102477
IDO1	ENSG00000131203	Indoleamine 2,3-dioxygenase 1	8	39902275-39928790
IFNAR1	ENSG00000142166	Interferon alpha and beta receptor subunit 1	21	33324429-33359864
IFNAR2	ENSG00000159110	Interferon alpha and beta receptor subunit 2	21	33229901-33265675
IFNG	ENSG00000111537	Interferon gamma	12	68154768-68159740
IFNGR1	ENSG00000027697	Interferon gamma receptor 1	6	137197485-137219449
IFNGR2	ENSG00000159128	Interferon gamma receptor 2	21	33402896-33479348
IGF1R	ENSG00000140443	Insulin like growth factor 1 receptor	15	98648539-98964530
IHH	ENSG00000163501	Indian hedgehog signaling molecule	2	219054424-219060921
IKBKB	ENSG00000104365	Inhibitor of nuclear factor kappa B kinase subunit beta	8	42271302-42332653
IL11RA	ENSG00000137070	Interleukin 11 receptor subunit alpha	9	34650702-34661902

IL12B	ENSG00000113302	Interleukin 12B	5	159314780- 159330487
IL17A	ENSG00000112115	Interleukin 17A	6	52186375- 52190638
IL1B	ENSG00000125538	Interleukin 1 beta	2	112829751- 112836816
IL1R1	ENSG00000115594	Interleukin 1 receptor type 1	2	102064544- 102179874
IL23A	ENSG00000110944	Interleukin 23 subunit alpha	12	56334174- 56340410
IL2RA	ENSG00000134460	Interleukin 2 receptor subunit alpha	10	6010689- 6062370
IL2RB	ENSG00000100385	Interleukin 2 receptor subunit beta	22	37125843- 37175054
IL2RG	ENSG00000147168	Interleukin 2 receptor subunit gamma	X	71107404- 71112108
IL3RA	ENSG00000185291	Interleukin 3 receptor subunit alpha	X	1336616- 1382689
IL5	ENSG00000113525	Interleukin 5	5	132541445- 132556838
IL6	ENSG00000136244	Interleukin 6	7	22725884- 22732002
IL6R	ENSG00000160712	Interleukin 6 receptor	1	154405193- 154469450
IL6ST	ENSG00000134352	Interleukin 6 signal transducer	5	55935095- 55995022
IMPDH1	ENSG00000106348	Inosine monophosphate dehydrogenase 1	7	128392277- 128410252
IMPDH2	ENSG00000178035	Inosine monophosphate dehydrogenase 2	3	49024325- 49029408
INH A	ENSG00000123999	Inhibin subunit alpha	2	219569162- 219575711
INHBA	ENSG00000122641	Inhibin subunit beta A	7	41667168- 41705834
INHBB	ENSG00000163083	Inhibin subunit beta B	2	120346136- 120351803
INHBC	ENSG00000175189	Inhibin subunit beta C	12	57434784- 57452062
INHBE	ENSG00000139269	Inhibin subunit beta E	12	57452323- 57459280
INSR	ENSG00000171105	Insulin receptor	19	7112255- 7294414
ITGA2B	ENSG00000005961	Integrin subunit alpha 2b	17	44372180- 44389649
ITGA4	ENSG00000115232	Integrin subunit alpha 4	2	181457202- 181538940
ITGAL	ENSG00000005844	Integrin subunit alpha L	16	30472719- 30523185
ITGAV	ENSG00000138448	Integrin subunit alpha V	2	186590056- 186680901
ITGB1	ENSG00000150093	Integrin subunit beta 1	10	32900318- 33005792
ITGB3	ENSG00000259207	Integrin subunit beta 3	17	47253827- 47313743
ITGB7	ENSG00000139626	Integrin subunit beta 7	12	53191323- 53207282
ITK	ENSG00000113263	IL2 inducible T cell kinase	5	157142933- 157255185
JAK1	ENSG00000162434	Janus kinase 1	1	64833229- 65067754

JAK2	ENSG00000096968	Janus kinase 2	9	4984390-5129948
JAK3	ENSG00000105639	Janus kinase 3	19	17824780-17848071
JUN	ENSG00000177606	Jun proto-oncogene, AP-1 transcription factor subunit	1	58780791-58784047
KCNA1	ENSG00000111262	Potassium voltage-gated channel subfamily A member 1	12	4909905-4918256
KCNA10	ENSG00000143105	Potassium voltage-gated channel subfamily A member 10	1	110517217-110519175
KCNA2	ENSG00000177301	Potassium voltage-gated channel subfamily A member 2	1	110519837-110631474
KCNA3	ENSG00000177272	Potassium voltage-gated channel subfamily A member 3	1	110672465-110674940
KCNA4	ENSG00000182255	Potassium voltage-gated channel subfamily A member 4	11	30009730-30017030
KCNA5	ENSG00000130037	Potassium voltage-gated channel subfamily A member 5	12	5043879-5046788
KCNA6	ENSG00000151079	Potassium voltage-gated channel subfamily A member 6	12	4809176-4813412
KCNA7	ENSG00000104848	Potassium voltage-gated channel subfamily A member 7	19	49067418-49072941
KCNB1	ENSG00000158445	Potassium voltage-gated channel subfamily B member 1	20	49293394-49484297
KCNB2	ENSG00000182674	Potassium voltage-gated channel subfamily B member 2	8	72537225-72938349
KCNC1	ENSG00000129159	Potassium voltage-gated channel subfamily C member 1	11	17734774-17856804
KCNC2	ENSG00000166006	Potassium voltage-gated channel subfamily C member 2	12	75040077-75209839
KCNC3	ENSG00000131398	Potassium voltage-gated channel subfamily C member 3	19	50311937-50333515
KCND1	ENSG00000102057	Potassium voltage-gated channel subfamily D member 1	X	48961378-48971844
KCND2	ENSG00000184408	Potassium voltage-gated channel subfamily D member 2	7	120273175-120750337
KCND3	ENSG00000171385	Potassium voltage-gated channel subfamily D member 3	1	111770662-111989155
KCNE1	ENSG00000180509	Potassium voltage-gated channel subfamily E regulatory subunit 1	21	34446688-34512210
KCNH2	ENSG00000055118	Potassium voltage-gated channel subfamily H member 2	7	150944961-150978321
KCNJ1	ENSG00000151704	Potassium inwardly rectifying channel subfamily J member 1	11	128836315-128867373
KCNJ11	ENSG00000187486	Potassium inwardly rectifying channel subfamily J member 11	11	17385859-17389331
KCNJ12	ENSG00000184185	Potassium inwardly rectifying channel subfamily J member 12	17	21376357-21419870
KCNJ8	ENSG00000121361	Potassium inwardly rectifying channel subfamily J member 8	12	21764955-21775600
KCNK2	ENSG00000082482	Potassium two pore domain channel subfamily K member 2	1	215005775-215237093
KCNK3	ENSG00000171303	Potassium two pore domain channel subfamily K member 3	2	26692690-26733420
KCNK9	ENSG00000169427	Potassium two pore domain channel subfamily K member 9	8	139600838-139704109
KCNMA1	ENSG00000156113	Potassium calcium-activated channel subfamily M alpha 1	10	76869601-77638369
KCNN4	ENSG00000104783	Potassium calcium-activated channel subfamily N member 4	19	43766533-43781257

KCNQ1	ENSG00000053918	Potassium voltage-gated channel subfamily Q member 1	11	2444684-2849105
KCNQ2	ENSG00000075043	Potassium voltage-gated channel subfamily Q member 2	20	63400210-63472677
KCNQ3	ENSG00000184156	Potassium voltage-gated channel subfamily Q member 3	8	132120859-132481095
KDM1A	ENSG00000004487	Lysine demethylase 1A	1	23019443-23083689
KDR	ENSG00000128052	Kinase insert domain receptor	4	55078481-55125595
KEAP1	ENSG00000079999	Kelch like ECH associated protein 1	19	10486125-10503558
KIF11	ENSG00000138160	Kinesin family member 11	10	92593130-92655395
KIT	ENSG00000157404	KIT proto-oncogene, receptor tyrosine kinase	4	54657918-54740715
KLKB1	ENSG00000164344	Kallikrein B1	4	186208979-186258471
KRAS	ENSG00000133703	KRAS proto-oncogene, GTPase	12	25205246-25250936
LAP3	ENSG00000002549	Leucine aminopeptidase 3	4	17577192-17607972
LCK	ENSG00000182866	LCK proto-oncogene, Src family tyrosine kinase	1	32251239-32286165
LDLR	ENSG00000130164	Low density lipoprotein receptor	19	11089462-11133820
LEPR	ENSG00000116678	Leptin receptor	1	65420652-65641559
LHCGR	ENSG00000138039	Luteinizing hormone/choriogonadotropin receptor	2	48686774-48755730
LIMK1	ENSG00000106683	LIM domain kinase 1	7	74082933-74122525
LIPF	ENSG00000182333	Lipase F, gastric type	10	88664441-88678814
LPL	ENSG00000175445	Lipoprotein lipase	8	19901717-19967259
LYN	ENSG00000254087	LYN proto-oncogene, Src family tyrosine kinase	8	55879835-56014169
M6PR	ENSG00000003056	Mannose-6-phosphate receptor, cation dependent	12	8940361-8949761
MAOA	ENSG00000189221	Monoamine oxidase A	X	43654907-43746824
MAOB	ENSG00000069535	Monoamine oxidase B	X	43766610-43882450
MAP1A	ENSG00000166963	Microtubule associated protein 1A	15	43510958-43531620
MAP2	ENSG00000078018	Microtubule associated protein 2	2	209424058-209734118
MAP2K1	ENSG00000169032	Mitogen-activated protein kinase kinase 1	15	66386837-66491544
MAP2K2	ENSG00000126934	Mitogen-activated protein kinase kinase 2	19	4090321-4124122
MAP3K7	ENSG00000135341	Mitogen-activated protein kinase kinase kinase 7	6	90513573-90587072
MAP3K8	ENSG00000107968	Mitogen-activated protein kinase kinase kinase 8	10	30434021-30461833
MAP4	ENSG00000047849	Microtubule associated protein 4	3	47850690-48089272
MAPK1	ENSG00000100030	Mitogen-activated protein kinase 1	22	21759657-21867680

MAPK11	ENSG00000185386	Mitogen-activated protein kinase 11	22	50263713- 50270767
MAPK14	ENSG00000112062	Mitogen-activated protein kinase 14	6	36027677- 36111236
MAPK3	ENSG00000102882	Mitogen-activated protein kinase 3	16	30114105- 30123506
MAPK8	ENSG00000107643	Mitogen-activated protein kinase 8	10	48306639- 48439360
MAPK9	ENSG00000050748	Mitogen-activated protein kinase 9	5	180233143- 180292099
MAPT	ENSG00000186868	Microtubule associated protein tau	17	45894382- 46028334
MC2R	ENSG00000185231	Melanocortin 2 receptor	18	13882044- 13915707
MCL1	ENSG00000143384	MCL1 apoptosis regulator, BCL2 family member	1	150574551- 150579738
MDM2	ENSG00000135679	MDM2 proto-oncogene	12	68808177- 68850686
MET	ENSG00000105976	MET proto-oncogene, receptor tyrosine kinase	7	116672196- 116798386
METAP2	ENSG00000111142	Methionyl aminopeptidase 2	12	95473520- 95515839
MGAM	ENSG00000257335	Maltase-glucoamylase	7	141907813- 142106747
MGMT	ENSG00000170430	O-6-methylguanine-DNA methyltransferase	10	129467190- 129770983
MME	ENSG00000196549	Membrane metalloendopeptidase	3	155024124- 155183729
MMP1	ENSG00000196611	Matrix metallopeptidase 1	11	102789919- 102798160
MMP10	ENSG00000166670	Matrix metallopeptidase 10	11	102770502- 102780628
MMP11	ENSG00000099953	Matrix metallopeptidase 11	22	23768226- 23784316
MMP12	ENSG00000262406	Matrix metallopeptidase 12	11	102862736- 102874982
MMP13	ENSG00000137745	Matrix metallopeptidase 13	11	102942995- 102955732
MMP14	ENSG00000157227	Matrix metallopeptidase 14	14	22836560- 22849027
MMP15	ENSG00000102996	Matrix metallopeptidase 15	16	58025754- 58046901
MMP16	ENSG00000156103	Matrix metallopeptidase 16	8	88032011- 88328025
MMP17	ENSG00000198598	Matrix metallopeptidase 17	12	131828393- 131851783
MMP19	ENSG00000123342	Matrix metallopeptidase 19	12	55835433- 55842966
MMP2	ENSG00000087245	Matrix metallopeptidase 2	16	55389700- 55506691
MMP20	ENSG00000137674	Matrix metallopeptidase 20	11	102576832- 102625332
MMP21	ENSG00000154485	Matrix metallopeptidase 21	10	125753580- 125775821
MMP23B	ENSG00000189409	Matrix metallopeptidase 23B	1	1632163- 1635263
MMP24	ENSG00000125966	Matrix metallopeptidase 24	20	35226690- 35276998
MMP25	ENSG00000008516	Matrix metallopeptidase 25	16	3046561- 3060726

MMP26	ENSG00000167346	Matrix metalloproteinase 26	11	4704927-4992429
MMP27	ENSG00000137675	Matrix metalloproteinase 27	11	102691487-102705769
MMP28	ENSG00000271447	Matrix metalloproteinase 28	17	35756249-35795707
MMP3	ENSG00000149968	Matrix metalloproteinase 3	11	102835801-102843609
MMP7	ENSG00000137673	Matrix metalloproteinase 7	11	102520508-102530750
MMP8	ENSG00000118113	Matrix metalloproteinase 8	11	102711796-102727050
MMP9	ENSG00000100985	Matrix metalloproteinase 9	20	46008908-46016561
MPL	ENSG00000117400	MPL proto-oncogene, thrombopoietin receptor	1	43337818-43354466
MR1	ENSG00000153029	Major histocompatibility complex, class I-related	1	181033425-181061938
MS4A1	ENSG00000156738	Membrane spanning 4-domains A1	11	60455846-60470752
MS4A2	ENSG00000149534	Membrane spanning 4-domains A2	11	60088261-60098467
MSLN	ENSG00000102854	Mesothelin	16	760734-768865
MST1R	ENSG00000164078	Macrophage stimulating 1 receptor	3	49887002-49903873
MTNR1A	ENSG00000168412	Melatonin receptor 1A	4	186533655-186555567
MTNR1B	ENSG00000134640	Melatonin receptor 1B	11	92969720-92985066
MTOR	ENSG00000198793	Mechanistic target of rapamycin kinase	1	11106535-11262551
MTR	ENSG00000116984	5-methyltetrahydrofolate-homocysteine methyltransferase	1	236795292-236921278
MTTP	ENSG00000138823	Microsomal triglyceride transfer protein	4	99563761-99623999
MUC5AC	ENSG00000215182	Mucin 5AC, oligomeric mucus/gel-forming	11	1157953-1201138
MUTT	ENSG00000146085	Methylmalonyl-CoA mutase	6	49430360-49463191
NAE1	ENSG00000159593	NEDD8 activating enzyme E1 subunit 1	16	66802875-66873256
NAMPT	ENSG00000105835	Nicotinamide phosphoribosyltransferase	7	106248298-106286326
NBN	ENSG00000104320	Nibrin	8	89933331-90003228
NCSTN	ENSG00000162736	Nicastrin	1	160343316-160358952
NEK11	ENSG00000114670	NIMA related kinase 11	3	131026850-131350465
NFKB1	ENSG00000109320	Nuclear factor kappa B subunit 1	4	102501331-102617302
NISCH	ENSG00000010322	Nischarin	3	52455118-52493068
NNMT	ENSG00000166741	Nicotinamide N-methyltransferase	11	114257787-114313285
NOS2	ENSG00000007171	Nitric oxide synthase 2	17	27756766-27800529
NOS3	ENSG00000164867	Nitric oxide synthase 3	7	150991017-151014588

NOTCH1	ENSG00000148400	Notch receptor 1	9	136494433- 136546048
NOTCH2	ENSG00000134250	Notch receptor 2	1	119911553- 120100779
NOTCH3	ENSG00000074181	Notch receptor 3	19	15159038- 15200995
NOTCH4	ENSG00000204301	Notch receptor 4	6	32194843- 32224067
NOXO1	ENSG00000196408	NADPH oxidase organizer 1	16	1978917- 1984192
NPC1L1	ENSG00000015520	NPC1 like intracellular cholesterol transporter 1	7	44512535- 44541315
NPEPPS	ENSG00000141279	Aminopeptidase puromycin sensitive	17	47522942- 47623276
NPR1	ENSG00000169418	Natriuretic peptide receptor 1	1	153678688- 153693992
NPR2	ENSG00000159899	Natriuretic peptide receptor 2	9	35792154- 35809732
NR1H4	ENSG00000012504	Nuclear receptor subfamily 1 group H member 4	12	100473708- 100564414
NR1I2	ENSG00000144852	Nuclear receptor subfamily 1 group I member 2	3	119780484- 119818485
NR3C1	ENSG00000113580	Nuclear receptor subfamily 3 group C member 1	5	143277931- 143435512
NR3C2	ENSG00000151623	Nuclear receptor subfamily 3 group C member 2	4	148078762- 148444698
NRAS	ENSG00000213281	NRAS proto-oncogene, GTPase	1	114704469- 114716771
NTRK1	ENSG00000198400	Neurotrophic receptor tyrosine kinase 1	1	156815640- 156881850
NTRK2	ENSG00000148053	Neurotrophic receptor tyrosine kinase 2	9	84668551- 85027070
NTRK3	ENSG00000140538	Neurotrophic receptor tyrosine kinase 3	15	87859751- 88256768
NTSR2	ENSG00000169006	Neurotensin receptor 2	2	11658178- 11670195
ODC1	ENSG00000115758	Ornithine decarboxylase 1	2	10439968- 10448327
OPRD1	ENSG00000116329	Opioid receptor delta 1	1	28812142- 28871267
OPRK1	ENSG00000082556	Opioid receptor kappa 1	8	53225716- 53251697
OPRM1	ENSG00000112038	Opioid receptor mu 1	6	154010496- 154246867
OXTR	ENSG00000180914	Oxytocin receptor	3	8750408- 8769628
P2RX4	ENSG00000135124	Purinergic receptor P2X 4	12	121209857- 121234106
P2RY12	ENSG00000169313	Purinergic receptor P2Y12	3	151336843- 151384753
P2RY2	ENSG00000175591	Purinergic receptor P2Y2	11	73218298- 73236352
PAH	ENSG00000171759	Phenylalanine hydroxylase	12	102836889- 102958410
PARP1	ENSG00000143799	Poly(ADP-ribose) polymerase 1	1	226360691- 226408093
PARP2	ENSG00000129484	Poly(ADP-ribose) polymerase 2	14	20343582- 20357905
PARP3	ENSG00000041880	Poly(ADP-ribose) polymerase family member 3	3	51942345- 51948867

PCSK9	ENSG00000169174	Proprotein convertase subtilisin/kexin type 9	1	55039447-55064852
PDCD1	ENSG00000188389	Programmed cell death 1	2	241849884-241858894
PDE10A	ENSG00000112541	Phosphodiesterase 10A	6	165327287-165988078
PDE3A	ENSG00000172572	Phosphodiesterase 3A	12	20369245-20684381
PDE4A	ENSG00000065989	Phosphodiesterase 4A	19	10416773-10469630
PDE4B	ENSG00000184588	Phosphodiesterase 4B	1	65792514-66374579
PDE4C	ENSG00000105650	Phosphodiesterase 4C	19	18208652-18248200
PDE4D	ENSG00000113448	Phosphodiesterase 4D	5	58969038-60522120
PDE5A	ENSG00000138735	Phosphodiesterase 5A	4	119494397-119628804
PDE7A	ENSG00000205268	Phosphodiesterase 7A	8	65714334-65842322
PDE7B	ENSG00000171408	Phosphodiesterase 7B	6	135851701-136195574
PDGFRA	ENSG00000134853	Platelet derived growth factor receptor alpha	4	54229280-54298245
PDGFRB	ENSG00000113721	Platelet derived growth factor receptor beta	5	150113839-150155872
PDXK	ENSG00000160209	Pyridoxal kinase	21	43719094-43762307
PGF	ENSG00000119630	Placental growth factor	14	74941834-74955626
PGR	ENSG00000082175	Progesterone receptor	11	101029624-101129813
PIGF	ENSG00000151665	Phosphatidylinositol glycan anchor biosynthesis class F	2	46580937-46617055
PIK3CA	ENSG00000121879	Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit alpha	3	179148114-179240093
PIK3CB	ENSG00000051382	Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit beta	3	138652698-138834928
PIK3CD	ENSG00000171608	Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta	1	9651731-9729114
PIK3CG	ENSG00000105851	Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma	7	106865278-106908980
PIM1	ENSG00000137193	Pim-1 proto-oncogene, serine/threonine kinase	6	37170152-37175428
PIM2	ENSG00000102096	Pim-2 proto-oncogene, serine/threonine kinase	X	48913182-48919024
PIM3	ENSG00000198355	Pim-3 proto-oncogene, serine/threonine kinase	22	49960768-49964072
PLA2G1B	ENSG00000170890	Phospholipase A2 group IB	12	120322115-120327779
PLA2G2A	ENSG00000188257	Phospholipase A2 group IIA	1	19975431-19980416
PLA2G4A	ENSG00000116711	Phospholipase A2 group IVA	1	186828949-186988981
PLA2G6	ENSG00000184381	Phospholipase A2 group VI	22	38111495-38214778
PLAT	ENSG00000104368	Plasminogen activator, tissue type	8	42174718-42207676
PLAU	ENSG00000122861	Plasminogen activator, urokinase	10	73909177-73917496

PLAUR	ENSG00000011422	Plasminogen activator, urokinase receptor	19	43646095- 43670547
PLCL1	ENSG000000115896	Phospholipase C like 1 (inactive)	2	197804593- 198572581
PLG	ENSG000000122194	Plasminogen	6	160702238- 160753315
PLIN3	ENSG000000105355	Perilipin 3	19	4838341- 4867694
PLK1	ENSG000000166851	Polo like kinase 1	16	23677656- 23690367
PLK2	ENSG000000145632	Polo like kinase 2	5	58453982- 58460139
PLK3	ENSG000000173846	Polo like kinase 3	1	44800377- 44805990
PNLIP	ENSG000000175535	Pancreatic lipase	10	116545931- 116567855
PNP	ENSG000000198805	Purine nucleoside phosphorylase	14	20468954- 20477089
POLA1	ENSG000000101868	DNA polymerase alpha 1, catalytic subunit	X	24693909- 24996986
POLB	ENSG000000070501	DNA polymerase beta	8	42338454- 42371808
POLE	ENSG000000177084	DNA polymerase epsilon, catalytic subunit	12	132623753- 132687376
POLE2	ENSG000000100479	DNA polymerase epsilon 2, accessory subunit	14	49643555- 49688422
POLE3	ENSG000000148229	DNA polymerase epsilon 3, accessory subunit	9	113407235- 113410675
POLE4	ENSG000000115350	DNA polymerase epsilon 4, accessory subunit	2	74958643- 74970128
PORCN	ENSG000000102312	Porcupine O-acyltransferase	X	48508962- 48520814
PPARA	ENSG000000186951	Peroxisome proliferator activated receptor alpha	22	46150521- 46243756
PPARD	ENSG000000112033	Peroxisome proliferator activated receptor delta	6	35342558- 35428191
PPARG	ENSG000000132170	Peroxisome proliferator activated receptor gamma	3	12287368- 12434356
PPP2CA	ENSG000000113575	Protein phosphatase 2 catalytic subunit alpha	5	134194332- 134226073
PPP3R2	ENSG000000188386	Protein phosphatase 3 regulatory subunit B, beta	9	101591604- 101595021
PRDX5	ENSG000000126432	Peroxisiredoxin 5	11	64318121- 64321811
PRKAA1	ENSG000000132356	Protein kinase AMP-activated catalytic subunit alpha 1	5	40759379- 40798374
PRKAB1	ENSG000000111725	Protein kinase AMP-activated non-catalytic subunit beta 1	12	119667864- 119681624
PRKCA	ENSG000000154229	Protein kinase C alpha	17	66302613- 66810743
PRKCB	ENSG000000166501	Protein kinase C beta	16	23835983- 24220611
PRKCE	ENSG000000171132	Protein kinase C epsilon	2	45651345- 46187990
PRKCG	ENSG000000126583	Protein kinase C gamma	19	53879190- 53907652
PRKCI	ENSG000000163558	Protein kinase C iota	3	170222424- 170305977
PRKDC	ENSG000000253729	Protein kinase, DNA-activated, catalytic subunit	8	47773111- 47960178

PRLR	ENSG00000113494	Prolactin receptor	5	35048756-35230487
PRMT5	ENSG00000100462	Protein arginine methyltransferase 5	14	22920525-22929408
PROC	ENSG00000115718	Protein C, inactivator of coagulation factors Va and VIIIa	2	127418427-127429242
PROS1	ENSG00000184500	Protein S	3	93873051-93980003
PSEN1	ENSG00000080815	Presenilin 1	14	73136418-73223691
PSENEN	ENSG00000205155	Presenilin enhancer, gamma-secretase subunit	19	35745600-35747519
PSMB1	ENSG00000080818	Proteasome 20S subunit beta 1	6	170535120-170553307
PSMB10	ENSG00000205220	Proteasome 20S subunit beta 10	16	67934506-67936864
PSMB2	ENSG00000126067	Proteasome 20S subunit beta 2	1	35599541-35641526
PSMB5	ENSG00000100804	Proteasome 20S subunit beta 5	14	23016543-23035230
PSMB8	ENSG00000204264	Proteasome 20S subunit beta 8	6	32840717-32844679
PSMB9	ENSG00000240065	Proteasome 20S subunit beta 9	6	32844136-32859851
PSMD1	ENSG00000173692	Proteasome 26S subunit, non-ATPase 1	2	231056864-231172827
PSMD2	ENSG00000175166	Proteasome 26S subunit, non-ATPase 2	3	184299198-184309050
PTCH1	ENSG00000185920	Patched 1	9	95442980-95517057
PTGER1	ENSG00000160951	Prostaglandin E receptor 1	19	14472466-14475354
PTGER2	ENSG00000125384	Prostaglandin E receptor 2	14	52314305-52328598
PTGER3	ENSG00000050628	Prostaglandin E receptor 3	1	70852353-71047808
PTGER4	ENSG00000171522	Prostaglandin E receptor 4	5	40679915-40693735
PTGFR	ENSG00000122420	Prostaglandin F receptor	1	78303884-78540701
PTGIR	ENSG00000160013	Prostaglandin I2 receptor	19	46620468-46625089
PTGIS	ENSG00000124212	Prostaglandin I2 synthase	20	49503874-49568137
PTGS1	ENSG00000095303	Prostaglandin-endoperoxide synthase 1	9	122370530-122395703
PTGS2	ENSG00000073756	Prostaglandin-endoperoxide synthase 2	1	186671791-186680423
PTH2R	ENSG00000144407	Parathyroid hormone 2 receptor	2	208359714-208854503
PTK2	ENSG00000169398	Protein tyrosine kinase 2	8	140657900-141002216
PTK6	ENSG00000101213	Protein tyrosine kinase 6	20	63528001-63537376
QPRT	ENSG00000103485	Quinolate phosphoribosyltransferase	16	29663279-29698699
RAC1	ENSG00000136238	Rac family small GTPase 1	7	6374527-6403967
RAD50	ENSG00000113522	RAD50 double strand break repair protein	5	132556019-132646349

RAF1	ENSG00000132155	Raf-1 proto-oncogene, serine/threonine kinase	3	12583601-12664226
RAMP1	ENSG00000132329	Receptor activity modifying protein 1	2	237858893-237912106
RAMP2	ENSG00000131477	Receptor activity modifying protein 2	17	42758447-42763041
RAMP3	ENSG00000122679	Receptor activity modifying protein 3	7	45157791-45186302
RARA	ENSG00000131759	Retinoic acid receptor alpha	17	40309180-40357643
RARB	ENSG00000077092	Retinoic acid receptor beta	3	25174332-25597932
RARG	ENSG00000172819	Retinoic acid receptor gamma	12	53210567-53232980
RBM39	ENSG00000131051	RNA binding motif protein 39	20	35701347-35742312
REN	ENSG00000143839	Renin	1	204154819-204190324
RET	ENSG00000165731	Ret proto-oncogene	10	43077064-43130351
RFK	ENSG00000135002	Riboflavin kinase	9	76385526-76394517
RICTOR	ENSG00000164327	RPTOR independent companion of MTOR complex 2	5	38937920-39074399
ROCK1	ENSG00000067900	Rho associated coiled-coil containing protein kinase 1	18	20946906-21111813
ROCK2	ENSG00000134318	Rho associated coiled-coil containing protein kinase 2	2	11179759-11348330
ROS1	ENSG00000047936	ROS proto-oncogene 1, receptor tyrosine kinase	6	117288300-117425855
RPL3	ENSG00000100316	Ribosomal protein L3	22	39312882-39320389
RPS6KB1	ENSG00000108443	Ribosomal protein S6 kinase B1	17	59893046-59950574
RPTOR	ENSG00000141564	Regulatory associated protein of MTOR complex 1	17	80544819-80966371
RRM1	ENSG00000167325	Ribonucleotide reductase catalytic subunit M1	11	4094707-4138932
RRM2	ENSG00000171848	Ribonucleotide reductase regulatory subunit M2	2	10120698-10211725
RRM2B	ENSG00000048392	Ribonucleotide reductase regulatory TP53 inducible subunit M2B	8	102204502-102238961
RXRA	ENSG00000186350	Retinoid X receptor alpha	9	134317098-134440585
RXRB	ENSG00000204231	Retinoid X receptor beta	6	33193588-33200688
RXRG	ENSG00000143171	Retinoid X receptor gamma	1	165400922-165445355
RYR1	ENSG00000196218	Ryanodine receptor 1	19	38433691-38587564
RYR2	ENSG00000198626	Ryanodine receptor 2	1	237042184-237833988
S1PR1	ENSG00000170989	Sphingosine-1-phosphate receptor 1	1	101236865-101243713
S1PR5	ENSG00000180739	Sphingosine-1-phosphate receptor 5	19	10512742-10517931
SCN10A	ENSG00000185313	Sodium voltage-gated channel alpha subunit 10	3	38696802-38816286
SCN11A	ENSG00000168356	Sodium voltage-gated channel alpha subunit 11	3	38845767-39051941

SCN1A	ENSG00000144285	Sodium voltage-gated channel alpha subunit 1	2	165984641- 166149214
SCN1B	ENSG00000105711	Sodium voltage-gated channel beta subunit 1	19	35030470- 35040449
SCN2A	ENSG00000136531	Sodium voltage-gated channel alpha subunit 2	2	165194993- 165392310
SCN2B	ENSG00000149575	Sodium voltage-gated channel beta subunit 2	11	118162806- 118176639
SCN3A	ENSG00000153253	Sodium voltage-gated channel alpha subunit 3	2	165087522- 165204067
SCN3B	ENSG00000166257	Sodium voltage-gated channel beta subunit 3	11	123629187- 123655244
SCN4A	ENSG00000007314	Sodium voltage-gated channel alpha subunit 4	17	63938554- 63972918
SCN4B	ENSG00000177098	Sodium voltage-gated channel beta subunit 4	11	118133377- 118152888
SCN5A	ENSG00000183873	Sodium voltage-gated channel alpha subunit 5	3	38548057- 38649687
SCN9A	ENSG00000169432	Sodium voltage-gated channel alpha subunit 9	2	166195185- 166376001
SCNN1A	ENSG00000111319	Sodium channel epithelial 1 subunit alpha	12	6346843- 6377730
SCNN1B	ENSG00000168447	Sodium channel epithelial 1 subunit beta	16	23278231- 23381294
SCNN1D	ENSG00000162572	Sodium channel epithelial 1 subunit delta	1	1280436- 1292029
SCNN1G	ENSG00000166828	Sodium channel epithelial 1 subunit gamma	16	23182745- 23216883
SCTR	ENSG00000080293	Secretin receptor	2	119439843- 119525301
SDHD	ENSG00000204370	Succinate dehydrogenase complex subunit D	11	112086824- 112120016
SERPINB2	ENSG00000197632	Serpin family B member 2	18	63871692- 63903888
SERPINC1	ENSG00000117601	Serpin family C member 1	1	173903804- 173917378
SERPIND1	ENSG00000099937	Serpin family D member 1	22	20774113- 20787720
SERPINE1	ENSG00000106366	Serpin family E member 1	7	101127104- 101139247
SH2B3	ENSG00000111252	SH2B adaptor protein 3	12	111405923- 111451623
SHH	ENSG00000164690	Sonic hedgehog signaling molecule	7	155799980- 155812463
SHMT1	ENSG00000176974	Serine hydroxymethyltransferase 1	17	18327860- 18363563
SI	ENSG00000090402	Sucrase-isomaltase	3	164978898- 165078496
SIGMAR1	ENSG00000147955	Sigma non-opioid intracellular receptor 1	9	34634722- 34637809
SIK1	ENSG00000142178	Salt inducible kinase 1	21	43414483- 43427131
SIRT1	ENSG00000096717	Sirtuin 1	10	67884656- 67918390
SIRT5	ENSG00000124523	Sirtuin 5	6	13574529- 13615158
SLAMF7	ENSG00000026751	SLAM family member 7	1	160739057- 160754821
SLC12A1	ENSG00000074803	Solute carrier family 12 member 1	15	48178438- 48304078

SLC12A2	ENSG00000064651	Solute carrier family 12 member 2	5	128083766- 128189677
SLC12A3	ENSG00000070915	Solute carrier family 12 member 3	16	56865207- 56915850
SLC12A4	ENSG00000124067	Solute carrier family 12 member 4	16	67943474- 67969601
SLC12A5	ENSG00000124140	Solute carrier family 12 member 5	20	46021690- 46060150
SLC18A1	ENSG00000036565	Solute carrier family 18 member A1	8	20144855- 20183206
SLC18A2	ENSG00000165646	Solute carrier family 18 member A2	10	117241093- 117279430
SLC22A11	ENSG00000168065	Solute carrier family 22 member 11	11	64555690- 64572875
SLC22A12	ENSG00000197891	Solute carrier family 22 member 12	11	64590641- 64602353
SLC22A6	ENSG00000197901	Solute carrier family 22 member 6	11	62936385- 62984983
SLC22A8	ENSG00000149452	Solute carrier family 22 member 8	11	62989154- 63015841
SLC25A4	ENSG00000151729	Solute carrier family 25 member 4	4	185143266- 185150382
SLC25A5	ENSG00000005022	Solute carrier family 25 member 5	X	119468422- 119471396
SLC25A6	ENSG00000169100	Solute carrier family 25 member 6	X	1386152- 1392113
SLC2A2	ENSG00000163581	Solute carrier family 2 member 2	3	170996347- 171026743
SLC52A2	ENSG00000185803	Solute carrier family 52 member 2	8	144354135- 144361272
SLC5A2	ENSG00000140675	Solute carrier family 5 member 2	16	31483002- 31490860
SLC6A1	ENSG00000157103	Solute carrier family 6 member 1	3	10992186- 11039247
SLC6A2	ENSG00000103546	Solute carrier family 6 member 2	16	55655604- 55706192
SLC6A3	ENSG00000142319	Solute carrier family 6 member 3	5	1392794- 1445440
SLC6A4	ENSG00000108576	Solute carrier family 6 member 4	17	30194319- 30236002
SLC6A8	ENSG00000130821	Solute carrier family 6 member 8	X	153687926- 153696588
SLC7A11	ENSG00000151012	Solute carrier family 7 member 11	4	138164097- 138242349
SLC8A1	ENSG00000183023	Solute carrier family 8 member A1	2	40097270- 40611053
SLCO2B1	ENSG00000137491	Solute carrier organic anion transporter family member 2B1	11	75100563- 75206549
SMO	ENSG00000128602	Smoothened, frizzled class receptor	7	129188633- 129213545
SMOX	ENSG00000088826	Spermine oxidase	20	4120980- 4187747
SMS	ENSG00000102172	Spermine synthase	X	21940709- 21994837
SNAP25	ENSG00000132639	Synaptosome associated protein 25	20	10218830- 10307418
SOAT1	ENSG00000057252	Sterol O-acyltransferase 1	1	179293714- 179358680
SQLE	ENSG00000104549	Squalene epoxidase	8	124998497- 125022283

SRC	ENSG00000197122	SRC proto-oncogene, non-receptor tyrosine kinase	20	37344685-37406050
SRD5A1	ENSG00000145545	Steroid 5 alpha-reductase 1	5	6633427-6674386
SRD5A2	ENSG00000277893	Steroid 5 alpha-reductase 2	2	31522480-31580938
SSTR1	ENSG00000139874	Somatostatin receptor 1	14	38207904-38213067
SSTR2	ENSG00000180616	Somatostatin receptor 2	17	73165010-73176633
SSTR5	ENSG00000162009	Somatostatin receptor 5	16	1078781-1080142
STAT3	ENSG00000168610	Signal transducer and activator of transcription 3	17	42313324-42388568
SV2A	ENSG00000159164	Synaptic vesicle glycoprotein 2A	1	149903318-149917844
SYK	ENSG00000165025	Spleen associated tyrosine kinase	9	90801787-90898549
SYT2	ENSG00000143858	Synaptotagmin 2	1	202590596-202710454
TAAR1	ENSG00000146399	Trace amine associated receptor 1	6	132644898-132646051
TACR1	ENSG00000115353	Tachykinin receptor 1	2	75046463-75199520
TBK1	ENSG00000183735	TANK binding kinase 1	12	64452092-64502114
TBXA2R	ENSG00000006638	Thromboxane A2 receptor	19	3594507-3606875
TBXAS1	ENSG00000059377	Thromboxane A synthase 1	7	139777051-140020325
TEK	ENSG00000120156	TEK receptor tyrosine kinase	9	27109141-27230174
TERT	ENSG00000164362	Telomerase reverse transcriptase	5	1253147-1295068
TFPI	ENSG00000003436	Tissue factor pathway inhibitor	2	187464230-187565760
TGFB1	ENSG00000105329	Transforming growth factor beta 1	19	41301587-41353922
TGFBR1	ENSG00000106799	Transforming growth factor beta receptor 1	9	99104038-99154192
TH	ENSG00000180176	Tyrosine hydroxylase	11	2163929-2171815
THRA	ENSG00000126351	Thyroid hormone receptor alpha	17	40058290-40093867
THRB	ENSG00000151090	Thyroid hormone receptor beta	3	24117153-24495756
TLR2	ENSG00000137462	Toll like receptor 2	4	153684070-153705702
TLR5	ENSG00000187554	Toll like receptor 5	1	223109404-223143248
TLR7	ENSG00000196664	Toll like receptor 7	X	12867072-12890361
TLR8	ENSG00000101916	Toll like receptor 8	X	12906620-12923169
TLR9	ENSG00000239732	Toll like receptor 9	3	52221080-52226163
TNF	ENSG00000232810	Tumor necrosis factor	6	31575565-31578336
TNFRSF8	ENSG00000120949	TNF receptor superfamily member 8	1	12063303-12144207

TNFSF11	ENSG00000120659	TNF superfamily member 11	13	42562736-42608013
TNFSF13B	ENSG00000102524	TNF superfamily member 13b	13	108251240-108308484
TNKS	ENSG00000173273	Tankyrase	8	9555912-9782346
TNNC1	ENSG00000114854	Troponin C1, slow skeletal and cardiac type	3	52451100-52454041
TOP1	ENSG00000198900	DNA topoisomerase I	20	41028822-41124487
TOP1MT	ENSG00000184428	DNA topoisomerase I mitochondrial	8	143304384-143359979
TOP2A	ENSG00000131747	DNA topoisomerase II alpha	17	40388525-40417896
TOP2B	ENSG00000077097	DNA topoisomerase II beta	3	25597905-25664907
TPH1	ENSG00000129167	Tryptophan hydroxylase 1	11	18017564-18042426
TPH2	ENSG00000139287	Tryptophan hydroxylase 2	12	71938845-72186618
TPK1	ENSG00000196511	Thiamin pyrophosphokinase 1	7	144451941-144836395
TPMT	ENSG00000137364	Thiopurine S-methyltransferase	6	18128311-18155077
TPO	ENSG00000115705	Thyroid peroxidase	2	1374066-1543711
TRHR	ENSG00000174417	Thyrotropin releasing hormone receptor	8	109086585-109121565
TRPA1	ENSG00000104321	Transient receptor potential cation channel subfamily A member 1	8	72019917-72075584
TRPM8	ENSG00000144481	Transient receptor potential cation channel subfamily M member 8	2	233917373-234019522
TRPV1	ENSG00000196689	Transient receptor potential cation channel subfamily V member 1	17	3565444-3609411
TRPV3	ENSG00000167723	Transient receptor potential cation channel subfamily V member 3	17	3510502-3557812
TSHR	ENSG00000165409	Thyroid stimulating hormone receptor	14	80954989-81146302
TSPO	ENSG00000100300	Translocator protein	22	43151547-43163242
TUBA1A	ENSG00000167552	Tubulin alpha 1a	12	49184795-49189080
TUBA4A	ENSG00000127824	Tubulin alpha 4a	2	219249710-219278170
TUBB	ENSG00000196230	Tubulin beta class I	6	30720352-30725426
TUBB1	ENSG00000101162	Tubulin beta 1 class VI	20	59019429-59026654
TUBB3	ENSG00000258947	Tubulin beta 3 class III	16	89921392-89938761
TUBB4B	ENSG00000188229	Tubulin beta 4B class IVb	9	137241287-137243707
TUBD1	ENSG00000108423	Tubulin delta 1	17	59859479-59892945
TUBE1	ENSG00000074935	Tubulin epsilon 1	6	112070663-112087529
TUBG1	ENSG00000131462	Tubulin gamma 1	17	42609683-42615238
TXN	ENSG00000136810	Thioredoxin	9	110243810-110256507

TXNRD1	ENSG00000198431	Thioredoxin reductase 1	12	104215779-104350307
TYK2	ENSG00000105397	Tyrosine kinase 2	19	10350529-10380572
TYMS	ENSG00000176890	Thymidylate synthetase	18	657653-673578
TYR	ENSG00000077498	Tyrosinase	11	89177875-89295759
UGCG	ENSG00000148154	UDP-glucose ceramide glucosyltransferase	9	111896814-111935369
VAMP1	ENSG00000139190	Vesicle associated membrane protein 1	12	6462237-6470987
VAMP2	ENSG00000220205	Vesicle associated membrane protein 2	17	8159149-8163546
VDR	ENSG00000111424	Vitamin D receptor	12	47841537-47943048
VEGFA	ENSG00000112715	Vascular endothelial growth factor A	6	43770184-43786487
VEGFB	ENSG00000173511	Vascular endothelial growth factor B	11	64234538-64238793
VKORC1	ENSG00000167397	Vitamin K epoxide reductase complex subunit 1	16	31090842-31095980
VKORC1L1	ENSG00000196715	Vitamin K epoxide reductase complex subunit 1 like 1	7	65873074-65959563
VWF	ENSG00000110799	Von Willebrand factor	12	5948874-6124770
WEE1	ENSG00000166483	WEE1 G2 checkpoint kinase	11	9573670-9593457
XDH	ENSG00000158125	Xanthine dehydrogenase	2	31334321-31414742
XIAP	ENSG00000101966	X-linked inhibitor of apoptosis	X	123859724-123913979
XPO1	ENSG00000082898	Exportin 1	2	61477849-61538626
YES1	ENSG00000176105	YES proto-oncogene 1, Src family tyrosine kinase	18	721588-812546

Table 5A. Gene targets of cancer therapeutic agents.

ABL1	CDK8	FANCL	HSPB1	MEF2B	PPP2CA	SMARCB1
ABL2	CDK9	FAS	IDH1	MEN1	PPP2R1A	SMO
ACPP (ACP3)	CDKN1A	FAT1	IDH2	MET	PRDM1	SNCAIP
ACVR1B	CDKN1B	FBXW7	IDO1	MGMT	PREX2	SOCS1
ADA	CDKN2A	FCGR1A	IFNAR1	MITF	PRKAR1A	SOX10
ADORA2A	CDKN2B	FGF1	IFNAR2	MLH1	PRKCA	SOX2
ADORA3	CDKN2C	FGF10	IGF1R	MPL	PRKCB	SOX9
AGXT	CEBPA	FGF14	IGF2	MRE11	PRKCE	SPEN
AKT1	CHD1	FGF19	IHH	MRE11A	PRKCG	SPOP
AKT2	CHD2	FGF2	IKBKB	MS4A1	PRKCI	SPTA1
AKT3	CHD4	FGF23	IKBKE	MSH2	PRKDC	SRC
ALK	CHEK1	FGF3	IKZF1	MSH6	PRLR	SSTR2
AMER1 (FAM123B)	CHEK2	FGF4	IL1B	MSLN	PRMT5	SSTR5
ANGPT1	CIC	FGF6	IL2RA	MST1R	PRSS8	STAG2

ANGPT2	CPT1A	FGFR1	IL2RB	MTOR	PSEN1	STAT3
ANPEP	CRBN	FGFR2	IL2RG	MUC5AC	PSENEN	STAT4
APC	CREBBP	FGFR3	IL6	MUTYH	PSMB1	STK11
APH1A	CRKL	FGFR4	IL6R	MYC	PSMB10	SUFU
APH1B	CRLF2	FGR	IL6ST	MYCL (MYCL1)	PSMB2	SYK
AR	CRTC1	FH	IL7R	MYCN	PSMB5	TAF1
ARAF	CRTC2	FKBP1A	INHA	MYD88	PSMB8	TBK1
ARFRP1	CSF1R	FLCN	INHBA	NAE1	PSMB9	TBX3
ARID1A	CSNK2A1	FLT1	INHBB	NAMPT	PSMD1	TEK
ARID1B	CSNK2A2	FLT3	INHBC	NBN	PSMD2	TERC
ARID2	CTCF	FLT4	INHBE	NCSTN	PTCH1	TERT
ASXL1	CTNNA1	FNTA	INPP4B	NEK11	PTEN	TET2
ATM	CTNNB1	FOLH1	IRF2	NF1	PTGS2	TGFB1
ATR	CUL3	FOLR1	IRF4	NF2	PTK2	TGFBR1
ATRX	CXCR1	FOLR2	IRS2	NFE2L2	PTK6	TGFBR2
AURKA	CXCR2	FOLR3	ITK	NFKBIA	PTPN11	TLR5
AURKB	CXCR4	FOXL2	JAK1	NKX2-I	QKI	TLR7
AURKC	CYLD	FOXP1	JAK2	NOTCH1	RAC1	TLR8
AXIN1	CYP11B1	FRK	JAK3	NOTCH2	RAD50	TMB
AXL	CYP11B2	FRS2	JUN	NOTCH3	RAD51	TNF
B4GALNT1	CYP17A1	FUBP1	KAT6A (MYST3)	NOTCH4	RAD51B	TNFAIP3
BAP1	CYP19A1	FYN	KDM1A	NPEPPS	RAD51C	TNFRSF14
BARD1	DDR2	FZD8	KDM5A	NPM1	RAD51D	TNFRSF8
BAX	DHFR	GABRA6	KDM5C	NR3C1	RAD54L	TNFSF11
BCL2	DHH	GART	KDM6A	NRAS	RAF1	TNFSF13B
BCL2L1	DHX9	GATA1	KDR	NSD1	RANBP2	TNKS
BCL2L2	DICER	GATA2	KEAP1	NTRK1	RARA	TOP1
BCL6	DNMT1	GATA3	KEL	NTRK2	RARB	TOP1MT
BCORL1	DNMT3A	GATA4	KIF11	NTRK3	RARG	TOP2A
BIRC5	DOTIL	GATA6	KIT	NUP93	RB1	TOP2B
BLK	DPP4	GID4 (C17ORF39)	KLHL6	PAK3	RBM10	TP53
BLM	DRD2	GLI1	KMT2A (MLL)	PALB2	RBM39	TSC1
BMX	DYRK1A	GNA11	KMT2C (MLL3)	PARK2	RET	TSC2
BRAF	DYRK1B	GNA13	KMT2D (MLL2)	PARP1	RICTOR	TSHR
BRCA1	DYRK2	GNAQ	KRAS	PARP2	RNF43	TUBA1A
BRCA2	DYRK3	GNAS	LAP3	PARP3	ROCK1	TUBA4A
BRD2	DYRK4	GNRH1	LCK	PAX5	ROCK2	TUBB
BRD3	EDNRA	GNRHR	LDLR	PBRM1	ROS1	TUBB1

BRD4	EGFR	GPR124	LHCGR	PDCD1LG2	RPL3	TUBB3
BRIP1	EHMT1	GRIN2A	LIMK1	PDE5A	RPS6KB1	TUBD1
BTG1	EHMT2	GRM3	LMO1	PDGFRA	RPTOR	TUBE1
BTK	EIF4E	GSK3A	LRP1B	PDGFRB	RRM1	TUBG1
C11orf30 (EMSY)	EP300	GSK3B	LYN	PDK1	RUNX1	TXN
CARD11	EPHA2	H3F3A	LZTR1	PGF	RUNX1T1	TYK2
CAXX	EPHA3	HCK	MAGI2	PIGF	RXRA	TYMS
CBFB	EPHA5	HDAC1	MAP1A	PIK3C2B	RXRB	U2AF1
CBL	EPHA7	HDAC10	MAP2	PIK3CA	RXRG	VDR
CCND1	EPHB1	HDAC11	MAP2K1	PIK3CB	S1PR1	VEGFA
CCND2	EPHB4	HDAC2	MAP2K1 (MEK1)	PIK3CD	SDHA	VEGFB
CCND3	ERBB2	HDAC3	MAP2K2	PIK3CG	SDHB	VHL
CCNE1	ERBB3	HDAC4	MAP2K2 (MEK2)	PIK3R1	SDHC	WEE1
CD19	ERBB4	HDAC5	MAP2K4 (MEK4)	PIK3R2	SDHD	WISP3
CD274	ERG	HDAC6	MAP3K1	PIM1	SETD2	WT1
CD38	ERRF11	HDAC7	MAP3K7	PIM2	SF3B1	XIAP
CD79A	ESR1	HDAC8	MAP3K8	PIM3	SH2B3	XPO1
CD79B	ESR2	HDAC9	MAPK1	PLCG2	SHH	YES1
CDC73	EZH2	HGF	MAPK11	PLK1	SIK1	ZBTB2
CDH1	F2R	HNF1A	MAPK14	PLK2	SIRT1	ZNF217
CDK1	FAM46C	HPRT1	MAPK3	PLK3	SLAMF7	ZNF703
CDK12	FANCA	HPSE	MAPK8	PMS2	SLC2A2	
CDK2	FANCC	HRAS	MAPK9	POLA1	SLIT2	
CDK4	FANCD2	HSD3B1	MCL1	POLD1	SMAD2	
CDK5	FANCE	HSP90AA1	MDM2	POLE	SMAD3	
CDK6	FANCF	HSPA1A	MDM4	PORCN	SMAD4	
CDK7	FANCG	HSPA1B	MED12	PPARG	SMARCA4	

Table 5B. Gene targets of cancer therapeutic agents.

ABL1	EPHB4	KIT	PSMB8
ABL2	ERBB2	KRAS	PSMB9
ACPP (ACP3)	ERBB3	LAP3	PSMD1
ADA	ERBB4	LCK	PSMD2
ADORA2A	ESR1	LDLR	PTCH1
ADORA3	ESR2	LHCGR	PTGS2
AGXT	EZH2	LIMK1	PTK2
AKT1	F2R	LYN	PTK6
AKT2	FCGR1A	MAP1A	RAC1
AKT3	FGF1	MAP2	RAD50
ALK	FGF2	MAP2K1	RAF1

ANGPT1	FGFR1	MAP2K2	RARA
ANGPT2	FGFR2	MAP3K7	RARB
ANPEP	FGFR3	MAP3K8	RARG
APH1A	FGFR4	MAPK1	RET
APH1B	FGR	MAPK11	RICTOR
AR	FKBP1A	MAPK14	ROCK1
ARAF	FLT1	MAPK3	ROCK2
ATR	FLT3	MAPK8	ROS1
AURKA	FLT4	MAPK9	RPL3
AURKB	FNTA	MCL1	RPS6KB1
AURKC	FOLH1	MDM2	RPTOR
AXL	FOLR1	MET	RRM1
B4GALNT1	FOLR2	MGMT	RXRA
BAX	FOLR3	MRE11	RXRB
BCL2	FRK	MS4A1	RXRG
BCL2L1	FYN	MSLN	S1PR1
BCL2L2	FZD8	MST1R	SH2B3
BIRC5	GART	MTOR	SHH
BLK	GNRH1	MUC5AC	SIK1
BMX	GNRHR	NAE1	SIRT1
BRAF	GSK3A	NAMPT	SLAMF7
BRD2	GSK3B	NCSTN	SLC2A2
BRD3	HCK	NEK11	SMO
BRD4	HDAC1	NOTCH1	SRC
BTK	HDAC10	NOTCH2	SSTR2
CCND1	HDAC11	NOTCH3	SSTR5
CCND2	HDAC2	NOTCH4	STAT3
CCND3	HDAC3	NPEPPS	SYK
CD19	HDAC4	NR3C1	TBK1
CD274	HDAC5	NRAS	TEK
CD38	HDAC6	NTRK1	TERT
CDK1	HDAC7	NTRK2	TGFB1
CDK2	HDAC8	NTRK3	TGFBR1
CDK4	HDAC9	PARP1	TLR5
CDK5	HPRT1	PARP2	TLR7
CDK6	HPSE	PARP3	TLR8
CDK7	HSP90AA1	PDE5A	TNF
CDK9	HSPA1A	PDGFRA	TNFRSF8
CHD1	HSPA1B	PDGFRB	TNFSF11
CHEK1	HSPB1	PGF	TNFSF13B
CHEK2	IDH1	PIGF	TNKS
CPT1A	IDH2	PIK3CA	TOP1
CRBN	IDO1	PIK3CB	TOP1MT
CRTC1	IFNAR1	PIK3CD	TOP2A
CRTC2	IFNAR2	PIK3CG	TOP2B
CSF1R	IGF1R	PIM3	TUBA1A

CSNK2A1	IHH	PLK1	TUBA4A
CSNK2A2	IKBKB	PLK2	TUBB
CXCR1	IL1B	PLK3	TUBB1
CXCR2	IL2RA	POLA1	TUBB3
CXCR4	IL2RB	PORCN	TUBD1
CYP17A1	IL2RG	PPARG	TUBE1
CYP19A1	IL6	PPP2CA	TUBG1
DDR2	IL6R	PRKCA	TXN
DHFR	INHA	PRKCB	TYK2
DHH	INHBA	PRKCE	TYMS
DHX9	INHBB	PRKCG	VDR
DNMT1	INHBC	PRKCI	VEGFA
DOT1L	INHBE	PRKDC	VEGFB
DPP4	ITK	PRLR	WEE1
DRD2	JAK1	PSEN1	XIAP
EDNRA	JAK2	PSENEN	XPO1
EGFR	JAK3	PSMB1	YES1
EHMT1	KDM1A	PSMB10	
EHMT2	KDR	PSMB2	
EPHA2	KIF11	PSMB5	

Table 5C. Gene targets of cancer therapeutic agents.

ABL1	EHMT1	KDM1A	PSMB1
ABL2	EHMT2	KDR	PSMB10
ACPP (ACP3)	EIF4E	KIF11	PSMB2
ADA	EPHA2	KIT	PSMB5
ADORA2A	EPHB4	KRAS	PSMB8
ADORA3	ERBB2	LAP3	PSMB9
AGXT	ERBB3	LCK	PSMD1
AKT1	ERBB4	LDLR	PSMD2
AKT2	ESR1	LHCGR	PTCH1
AKT3	ESR2	LIMK1	PTGS2
ALK	EZH2	LYN	PTK2
ANGPT1	F2R	MAP1A	PTK6
ANGPT2	FCGR1A	MAP2	RAC1
ANPEP	FGF1	MAP2K1	RAD50
APH1A	FGF2	MAP2K2	RAF1
APH1B	FGFR1	MAP3K7	RARA
AR	FGFR2	MAP3K8	RARB
ARAF	FGFR3	MAPK1	RARG
ATR	FGFR4	MAPK11	RBM39
AURKA	FGR	MAPK14	RET
AURKB	FKBP1A	MAPK3	RICTOR
AURKC	FLT1	MAPK8	ROCK1
AXL	FLT3	MAPK9	ROCK2
B4GALNT1	FLT4	MCL1	ROS1

BAX	FNTA	MDM2	RPL3
BCL2	FOLH1	MET	RPS6KB1
BCL2L1	FOLR1	MGMT	RPTOR
BCL2L2	FOLR2	MS4A1	RRM1
BIRC5	FOLR3	MSLN	RXRA
BLK	FRK	MST1R	RXRB
BMX	FYN	MTOR	RXRG
BRAF	FZD8	MUC5AC	S1PR1
BRD2	GART	NAE1	SH2B3
BRD3	GNRH1	NAMPT	SHH
BRD4	GNRHR	NBN	SIK1
BTK	GSK3A	NCSTN	SIRT1
CCND1	GSK3B	NEK11	SLAMF7
CCND2	HCK	NOTCH1	SLC2A2
CCND3	HDAC1	NOTCH2	SMO
CD19	HDAC10	NOTCH3	SRC
CD274	HDAC11	NOTCH4	SSTR2
CD38	HDAC2	NPEPPS	SSTR5
CDK1	HDAC3	NR3C1	STAT3
CDK2	HDAC4	NRAS	SYK
CDK4	HDAC5	NTRK1	TBK1
CDK5	HDAC6	NTRK2	TEK
CDK6	HDAC7	NTRK3	TERT
CDK7	HDAC8	PARP1	TGFB1
CDK9	HDAC9	PARP2	TGFBR1
CHD1	HPRT1	PARP3	TLR5
CHEK1	HPSE	PDE5A	TLR7
CHEK2	HSP90AA1	PDGFRA	TLR8
CPT1A	HSPA1A	PDGFRB	TNF
CRBN	HSPA1B	PGF	TNFRSF8
CRTC1	HSPB1	PIGF	TNFSF11
CRTC2	IDH1	PIK3CA	TNFSF13B
CSF1R	IDH2	PIK3CB	TNKS
CSNK2A1	IDO1	PIK3CD	TOP1
CSNK2A2	IFNAR1	PIK3CG	TOP1MT
CXCR1	IFNAR2	PIM1	TOP2A
CXCR2	IGF1R	PIM2	TOP2B
CXCR4	IHH	PIM3	TUBA1A
CYP17A1	IKBKB	PLK1	TUBA4A
CYP19A1	IL1B	PLK2	TUBB
DDR2	IL2RA	PLK3	TUBB1
DHFR	IL2RB	POLA1	TUBB3
DHH	IL2RG	PORCN	TUBD1
DHX9	IL6	PPARG	TUBE1
DNMT1	IL6R	PPP2CA	TUBG1
DOT1L	IL6ST	PRKCA	TXN

DPP4	INHA	PRKCB	TYK2
DRD2	INHBA	PRKCE	TYMS
DYRK1A	INHBB	PRKCG	VDR
DYRK1B	INHBC	PRKCI	VEGFA
DYRK2	INHBE	PRKDC	VEGFB
DYRK3	ITK	PRLR	WEE1
DYRK4	JAK1	PRMT5	XIAP
EDNRA	JAK2	PSEN1	XPO1
EGFR	JAK3	PSENEN	YES1

Table 5D. Gene targets of cancer therapeutic agents.

BIRC5	CYP11B2	JAK2	MDM2	RPL3
BRAF	EGFR	KIF11	MET	TOP2A
CDK4	FLT3	KIT	MTOR	TUBG1
CDK6	GART	MAP2K1	PIK3CA	
CYP11B1	JAK1	MAP2K2	PSMB5	

[00283] Tables 6A-6C provide lists of gene modulatory reagents, one or more of which may be used in a method of cell editing described herein.

Table 6A. Library of gene modulatory reagents.

Target Gene Symbol	Transcript	SEQ ID NO.	Sequences	gRNA coordinates
ABL1	ENST00000372348.6	1	GGACACAGGCCCATGGTACC	chr9:130854923-130854946_-
		2	ATCATTCAACGGTGGCCGAC	chr9:130862814-130862837_+
		3	CATCACGCCAGTCAACAGTC	chr9:130854891-130854914_+
		4	ATCTCAGCGAGATGGACCTC	chr9:130855023-130855046_-
		5	AAGAAGGAATCATCGAGGCA	chr9:130714400-130714423_+
ABL2	ENST00000502732.5	6	CCTCAGCCCCGCGGGATCCG;	chr1:179229326-179229349_-
		7	TTACCATGAAGCACAACTT	chr1:179121669-179121692_-
		8	GGTGAAGCTACGAGTCCT	chr1:179126650-179126673_-
		9	GGAGTACGCGAGAGCAGGGA	chr1:179229393-179229416_-
		10	GAGTACGCGAGAGCAGGGAT	chr1:179229392-179229415_-
ACPP (ACP3)	ENST00000336375.9	11	GCAGCCCTGTTTCCCCCAGA	chr3:132332248-132332271_+
		12	CCTACTCTGGCAGCCCATCC	chr3:132332292-132332315_+
		13	GAAAGAGGAAGTGTGTGCAC	chr3:132332311-132332334_-
		14	AGTCACAACTTCAACTCCT	chr3:132317550-132317573_-
		15	CCAGATGCTGACACCTTCTG	chr3:132332261-132332284_-
ADA	ENST00000372874.8	16	GAGACTTCGGGGTCAAGGCC	chr20:44625599-44625622_-
		17	CAGGCTTGATGGATCCGTCT	chr20:44636248-44636271_+
		18	AAACCATCTTATACTATGGC	chr20:44636225-44636248_-
		19	CCAAAGTGGAGCCAATCCCC	chr20:44626466-44626489_-
		20	CTCCCAGCTAACACAGCAGA	chr20:44629130-44629153_-
ADORA2A	ENST00000611543.4	21	GAACGTCACCAACTACTTTG	chr22:24433517-24433540_+
		22	TTGCCATCCGCATCCCGCTC	chr22:24433714-24433737_+
		23	CATGGCCACAGACGACAGGC	chr22:24433384-24433407_-
		24	TGGGCATGGCCACAGACGAC	chr22:24433388-24433411_-
		25	AGCACACCAGCACATTGCCC	chr22:24433466-24433489_-

ADORA3	ENST00000241356.4	26	TGGGCATCTTGCCTTCCCAG	chr1:111503347-111503370_+
		27	GACAGAGCAGTGTGTGTT	chr1:111503328-111503351_+
		28	AATAGAAGGTGGTGGTCTGC	chr1:111503206-111503229_+
		29	CAAGGACATGATGGAGGCGT	chr1:111503051-111503074_+
		30	GTCCTTGCTGGCCATCGCTG	chr1:111503035-111503058_-
AGXT	ENST00000307503.3	31	GGACCCCCCTTTACATGGAC	chr2:240873022-240873045_+
		32	CAACCTGCCTCCTCGCATCA	chr2:240868957-240868980_+
		33	CCCCGGGCTGCCATGATGCG	chr2:240868967-240868990_-
		34	TCCAGTACGTGTTCCAGACC	chr2:240869194-240869217_+
		35	CATTGTGGGGCAGCGAGCCG	chr2:240869321-240869344_+
AKT1	ENST00000349310.7	36	TGGCACCTTCATTGGCTACA	chr14:104780144-104780167_-
		37	GGCTCACCCAGTGACAACCTC	chr14:104775697-104775720_-
		38	GCCGTCAGCCACAGTCTGGA	chr14:104775759-104775782_+
		39	CGACGTGGCTATTGTGAAGG	chr14:104792615-104792638_-
		40	GGAGGAGATGGACTTCCGGT	chr14:104775719-104775742_-
AKT2	ENST00000392038.6	41	ATGACAAAGGTGTTGGGTCTG	chr19:40255220-40255243_+
		42	CTGGTGCGGGAGAAGGCCAC	chr19:40241986-40242009_-
		43	CAGGAAGTACCGTGGCCTCC	chr19:40257016-40257039_+
		44	GTCCATGGGGTCTCGCCTG	chr19:40242611-40242634_+
		45	TGTCTGTCATCAAAGAAGGC	chr19:40265234-40265257_-
AKT3	ENST00000366539.5	46	TTTGACTATTTGAACTACT	chr1:243637707-243637730_-
		47	TTACCATTTGTGAAAGAAGGT	chr1:243843137-243843160_-
		48	GATGTTACCATTTGTGAAAGA	chr1:243843141-243843164_-
		49	TCTCTATAACAGTAGTCCAC	chr1:243664802-243664825_+
		50	TCCCCTCAACAACTTTTCAG	chr1:243695593-243695616_-
ALK	ENST00000389048.7	51	GACCTGCCATTGAGGAGTGT	chr2:29320787-29320810_+
		52	CCCCTCCACTGCATGACCTC	chr2:29694949-29694972_-
		53	GTCCAGAGCTAGCGAGCCGC	chr2:29920377-29920400_+
		54	TCAGCGAGCTGTTCAAGTTGG	chr2:29920128-29920151_-
		55	ATTCCAGGGCCACTCGAAAT	chr2:29383797-29383820_+
ANGPT1	ENST00000517746.5	56	CTGCCATTCTGACTCACATA	chr8:107497504-107497527_-
		57	ACAGTGGGAGAAGATATAAC	chr8:107497453-107497476_-
		58	TCGTCAAACATATATAATCC	chr8:107322009-107322032_-
		59	GAGAAATCCGGTTCACGTG	chr8:107497322-107497345_+
		60	GCACCCTATGTGAGTCAGAA	chr8:107497501-107497524_+
ANGPT2	ENST00000325203.9	61	GGCAGTTGTCCATCTCTGGC	chr8:6562774-6562797_+
		62	CGGAAGAGCATGGACAGCAT	chr8:6562845-6562868_-
		63	AGCAATATCAGGTCCAGCAT	chr8:6562817-6562840_-
		64	AAGCAATATCAGGTCCAGCA	chr8:6562818-6562841_-
		65	CAGGAGGAAAGTGTAGCTGC	chr8:6562793-6562816_+
ANPEP	ENST00000300060.6	66	CCACGCTTTACTTTGGTCCA	chr15:89806370-89806393_+
		67	CCCGCTGTCCACACCCGCCT	chr15:89803702-89803725_-
		68	CGCCGGCGTTGAAGTCTGGC	chr15:89804374-89804397_+
		69	TTGAACTCGGCCTTCATGGC	chr15:89805376-89805399_+
		70	CTCAGTCTTGTC AATGTCCG	chr15:89806121-89806144_+
APH1A	ENST00000369109.7	71	GCCATCTGGCGGATGGAGAT	chr1:150267720-150267743_+
		72	TGACCGACCGGTCAGATGCC	chr1:150268042-150268065_-
		73	TCTTGGTCCATGTGACCGAC	chr1:150268054-150268077_-
		74	ACCCATCTCCATCCGCCAGA	chr1:150267721-150267744_-
		75	TTAGCATCGCTGAGTGAGGA	chr1:150267750-150267773_-
APH1B	ENST00000261879.9	76	ATCAGCAGATATTTCTGTGT	chr15:63279242-63279265_-
		77	CTCTTGCCATGAACCAAACA	chr15:63279196-63279219_-
		78	TCTTGCCATGAACCAAACAA	chr15:63279195-63279218_-

AR	ENST00000374690.8	79	TAGGCCAGCAGTCGCATAGA	chr15:63286603-63286626_-
		80	ATAGGCCAGCAGTCGCATAG	chr15:63286604-63286627_-
		81	TAGAGGCCCCACAGGCTACC	chrX:67545448-67545471_+
		82	GCAGCTGAGTCATCCTCGTC	chrX:67545602-67545625_-
		83	GCCCATCGTAGAGGCCCCAC	chrX:67545440-67545463_+
		84	CAGCAGGGACAACGTGGATG	chrX:67545624-67545647_-
ARAF	ENST00000377045.8	85	TCCAGGACCAGGTAGCCTGT	chrX:67545455-67545478_-
		86	TGGAGCGGATGCGCTGTAGG	chrX:47566695-47566718_-
		87	ACAAAATTGTGCATGGTCAG	chrX:47564878-47564901_-
		88	ACAGACTGTGGGGACCTTGG	chrX:47565090-47565113_-
		89	GTGGAGCGGATGCGCTGTAG	chrX:47566696-47566719_-
ATR	ENST00000350721.8	90	GTGGTCTACCGACTCATCAA	chrX:47563306-47563329_+
		91	CAAGAAGAATATTCCTTGAG	chr3:142556507-142556530_-
		92	CGCACGTCAGCATTCTGGCA	chr3:142550228-142550251_+
		93	CAACTTGTCTGTACTCTTCA	chr3:142556058-142556081_-
		94	TCCAGAGACAGATGCTGACT	chr3:142553316-142553339_+
AURKA	ENST00000395913.7	95	ACATGTCCGTGTTTCAGAGAA	chr3:142556004-142556027_+
		96	GTGCTTGCAAAGGAATGCGC	chr20:56386391-56386414_+
		97	ATTACCTGTAAATAGTGGCC	chr20:56386445-56386468_-
		98	ATGCGCTGGGAAGAATTTGA	chr20:56386405-56386428_+
		99	TGCTTGCAAAGGAATGCGCT	chr20:56386392-56386415_+
AURKB	ENST00000585124.5	100	TGAGTCACGAGAACACGTTT	chr20:56386489-56386512_+
		101	TCCCCCTTTCTCTTAAGGA	chr17:8210220-8210243_-
		102	AACTCCTACCCCTGGCCCTA	chr17:8210186-8210209_-
		103	GGGCCATCCTTAGAGAGAAA	chr17:8210217-8210240_+
		104	CTCCATCACCTTCTGGCCAG	chr17:8207599-8207622_+
AURKC	ENST00000302804.11	105	GGACATTGGAGCGGCTCATG	chr17:8207746-8207769_+
		106	AATCGGGCGTCCCCTGGGCA	chr19:57232059-57232082_+
		107	ATCGGGCGTCCCCTGGGCAA	chr19:57232060-57232083_+
		108	TTTGAAATCGGGCGTCCCCT	chr19:57232054-57232077_+
		109	CAGTCGATGACTTTGAAATC	chr19:57232043-57232066_+
AXL	ENST00000301178.8	110	CCAAATTTCCCCTTGCCCAG	chr19:57232069-57232092_-
		111	GAGTAGGTCCACGGGCTCTG	chr19:41221963-41221986_-
		112	TGCCACACACACTGTCAGAT	chr19:41239227-41239250_-
		113	GCCTAGCCGAAGCTGATGGG	chr19:41238028-41238051_-
		114	CCACCTCCAGTCCGTGGGT	chr19:41231222-41231245_-
B4GALNT1	ENST00000341156.8	115	AGTAGGTCCACGGGCTCTGG	chr19:41221962-41221985_-
		116	CCAGTACCCCTACAGGGTG	chr12:57631012-57631035_-
		117	CCCACGGCGCAAGAGGTAGC	chr12:57632011-57632034_+
		118	GCAGTTGTGAGTCCAGTGGG	chr12:57631321-57631344_-
		119	TGGCAGGGGCTATGAGCAGC	chr12:57631045-57631068_+
BAX	ENST00000345358.11	120	GGGGGCGCCACGGCGCAAG	chr12:57632004-57632027_+
		121	ATGATCTGCTCAGAGCTGGT	chr19:48955549-48955572_-
		122	GCAGCTGACATGTTTTCTGA	chr19:48956249-48956272_+
		123	GTTTCATCCAGGATCGAGCA	chr19:48955685-48955708_+
		124	TCTGACGGCAACTTCAACTG	chr19:48956264-48956287_+
BCL2	ENST00000398117.1	125	GGCGGTGATGGACGGGTCCG	chr19:48954921-48954944_+
		126	CCATTATAAGCTGTCGAGA	chr18:63318587-63318610_-
		127	TCCAGCCGCATCCCGGGACC	chr18:63318470-63318493_-
		128	CGCGCGGGGACGCTTTGCCA	chr18:63318269-63318292_-
		129	GCGGCGAGGTCTGGCGACC	chr18:63318452-63318475_+
BCL2L1	ENST00000307677.4	130	CACACCTGGATCCAGGATAA	chr18:63318088-63318111_-
		131	TCCCAGCTCCACATCACCCC	chr20:31721868-31721891_-
		132	AGCAGTAAAGCAAGCGCTGA	chr20:31721944-31721967_-

BCL2L2	ENST00000250405.9	133	TGGCAACCCATCCTGGCACC	chr20:31722040-31722063_-
		134	TCCTACAAGCTTTCCCAGAA	chr20:31722156-31722179_-
		135	CAGCAGCAGTTTGGATGCC	chr20:31721983-31722006_-
		136	CTGAGCCGCCAGATCAGAGA	chr14:23307945-23307968_-
		137	GACCTGGGTGAAGCGTTGTT	chr14:23307990-23308013_-
		138	AGGCAGAAGGGTTATGTCTG	chr14:23307833-23307856_+
		139	GGTTATAAGCTGAGGCAGAA	chr14:23307821-23307844_+
BIRC5	ENST00000350051.7	140	GCGTTGTTGGGCTGAGCCTG	chr14:23307978-23308001_-
		141	CCAGGCAGGGGGCAACGTCG	chr17:78214323-78214346_-
		142	ATGCGGTGGTTCCTTGAGAAA	chr17:78214349-78214372_-
		143	GCTGCGCCTGCACCCCGGAG	chr17:78214404-78214427_+
		144	GAACATAAAAAGCATTTCGTC	chr17:78216667-78216690_+
BLK	ENST00000259089.8	145	CAGGCGCAGCCCTCCAAGAA	chr17:78214391-78214414_-
		146	CTGGCCAGGTCACCTCGTCAC	chr8:11549039-11549062_+
		147	GAGAAGCTACAGGTCCTGAA	chr8:11548102-11548125_+
		148	CTTTAGATCACAGGTCGGA	chr8:11550164-11550187_+
		149	AGGTGGTTCTTTAGATCACA	chr8:11550156-11550179_+
BMX	ENST00000357607.6	150	GAAGGTCAGCGCCCAAGACA	chr8:11543301-11543324_+
		151	TGTCATATTCATAGTAGGAA	chrX:15508463-15508486_-
		152	ACTGCATGTTGAAGTTTGGC	chrX:15522512-15522535_-
		153	TGGTACTTGAAGATGGTGGC	chrX:15522446-15522469_-
		154	GGTACTTGAAGATGGTGGCT	chrX:15522445-15522468_-
BRAF	ENST00000646891.1	155	TGGTACTTGACCAGCAGGTG	chrX:15516125-15516148_-
		156	AGAGAAGAAACCAATTGGTT	chr7:140808039-140808062_-
		157	GAGAGAAGAAACCAATTGGT	chr7:140808040-140808063_-
		158	CAACAGTTATTGGAATCTCT	chr7:140834801-140834824_-
		159	GTGCTTTCTTTAGACTGTCT	chr7:140808946-140808969_+
BRD2	ENST00000374825.8	160	TGGGTGGTGTTCAAAGAACT	chr7:140800444-140800467_+
		161	GCAGGCACCGAAGCCATTGT	chr6:32974567-32974590_-
		162	TGGACATGGGTACTATTAAG	chr6:32975411-32975434_+
		163	AAGAGACGGCAGGCACCTGA	chr6:32976274-32976297_-
		164	GGGCACTGGTAACACTGCCC	chr6:32976253-32976276_-
BRD3	ENST00000303407.11	165	GTGTCCAATCCCAAAAAGCC	chr6:32974627-32974650_+
		166	TCGTGGCGGTGGACATCCTC	chr9:134053461-134053484_+
		167	ATTTGATTGCGTCCACGGGC	chr9:134053275-134053298_+
		168	ACCTTTGCCCTTTGGAGCAG	chr9:134051592-134051615_+
		169	GAGTGCAAGCGAATGTATGC	chr9:134052346-134052369_-
BRD4	ENST00000263377.6	170	CGCCACGACAGTCGCCCCCG	chr9:134053446-134053469_-
		171	GGGTGGCCGCGATGATGGGT	chr19:15265367-15265390_+
		172	TCTTTGGAGGTTTCACAGGC	chr19:15264618-15264641_+
		173	GAGCAGGTATTGCAGTTGGT	chr19:15272898-15272921_+
		174	TTCAGCTTGACGGCATCCAC	chr19:15272821-15272844_+
BTK	ENST00000308731.7	175	TGGCTCGTGAATGGGGTCAA	chr19:15264697-15264720_+
		176	CTTCCTTAGTTCTTCAGTTG	chrX:101370022-101370045_+
		177	TCTCCCCAACTGAAGAACTA	chrX:101370025-101370048_-
		178	GAACCAGATCACTGTTGTAC	chrX:101362662-101362685_+
		179	GCCCTTCATCATATACAACC	chrX:101370060-101370083_+
CCND1	ENST00000227507.2	180	AATCCGGTACAACAGTGATC	chrX:101362665-101362688_-
		181	TGGTTTCCACTTCGCAGCAC	chr11:69641327-69641350_-
		182	ATGCCAACCTCCTCAACGAC	chr11:69641368-69641391_+
		183	GCACAGGAGCTGGTGTCCA	chr11:69641311-69641334_-
		184	GCGACGATCTCCGCATGGA	chr11:69641472-69641495_-
CCND2	ENST00000261254.7	185	GGTTGGCATCGGGGTACGCG	chr11:69641354-69641377_-
		186	TGCAGATGGGACTTCGGAGT	chr12:4276082-4276105_-

		187	CTCGTGGCACAGCAGCTCCA	chr12:4274038-4274061_-
		188	CCAGGTAATTCATGGCCAGA	chr12:4276039-4276062_-
		189	CAGCTCCATGGCCAGCCCGG	chr12:4274026-4274049_-
		190	GCAGAACCTGCTCACCATCG	chr12:4274120-4274143_+
CCND3	ENST00000372991.8	191	TACTCGGGCAGCGAACAGGC	chr6:41941648-41941671_+
		192	GGGGTACGTAGCGCTCCTCC	chr6:41941528-41941551_+
		193	AACACAGCAGCTCCATACTC	chr6:41941633-41941656_+
		194	GTCTTGCGTCCCCACCCGAA	chr6:41940494-41940517_-
		195	ATGGAGCTGCTGTGTGCGA	chr6:41941626-41941649_-
CD19	ENST00000324662.7	196	ATTACCCACATATCTCTGGC	chr16:28933376-28933399_-
		197	CTGGACCCATGTGCACCCCA	chr16:28933312-28933335_+
		198	GTGACGCCTCCCCAGGAAG	chr16:28936521-28936544_+
		199	AGAGCTGAAGGACGATCGCC	chr16:28933357-28933380_+
		200	CGGGCCACAGCTCAAGACGC	chr16:28933421-28933444_+
CD274	ENST00000381577.3	201	TCTGAAGTGCAGCATTTCCC	chr9:5457304-5457327_-
		202	TTGAAGGACCAGCTCTCCCT	chr9:5457287-5457310_+
		203	TACCGCTGCATGATCAGCTA	chr9:5457359-5457382_+
		204	TGAACATGAACTGACATGTC	chr9:5462885-5462908_+
		205	TGAACTGACATGTCAGGCTG	chr9:5462891-5462914_+
CD38	ENST00000226279.7	206	TATCAGCCACTAATGAAGTT	chr4:15816592-15816615_+
		207	TGAAAGCATCCCATACACTT	chr4:15816522-15816545_-
		208	CCGGGGACAAACCCTGCTGC	chr4:15778442-15778465_+
		209	CTCCTAGAGAGCCGGCAGCA	chr4:15778453-15778476_-
		210	CTGGACCTGTGTGAACTGAT	chr4:15824911-15824934_-
CDK1	ENST00000395284.7	211	CCATAGTTAGTCAATGGGTA	chr10:60780146-60780169_-
		212	AAGGGTAGACACAAAACCTAC	chr10:60784724-60784747_+
		213	ACACAAAACCTACAGGTCAAG	chr10:60784732-60784755_+
		214	TATCCCTCCTGGTCAGTACA	chr10:60785747-60785770_+
		215	AGATCTCCAGAAGTATTGCT	chr10:60791907-60791930_+
CDK2	ENST00000266970.8	216	CCTTAAGCAGAGAGATCTCT	chr12:55967886-55967909_-
		217	AAGCAGAGAGATCTCTCGGA	chr12:55967882-55967905_-
		218	TGGAATAATATTTGCAGCCC	chr12:55969509-55969532_-
		219	CGAGCTCCTGAAATCCTCCT	chr12:55969492-55969515_+
		220	AATAATATTTGCAGCCCAGG	chr12:55969506-55969529_-
CDK4	ENST00000257904.10	221	CTTGCCAGCCGAAACGATCA	chr12:57751205-57751228_-
		222	ACCTCACGACTGTGCTGAT	chr12:57751547-57751570_+
		223	TGCCTATGGGACAGTGTACA	chr12:57751650-57751673_-
		224	CACGAACTGTGCTGATGGGA	chr12:57751551-57751574_+
		225	AGCATGTAGACCAGGACCTA	chr12:57751257-57751280_-
CDK5	ENST00000485972.5	226	ATCTCCCGGAGGGCGGAAC	chr7:151056946-151056969_+
		227	TCTGCATCGCGCGGCCGCG	chr7:151057841-151057864_+
		228	GAGGCTGGATGACGATGATG	chr7:151057070-151057093_-
		229	TTTCTCGTATTTCTGCATCG	chr7:151057830-151057853_+
		230	TCCATCGACATGTGGTCAGC	chr7:151055290-151055313_-
CDK6	ENST00000265734.8	231	GAAGAACGGAGGCCGTTTCG	chr7:92833202-92833225_-
		232	CCACTGAGGTTAGAGCCATC	chr7:92725624-92725647_+
		233	AGTTCAGATGTTGATCAACT	chr7:92623047-92623070_-
		234	AACATTCTGGTGACCAGCAG	chr7:92725692-92725715_-
		235	CCGCATCTATAGTTTCCAGA	chr7:92725639-92725662_-
CDK7	ENST00000256443.7	236	TCGGGCTTTACGGCGCCGGA	chr5:69234956-69234979_+
		237	ATTTATGTCCAAAAGCATCA	chr5:69255461-69255484_-
		238	ACTTCACGTCCAGAGCCATC	chr5:69234971-69234994_-
		239	CAATAGAGCTTATACACATC	chr5:69259903-69259926_+
		240	AACTTTGGGCACACCAACTG	chr5:69269259-69269282_+

CDK9	ENST00000373264.4	241	GCTTCTAAAAACACGAGAATG	chr9:127787555-127787578_+
		242	CGAGCAACAGCTCCGGGGGC	chr9:127788362-127788385_-
		243	TCTGCGAGCATGACCTTGCT	chr9:127787994-127788017_+
		244	CGGCCCCCGAGCTGTTGCT	chr9:127788363-127788386_+
		245	TACCCTTGCAGCGTTATAG	chr9:127787950-127787973_-
CHD1	ENST00000614616.4	246	ATAGGATGGCTGCTTCTTCA	chr5:98897269-98897292_+
		247	ATTCCTTGGAGGTCTAAATT	chr5:98893581-98893604_-
		248	GGCTTCTCAAATGAATGCTG	chr5:98896257-98896280_-
		249	TATTATCTGGTGGTTTAATG	chr5:98889107-98889130_+
		250	GCATTGATGAGTATTTTACG	chr5:98898291-98898314_-
CHEK1	ENST00000428830.6	251	CCAGTTGATGTTTGGTCCTG	chr11:125633299-125633322_+
		252	CAAAATCTCAGACTTTGGCT	chr11:125633169-125633192_+
		253	TTATTTCTGGAGTACTGTAG	chr11:125627784-125627807_+
		254	GAGATTCTTCCATCAACTCA	chr11:125629265-125629288_+
		255	ATGGTATTGGAATAACTCAC	chr11:125629400-125629423_+
CHEK2	ENST00000328354.10	256	GTTGAGGCTCAGCAGTCTCA	chr22:28734680-28734703_-
		257	CGATTATGGGCCCTTCAGGA	chr22:28734416-28734439_-
		258	TGCCGTGGAGAGGTAAAGC	chr22:28711991-28712014_-
		259	TGATCAGTCAGTTTATCTA	chr22:28719434-28719457_-
		260	AATACAGAGCTTGTAGGGAA	chr22:28725035-28725058_-
CPT1A	ENST00000265641.9	261	TGCAAAAATCAATCGGACTC	chr11:68812443-68812466_-
		262	CATCATCACTGGCGTGTACC	chr11:68812548-68812571_-
		263	GTGTCTTTGACAGCCGGGAC	chr11:68804009-68804032_+
		264	GTCGGTGAGGCCTCTTATGA	chr11:68799324-68799347_-
		265	TTTAATACTTCCCGGATCCC	chr11:68793325-68793348_-
CRBN	ENST00000231948.8	266	GCACGATGACGACAGCTGTC	chr3:3174197-3174220_-
		267	GCCACCATTATATGAACAT	chr3:3167647-3167670_+
		268	TGTATGTGATGTCGGCAGAC	chr3:3175162-3175185_+
		269	CCATGCTGTATTACCCGCAA	chr3:3179683-3179706_+
		270	CGCACCATACTGACTTCTTG	chr3:3174103-3174126_+
CRTC1	ENST00000321949.12	271	TGGTGTCCAGGCCCGAGGAT	chr19:18745830-18745853_-
		272	CGTCATTGTGCTCTGGTGCA	chr19:18749797-18749820_-
		273	TGGTGTCCGCGGGTGGTGAG	chr19:18747081-18747104_-
		274	CGCGGGTGGTGAGAGGTACA	chr19:18747074-18747097_-
		275	CCTCGGGCCTGGACACCAGC	chr19:18745835-18745858_+
CRTC2	ENST00000368633.1	276	TAACCAGATTGGCTCTGGCC	chr1:153955075-153955098_-
		277	GAGCCAATCTGGTTAACATT	chr1:153955083-153955106_+
		278	CATCCTGCCAGCCGACGTG	chr1:153953265-153953288_-
		279	AGAGCCAATCTGGTTAACAT	chr1:153955082-153955105_+
		280	AGTCCCCAGGATACCTACCC	chr1:153953303-153953326_-
CSF1R	ENST00000286301.7	281	GGCCACGCAGGAGTAGTTGC	chr5:150077324-150077347_+
		282	TCCTTCCTGGCCAGAAACCC	chr5:150070493-150070516_-
		283	TCCTGTGCTAGCACGTTCCA	chr5:150080302-150080325_+
		284	ATCCCAGACCTGCAGCACTT	chr5:150070029-150070052_+
		285	AACGGTGACCTTGCGATGTG	chr5:150080943-150080966_-
CSNK2A1	ENST00000646561.1	286	GATCATAATTGTCATGTCCA	chr20:489781-489804_+
		287	CATCATATTGGCGCTGCTGA	chr20:486379-486402_+
		288	AGCAGCGCCAATATGATGTC	chr20:486374-486397_-
		289	GCTTACTGCAAGAGAGGCAA	chr20:487441-487464_-
		290	TGAGGATAGCCAAGGTTCTG	chr20:488751-488774_-

CSNK2A2	ENST00000262506.7	291	TAATCAAGATGATTACCAAC	chr16:58196821-58196844_-
		292	GACCAAGTTTTCGAACCAGT	chr16:58196806-58196829_+
		293	TTGTCCTGTCCATGGAAGAA	chr16:58167216-58167239_+
		294	GGAACCATTCTTCCATGGAC	chr16:58167220-58167243_-
		295	AGCAAGCATGATCTTTTCGAA	chr16:58167241-58167264_-
CXCR1	ENST00000295683.2	296	TATTACAGATCCACAGATGT	chr2:218165180-218165203_-
		297	TCATCAAAATCCCACATCTG	chr2:218165170-218165193_+
		298	CAGGCTCAGCAGGAACACTA	chr2:218165049-218165072_+
		299	CAGCAGGTAGACATCAGTGA	chr2:218164974-218164997_+
		300	TCTCAGTTTCTAGCATACAG	chr2:218165105-218165128_+
CXCR2	ENST00000318507.6	301	GGCGGCATCTAGTAGAAAAG	chr2:218134889-218134912_-
		302	GGTCAGGGCAAAGAGTAGGT	chr2:218135078-218135101_-
		303	CAGGCTCAGCAGGAATACCA	chr2:218134967-218134990_-
		304	CAGCAGGTAGACATCAGTGA	chr2:218135042-218135065_-
		305	GCGGCATCTAGTAGAAAAGG	chr2:218134888-218134911_-
CXCR4	ENST00000409817.1	306	CTTCTGGGCAGTTGATGCCG	chr2:136115629-136115652_-
		307	AGGGAAGCGTGATGACAAAG	chr2:136115650-136115673_+
		308	GCATTTCTTCACGGAAACA	chr2:136115826-136115849_+
		309	AGGGGACTATGACTCCATGA	chr2:136115851-136115874_-
		310	GAAGCGTGATGACAAAGAGG	chr2:136115653-136115676_+
CYP17A1	ENST00000369887.3	311	TCGCTGACTCTGGCGCACAC	chr10:102835326-102835349_-
		312	TGGGCCAAAACAAATAAGCT	chr10:102837306-102837329_+
		313	GCCTGGTGGACCTAGTCCCC	chr10:102834790-102834813_-
		314	GGTATCGCCTTCGCTGACTC	chr10:102835336-102835359_-
		315	GATTGTGCGCCACCACCAGC	chr10:102837117-102837140_-
CYP19A1	ENST00000396402.5	316	CCAATTCCCATGCAGTAGCC	chr15:51236984-51237007_+
		317	CATTATGTGGAACATACTTG	chr15:51227908-51227931_+
		318	GCGAGTCTGGATCTCTGGAG	chr15:51236877-51236900_-
		319	GTGACCATACGAACAAGGCC	chr15:51222491-51222514_+
		320	TGTGACCATACGAACAAGGC	chr15:51222490-51222513_+
DDR2	ENST00000367922.7	321	TCTCTTGGCGGAACCGTCAT	chr1:162754826-162754849_+
		322	AGATAAATGATGGAACCTCC	chr1:162755710-162755733_-
		323	TGTCTTACAATGCTCCAGCT	chr1:162755672-162755695_+
		324	CGATGCCATGACCTCCTGCA	chr1:162754752-162754775_-
		325	TCACTCTGGTGGGGACCCAG	chr1:162754727-162754750_+
DHFR	ENST00000439211.6	326	GTAGACATGGTCTGGATAGT	chr5:80637901-80637924_-
		327	CCTCCCGCTGCTGTCATGGT	chr5:80654481-80654504_-
		328	GACATGGTCTGGATAGTTGG	chr5:80637898-80637921_-
		329	CGAACCAACCATGACAGCAG	chr5:80654477-80654500_+
		330	CCAACCATGACAGCAGCGGG	chr5:80654481-80654504_+
DHH	ENST00000649637.1	331	CCTGGGCGCCAGTGGGCCAG	chr12:49094322-49094345_-
		332	AGCGGACCCTGGGCGCCAGT	chr12:49094329-49094352_-
		333	TTGTGCCCGCGTGCCAGAG	chr12:49094347-49094370_-
		334	GCCATGGATACAGCGGACCT	chr12:49094507-49094530_+
		335	TAGATTGGTCAGGAGAGCCA	chr12:49094491-49094514_+
DHX9	ENST00000367549.3	336	CAAGGATTCCAGTTGGATTG	chr1:182858834-182858857_-
		337	GTCAGACAACCTGTACCATCT	chr1:182858168-182858191_+
		338	TGGTGTTCCTGGGCCCCACCT	chr1:182853336-182853359_+
		339	ACTTGGTTTGTGCTGAGA	chr1:182858789-182858812_-
		340	GCGACAAAACCAAGTGGGTG	chr1:182858797-182858820_+
DNMT1	ENST00000340748.8	341	CCTGAGGTTTCCGTTTGGCA	chr19:10175595-10175618_+
		342	ATAAATGAATGGTGGATCAC	chr19:10155893-10155916_-
		343	ACTGAATGCACTTGGGAGGG	chr19:10159897-10159920_+

DOT1L	ENST00000398665.7	344	CTGAATGCACTTGGGAGGGT	chr19:10159898-10159921_+
		345	GAAGCAGGTCAGTTTGTGCT	chr19:10159659-10159682_+
		346	GTCGATAGTGTGCAGGTAGT	chr19:2207648-2207671_-
		347	CGGCAGCGGCCACGGGTAGA	chr19:2164236-2164259_-
		348	CAGAGGTGCAAAGGGTTTCG	chr19:2206743-2206766_-
		349	AGTTGGTGGCAGCAGCAACC	chr19:2193707-2193730_-
DPP4	ENST00000360534.7	350	ATAGTGATGTTTGCAGTTGG	chr19:2193721-2193744_-
		351	AGTTACAGAATCACATGGAC	chr2:162038348-162038371_-
		352	GTCCATGTGATTCTGTAAC	chr2:162038351-162038374_+
		353	ATGATGAATCCAGTGGAAGA	chr2:162024815-162024838_-
		354	GATTATTCAATATCTCCTGA	chr2:162045565-162045588_-
DRD2	ENST00000362072.7	355	CCCGTGGTTCTGCTGAACAA	chr2:162073400-162073423_-
		356	TTCCCGTCTGACCCGTTGAA	chr11:113424568-113424591_+
		357	CTTCAACGGGTCAGACGGGA	chr11:113424566-113424589_-
		358	CGGCCCTTCAACGGGTCAGA	chr11:113424571-113424594_-
		359	GAGGCTGACGATCAGGTAGT	chr11:113424423-113424446_+
EDNRA	ENST00000324300.10	360	TGTGTGCCATCAGCATCGAC	chr11:113418025-113418048_-
		361	TGGGTTGATGAGTGGTAACC	chr4:147485821-147485844_-
		362	GAAGTAATTTTAGTCTGCTG	chr4:147485888-147485911_-
		363	TCCATCTTGAGGCAAATTTG	chr4:147485663-147485686_-
		364	ATTTTCATCGTGGAATGGT	chr4:147485948-147485971_+
EGFR	ENST00000275493.6	365	TCTGCGCTCTTAGTGTGAC	chr4:147519956-147519979_+
		366	TAAATGCCACCGGCAGGATG	chr7:55156632-55156655_-
		367	ATCCCAAGGATGTTATGTTT	chr7:55160165-55160188_-
		368	AGCTGTCCGGCCCCACAGGCT	chr7:55155863-55155886_-
		369	CCTTGACGCTGGCTTCGTCT	chr7:55154024-55154047_-
EHMT1	ENST00000460843.5	370	GCAGCGCCCGGAGCACTGCT	chr7:55152563-55152586_-
		371	TCCCGTTGGATCAAAGCCCT	chr9:137777940-137777963_-
		372	CGGTGAGAGATGCTGCTCTC	chr9:137776638-137776661_-
		373	TTGATCCAACGGGACCTGCT	chr9:137777949-137777972_+
		374	CTCCAGCACATCTGGACCGT	chr9:137762680-137762703_-
EHMT2	ENST00000375537.8	375	AGCACTCCCCCTCCCAAGGG	chr9:137717069-137717092_-
		376	GACCATCCCCCGGGTGACG	chr6:31888125-31888148_-
		377	GAGTGATGATGTCCACTCAC	chr6:31892840-31892863_-
		378	CGGGCCAAGATGTCAATGAC	chr6:31896437-31896460_-
		379	GCCTCATGGTCTCCCGCTTG	chr6:31888460-31888483_+
EPHA2	ENST00000358432.7	380	GAGGAGTGGGAGACGGTGGT	chr6:31892470-31892493_-
		381	TCGCGGCCCGCTGTCCCTG	chr1:16138091-16138114_+
		382	GTGTGCAAGGCATCGACGCT	chr1:16138274-16138297_+
		383	GCTCACTGTCACTGGTGC	chr1:16137964-16137987_+
		384	GAGGTGGCACCTCAGGGGA	chr1:16138336-16138359_+
EPHB4	ENST00000358173.7	385	CGTCCAGCGCAGCTCCACCT	chr1:16138117-16138140_+
		386	GTGTTAGAGTGGCTATTGGC	chr7:100820217-100820240_+
		387	CAGGGCTCCACCAGGTCCCG	chr7:100819684-100819707_+
		388	TCCTGCAGTGTCTGACATCC	chr7:100818617-100818640_-
		389	TCCGGGGTTTCGAGGCAGCTG	chr7:100822288-100822311_-
ERBB2	ENST00000269571.9	390	GCTGTGATGTTCTGGCCGA	chr7:100817207-100817230_+
		391	AGCTCTCCGGCAGAAATGCC	chr17:39712418-39712441_-
		392	GCCGAATGTATACCGGCCCT	chr17:39710433-39710456_-
		393	CCAGAACCTGCAAGTAATCC	chr17:39715497-39715520_+
		394	GGAGCACTTGCCGAGAGGTGA	chr17:39712340-39712363_-
		395	TGCGCCCGAGGGCACTGCTG	chr17:39716329-39716352_+

ERBB3	ENST00000267101.7	396	GTGGTAGCAGAGCTGCCTAT	chr12:56093442-56093465_-
		397	GGCCTGTCCTCCTGACAAGA	chr12:56088576-56088599_+
		398	ACTGTCATTGAAAGTGCCGGC	chr12:56088021-56088044_-
		399	CGTAGGCCCCCGAAGCACCT	chr12:56093481-56093504_-
		400	CCAACCTCCGCGTGGTGCGA	chr12:56085058-56085081_+
ERBB4	ENST00000342788.8	401	TGTGTTCAGTGATGGCTGT	chr2:211679134-211679157_-
		402	TTTTCTAACCTGGTGACCAT	chr2:211704121-211704144_-
		403	TTCTAGTCACTGGTATTCAT	chr2:211712048-211712071_-
		404	TGGAGGCTGCTCAGGACCTA	chr2:211725089-211725112_-
		405	GCTTGTGATGGCATTGGCAC	chr2:211712154-211712177_-
ESR1	ENST00000440973.5	406	CCCCTACGGCCCCGGGTCTG	chr6:151808145-151808168_+
		407	AGCCTCAGACCCGGGGCCGT	chr6:151808147-151808170_-
		408	GCTGCGGCGTTCCGGCTCCAA	chr6:151808167-151808190_+
		409	AAATTCAGATAATCGACGCC	chr6:151842599-151842622_+
		410	CCCTTGGATCTGATGCAGTA	chr6:151807949-151807972_-
ESR2	ENST00000341099.5	411	AACTGGCGATGGACCACTAA	chr14:64282701-64282724_+
		412	TAGCGATCTTGCTTCACACC	chr14:64282646-64282669_+
		413	AGTGTACAATCGATAAAAC	chr14:64268855-64268878_-
		414	AATGTGTTGTGGCCAACACC	chr14:64282734-64282757_-
		415	CAGTAACAGGGCTGGCGCAA	chr14:64280100-64280123_+
EZH2	ENST00000320356.6	416	GCAATGAGCTCACAGAAGTC	chr7:148846483-148846506_+
		417	TTAATGGGATGACTTGTGT	chr7:148832700-148832723_+
		418	CTCACCGAACAGCAGCTCCC	chr7:148826599-148826622_-
		419	TGTTGGAAAATCCAAGTCAC	chr7:148832717-148832740_+
		420	ACTTCTGTGAGCTCATTGCG	chr7:148846479-148846502_-
F2R	ENST00000319211.4	421	GCTGTTGTCTGCCCCGACCC	chr5:76716360-76716383_+
		422	CCATTGTCCC GGCTCTGCG	chr5:76716288-76716311_-
		423	CGGGTGCGGGCAGACAACAG	chr5:76716358-76716381_-
		424	GCCGCCTGCTTCAGTCTGTG	chr5:76716334-76716357_+
		425	CCGGGACAATGGGGCCGCGG	chr5:76716299-76716322_+
FCGR1A	ENST00000369168.4	426	CTGGGAGCAGCTCTACACAG	chr1:149784095-149784118_+
		427	TAGAGCTGCTCCAGGCAGA	chr1:149784087-149784110_-
		428	ACCAGCTTGGAGACAACATG	chr1:149782726-149782749_+
		429	AACCGTAACCTTGCACTGTG	chr1:149784060-149784083_+
		430	GCATGACACCTCAAGGCCAG	chr1:149788412-149788435_-
FGF1	ENST00000621536.4	431	TTCCGGATGGCACAGTGGAT	chr5:142613983-142614006_-
		432	ACTTGCCATGGACACCGAC	chr5:142600716-142600739_-
		433	CAGATTAAACTTCTCGGTCA	chr5:142614073-142614096_+
		434	TACTTGCCATGGACACCGA	chr5:142600717-142600740_-
		435	GGCCCCCGTTGCTACAGTAG	chr5:142614021-142614044_+
FGF2	ENST00000644866.2	436	CTGCCCGCCTTGCCCGAGGA	chr4:122827198-122827221_+
		437	GCCGCTTGGGGTCCCTGAAG	chr4:122827245-122827268_-
		438	CGGCTGCCATGGTCCCTGCG	chr4:122827161-122827184_-
		439	TAACCGTTACCTGGCTATGA	chr4:122876378-122876401_+
		440	TTGGGGTCCCTGAAGTGGCC	chr4:122827240-122827263_-
FGFR1	ENST00000447712.6	441	AAGCACCTCCATCTCTTGT	chr8:38421899-38421922_+
		442	GGTTTGGGGTCCCACTGGAA	chr8:38427985-38428008_+
		443	ACCCTGCTTGCAGGATGGGC	chr8:38424663-38424686_+
		444	GACTCCGTGCGCGCAGACTC	chr8:38429749-38429772_-
		445	CAAGGTCGGGGACGGCCTAG	chr8:38457365-38457388_+
FGFR2	ENST00000457416.6	446	CAAGTTTCGCTGCCAGCCG	chr10:121551366-121551389_-
		447	CGCACCTCTAGCGACTCCCC	chr10:121565631-121565654_+

FGFR3	ENST00000440486.7	448	ACCCCAGCTGACCATGGTTA	chr10:121593802-121593825 +
		449	GGTTGGCATTGGGTTCCCCC	chr10:121551349-121551372 +
		450	CACCGGCCCATCCTCCAAGC	chr10:121520135-121520158 -
		451	GGGGACGGAGCAGCGCGTCG	chr4:1794008-1794031 +
		452	GCGGAAGCGGACGGTGTGG	chr4:1801423-1801446 -
		453	AATAGAATTGCCCGCCAGGC	chr4:1803773-1803796 -
		454	CTTCGGCAGCGGGGATGCTG	chr4:1799293-1799316 +
FGFR4	ENST00000292408.8	455	ACTCCGGGGCCTACAGCTGC	chr4:1799451-1799474 +
		456	GATGGAGAGCGTGGTGCCCT	chr5:177091710-177091733 +
		457	CGCTACCTCTGCCTGGCACG	chr5:177090589-177090612 +
		458	GCCAGCGGATGGTGGGCGTG	chr5:177091031-177091054 -
		459	AGCTGGACAGCGGAATTGA	chr5:177091000-177091023 -
FGR	ENST00000374005.7	460	GTACACGGCCAGCAGGTGCC	chr5:177090513-177090536 -
		461	GAGAGGCAGCTGCTTTCACC	chr1:27617239-27617262 -
		462	CTTTCACCAGGCAACCCCA	chr1:27617227-27617250 -
		463	ATGTGGCAAATGAGGATGC	chr1:27623767-27623790 +
		464	CTCGCTTCCCGAATGAGAA	chr1:27617202-27617225 +
FKBP1A	ENST00000400137.8	465	GAGGCTCGGTCTCTCAGCTC	chr1:27621618-27621641 -
		466	GGGCGCACCTTCCCAAGCG	chr20:1392859-1392882 -
		467	TCAGCGTCCGCCGCCCAT	chr20:1392993-1393016 -
		468	GCGAGGTCTGGCCGCGCTTG	chr20:1392848-1392871 +
		469	CACCTGCACTCCCATGGCGG	chr20:1392983-1393006 +
FLT1	ENST00000282397.8	470	CAAGCGCGGCCAGACCTGCG	chr20:1392845-1392868 -
		471	GTAAGACCGCTTGCCAGCTA	chr13:28430096-28430119 +
		472	TCCCCGAGCCTCAGATCACT	chr13:28384918-28384941 -
		473	GTTAGGTGACGTAACCCGGC	chr13:28438241-28438264 +
		474	CTTGACACTTTGATCCCTGA	chr13:28434191-28434214 -
FLT3	ENST00000241453.11	475	CAGGTGCTTGAAACCGTAGC	chr13:28430109-28430132 -
		476	GTCCACGTACATCTGATTTG	chr13:28048328-28048351 +
		477	GGTAACCAAAGCTGATTGAC	chr13:28049390-28049413 +
		478	TCCACGTACATCTGATTTGT	chr13:28048329-28048352 +
		479	CCCAGGTGAGCCCGAATCCA	chr13:28049660-28049683 +
FLT4	ENST00000261937.10	480	GAGCAAAAGGGTCTTGATAA	chr13:28048280-28048303 -
		481	GACGTAGCTGCCTGTGTCGT	chr5:180630624-180630647 +
		482	GTCAAGTTCTGCGTGAGCCG	chr5:180621218-180621241 +
		483	CCCGTAGGCCGTGCAGGTGA	chr5:180625942-180625965 +
		484	GGCATGTGGACTGTGGCGCC	chr5:180626219-180626242 +
FNTA	ENST00000302279.7	485	TCTTTGTACCACACGATGCT	chr5:180621131-180621154 +
		486	GTGACTTCAAAAGAACTCTC	chr8:43069560-43069583 -
		487	CTACATCACTGCAATAATTG	chr8:43069611-43069634 +
		488	TGTGGACCAACTTCTGAAAG	chr8:43077247-43077270 +
		489	GGGTCGGGGAGGCTGCGCAA	chr8:43056362-43056385 +
FOLH1	ENST00000256999.6	490	TCTTTTGAAGTCACTTCAGA	chr8:43069569-43069592 +
		491	CCCGCGCTGGCTGTGCGCTG	chr11:49208336-49208359 -
		492	TCACGAAACCGACTCGGCTG	chr11:49208372-49208395 -
		493	GTGCTAGCTCAACAGAATCC	chr11:49200331-49200354 +
		494	TCTCCTTACGAAACCGACT	chr11:49208378-49208401 -
FOLR1	ENST00000312293.9	495	CAGCCGAGTCGGTTTCGTGA	chr11:49208375-49208398 +
		496	AGTGTGGGTGGCTGTAGTAG	chr11:72192211-72192234 +
		497	ATGAAATGCCGTTTGACGGC	chr11:72195381-72195404 -
		498	CCAGTTGAATCTATATAGGT	chr11:72195337-72195360 -
		499	CTGCAAACGGCATTTCATCC	chr11:72195386-72195409 +

FOLR2	ENST00000298223.10	500	GACATTGAGAAGCTCAGTCC	chr11:72192258-72192281_-
		501	CTGGGACCACTGCGGCAAGA	chr11:72220955-72220978_+
		502	CGGGCTCCATCTTGCCGAG	chr11:72220961-72220984_-
		503	TGGCATCCATACAGACATTG	chr11:72218664-72218687_-
		504	GTCCTGGGCACTGCACATGG	chr11:72218630-72218653_-
FOLR3	ENST00000611028.2	505	TGATCTCCTCAATGTCTGTA	chr11:72218658-72218681_+
		506	CCTGGGGGCCCTGGATCCGGC	chr11:72139127-72139150_+
		507	ATAAAGTGGCGCTTGCAGGT	chr11:72139071-72139094_-
		508	GGCCATACAGCTCGTCCTCG	chr11:72136095-72136118_-
		509	TGGCTTTGGTGACTGCTGCG	chr11:72135989-72136012_+
FRK	ENST00000606080.1	510	GTTAAAGTTGTACAGGCGGG	chr11:72139024-72139047_-
		511	AGATGTTGCTCATTGTGCCT	chr6:116060298-116060321_+
		512	GGCTGAGGACAGAAGCCTAC	chr6:116059974-116059997_-
		513	TCAACCGTGATTGAAAATCC	chr6:116060213-116060236_-
		514	GTTGCTCATTGTGCCTTGGT	chr6:116060302-116060325_+
FYN	ENST00000354650.7	515	GGCTCCAGTCAGCAACTACA	chr6:116060018-116060041_-
		516	CGAAGCTGGGGTAGTGCTGA	chr6:111719924-111719947_+
		517	TTACATTCCCAGCAATTATG	chr6:111707949-111707972_-
		518	GTCCTTGCCCCCGGCTGCG	chr6:111719870-111719893_+
		519	CCGAAGCTGGGGTAGTGCTG	chr6:111719923-111719946_+
FZD8	ENST00000374694.2	520	AATGGGCTGTGTGCAATGTA	chr6:111720029-111720052_-
		521	GCGCCGCTCATGCGCCAGTA	chr10:35641052-35641075_-
		522	GCAGCGCTCTAGCGGCGCTG	chr10:35641350-35641373_-
		523	GAGGCGCACAGCATGGAGTG	chr10:35641418-35641441_-
		524	GATGCCCTTACACAGCGGCA	chr10:35641291-35641314_+
GART	ENST00000381839.7	525	TAGCCGATGCCCTTACACAG	chr10:35641286-35641309_+
		526	TCGCTTATGGTCCTGTGCTG	chr21:33530821-33530844_+
		527	CACCGCCCTAACTGTTGTCA	chr21:33528214-33528237_-
		528	GGAATAATGCTGACCAAGAA	chr21:33528567-33528590_-
		529	AAACAAGTGTGGTTGCCCC	chr21:33539211-33539234_-
GNRH1	ENST00000276414.4	530	CGCTTATGGTCCTGTGCTGG	chr21:33530822-33530845_+
		531	TCCTCCAGGGCGCAGTCCAT	chr8:25423228-25423251_+
		532	CTACTGACTTGGTGCGTGGA	chr8:25423271-25423294_-
		533	TATTCTACTGACTTGGTGCG	chr8:25423275-25423298_-
		534	AGCTCCTTTCAGGTCTCGGA	chr8:25421575-25421598_+
GNRHR	ENST00000226413.4	535	GGGAGAACGTGGCTGGTGCG	chr8:25421596-25421619_+
		536	CTGATTGTCATGCCACTGGA	chr4:67754039-67754062_-
		537	TCATGCCAAGTGATGGGATG	chr4:67754032-67754055_-
		538	GTAACCTCCAGCATACCAT	chr4:67753998-67754021_+
		539	TGATTGTCATGCCACTGGAT	chr4:67754038-67754061_-
GSK3A	ENST00000222330.7	540	AAAGACACTACTGAGGATCC	chr4:67753825-67753848_+
		541	TACACGGACATCAAAGTGAT	chr19:42240048-42240071_-
		542	CTCTGGGCCCTTGGCCTAGAG	chr19:42240089-42240112_+
		543	CACTAGCTTCCCGCCGCCCG	chr19:42242194-42242217_-
		544	TTGGGGTTCGTGTACCAGGCA	chr19:42240014-42240037_-
GSK3B	ENST00000316626.5	545	TCACGGCCCAGCTTACCCCC	chr19:42242178-42242201_+
		546	CGTTATTTCTTCTACTCCAG	chr3:119947274-119947297_-
		547	CGGCTTGACAGCTCTCCGAA	chr3:120093386-120093409_+
		548	CTCCTGGGCAGGGTCCAGAC	chr3:120002177-120002200_-
		549	TTCATGCTGCCAAAAGCTGA	chr3:120093354-120093377_+
HCK	ENST00000534862.6	550	CAACAGTGGTGGCAACTCCT	chr3:120002192-120002215_-
		551	GCTGCCCGCAGACGAGGAG	chr20:32052455-32052478_+
		552	AGGACAGTGTGGGCTGGCGC	chr20:32071723-32071746_-
		553	AGGCTCGATCCCTGGCCACC	chr20:32074639-32074662_+

HDAC1	ENST00000373548.7	554	AGAATGTATTGCCTCCGACC	chr20:32071688-32071711_-
		555	GCGCCCGCTCCTCGTCTCGC	chr20:32052459-32052482_-
		556	TTCGGTGAGGCTTCATTGGG	chr1:32302651-32302674_-
		557	CCCAGGAACTGGGGACCTAC	chr1:32327655-32327678_+
		558	AGTAGTAACAGACTTTCCTC	chr1:32292189-32292212_-
		559	GTACTCTCCATACTTATGAA	chr1:32327630-32327653_-
HDAC10	ENST00000216271.9	560	TTACGTCAATGATATCGTCT	chr1:32327035-32327058_+
		561	GTGTAGCCCGTGTTCCTGCT	chr22:50249861-50249884_+
		562	CTCCCGGGCACCATGGCCAG	chr22:50249939-50249962_-
		563	TGTGCAAAATGGGCTTGCCC	chr22:50250066-50250089_-
		564	GAGTCAGATGCAGACGCAGT	chr22:50249373-50249396_-
HDAC11	ENST00000295757.7	565	CAGCGTTTCCCATCCCAACC	chr22:50249149-50249172_+
		566	CAACATCACCTTCATGGGCC	chr3:13481314-13481337_+
		567	CAAAGGGATGCAGCTTCTCC	chr3:13481332-13481355_-
		568	CCCTTTGATGCCGAAAATG;	chr3:13481348-13481371_+
		569	AAGCTGCATCCCTTTGATGC	chr3:13481339-13481362_+
HDAC2	ENST00000519065.5	570	AACGGGGGGGATTTCTGTGA	chr3:13496754-13496777_-
		571	GATATGGCTGTTAATTGGGC	chr6:113956096-113956119_-
		572	GAGCCCATGGCGTACAGTCA	chr6:113970891-113970914_-
		573	GGGGAATACTTTCCTGGCAC	chr6:113953286-113953309_-
		574	TCTTCGGCAGTGGCTTTATG	chr6:113958740-113958763_+
HDAC3	ENST00000305264.7	575	TTCTGGCACAGGAGACTTG	chr6:113953276-113953299_-
		576	CGAGCAGAACTCAAAGAGCC	chr5:141630091-141630114_+
		577	TCATGTTGGGAGGCCTGGTA	chr5:141634921-141634944_+
		578	TGGTGGGGCTGACTCTCTGC	chr5:141634862-141634885_+
		579	CCAGGCGATGGGGCTTCATA	chr5:141636597-141636620_+
HDAC4	ENST00000345617.7	580	GATATTGCCATTAACCTGGGC	chr5:141629887-141629910_-
		581	GTCGACACTCCGCTCTGGGG	chr2:239156716-239156739_+
		582	GCCTGGGGCGCTGCTGCACG	chr2:239139770-239139793_+
		583	GTGACGAGGGGTGCTTGTGC	chr2:239134246-239134269_+
		584	CAAGGGCGAGGTGCTCAGGT	chr2:239134332-239134355_+
HDAC5	ENST00000225983.10	585	CTCCACGCACAGTCCTTGGT	chr2:239126639-239126662_-
		586	TGTGCAGAGAAGTCCGCGGC	chr17:44110743-44110766_+
		587	AGCAGGGAGGCATGCCCCGTG	chr17:44091322-44091345_+
		588	CGGGCAGTCCCCACTAGTGA	chr17:44088565-44088588_-
		589	GCCCTCCAGTCCCTGCGGCA	chr17:44091427-44091450_-
HDAC6	ENST00000334136.10	590	CACGTTACCCGTCCTACTAGT	chr17:44088556-44088579_+
		591	GTTAGTGGGCGAACCCCTGC	chrX:48814979-48815002_-
		592	CTGGTTCCAAGGCACATTGA	chrX:48814543-48814566_-
		593	CTGAGTCGTAGGTGTCTGCT	chrX:48806427-48806450_-
		594	GATATACCATCAATGTGCCT	chrX:48814537-48814560_+
HDAC7	ENST0000080059.11	595	CTTGAGGCTGAAGCACTGGC	chrX:48803136-48803159_+
		596	TGACCACCGAGCGGCTCTCT	chr12:47795312-47795335_-
		597	GTGGGCACCCGGGCTCACCT	chr12:47802245-47802268_+
		598	TAAGGACTGGGCAAAGTGGA	chr12:47795336-47795359_+
		599	GGCTGCAGTAGTGGGCACCC	chr12:47802235-47802258_+
HDAC8	ENST00000647594.1	600	CAGCGGGGCATGAGAGCCTG	chr12:47795593-47795616_+
		601	GCTGCCCAATGCCTGATTGA	chrX:72567939-72567962_-
		602	ACATTCCGTCAATCAGGCAT	chrX:72567934-72567957_+
		603	CATTCCGTCAATCAGGCATT	chrX:72567935-72567958_+
		604	ATCCGGACTCCATAGAATAT	chrX:72568757-72568780_-
HDAC9	ENST00000417496.6	605	CCTGGCCAAGATCCCCAAAC	chrX:72572649-72572672_-
		606	AGGTCTGTCTTAGGTCTAA	chr7:18585324-18585347_-
		607	CTAAAGGTGAGATGGGCTCC	chr7:18585308-18585331_-

		608	CTTAGGTCTAAAGGTGAGAT	chr7:18585315-18585338_-
		609	CCATCTCACCTTTAGACCTA	chr7:18585316-18585339_+
		610	TCAGTTCAGGAGCATATCA	chr7:18585500-18585523_+
		611	GTCGCCATAACGGAGCCGGC	chrX:134460296-134460319_-
HPRT1	ENST00000298556.7	612	GCGGGTCGCCATAACGGAGC	chrX:134460300-134460323_-
		613	CTCATGGACTAATTATGGAC	chrX:134473443-134473466_+
		614	AAAATCTACAGTCATAGGAA	chrX:134475320-134475343_-
		615	GCCCCCTTGAGCACACAGA	chrX:134475236-134475259_-
HPSE	ENST00000405413.6	616	CTGGCAATCTCAAGTCAACC	chr4:83322218-83322241_-
		617	CCTTGGAAGAGCAGTAGTCC	chr4:83313143-83313166_+
		618	TGGCGTCAATGGTGACGGAC	chr4:83334592-83334615_+
		619	ACGACGTCTGTGCTTGCGC	chr4:83334666-83334689_+
		620	CATTGACGCCAACCTGGCCA	chr4:83334580-83334603_-
HSP90AA1	ENST00000216281.12	621	ACGATGATGAGCAGTACGCT	chr14:102085800-102085823_-
		622	GATCAAAAGGAGCACGTCGT	chr14:102084494-102084517_+
		623	TCTCACGGGATATGTTTGA	chr14:102083926-102083949_+
		624	AGATCAAAAGGAGCACGTCG	chr14:102084493-102084516_+
		625	CGATGATGAGCAGTACGCTT	chr14:102085799-102085822_-
HSPA1A	ENST00000375651.6	626	CACCACCTACTCCTGCGTGG	chr6:31815791-31815814_+
		627	GTGTTGGAACACCCCCACGC	chr6:31815802-31815825_-
		628	GACCAAGGCATTCTACCCCG	chr6:31816085-31816108_+
		629	CAACGACGGAGACAAGCCCA	chr6:31816040-31816063_+
		630	GGACACCGAGCGGCTCATCG	chr6:31815890-31815913_+
HSPA1B	ENST00000375650.4	631	CAGGTCGATGCCGATCGCCG	chr6:31827960-31827983_-
		632	CACCACCTACTCCTGCGTGG	chr6:31827985-31828008_+
		633	GTGTTGGAACACCCCCACGC	chr6:31827996-31828019_-
		634	CAACGACGGAGACAAGCCCA	chr6:31828234-31828257_+
		635	GGACACCGAGCGGCTCATCG	chr6:31828084-31828107_+
HSPB1	ENST00000248553.6	636	GCATAGCCGCCTCTTCGACC	chr7:76302783-76302806_+
		637	GAGTGGTCGCAGTGGTTAGG	chr7:76302832-76302855_+
		638	TGCCGGAGGAGTGGTCGCAG	chr7:76302824-76302847_+
		639	CAGCCGGCAACTCAGCAGCG	chr7:76302942-76302965_+
		640	CGGGCTGCCCCGGCTGCCGG	chr7:76302810-76302833_+
IDH1	ENST00000345146.6	641	TGGGTAACCTATCATCAT	chr2:208248390-208248413_-
		642	ACCCATCCACTCACAAGCCG	chr2:208248408-208248431_+
		643	AATATCCCCCGGCTTGTGAG	chr2:208248414-208248437_-
		644	CCCCCGGCTTGTGAGTGGAT	chr2:208248409-208248432_-
		645	CCCATCCACTCACAAGCCGG	chr2:208248409-208248432_+
IDH2	ENST00000330062.7	646	GATGTTCCGGATAGTTCCAT	chr15:90088694-90088717_+
		647	CCAAGCCCATCACCATTGGC	chr15:90088604-90088627_-
		648	GTTCGCTCTCCAGCTTGGA	chr15:90102386-90102409_-
		649	TTGGGATGGCCGGCTACCTG	chr15:90102372-90102395_-
		650	AACATCCCACGCCTAGTCCC	chr15:90088632-90088655_-
IDO1	ENST00000522495.5	651	CACACGCTATGGAAAATCC	chr8:39913926-39913949_+
		652	ATGGCATATGTGTGGGGCAA	chr8:39918165-39918188_+
		653	CTTGCTCTGCCAAATCCAC	chr8:39913987-39914010_+
		654	GCATCACCATGGCATATGTG	chr8:39918157-39918180_+
		655	CATCACCATGGCATATGTGT	chr8:39918158-39918181_+
IFNAR1	ENST00000270139.7	656	TGGGTGTTGTCCGCAGCCGC	chr21:33325109-33325132_+
		657	AGTGTATGTGGGCTTTGGA	chr21:33343347-33343370_+
		658	ATAGTGATACACATCTCTCC	chr21:33343314-33343337_+

IFNAR2	ENST00000342136.8	659	GAACAAAAGATAGTGTTATG	chr21:33343336-33343359_+
		660	AAGCAGCACTACTTACGTCA	chr21:33343610-33343633_+
		661	TACAGCAATGTATAGTGAGT	chr21:33245039-33245062_-
		662	TGTATAGTGAGTTGGTACAA	chr21:33245031-33245054_-
		663	AGTGAGTTGGTACAATGGAG	chr21:33245026-33245049_-
		664	CATATGAAATACCAAACACG	chr21:33243682-33243705_-
IGF1R	ENST00000650285.1	665	AAACCAACAATCTCAAACCTC	chr21:33248722-33248745_-
		666	CTCTCGCTCTGGCCGACGAG	chr15:98649647-98649670_+
		667	CAGCCCATGTAGTAAGATGC	chr15:98913144-98913167_-
		668	GTTTTGGGGCAGGCGCAGCA	chr15:98916766-98916789_-
		669	GTAAACGGCGTACTGAGTCC	chr15:98913171-98913194_-
IHH	ENST00000295731.6	670	ACACATCGGCTTCTCCTCCA	chr15:98708020-98708043_-
		671	CTGAACTGCTTGTAGGCGAG	chr2:219060309-219060332_+
		672	GCAGCTTCACACCGGGCCAC	chr2:219057627-219057650_+
		673	CCGCAATAAGTATGGACTGC	chr2:219057510-219057533_-
		674	TGTGAAGCTGCGGGTGACCG	chr2:219057615-219057638_-
IKBKB	ENST00000520810.6	675	GTGAAGCTGCGGGTGACCGA	chr2:219057614-219057637_-
		676	AGTCTTGCACATCATTCGT	chr8:42306393-42306416_+
		677	ACTGCCAAGGAGGAGATCTC	chr8:42290247-42290270_+
		678	ATCTCGGGCAGCCACCACAT	chr8:42290166-42290189_-
		679	TGAAAGAGCGCCTTGGGACA	chr8:42272149-42272172_+
IL1B	ENST00000263341.6	680	GGGCAGCCACCACATTGGGG	chr8:42290161-42290184_-
		681	GATCACTGAACTGCACGCTC	chr2:112832746-112832769_-
		682	GCAGGCCGCGTCAGTTGTTG	chr2:112833466-112833489_-
		683	TCCCATGTGTGCGAAGAAGAT	chr2:112832801-112832824_+
		684	CTACAGCAAGGGCTTCAGGC	chr2:112833484-112833507_-
IL2RA	ENST00000379959.7	685	GTGCAGTTCAGTGATCGTAC	chr2:112832753-112832776_+
		686	CTCACGTTTCATCATGGTGCC	chr10:6062098-6062121_-
		687	TCACTCTATATGCTCTGTAC	chr10:6025883-6025906_-
		688	GGGACTGCTCACGTTTCATCA	chr10:6062105-6062128_-
		689	ATGGCTTTGAATGTGGCGTG	chr10:6025973-6025996_+
IL2RB	ENST00000216223.9	690	GCAAAGTCCAATGCAGCCAG	chr10:6024261-6024284_-
		691	CGGCCAGGCATGGACTTGGC	chr22:37143528-37143551_+
		692	GGCCCAGGATGCTTGACTCA	chr22:37142460-37142483_+
		693	CCCATCTTGGCTCCAGACAC	chr22:37143567-37143590_+
		694	ACTCAGGGGAGCAGCTCAC	chr22:37142475-37142498_+
IL2RG	ENST00000374202.6	695	CTGTGCTGGAGCCAAGATG	chr22:37143566-37143589_-
		696	TTGTTTCAGTCCAGGACCCA	chrX:71110549-71110572_-
		697	AAACACTGAACCTCTGGGAG	chrX:71110977-71111000_+
		698	CCTGTCTCCTGGGTTCCCGT	chrX:71110533-71110556_+
		699	AAAACACTGAACCTCTGGGA	chrX:71110976-71110999_+
IL6	ENST00000404625.5	700	TTTCTTCAGAGAATAGATAG	chrX:71110626-71110649_+
		701	GTTTCATAGCTGGGCTCCTGG	chr7:22727245-22727268_-
		702	TGGAGAAGGAGTTCATAGCT	chr7:22727255-22727278_-
		703	GGAAGGCAGCAGGCAACACC	chr7:22727480-22727503_-
		704	TTTGTCAATTCGTTCTGAAG	chr7:22727566-22727589_-
IL6R	ENST00000368485.7	705	CTTCCAATCTGGATTCAATG	chr7:22728784-22728807_+
		706	CAGCAATGTTGTTGTGAGT	chr1:154430528-154430551_+
		707	GCACGGCTCCTGGAAGTCTT	chr1:154434532-154434555_-
		708	AGCCTTTGTCGTCAGGGATG	chr1:154430563-154430586_-
		709	AGCAATGTTGTTGTGAGTG	chr1:154430529-154430552_+
INHA	ENST00000243786.2	710	TTGTTTGTGAGTGGGGTCCT	chr1:154430536-154430559_+
		711	GGGGCCCCCGCGGTGACCA	chr2:219572496-219572519_+
		712	GGGGCAGCCGCTGACTCCA	chr2:219572529-219572552_-

INHBA	ENST00000242208.4	713	GTGCAGCACCATAGCTCACC	chr2:219572363-219572386_-
		714	TAGCAGGGCCAGGTGAGCTA	chr2:219572355-219572378_+
		715	CCTGTGTGTGAAGCCCCCA	chr2:219572561-219572584_-
		716	TTCCCCCAGGATCCG	chr7:41700292-41700315_-
INHBB	ENST00000295228.3	717	TTGGCTGAGAGGATTTCTGT	chr7:41700340-41700363_-
		718	AGTCGGGGAGAACGGGTATG	chr7:41700070-41700093_-
		719	AGATAGAGGATGACATTGGA	chr7:41700047-41700070_-
		720	GTGAGGAGTTCCCCACCCC	chr7:41700300-41700323_-
INHBB	ENST00000295228.3	721	CGGCGTGCGTGATGTTGGGC	chr2:120346457-120346480_-
		722	TCGTCGCCAGCGGCGCACCA	chr2:120346169-120346192_+
		723	CGTCGTGCGGCGGCTTCCGG	chr2:120346354-120346377_+
		724	GACACCTGTACGTCGTGCGG	chr2:120346344-120346367_+
INHBC	ENST00000309668.2	725	CAGGACACCTGTACGTCGTG	chr2:120346341-120346364_+
		726	CTCAAAGCAGCTCTGGACAC	chr12:57435081-57435104_-
		727	CCGCTGGCTCTCCAGTTCCA	chr12:57434983-57435006_-
		728	GGTCAGTGTCCAGCATGTGG	chr12:57434955-57434978_+
INHBE	ENST00000266646.2	729	TGGCTCTCCAGTTCCAAGGT	chr12:57434979-57435002_-
		730	GTCAGTGTCCAGCATGTGGG	chr12:57434956-57434979_+
		731	TTATTCTGGGACGACTGGTC	chr12:57455703-57455726_-
		732	TGGTGCAGACAGGGGACA	chr12:57455582-57455605_+
ITK	ENST00000422843.7	733	GCCCTCCGAGACTACAGCC	chr12:57455758-57455781_+
		734	ATGAGTTATTCTGGGACGAC	chr12:57455708-57455731_-
		735	GGCCATTACCAGGAGCATG	chr12:57455519-57455542_+
		736	GAAGCGGACTTTAAAGTTTCG	chr5:157181044-157181067_-
JAK1	ENST00000342505.4	737	CTACCAAACCAATGATCCTC	chr5:157222909-157222932_+
		738	GACGATCTTCAAAGTATGCC	chr5:157181087-157181110_-
		739	TGGACAGTTCTGAGATTAC	chr5:157222968-157222991_+
		740	ATCTTCAAAGTATGCCAGGC	chr5:157181083-157181106_-
JAK2	ENST00000381652.3	741	GTCCATCCTGCTCGGTCTTG	chr1:64869410-64869433_+
		742	TGGGGTCTCGAATAGGAGCC	chr1:64869428-64869451_+
		743	CAGCTGGCTCATGGGGTAGA	chr1:64850839-64850862_+
		744	TCGAAACTCAGCTGGCTCAT	chr1:64850831-64850854_+
JAK3	ENST00000458235.5	745	GATATTGAGAACGAGTGTCT	chr1:64869385-64869408_-
		746	TGTATATTTCAAGCACGGC	chr9:5064993-5065016_-
		747	TCTTTTGAATTGTTACCAGA	chr9:5069122-5069145_+
		748	GTTCTGAAAAAGACTCTGCA	chr9:5021968-5021991_+
KDM1A	ENST00000356634.7	749	AAGAAAGCAGGTAATCAGAC	chr9:5066702-5066725_+
		750	TGTACTTCGATGCAGTCTTA	chr9:5066731-5066754_+
		751	CGGCGGCATCGCCTGGACCC	chr19:17842326-17842349_-
		752	CAGCCCACCCACATCATCCT	chr19:17838333-17838356_-
KDR	ENST00000645273.1	753	CATGTGCTGCTGCCCGCTCG	chr19:17844316-17844339_-
		754	GGCGGCATCGCCTGGACCCA	chr19:17842325-17842348_-
		755	GCAAAGAGGGAGTGGTACAC	chr19:17843869-17843892_+
		756	TGTCCGTTGGCTTCATAAAG	chr1:23059140-23059163_-
KIF11	ENST00000260731.4	757	GCTGGGCCCCGACAGGCCCGC	chr1:23019716-23019739_-
		758	GCGGTTCCGCCAGGCCCGCG	chr1:23019805-23019828_-
		759	CGGAACCGCCGGGGTCCGCA	chr1:23019819-23019842_+
		760	CTGCTTCTTGAGAAAGTCATC	chr1:23050426-23050449_-
KDR	ENST00000645273.1	761	ATGTCTGCCTTGCTCAAGAC	chr4:55104688-55104711_-
		762	GTATCCAAGTTCTTGCAAAC	chr4:55104806-55104829_+
		763	CTGCACAGGTGTACAATCCT	chr4:55113354-55113377_+
		764	ACCATTTTATTTCTGGGGGT	chr4:55110651-55110674_+
KIF11	ENST00000260731.4	765	TACTTGTCGTCTGATTCTCC	chr4:55102457-55102480_+
		766	TCCTGCATCTCTCAATCTTG	chr10:92613597-92613620_+

		767	ACGTGGAATTATACCAGCCA	chr10:92609023-92609046_-
		768	TAGTGTACGAACTGGAGGAT	chr10:92606336-92606359_+
		769	AATCCCTGTTGACTTTGGGA	chr10:92613455-92613478_+
		770	TGAAGAGTATACCTGGGAAG	chr10:92607215-92607238_+
KIT	ENST00000288135.5	771	ACCAATCTATTGTGGGCTCT	chr4:54723650-54723673_-
		772	CTCATCGCGGTAGCTGCGAT	chr4:54657996-54658019_-
		773	TGACTTCAATTATGAACGTC	chr4:54703761-54703784_+
		774	CTACTGCTTCGCGTCCAGAC	chr4:54658059-54658082_+
		775	CAGAACGCAGAGAAAAATCCC	chr4:54658033-54658056_-
KRAS	ENST00000256078.8	776	AGGGACCAGTACATGAGGAC	chr12:25227299-25227322_-
		777	TCTCGACACAGCAGGTCAAG	chr12:25227336-25227359_-
		778	CAATGAGGGACCAGTACATG	chr12:25227304-25227327_-
		779	GGACCAGTACATGAGGACTG	chr12:25227297-25227320_-
		780	GGACTCTGAAGATGTACCTA	chr12:25225729-25225752_-
LAP3	ENST00000226299.8	781	CCTCCACAGACGAGAGCTCC	chr4:17583504-17583527_-
		782	ACGACTACTCGCCCCGAGC	chr4:17577483-17577506_-
		783	GCAAGAACATCTTGTCGGCT	chr4:17577452-17577475_-
		784	CTGGACCACCTCTGAAGGCA	chr4:17581761-17581784_+
		785	GAACAGGAAAACCTGGCATGA	chr4:17582341-17582364_+
LCK	ENST00000336890.9	786	TTGCCATCCAGTGGGACTAT	chr1:32274404-32274427_-
		787	TCCCTGACCACGGGCCAGGA	chr1:32275345-32275368_+
		788	TGTGGCCAAAGCGAACAGCC	chr1:32275386-32275409_+
		789	CGGGAGAGCGAGAGCACCGC	chr1:32275650-32275673_+
		790	AAGGCGCAGTCCCTGACCAC	chr1:32275336-32275359_+
LDLR	ENST00000558518.5	791	CGCGGCGAGGAGCAAGGCGA	chr19:11089579-11089602_-
		792	CCCCGCCGCGGCGAGGAGCA	chr19:11089585-11089608_-
		793	AGGGGTCTTTACGTGTTCCA	chr19:11105458-11105481_+
		794	CCTGGGGCTGGAAATTGCGC	chr19:11089555-11089578_+
		795	GCGGGACCACAGGTGAGCAC	chr19:11105335-11105358_-
LHCGR	ENST00000294954.11	796	GCTGCCACGAGCGCTGCGCG	chr2:48755589-48755612_-
		797	AGCTTTCAGAGGACTTAATG	chr2:48731236-48731259_-
		798	GGAAGATTTATAAATGCTCC	chr2:48725690-48725713_+
		799	AGTCGAGTGAGACCGGCCGT	chr2:48755510-48755533_+
		800	GATCACTTTGACAGGGAGGT	chr2:48731267-48731290_+
LIMK1	ENST00000336180.6	801	TCTCATAGTACTGGTGCGAC	chr7:74096642-74096665_-
		802	CGCTTGCCATGAGATGAGGC	chr7:74099134-74099157_-
		803	TGACGGGGGTCACCACAGTC	chr7:74099046-74099069_-
		804	GCCCATCCGAAATGTGCCCC	chr7:74105952-74105975_+
		805	GATCCGGTCTCCGACGTGGA	chr7:74105912-74105935_-
LYN	ENST00000519728.5	806	TAACCAGGAAGGACGCAGAA	chr8:55950697-55950720_+
		807	CTTTGCTGTTTATTGGACGT	chr8:55941964-55941987_-
		808	TTTCAAGGATATAACCAGGA	chr8:55950686-55950709_+
		809	AAAGACAGCTTGAGTGACGA	chr8:55941883-55941906_+
		810	CAACGTCCAATAAACAGCAA	chr8:55941965-55941988_+
MAP1A	ENST00000300231.5	811	CTCTAGCAGTTACAGCGACT	chr15:43521820-43521843_+
		812	TCCACTGGGGACTGATGAAA	chr15:43524497-43524520_-
		813	CTCCCGTACTGAAGCTACGC	chr15:43524103-43524126_+
		814	AGAAATGGGGCATCTGATGC	chr15:43525177-43525200_+
		815	TGAGGCAGGTCGTGGCAGAT	chr15:43528206-43528229_-
MAP2	ENST00000360351.8	816	AAAGTTAAATCCAAGGGCTA	chr2:209694301-209694324_-
		817	AATTAGTGACTTTGGACAGA	chr2:209695316-209695339_+
		818	TATTTCCACTGACAATTTGA	chr2:209695666-209695689_-
		819	ACTTTGGACAGATGGCTTCA	chr2:209695324-209695347_+
		820	TGTCTCTGGCTGAGAAACTA	chr2:209692756-209692779_-

MAP2K1	ENST00000307102.9	821	CGTTAACTGCAGAGCCGTCG	chr15:66387388-66387411_-
		822	GACGCCCATCCAGCTGAACC	chr15:66387364-66387387_+
		823	GTTAACTGCAGAGCCGTCGG	chr15:66387387-66387410_-
		824	CAGCCGCATCTCCTTCCACC	chr15:66485126-66485149_-
		825	TGGAGATCAAACCCGCAATC	chr15:66436755-66436778_+
MAP2K2	ENST00000262948.9	826	GGGCCAGCATCGGGGCTCCG	chr19:4123865-4123888_+
		827	CAGCATTTGCATGGAACACA	chr19:4110507-4110530_-
		828	CGAGCAGCAGAAGAAGCGGC	chr19:4117558-4117581_-
		829	CGGGGAGATCAGCATTTGCA	chr19:4110516-4110539_-
		830	CTTCTCCGGGCCAGCATCG	chr19:4123857-4123880_+
MAP3K7	ENST00000369329.7	831	TGTGAAGATAAGCCACTCCT	chr6:90560121-90560144_+
		832	CGAGTCATCAGGCTCTCAAT	chr6:90552121-90552144_+
		833	TTTACAGTGTTCCTCAAGGAG	chr6:90560133-90560156_-
		834	GTGAAGATAAGCCACTCCTT	chr6:90560122-90560145_+
		835	TCCATTGAAGGGCGCTGGGA	chr6:90552082-90552105_+
MAP3K8	ENST00000263056.5	836	TCCTCGGGGCGCCTTTGGAA	chr10:30447876-30447899_+
		837	TTCCTGTAAGTCAGCTTCCA	chr10:30447835-30447858_-
		838	ATGACAACCATGGTACCTCT	chr10:30439138-30439161_-
		839	CCGATGTTCTCTGATCCCC	chr10:30447818-30447841_+
		840	GTAATGGAGTACATGAGCAC	chr10:30438935-30438958_+
MAPK1	ENST00000215832.10	841	CGGGCCCGGAGATGGTCCGC	chr22:21867392-21867415_-
		842	GCGGGCCCGGAGATGGTCCG	chr22:21867393-21867416_-
		843	CCGCGGGCAGGTGTTGACG	chr22:21867376-21867399_-
		844	TTCTCTACCAGATCCTCAGA	chr22:21805933-21805956_-
		845	GTGTGGCCACATATTCTGTC	chr22:21799049-21799072_+
MAPK11	ENST00000330651.10	846	GACATGTCGGGCCCTCGCGC	chr22:50270272-50270295_-
		847	GCCGGTAGAAGCCGGCGCGA	chr22:50270261-50270284_+
		848	ACTCGGCCGGGATCATCCAC	chr22:50267256-50267279_-
		849	CGGTCTTGTTTCACTCCTGC	chr22:50270243-50270266_+
		850	CTCGGCCGGGATCATCCACC	chr22:50267255-50267278_-
MAPK14	ENST00000229794.8	851	GCATGAATGATGGACTGAAA	chr6:36052753-36052776_-
		852	AAGTAACCGCAGTTCTCTGT	chr6:36052784-36052807_-
		853	ATTCAGCTGACATAATTCAC	chr6:36073697-36073720_+
		854	TACACCTGCAAGGTCTCTGG	chr6:36059311-36059334_+
		855	TACCAGAACCTGTCTCCAGT	chr6:36028226-36028249_+
MAPK3	ENST00000263025.8	856	TTTGATTTTCGGCCTGGCC	chr16:30118139-30118162_-
		857	GGGGAGCCCCGTAGAACCGA	chr16:30123153-30123176_-
		858	CACATACTCCGTAGGAAGC	chr16:30118091-30118114_+
		859	GCGTAGCCACATACTCCGTC	chr16:30118084-30118107_+
		860	CCACGCGAGTCTTGCGCACG	chr16:30121971-30121994_+
MAPK8	ENST00000374176.8	861	TAGTAGCGAGTCACTACATA	chr10:48420253-48420276_-
		862	GAATCAGACTCATGCCAAGC	chr10:48404914-48404937_+
		863	ACTTTGAAGATTCTTGACTT	chr10:48420193-48420216_+
		864	GCCCATGCCAAGGATGACCT	chr10:48420284-48420307_-
		865	GAGTCTGATTCTGAAATGGT	chr10:48404902-48404925_-
MAPK9	ENST00000452135.6	866	TCAGTTTATAGTGTCGAAG	chr5:180280515-180280538_-
		867	AAGCATCTGGTAAAGAAGGT	chr5:180261725-180261748_+
		868	GTAACGTTTTAGGACAGTGA	chr5:180280483-180280506_+
		869	GCTGAAACCAATTGGCTCTG	chr5:180280455-180280478_-
		870	GTCACCCATACATCACTGTT	chr5:180241054-180241077_-
MCL1	ENST00000369026.2	871	CTGGAGACCTTACGACGGGT	chr1:150578880-150578903_-
		872	CCACCCTACGCCAGACTCC	chr1:150579308-150579331_-
		873	GGGACCTCGGCGCCAATGGG	chr1:150579270-150579293_+
		874	ACCTTACGACGGGTTGGGGA	chr1:150578874-150578897_-

MDM2	ENST00000539479.6	875	GCCATCCCCAACCCGTCGTA	chr1:150578873-150578896_+
		876	TTGAAGTTATTAAAGTCTGT	chr12:68813574-68813597_+
		877	AGACACTTATACTATGAAAG	chr12:68813606-68813629_+
		878	TACCATGATCTACAGGAACT	chr12:68820333-68820356_+
		879	ATCAGTAGGTACAGACATGT	chr12:68809221-68809244_-
MET	ENST00000397752.7	880	GCTTCTCTGTGAAAGAGCAC	chr12:68816923-68816946_+
		881	TCCTGTTTACCTTGGTGCAG	chr7:116699124-116699147_+
		882	TTACTTCTTGACGGTCCAAA	chr7:116699860-116699883_+
		883	CAAGGCTGACCATATGTGGC	chr7:116755388-116755411_+
		884	AAGAAACTAGAGTTCTCCT	chr7:116755447-116755470_+
MGMT	ENST00000306010.7	885	CTACAAAGAAGTTGATGAAC	chr7:116699653-116699676_-
		886	TGCGCACCGCGAGGACCTGC	chr10:129467259-129467282_-
		887	CTTTGCGTCCCGACGCCCGC	chr10:129467244-129467267_+
		888	GAAATAAAGCTCCTGGGCAA	chr10:129536339-129536362_+
		889	GTGCGCACCGCGAGGACCTG	chr10:129467260-129467283_-
MRE11	ENST00000323929.7	890	GCAAAGCGTTCTAGGGGCGC	chr10:129467227-129467250_-
		891	TTTTCTTAATAACTCGAGGC	chr11:94485994-94486017_+
		892	TTCATGAAAAATAAGCCCTCA	chr11:94486030-94486053_-
		893	CTGTTTTATATCTCACAACC	chr11:94471618-94471641_-
		894	GGCAATCATGACGATCCAC	chr11:94479674-94479697_-
MS4A1	ENST00000345732.8	895	CTTTGGACGTTCATGTCTG	chr11:94478800-94478823_-
		896	GTCCAAAACCACTCTTCAGG	chr11:60462450-60462473_+
		897	TGTAACAGTATTGGGTAGAT	chr11:60466114-60466137_-
		898	CGGATCACTCCTGGCAGCAA	chr11:60464298-60464321_+
		899	CTCATGAAGAAGCTTTGCGT	chr11:60462491-60462514_-
MSLN	ENST00000382862.7	900	TGAGGGAATCTAAGACTTTG	chr11:60462510-60462533_+
		901	CAATGTGGACCTGCTCCCGA	chr16:764966-764989_+
		902	GGGGCCCCGAGAACGCATCT	chr16:764906-764929_-
		903	AAGAAACGGGTGCAGGCCTG	chr16:764925-764948_-
		904	GACTCGGCCACAAAGCGCCC	chr16:765175-765198_-
MST1R	ENST00000296474.7	905	GACCCCTGTTGGGGTCCTGT	chr16:762699-762722_+
		906	AAGTCGCGAGAGGCCGCGTA	chr3:49903490-49903513_+
		907	ACAAAGTCTTTCCGGGGCAC	chr3:49897661-49897684_+
		908	CCGTGCCAGGCGTGTGTGCA	chr3:49902763-49902786_+
		909	TTTGAGCTGTCTTGGGCAG	chr3:49898056-49898079_+
MTOR	ENST00000361445.8	910	CTAAGGGCATGGCATTTTCAT	chr3:49898605-49898628_-
		911	CCAATTCTCTATTGTTGCC	chr1:11233402-11233425_+
		912	ACAGCTTAGGACATGGTTCA	chr1:11243256-11243279_+
		913	CAAGTACTGCAAAGATCTCA	chr1:11248021-11248044_-
		914	TCGCCACCCAGGCATGCCCA	chr1:11240410-11240433_-
MUC5AC	ENST00000621226.2	915	GCAGCTCCTTGATATCCTGC	chr1:11241580-11241603_+
		916	CATGGGAAGCTGAGCTGCAT	chr11:1175227-1175250_+
		917	TGGGCTGGCAGGTGCTGACA	chr11:1174924-1174947_-
		918	GCCGGCTGCTTCTGCCCTGA	chr11:1164510-1164533_+
		919	AAGGCCATCAAGATTTTCCT	chr11:1177320-1177343_+
NAE1	ENST00000290810.7	920	GCGTGACACTGAGCCTGGAT	chr11:1167955-1167978_+
		921	TTCCTTCAAAGAAGCAGTAT	chr16:66824858-66824881_-
		922	CTTAAAACTTGGTACTACC	chr16:66826675-66826698_-
		923	GAACCGAGCTGAAGCTGCCA	chr16:66823578-66823601_-
		924	TATGTCCTACAGATCAAAAG	chr16:66821493-66821516_+
NAMPT	ENST00000222553.7	925	AGGACCACAGTCATACTCCA	chr16:66817466-66817489_-
		926	TCTGCCGACGATTTCATCTC	chr7:106284867-106284890_+

		927	CATCTCGGGCCGAGGACAG	chr7:106284881-106284904 +
		928	CCGCAGGATTCATCTCGGGC	chr7:106284871-106284894 +
		929	CCGGCCCCGAGATGAATCCTG	chr7:106284871-106284894 -
		930	GCTCACTTGGTTAACTTCAA	chr7:106268556-106268579 -
NCSTN	ENST00000294785.9	931	TCTTTCTGCGTCCTACTAGC	chr1:160343459-160343482 +
		932	AGAAATACAGTGGAATTCGC	chr1:160350147-160350170 +
		933	TCCACACATTGTAATCAGAC	chr1:160351711-160351734 -
		934	GGACATTAAGCCTGACGAC	chr1:160351761-160351784 +
		935	CAGTGGAATTCGCTGGGCAA	chr1:160350154-160350177 +
NEK11	ENST00000383366.8	936	ATTGAGGAATATAACAAGC	chr3:131109823-131109846 +
		937	TTCCAGTTAAAGTTGTGGCC	chr3:131133869-131133892 -
		938	TGGTTTATCCAGCTGCTGCT	chr3:131109877-131109900 +
		939	CAAGAAAGCCAAACGAGGAG	chr3:131029851-131029874 +
		940	CCGACTTTGTGTCATAGCCT	chr3:131133926-131133949 -
NOTCH1	ENST00000277541.7	941	TCCAGGTTGATCTCGCAGTT	chr9:136515375-136515398 +
		942	GTTGATGTTGGTCTGGCAGT	chr9:136513108-136513131 +
		943	CGCAGGGGTTGGAGGCGCAC	chr9:136523143-136523166 +
		944	TTGATGTTGGTCTGGCAGTT	chr9:136513109-136513132 +
		945	GGCCCGCGATGCTCCAGCC	chr9:136544080-136544103 -
NOTCH2	ENST00000256646.6	946	AGTACAGTTTCCATGGATGC	chr1:119955053-119955076 +
		947	ATGCTCACAAGGATTGCTAT	chr1:119967598-119967621 +
		948	GCTACCTGTCTGGATAAGAT	chr1:119967458-119967481 -
		949	CAGGTGCTCCCTTCAAAACC	chr1:119987063-119987086 +
		950	TCAGAAATGGAGGGGTTTGTG	chr1:119987004-119987027 -
NOTCH3	ENST00000263388.6	951	CATGTCCCACCGGCCCTGCA	chr19:15185306-15185329 +
		952	CAAATGGCCCGGCCGTTTAC	chr19:15189334-15189357 +
		953	GGTCGCGGCCCGGCCCATG	chr19:15200899-15200922 -
		954	GCACCTGCCCAAGTGCTCGC	chr19:15189142-15189165 +
		955	GTGAACGTGGACGACTGTCC	chr19:15191821-15191844 -
NOTCH4	ENST00000375023.3	956	CAGAGGCAAAAGAAGGCTCC	chr6:32216961-32216984 +
		957	TCCTAGGGGCTGTTTCAATG	chr6:3221037-3221060 -
		958	TATGGCAGGAGGTGCCTTTG	chr6:32221139-32221162 +
		959	CCACGTTGTGAGCTGCGGGC	chr6:32221069-32221092 -
		960	GCACAGGTTGGGAGCACACA	chr6:32215344-32215367 +
NPEPPS	ENST00000322157.8	961	TGTAGACATAACAGGTGTGC	chr17:47585557-47585580 -
		962	TCGCTCCATAGCATATAATT	chr17:47605395-47605418 -
		963	AATACCTGACCAAAACAAT	chr17:47596408-47596431 +
		964	CAGCATGGCAGAGCTGTACT	chr17:47603945-47603968 -
		965	AGAGAAAGGTACGAATGCC	chr17:47603980-47604003 -
NR3C1	ENST00000343796.6	966	CAGTGTGCTTGCTCAGGAGA	chr5:143400769-143400792 -
		967	GACTTCTATAAAACCCTAAG	chr5:143400735-143400758 -
		968	TTTGGAAGGAAACTCGAATG	chr5:143400109-143400132 -
		969	TCATCGAACTCTGCACCCCT	chr5:143399969-143399992 -
		970	TCCAAAGAATCATTAATCC	chr5:143400810-143400833 -
NRAS	ENST00000369535.4	971	TGAAATGACTGAGTACAAAC	chr1:114716141-114716164 -
		972	AGAGACCAATACATGAGGAC	chr1:114713865-114713888 -
		973	TGAATATGATCCCACCATAG	chr1:114716048-114716071 -
		974	GATCATATTCTCTACAAAG	chr1:114716060-114716083 +
		975	GAGTACAACTGGTGGTGGT	chr1:114716131-114716154 -
NTRK1	ENST00000524377.5	976	GTGTGCAGCTGCACACTGGC	chr1:156873634-156873657 -
		977	GCATCCCTTCTCTGTGGAT	chr1:156873680-156873703 +
		978	CTCTCTGGAAAACTGTGCA	chr1:156866937-156866960 +
		979	CGGCGGTGGAGATGCACCAC	chr1:156873656-156873679 +
		980	CCAGCGCTGTAGCCAGCGCA	chr1:156868138-156868161 -

NTRK2	ENST00000277120.7	981	TTATAGAACCACTGAAGCGC	chr9:84727736-84727759_-
		982	GGATTCTGGATTAAAATTTG	chr9:84702356-84702379_+
		983	CCCCCATGGCGCGGCTCTG	chr9:84670775-84670798_+
		984	GAAGCCCCAGAGCCGCGCCA	chr9:84670779-84670802_-
		985	GCCGTGGTACTCCGTGTGAT	chr9:84727809-84727832_-
NTRK3	ENST00000394480.6	986	CACCCCTTCCTGATGTGGAC	chr15:88136502-88136525_-
		987	GCAAGACTGAGATCAATTGC	chr15:88256015-88256038_-
		988	ACTGCAGCTGTGACATCCGC	chr15:88137515-88137538_-
		989	GCCAGAACTACACTTGGCT	chr15:88256113-88256136_+
		990	CTGATGTTTCATGCGGAAGAG	chr15:88137411-88137434_+
PARP1	ENST00000366794.9	991	GAACAACCTCCTGAAGGCTCT	chr1:226380045-226380068_+
		992	CCACCTCAACGTCAGGGTGC	chr1:226402285-226402308_+
		993	ACGGAGGCGCTGGTTTCTGG	chr1:226383100-226383123_+
		994	GCAAGTGCCTTCTGGGGAGT	chr1:226386327-226386350_-
		995	GTAGCTGATGGCATGGTGT	chr1:226385645-226385668_-
PARP2	ENST00000250416.9	996	AACTCGTAGATGCCAGAGAC	chr14:20344998-20345021_+
		997	ATGGTATGCCAGGAAGGTCA	chr14:20345084-20345107_+
		998	ATCTACGAGTTTCTTGCA	chr14:20344986-20345009_-
		999	AGCTTTGCCCTTTAACAGCA	chr14:20345405-20345428_-
		1000	AGCAAGATGGTATGCCAGGA	chr14:20345078-20345101_+
PARP3	ENST00000431474.5	1001	CATCTTCTAGCCTTGTGAAG	chr3:51944415-51944438_-
		1002	GGACCACTTTGTGTCTCACC	chr3:51944496-51944519_+
		1003	TGATGAGCTTCTGCGTGGCT	chr3:51944833-51944856_-
		1004	TGTCCACTCAGCAGCAACCC	chr3:51943508-51943531_+
		1005	CGATAAGTGTGTACTTGCCC	chr3:51944514-51944537_-
PDE5A	ENST00000264805.9	1006	GAAATGCACCATTTTCATAG	chr4:119562846-119562869_-
		1007	TCTTAGACCCATTGTTGTCA	chr4:119607100-119607123_-
		1008	TATGCCAATTAAGAATCATA	chr4:119596527-119596550_-
		1009	GCACGAGGACTCTGCTGCAA	chr4:119607183-119607206_+
		1010	CAAGGGACAAGAGCAAGATT	chr4:119607200-119607223_+
PDGFRA	ENST00000257290.9	1011	CGGAGATCCACTCCCAGAC	chr4:54273592-54273615_+
		1012	TGCGGGCCTACCCACCTCCC	chr4:54267635-54267658_+
		1013	TGCCTCCTACGACAGCAGAC	chr4:54263805-54263828_+
		1014	GTGCCTCGGCGGCCACACA	chr4:54261310-54261333_+
		1015	ATGATCACCATGGCTCAACT	chr4:54272420-54272443_+
PDGFRB	ENST00000261799.8	1016	CGCGCAACGTGTCGGAGACC	chr5:150132748-150132771_-
		1017	CAGGACAGTGGGCGGTGGGT	chr5:150132829-150132852_+
		1018	GCATCGGAGCCGACACTGC	chr5:150132864-150132887_-
		1019	CTACTATGTCTACAGACTCC	chr5:150134749-150134772_-
		1020	GTGACACTGCACGAGAAGAA	chr5:150134886-150134909_-
PGF	ENST00000555567.5	1021	TGCTGGGAACGGCTCGTCAG	chr14:74953909-74953932_-
		1022	CGAGCCGTTCCAGCAGACA	chr14:74953916-74953939_+
		1023	TAAAGATCCGTTCTGGGGAC	chr14:74948556-74948579_-
		1024	GGCTTCATCTTCTCCCGCAG	chr14:74946384-74946407_+
		1025	TCAGCTCCACGTAGGAGGGC	chr14:74948537-74948560_+
PIGF	ENST00000281382.10	1026	GGTCTTAACAAACATAAGCA	chr2:46612266-46612289_+
		1027	GGATTGGGAAAGACCATGGC	chr2:46592473-46592496_-
		1028	CACTGGATTGGGAAAGACCA	chr2:46592477-46592500_-
		1029	CATGGTCTTCCCAATCCAG	chr2:46592478-46592501_+
		1030	AAGTTCTCCAAGAAGAGTGA	chr2:46615063-46615086_+
PIK3CA	ENST00000263967.3	1031	ATGCCTCCACGACCATCATC	chr3:179198825-179198848_+
		1032	CTTCAATCACTGACATATCT	chr3:179210483-179210506_-
		1033	TGCACTATTTATAACCCAAA	chr3:179203706-179203729_-
		1034	GAGTACCTTGTTCCAATCCC	chr3:179204566-179204589_+

PIK3CB	ENST00000477593.5	1035	GGTTAAAGATCCAGAAGTAC	chr3:179199726-179199749_+
		1036	CCTGCCCCATTTTATACTTG	chr3:138734752-138734775_-
		1037	ATCGTATTTACCCACGCTAC	chr3:138712275-138712298_+
		1038	ACTTGTGGGATTGTCTTGGA	chr3:138742670-138742693_-
		1039	TATAGGAGTCAATATCCATA	chr3:138755915-138755938_+
		1040	CACTGGGATTTATATCCAGT	chr3:138759210-138759233_-
PIK3CD	ENST00000377346.8	1041	TACAAGGACCAGCTTAAGAC	chr1:9719959-9719982_+
		1042	CCGCAGGGTACCAGGCCCCC	chr1:9716007-9716030_-
		1043	ATGGGAGGTGGTTTGGCACG	chr1:9717072-9717095_-
		1044	ACGCAGGATGCCCCCTGGGG	chr1:9710448-9710471_+
		1045	GATGCGGAACGGCTGCTCCA	chr1:9717558-9717581_-
PIK3CG	ENST00000496166.5	1046	CCTCCTCTGTGAAGGGTTTG	chr7:106868760-106868783_-
		1047	CAGAGAGCGATTTAATATCA	chr7:106872888-106872911_-
		1048	GATGACTGCACGGGAGTCAC	chr7:106868539-106868562_+
		1049	TTTAGAGTTCCATATGATCC	chr7:106874758-106874781_+
		1050	GGACGTCACCCACGGGTGCA	chr7:106868150-106868173_-
PIM3	ENST00000360612.4	1051	GCCGCTCGAACCAGTCCAGC	chr22:49961518-49961541_-
		1052	AAGGAGCGGGTGACCGAGTG	chr22:49961338-49961361_+
		1053	GAAGGAGCGGGTGACCGAGT	chr22:49961337-49961360_+
		1054	TGAAGGAGCGGGTGACCGAG	chr22:49961336-49961359_+
		1055	GGTGGTGCTGCTGCGCAAGG	chr22:49961464-49961487_+
PLK1	ENST00000300093.8	1056	CGTAGGTAGTATCGGGCCTC	chr16:23680125-23680148_-
		1057	CAACCAAAGTCAATATGAC	chr16:23680928-23680951_+
		1058	TGGTGTGGAGCTCTGCCGC	chr16:23679314-23679337_+
		1059	AGGTGGATGTGTGGTCCATT	chr16:23681027-23681050_+
		1060	AAGTCAATATGACGGGGAG	chr16:23680934-23680957_+
PLK2	ENST00000274289.7	1061	GCAGTAGCGTTCCCAGTCG	chr5:58459710-58459733_+
		1062	GAGTAGCTAAACCTCATCAA	chr5:58458990-58459013_-
		1063	CAGAAGTTTCGATACTACCTC	chr5:58458462-58458485_-
		1064	AGTAGCTAAACCTCATCAAA	chr5:58458989-58459012_-
		1065	ACTCGGGGCCGAGATCTCG	chr5:58459746-58459769_-
PLK3	ENST00000372201.4	1066	AGCCCCGAAGGATGGCGGCC	chr1:44803074-44803097_-
		1067	CTTGACCCGGGACCTCAAGT	chr1:44801728-44801751_+
		1068	CTGCTCCGGAGGCTCCAACC	chr1:44801901-44801924_-
		1069	GGCTTGGCGACGCGGCTCTG	chr1:44800908-44800931_-
		1070	CTTCAGTCAAGCCGTCTCAA	chr1:44802980-44803003_-
POLA1	ENST00000379068.7	1071	TCACAGTCGTGCGCGTGAC	chrX:24693967-24693990_-
		1072	GTCACCTAGCAGACCATCCT	chrX:24715156-24715179_-
		1073	TGGGACCAACACATCTAGCC	chrX:24726988-24727011_+
		1074	TCAACTTTACACCAACTGAC	chrX:24727795-24727818_-
		1075	GTCGCCGTGCACAGGTGCCA	chrX:24693959-24693982_-
PORCN	ENST00000326194.10	1076	CATCCTCATCTACCTACTCA	chrX:48511463-48511486_+
		1077	CATGCAAGCACCGTGGCAGG	chrX:48511314-48511337_+
		1078	GGCGGCCTTGGACAGCTTGT	chrX:48512479-48512502_-
		1079	CCATCCGTGGGGGTCTGCAA	chrX:48509801-48509824_+
		1080	AATGGCCACCTTTAGCCGCC	chrX:48509819-48509842_+
PPARG	ENST00000287820.10	1081	CCCATAACAGCATGGAATAG	chr3:12351574-12351597_-
		1082	ACGACATTCAATTGCCATGA	chr3:12381408-12381431_-
		1083	AGAGCCTTCCAACCTCCCTCA	chr3:12381394-12381417_+
		1084	TCATGCTTGTGAAGGATGCA	chr3:12381469-12381492_+
		1085	AGTGAAGGGCTTGATATCAA	chr3:12379796-12379819_-
PPP2CA	ENST00000481195.5	1086	AAAAGAATCCAACGTGCAAG	chr5:134206091-134206114_-
		1087	AACGCATCACCATTCTTCGA	chr5:134201985-134202008_-
		1088	ACATCGAACCTCTGCACGT	chr5:134206083-134206106_+

PRKCA	ENST00000413366.7	1089	GACCACAGCAAGTCACACAT	chr5:134200470-134200493_+
		1090	AGCTCACCAGCTAGTGATGG	chr5:134200333-134200356_-
		1091	AGTCGTCGGTCTTTGTCTGA	chr17:66688311-66688334_-
		1092	TGTCCCCAGCCTCTGCGGAA	chr17:66645419-66645442_+
		1093	CTTGTGAACGTTTCATATCGC	chr17:66645382-66645405_-
		1094	CAACCGCTTCGCCCGCAAAG	chr17:66302901-66302924_+
PRKCB	ENST00000643927.1	1095	GAGGGGGCGGATTTACCTAA	chr17:66645455-66645478_+
		1096	GGGTCAGCCATCTTGCGCGC	chr16:23836163-23836186_-
		1097	GTGCTCTCCTCGCCCTCGCT	chr16:23836202-23836225_-
		1098	TGGTCCGTGCCACACAGGCT	chr16:24035459-24035482_-
		1099	GGTCAGCCATCTTGCGCGCG	chr16:23836162-23836185_-
PRKCE	ENST00000306156.7	1100	CCACGTTTTGTGACCACTGT	chr16:24032181-24032204_+
		1101	CGACTCGCGCATCGGCCAAA	chr2:45652240-45652263_+
		1102	TGGCGCAGCGACCAGGCTGT	chr2:45652157-45652180_-
		1103	ATGCGGCCGAGGAAGCGGCA	chr2:45976466-45976489_+
		1104	GAACGGGAGCCGCCACTTCG	chr2:45652420-45652443_+
PRKCG	ENST00000263431.3	1105	AACTACCATGGTCGGGGCG	chr2:45652087-45652110_-
		1106	TTTCTGAAAACAGGGGCCG	chr19:53882536-53882559_-
		1107	GCGATTACAGAGGGGGACCC	chr19:53882519-53882542_+
		1108	GGAGCTGCTCAAGGCGCCCG	chr19:53892613-53892636_+
		1109	CGGCGTAGGCGATTACAGAGG	chr19:53882511-53882534_+
PRKCI	ENST00000295797.4	1110	TACGTGGATCTCATCTGCTG	chr19:53889990-53890013_-
		1111	CTCATTGCAAAGGCCCTCAA	chr3:170235264-170235287_-
		1112	AAACTCGTCACAATTGAATG	chr3:170270519-170270542_+
		1113	AACTCGTCACAATTGAATGT	chr3:170270520-170270543_+
		1114	CACCATGAAATGGATAGATG	chr3:170235325-170235348_+
PRKDC	ENST00000314191.6	1115	TTAAATTATCTTCATGAGCG	chr3:170284488-170284511_+
		1116	CGCTTATAGAGCTGGTACAT	chr8:47912452-47912475_+
		1117	CTGTGAACTTTTACATAGCA	chr8:47912531-47912554_-
		1118	AAGCCACGCAGATGCCAGAA	chr8:47912490-47912513_-
		1119	TGTAGCACTCCAACGCGGCC	chr8:47893183-47893206_+
PRLR	ENST00000618457.4	1120	TGATGAAGAGCTATGTGGCC	chr8:47914023-47914046_-
		1121	TGTCCCAGGCCTCCACCAGC	chr5:35086254-35086277_+
		1122	GGAAGTCCTCCATCTGTCCC	chr5:35086240-35086263_+
		1123	ATTATTCAGTACTTACCAC	chr5:35086212-35086235_-
		1124	ATAAGGAAACATTACCTGC	chr5:35086269-35086292_-
PSEN1	ENST00000324501.9	1125	AAACATTCACCTGCTGGTGG	chr5:35086263-35086286_-
		1126	ATTATCTAATGGACGACCCC	chr14:73170855-73170878_+
		1127	AAAGAGCATGATCACATGCT	chr14:73170944-73170967_-
		1128	GGCAGGAGCACAACGACAGA	chr14:73170812-73170835_+
		1129	GCTTTTATACCCGGAAGGAT	chr14:73171019-73171042_+
PSENEN	ENST00000587708.6	1130	ACCCAGGGTAACCTCCCGGC	chr14:73170870-73170893_+
		1131	CCAGGTTTCATAGCTGCGCTG	chr19:35745917-35745940_-
		1132	CTGTGCCGGAAGTACTACCT	chr19:35745969-35745992_+
		1133	ATGTTGACCAACCAGAGAAA	chr19:35746435-35746458_-
		1134	GATTTGGCTCTGTTCTGTGT	chr19:35746493-35746516_-
PSMB1	ENST00000262193.6	1135	GTTCTGTGTAGGCTGGGACA	chr19:35746482-35746505_-
		1136	ACAGCCATGTATTCGGCTCC	chr6:170553207-170553230_-
		1137	GGCGAAAATCGCAGCTGCAA	chr6:170553147-170553170_+
		1138	TCGCAGCTGCAAAGGGCCCG	chr6:170553155-170553178_+
		1139	GATGGAACCGCACAGAGCCG	chr6:170553172-170553195_-
PSMB10	ENST00000358514.8	1140	TCTGATACTCGATTGAGTGA	chr6:170549047-170549070_-
		1141	GTCCCGGTCTTGCGTGCGTG	chr16:67936422-67936445_+
		1142	ACGCGTCCTCCCGGGCTCA	chr16:67936447-67936470_-

PSMB2	ENST00000373237.3	1143	TCTCGAAGGAGAAGCCCCCT	chr16:67936703-67936726_+
		1144	GGGCTGGCTTCAGCATCTTG	chr16:67936733-67936756_+
		1145	TCCCGGTCTTGCGTGCGTGA	chr16:67936423-67936446_+
		1146	GGAGGCGACAAGAACATAGT	chr1:35641381-35641404_+
PSMB5	ENST00000361611.10	1147	AAGATATTACTCCTGTGTGT	chr1:35636380-35636403_-
		1148	GCCACCATGGAGTACCTCAT	chr1:35641415-35641438_-
		1149	AGGTACTCCATGGTGGCGGA	chr1:35641421-35641444_+
		1150	GATACCGATGAGGTACTCCA	chr1:35641411-35641434_+
PSMB8	ENST00000374882.7	1151	AAAAACCCGCGCTGGTTCAC	chr14:23034825-23034848_+
		1152	CGCTACCGGTGAACCAGCGC	chr14:23034830-23034853_-
		1153	TGGGACACCCCAGCCTGGCG	chr14:23034734-23034757_+
		1154	CAAGTCCGAAAAACCCGCGC	chr14:23034817-23034840_+
PSMB9	ENST00000374859.2	1155	GCTTCATGGAACAACCACCC	chr14:23034691-23034714_-
		1156	ATTCTTCCAGTCCCTGGGTG	chr6:32843058-32843081_-
		1157	GATTCCGCGCCGCTGCCCTCG	chr6:32843946-32843969_+
		1158	CCCCGGGGTAAAGCGAGCTC	chr6:32843856-32843879_+
PSMB9	ENST00000374859.2	1159	ACAGAATTCTTCCAGTCCCT	chr6:32843063-32843086_-
		1160	ATTCCGCGCCGCTGCCCTCGG	chr6:32843947-32843970_+
		1161	CCTTGCAGGGATGCTGCGGG	chr6:32854219-32854242_+
		1162	CCGCCCCGAGCATCCCTGCA	chr6:32854219-32854242_-
PSMD1	ENST00000308696.10	1163	GCCCGGGGTAAAGTCCCCGGT	chr6:32854247-32854270_-
		1164	GTGTGGACTTCTCCCGCCCG	chr6:32854262-32854285_-
		1165	GCGGGCGGGAGCACCAACCG	chr6:32854234-32854257_+
		1166	GAGGTTTTATACGAAGATGA	chr2:231062506-231062529_+
PSMD2	ENST00000310118.8	1167	GGCTATAAGCTAACATTCCT	chr2:231070032-231070055_-
		1168	AAGATGAAGTTTTCCGGAGT	chr2:231062519-231062542_+
		1169	AGGCTGCAAAGTGCCTGACTC	chr2:231062532-231062555_-
		1170	CAATGATAACTCTGAATATG	chr2:231062640-231062663_+
PTCH1	ENST00000331920.10	1171	GGACGAGAAGCCGAGCGGCA	chr3:184299337-184299360_+
		1172	ATGCCAATCTCAGAGCTTCA	chr3:184302450-184302473_-
		1173	CTTCTCGTCCGTGCCGCCGG	chr3:184299324-184299347_-
		1174	GTATCGGCTAGTGGGCTCCC	chr3:184301601-184301624_+
PTGS2	ENST00000367468.9	1175	GCTTCTCGTCCGTGCCGCCG	chr3:184299325-184299348_-
		1176	CAGAGACTCTTATTAAACT	chr9:95506528-95506551_-
		1177	GCCTCCAGCCGCGCTCCCG	chr9:95508271-95508294_+
		1178	ATTCTGTCTGTTTCACTGA	chr9:95476776-95476799_+
PTK2	ENST00000522684.5	1179	TATCACAGAAACAGGTTACA	chr9:95482138-95482161_-
		1180	CTGGCAGGAGGAGTTGATTG	chr9:95480005-95480028_-
		1181	GGGTACAATCGCACTTATAC	chr1:186679354-186679377_+
		1182	TTTCTCCATAGAATCCTGTC	chr1:186679333-186679356_+
PTK6	ENST00000542869.2	1183	TTCTCCATAGAATCCTGTCC	chr1:186679334-186679357_+
		1184	CCGACTCCCTTGGGTGTCAA	chr1:186678259-186678282_-
		1185	CCATAGTCAGCATTGTAAGT	chr1:186678355-186678378_+
		1186	GAATGCTTCAAGTGTGCTCT	chr8:140818880-140818903_-
RAC1	ENST00000356142.4	1187	ATTTGGTGTGTGATTCAAGT	chr8:140890692-140890715_+
		1188	GGGTACTGCCGGCTGGTGAA	chr8:140800493-140800516_-
		1189	CAAATCTGTAGACTGGAGAC	chr8:140818908-140818931_+
		1190	GGCGATCATACTGGGAGATG	chr8:140846300-140846323_-
PTK6	ENST00000542869.2	1191	CCGCCTCGTTCAGGTGCAGC	chr20:63534240-63534263_+
		1192	AAGATCTGGCGGCGTGCCGG	chr20:63534263-63534286_-
		1193	TCCCGGGACACCATGGCGGG	chr20:63537300-63537323_+
		1194	CCGACGCACAGCTTCCGAGC	chr20:63535016-63535039_+
RAC1	ENST00000356142.4	1195	GGGCCGGCTGCACCTGAACG	chr20:63534243-63534266_-
		1196	CGGTAAGGATATAACCTCCC	chr7:6398675-6398698_+

		1197	ACGGTAAGGATATAACCTCC	chr7:6398674-6398697_+
		1198	CGGCTTGTCTTTGCCCCGGG	chr7:6398689-6398712_-
		1199	GGTAAGGATATAACCTCCCG	chr7:6398676-6398699_+
		1200	AATCGGCTTGTCTTTGCCCC	chr7:6398692-6398715_-
RAD50	ENST00000378823.7	1201	GATGAATTAACCTCACTGTT	chr5:132591921-132591944_+
		1202	TGATGAATTAACCTCACTGT	chr5:132591920-132591943_+
		1203	TCTAATTGGCCTTTAAGTGA	chr5:132579434-132579457_+
		1204	TTGCTTCTTTTCGGCTATCCA	chr5:132587625-132587648_-
		1205	AAACGTTTGCAAACATGTCC	chr5:132557310-132557333_+
RAF1	ENST00000251849.8	1206	TGGAGCACATACAGGGAGCT	chr3:12618697-12618720_-
		1207	GCAGTTTGGCTATCAGCGCC	chr3:12618597-12618620_-
		1208	GGATGTGACCTCTGCCCTCT	chr3:12604192-12604215_+
		1209	GTATGCGAGAGTCTGTTTCC	chr3:12606211-12606234_-
		1210	GTGTAAAGGTGAAGGCGTG	chr3:12604244-12604267_+
RARA	ENST00000254066.9	1211	CGGGCACCTCAATGGGTACC	chr17:40331256-40331279_+
		1212	GGGGAGAGTCCACCCAGCAT	chr17:40331305-40331328_-
		1213	GCAGCTCCTGCCGACACCT	chr17:40331231-40331254_+
		1214	GGGGGAAGAAGAAGGCGTA	chr17:40331284-40331307_-
		1215	AAAGCAAGGCTTGTAGATGC	chr17:40348381-40348404_-
RARB	ENST00000330688.8	1216	GACTCGCAGTGTAGAAATCC	chr3:25428775-25428798_-
		1217	GCTCTCAAAGCATGCTTCAG	chr3:25428824-25428847_+
		1218	CAAACCCTGCTTCGTCTGCC	chr3:25461268-25461291_+
		1219	AGCTTCTCCTGGAGCATGC	chr3:25428804-25428827_-
		1220	TTGTCTGGCAGACGAAGCA	chr3:25461272-25461295_-
RARG	ENST00000425354.6	1221	CCTTCCCAGGGGCACTCAGG	chr12:53227440-53227463_-
		1222	TTGTCATTGCACACGAAGCA	chr12:53215691-53215714_+
		1223	GCCTTCCCAGGGGCACTCAG	chr12:53227441-53227464_-
		1224	CTAGGGCTCAGCATCTCGAA	chr12:53227411-53227434_+
		1225	AAGCATGGCTTGTAGACCCG	chr12:53215706-53215729_+
RET	ENST00000355710.7	1226	TGCAGTCAGCAAGAGACGGC	chr10:43112132-43112155_+
		1227	AAGTATACGCGGGCACAGCC	chr10:43102421-43102444_-
		1228	AGCAGAGCTCCCGGGGCTTG	chr10:43102480-43102503_-
		1229	GACGTACAGCAAGGGCGTGC	chr10:43100521-43100544_-
		1230	AGGCCAACGGCAGCTTCGTG	chr10:43106529-43106552_+
RICTOR	ENST00000357387.7	1231	AAATAATTATCCATGAGGTC	chr5:38967203-38967226_+
		1232	TCCTCTACCTGTTGTGACTG	chr5:38967969-38967992_-
		1233	CGGCGAGGAGAACGTCCCGC	chr5:39074122-39074145_-
		1234	CCCGTCAATATGGCGCGAT	chr5:39074363-39074386_-
		1235	GACAGTTGGAGGCTTTCAGA	chr5:38967387-38967410_-
ROCK1	ENST00000399799.2	1236	TGCAGAAGTAGTTCCTGCAT	chr18:21045322-21045345_-
		1237	TGTAGAGATAACGATCATCT	chr18:21045430-21045453_+
		1238	TTTGTGCCTTCTTACTGAC	chr18:21042095-21042118_-
		1239	GAATGTGACTGGTGGTTCGGT	chr18:21042590-21042613_-
		1240	TTGGATGCAATCCATTCCAT	chr18:21045303-21045326_-
ROCK2	ENST00000315872.10	1241	TTTTGGCACGTGTATGAAGA	chr2:11235706-11235729_-
		1242	GAAGCCTGACAACATGCTCT	chr2:11235757-11235780_-
		1243	AATCAGAGGTCTACAGATGA	chr2:11286597-11286620_-
		1244	TCCACGTTGATGGGGGAGCG	chr2:11344005-11344028_+
		1245	CGCCCCGAGACCGCGCCGG	chr2:11344078-11344101_-
ROS1	ENST00000368508.7	1246	GCTGGGTCACCTTCTCTACT	chr6:117385699-117385722_-
		1247	GTCCTGTAACCTGGGACTTGG	chr6:117403152-117403175_+
		1248	CCCTGGTCAGAGCCCTCAGT	chr6:117387796-117387819_-
		1249	GTAGATAGTATTTGGTAAAG	chr6:117396916-117396939_+
		1250	CAGCAAAGGGGATGCGAGGT	chr6:117389616-117389639_+

RPL3	ENST00000216146.8	1251	ATCACGCCATCAAATCCCGC	chr22:39319595-39319618_+
		1252	CCACCGAGGCCTGCGCAAGG	chr22:39314780-39314803_-
		1253	ACAGAGAAGGCTACACGAGC	chr22:39314737-39314760_+
		1254	CATGGGTGGTGTCTCTACAA	chr22:39317573-39317596_+
		1255	TGAGATGATCGACGTCATCG	chr22:39315392-39315415_-
RPS6KB1	ENST00000225577.8	1256	CATGAGGCGACGAAGGAGGC	chr17:59893183-59893206_+
		1257	TAAATGAAAGCATGGACCAT	chr17:59910568-59910591_+
		1258	GCGGCGGGTCCGGGCCCATG	chr17:59893167-59893190_+
		1259	AAGTAACAGGAGCAAAATACT	chr17:59914650-59914673_+
		1260	AGGCGACGAAGGAGGCGGGA	chr17:59893187-59893210_+
RPTOR	ENST00000306801.7	1261	AGGCACTGTGAGAAAATTGA	chr17:80545728-80545751_+
		1262	ATAGGTCAGCCGGGAGGTCG	chr17:80754119-80754142_-
		1263	CTTCTGTAAATTTGCACCGA	chr17:80643763-80643786_-
		1264	GGGGATCATGGGCAGCAGCT	chr17:80754100-80754123_-
		1265	GATGGGTCCTCAGAAAGCTC	chr17:80643737-80643760_+
RRM1	ENST00000300738.9	1266	GTGAGTTGTATTGCGGCTAC	chr11:4118422-4118445_+
		1267	AATGTTGACTTGCCACCAT	chr11:4107487-4107510_-
		1268	CAATGTTGACTTGCCACCA	chr11:4107488-4107511_-
		1269	ACAGCTCGATATGTGGATCA	chr11:4119895-4119918_+
		1270	CTCGATATGTGGATCAAGGT	chr11:4119899-4119922_+
RXRA	ENST00000481739.1	1271	CAGGGACGGGTGCAGCGAGG	chr9:134401691-134401714_-
		1272	GGAGCCGATGCCAGGCCCA	chr9:134401709-134401732_-
		1273	CCTCGCTGCACCCGTCCCTG	chr9:134401694-134401717_+
		1274	AGGAAGCCATGTTTCCTGAG	chr9:134408234-134408257_-
		1275	TGGCGCCACCCCTGCGCTG	chr9:134429207-134429230_-
RXRB	ENST00000374680.3	1276	ATTTCTTTTCGCACCCCCAC	chr6:33200393-33200416_+
		1277	CCCATGGAAGAACTGATGAC	chr6:33199229-33199252_+
		1278	AGGCCCCGGACCCCTAAGAC	chr6:33198381-33198404_+
		1279	CTCCCTTGCTCCGGCTCCG	chr6:33200275-33200298_+
		1280	CCTGGCCACTGGCATGAAGA	chr6:33197764-33197787_-
RXRG	ENST00000359842.9	1281	TTTCCAATCCCGGAAGCCC	chr1:165419943-165419966_+
		1282	CTGCAAGTGCTCCTGAGGGT	chr1:165428759-165428782_+
		1283	CTGTGGACAAGGCTGCTGAT	chr1:165428909-165428932_+
		1284	CCCTCTTATGCCCATGACA	chr1:165417043-165417066_+
		1285	GAGAGCCCAGGGCATTGAGG	chr1:165428810-165428833_+
S1PR1	ENST00000305352.6	1286	CAATAAAATAGTACATGGGT	chr1:101239214-101239237_-
		1287	TAAAATAGTACATGGGTCGG	chr1:101239211-101239234_-
		1288	CGTCCGGCATTACAACCTACA	chr1:101239058-101239081_+
		1289	GTCCGGCATTACAACCTACAC	chr1:101239059-101239082_+
		1290	TTGCCAATAAAATAGTACAT	chr1:101239218-101239241_-
SH2B3	ENST00000341259.6	1291	GCTCCAGCATCCAGGAGGTC	chr12:111446780-111446803_+
		1292	CTCGGCCGGGGAGCTGCCAG	chr12:111418591-111418614_+
		1293	GTGTCCCGGTAGTCGCGGCC	chr12:111418397-111418420_-
		1294	CTGGCAGCTCCCGGCCGAG	chr12:111418588-111418611_-
		1295	CTGTGAGTTGCACGCCGTAG	chr12:111418231-111418254_+
SHH	ENST00000297261.6	1296	AAGAAAACACCGGAGCGGAC	chr7:155811834-155811857_-
		1297	AGACCCTAGCGCCAGCGGA	chr7:155811939-155811962_-
		1298	GGTGAGTTCCTTAAATCGCT	chr7:155811891-155811914_+
		1299	GTATGCTCGGGACTGGCGTG	chr7:155812048-155812071_-
		1300	GGATGAAGAAAACACCGGAG	chr7:155811839-155811862_-
SIK1	ENST00000270162.7	1301	TGGCGGGGGCCTGGCACACC	chr21:43417666-43417689_+

		1302	GTGCCAGGCCCCGCCAGCC	chr21:43417660-43417683_-
		1303	CAGGAGAGCCTCTGTCCACG	chr21:43421317-43421340_-
		1304	CCCCTCAAAGACTTCCGGGG	chr21:43421275-43421298_+
		1305	AGTCGTCTCCCCCTCCACCA	chr21:43418514-43418537_-
SIRT1	ENST00000212015.10	1306	CGCAAGAGGCCGCGGAGAGA	chr10:67884820-67884843_+
		1307	TGTCGGCCCCCGCCGCCGAG	chr10:67884762-67884785_-
		1308	CACATGCAAGCTCTAGTGAC	chr10:67887491-67887514_+
		1309	GGCCGCGTCTGTCCTCCCGCCG	chr10:67884789-67884812_+
		1310	TGGGGCGGCCCCAGAGCGTG	chr10:67884876-67884899_+
SLAMF7	ENST00000368043.7	1311	GAACCAGCCATATTGCTCTC	chr1:160739289-160739312_-
		1312	GCTGGTTCGGTTCGGTTGGTG	chr1:160748221-160748244_+
		1313	TATATCCTTTGGCAGCTCAC	chr1:160739334-160739357_+
		1314	CTTCCAGAGAGCAATATGGC	chr1:160739286-160739309_+
		1315	GCTTTACTTTGGACTTCAGG	chr1:160748254-160748277_-
SLC2A2	ENST00000314251.7	1316	CTCAACTAATCACCATGCTC	chr3:171014548-171014571_-
		1317	GGCCTGGTTCCTATGTATAT	chr3:171007229-171007252_-
		1318	CAGTCTCTTCCTCAGCCCAA	chr3:171014580-171014603_+
		1319	GTTTCATTGAGTATGAGATTG	chr3:171014614-171014637_+
		1320	CTGCAAAGCTGGATACAGAC	chr3:171014523-171014546_+
SMO	ENST00000249373.7	1321	GCCCCGTGTCATCGTGGAG	chr7:129203506-129203529_+
		1322	CCGCTGCCCGCCAGCGCGG	chr7:129189155-129189178_+
		1323	TGGCTGGCCAGTTCATGGA	chr7:129205702-129205725_+
		1324	CCCCGTGTCATCGTGGAGA	chr7:129203507-129203530_+
		1325	AGCAGCGGGGGCATTCCGG	chr7:129203384-129203407_-
SRC	ENST00000373578.6	1326	CGTCACCTCCCCGAGAGGG	chr20:37384368-37384391_+
		1327	GGCGCCCTCCGACTCCATCC	chr20:37393963-37393986_+
		1328	CAGCGGGCCCGCCCTCTGCG	chr20:37384376-37384399_-
		1329	CTGGCCCACTCGCTCAGCAC	chr20:37393910-37393933_+
		1330	TCCTAGACTCATAGTCATAG	chr20:37386096-37386119_-
SSTR2	ENST00000357585.3	1331	TTGACACCACAGAGCCATTG	chr17:73169378-73169401_-
		1332	TTGCTTGTCAGGTCATAGTA	chr17:73169424-73169447_-
		1333	ATTTGACCTCAATGGCTCTG	chr17:73169372-73169395_+
		1334	CACTCAATGGAAGCCACACA	chr17:73169338-73169361_+
		1335	AAAAGCAGCCATGGACATGG	chr17:73169309-73169332_+
SSTR5	ENST00000293897.5	1336	GCTGGAACGCCTCCTCCCCG	chr16:1078899-1078922_+
		1337	GCCTCCAGAGGCAGCCCCCG	chr16:1078914-1078937_-
		1338	AGGCGGTGACAACAGGACGC	chr16:1078933-1078956_+
		1339	GCTGTACCTGCTGGTGTGTG	chr16:1079002-1079025_+
		1340	CTGGAACGCCTCCTCCCCGG	chr16:1078900-1078923_+
STAT3	ENST00000264657.9	1341	CTGCTGTAGCTGATTCCATT	chr17:42348489-42348512_+
		1342	GAAACTGCCGCAGCTCCATT	chr17:42348416-42348439_+
		1343	AGCCGATCTAGGCAGATGTT	chr17:42337443-42337466_+
		1344	TCCAGTTCACCTAAAGTC	chr17:42333671-42333694_-
		1345	GACCCCTGATTTTAGCAGGA	chr17:42348512-42348535_-
SYK	ENST00000375754.8	1346	CCCTTCGTGCAGCAGGCACA	chr9:90862237-90862260_-
		1347	AGCCGTTGTTGTCTCTGGCT	chr9:90862208-90862231_-
		1348	GCCATGCTTCAGGGGCCGGA	chr9:90843880-90843903_-
		1349	CAGAAGATTACCTGGTCCAG	chr9:90843971-90843994_+
		1350	GGTTCCATGGAATAATCTCT	chr9:90845518-90845541_+
TBK1	ENST00000331710.9	1351	ATGTCTCCACTCCAGTCAAT	chr12:64480075-64480098_-
		1352	CAAATTATTGCTATTGAAG	chr12:64460304-64460327_+
		1353	CGACGCTTAGTCTTAGAACC	chr12:64484378-64484401_+
		1354	ATCAAGAACTTATCTACGAA	chr12:64484355-64484378_+
		1355	ATGCGTGTATAGGGGAAGA	chr12:64466965-64466988_+

TEK	ENST00000380036.8	1356	AGGGGGGAGGATCCGGTGGGA	chr9:27185530-27185553_-
		1357	TCTTCACCTCGGCCTTCACC	chr9:27169593-27169616_+
		1358	ACAGTCATAGTTAAAGTAGC	chr9:27168505-27168528_-
		1359	ATGCTGGAGTGTACTCGGCC	chr9:27169554-27169577_+
		1360	CTGGAGAGCAGAGACATCCT	chr9:27180315-27180338_-
TERT	ENST00000310581.9	1361	CGAAGAAGCCACCTCTTTGG	chr5:1294026-1294049_-
		1362	CCCGCGCCTCCTCGCACCCG	chr5:1294210-1294233_+
		1363	CTGGCGGCTGGTGCAGCGCG	chr5:1294862-1294885_-
		1364	AGCAGCCGGTGTCTGTGCC	chr5:1293600-1293623_-
		1365	GGTCCACTAGCGTGTGGCGG	chr5:1294307-1294330_+
TGFB1	ENST00000221930.5	1366	TGGATAGTCCCGCGGCCGCG	chr19:41352950-41352973_+
		1367	TGGTTATCTTTTGATGTCAC	chr19:41344775-41344798_-
		1368	TCACCGGAGTTGTGCGGCAG	chr19:41344759-41344782_-
		1369	TACTGGTGCTGACGCCTGGC	chr19:41352969-41352992_-
		1370	CAACCACTGCCGCACAACCTC	chr19:41344756-41344779_+
TGFBRI	ENST00000374994.8	1371	GTTACGTCATGAAAACATCC	chr9:99138042-99138065_+
		1372	CCTCTTCATTTGGCACTCGA	chr9:99132629-99132652_-
		1373	GTTTGGAGAGGAAAGTGGCG	chr9:99137938-99137961_+
		1374	TGTCTGCTGCTATAAATCCC	chr9:99138060-99138083_-
		1375	TTACGTCATGAAAACATCCT	chr9:99138043-99138066_+
TLR5	ENST00000642603.1	1376	CGGCCATCAAAGGAGCAGGA	chr1:223112945-223112968_+
		1377	ATGAGCTCGAGCCCCTACAA	chr1:223112446-223112469_-
		1378	CCTCCTTGTCATAAGTCAAG	chr1:223112763-223112786_+
		1379	CTCCTTGTCATAAGTCAAGG	chr1:223112764-223112787_+
		1380	TATACAAGCTATTAGCTGCG	chr1:223112403-223112426_+
TLR7	ENST00000380659.3	1381	ATGTTCTTAAACCATCTTGG	chrX:12886423-12886446_-
		1382	ACATCCAGAGTGACATCACA	chrX:12885610-12885633_-
		1383	CAGTCTGTGAAAGGACGCTG	chrX:12885749-12885772_-
		1384	CAGCTACTAGAGATACCGCA	chrX:12885919-12885942_+
		1385	ACTGTGTACCTATTCCACTG	chrX:12885803-12885826_+
TLR8	ENST00000311912.5	1386	CAAAATAGCTCCTGCAGCCT	chrX:12910403-12910426_+
		1387	ATTGAAGCACCACCATCACA	chrX:12919844-12919867_-
		1388	AAAGACTCTGGCAAACCAGA	chrX:12919460-12919483_-
		1389	ACAAGGCACGCATGGAAATG	chrX:12919827-12919850_-
		1390	AAGTCAAGTATTTCTAAGCG	chrX:12920048-12920071_-
TNF	ENST00000449264.2	1391	TGGAGTGTGCGCCCCCAGA	chr6:31575899-31575922_+
		1392	GCTCATGGTGTCTTCCAG	chr6:31575724-31575747_-
		1393	AAGCACCGCCTGGAGCCCTG	chr6:31575810-31575833_-
		1394	TGGAGTGATCGGCCCCCAG	chr6:31575898-31575921_+
		1395	TGGGCTACAGGCTTGTCCT	chr6:31576783-31576806_-
TNFRSF8	ENST00000263932.6	1396	TAGAAGCAGCTTCCTGGGCG	chr1:12110124-12110147_-
		1397	ACTACTATGACAAGGCTGTC	chr1:12084503-12084526_+
		1398	GCCTCATCCAGGTAGTAGTC	chr1:12097159-12097182_-
		1399	CCAGCACCATGCCTGTAAGA	chr1:12110093-12110116_+
		1400	TCTGTGAGCCGCTTCCCCA	chr1:12109586-12109609_+
TNFSF11	ENST00000398795.6	1401	CTGCGTGGCTCGGAGGAGAT	chr13:42574336-42574359_+
		1402	GGCCACGAACATGGAGCGGG	chr13:42574433-42574456_-
		1403	CCTAATAGAATATCAGAAGA	chr13:42581131-42581154_+
		1404	AATTAATACCTGATTCATGT	chr13:42581234-42581257_+
		1405	GACTACACCAAGTACCTGCG	chr13:42574321-42574344_+
TNFSF13B	ENST00000375887.8	1406	GCTTTCGCTTTTGAGGAT	chr13:108270011-108270034_-
		1407	GAAGCTCCAGCTGTCACCGC	chr13:108270204-108270227_+
		1408	TCTTTGGAGGATCGGACAGA	chr13:108270003-108270026_-

TNKS	ENST00000310430.10	1409	TGTTTCTTCTGGACCCTGAA	chr13:108270400-108270423_-
		1410	GTCTTTGGAGGATCGGACAG	chr13:108270004-108270027_-
		1411	CAGCGCTAGGCCGTGCCGCG	chr8:9556111-9556134_-
		1412	CCCTTCGCCTCCCCGCGCA	chr8:9556101-9556124_+
		1413	ACGGCCTAGCGCTGCCGGAG	chr8:9556120-9556143_+
		1414	GTAACCTAGCAGGAGGCGGC	chr8:9720440-9720463_-
		1415	TCCCGACTGCCATCCCCCTC	chr8:9556134-9556157_-
TOP1	ENST00000361337.2	1416	CCCACTCATGTTCGGCCCGGA	chr20:41029053-41029076_-
		1417	GGTCCCCACTCATGTTCGGCC	chr20:41029057-41029080_-
		1418	TAGCTACTTCCTCTGCTTTG	chr20:41097238-41097261_-
		1419	CCCCACTCATGTTCGGCCCGG	chr20:41029054-41029077_-
		1420	GAAGAAGAGCGCTATCCTGA	chr20:41092475-41092498_+
TOP1MT	ENST00000329245.8	1421	GGGCTCGCGCAGGACGCAGA	chr8:143334752-143334775_-
		1422	CGATAACACCGTCACGTGGC	chr8:143324552-143324575_-
		1423	CGTGGCGACCATCCCAAGAT	chr8:143325396-143325419_-
		1424	GCCGGCGGGGACCAAGTGA	chr8:143324585-143324608_-
		1425	CCACGGCCACGGAACAAGCC	chr8:143325414-143325437_+
TOP2A	ENST00000423485.5	1426	GATAATGATTATGACAGATC	chr17:40407547-40407570_-
		1427	CTCCGCCAGACACCTACAT	chr17:40416761-40416784_-
		1428	CAGAACCAATGTAGGTGTCT	chr17:40416756-40416779_+
		1429	TTGGGACACCAGCACATCAA	chr17:40406469-40406492_-
		1430	AGACACCTACATTGGTTCTG	chr17:40416753-40416776_-
TOP2B	ENST00000435706.6	1431	CGGCGTGGGCGGCGCAACG	chr3:25664242-25664265_-
		1432	CGGAGACAGCGTAGGCTACA	chr3:25626781-25626804_-
		1433	CATAATCTTCCATAGCGTA	chr3:25630043-25630066_+
		1434	CATGTAGCCTACGCTGTCTC	chr3:25626782-25626805_+
		1435	GATTTGGCTGGTTCGTGTAG	chr3:25635969-25635992_-
TUBA1A	ENST00000301071.11	1436	TGCCGTGATAAGTTGCTCA	chr12:49186398-49186421_+
		1437	CACCTTCTTCAGTGAGACGG	chr12:49186664-49186687_-
		1438	ACACCTTCTTCAGTGAGACG	chr12:49186665-49186688_-
		1439	CACCCTGAGCAACTTATCAC	chr12:49186400-49186423_-
		1440	GGAGATCATTGACCTCGTGT	chr12:49186326-49186349_-
TUBA4A	ENST00000248437.8	1441	GAGCTCTATTGCTTGGAACA	chr2:219252147-219252170_-
		1442	CAGATCCACAAAACTGCCC	chr2:219252023-219252046_+
		1443	GTGCTGGAAAACACGTACCC	chr2:219252041-219252064_-
		1444	CTGCTGGGAGCTCTATTGCT	chr2:219252154-219252177_-
		1445	ACCCAGAGCAGCTCATCACT	chr2:219251654-219251677_-
TUBB	ENST00000327892.12	1446	ATATGTTCTCGTGCCATCC	chr6:30722924-30722947_+
		1447	CATTGTAGTACACAGAGATG	chr6:30722613-30722636_-
		1448	TGTTCTCTCGTGCCATCCTGG	chr6:30722927-30722950_+
		1449	AGGTTCTAGATCCACCAGGA	chr6:30722938-30722961_-
		1450	AGATCCACCAGGATGGCACG	chr6:30722931-30722954_-
TUBB1	ENST00000217133.1	1451	CGAATGCTGTCCATCGTCCC	chr20:59023530-59023553_-
		1452	GACTTGGCTGGGAGCGACCG	chr20:59022877-59022900_+
		1453	GGACCTAGAACCTGGGACGA	chr20:59023520-59023543_+
		1454	GCTGCAAGGCCGAGGCCCG	chr20:59022894-59022917_-
		1455	GCTGATTCTCTCCAGCTGCA	chr20:59022908-59022931_-
TUBB3	ENST00000315491.11	1456	TACTGGGCGCGTCTGGCGGG	chr16:89923379-89923402_-
		1457	ATTCTGGTGGACCTGGAACC	chr16:89933490-89933513_+
		1458	AGGCCTGAAGAGATGTCCAA	chr16:89933539-89933562_-
		1459	GATGTCCAAAGGCCCTGAG	chr16:89933528-89933551_-
		1460	CCATGGACAGTGTCCGCTCA	chr16:89933515-89933538_+
TUBD1	ENST00000325752.7	1461	TAGTGACTCACACAGTCCC	chr17:59890908-59890931_-
		1462	CATCATAATGAGTATGGCTG	chr17:59880997-59881020_-

TUBE1	ENST00000368662.9	1463	TCATCATAATGAGTATGGCT	chr17:59880998-59881021_-
		1464	ATATTTCCATTGGCCAGACT	chr17:59886138-59886161_+
		1465	TCAATTGTAAACAGTGCAACT	chr17:59890976-59890999_-
		1466	TACGACCACCGACTGGGTCA	chr6:112087413-112087436_+
TUBG1	ENST00000251413.7	1467	GACCACCGACTGGGTCATGG	chr6:112087416-112087439_+
		1468	GCGCACCACCATGACCCAGT	chr6:112087421-112087444_-
		1469	GACACGAGATAATGAAGTTG	chr6:112074760-112074783_+
		1470	CATTAGCAAAATCGACCTCA	chr6:112076075-112076098_-
TXN	ENST00000374517.5	1471	GCCGCACTGGCCCAACTGTA	chr17:42609756-42609779_-
		1472	TCTTAGAACGGCTGAATGAC	chr17:42612484-42612507_+
		1473	TGTCATTACAGCCGTTCTAAG	chr17:42612482-42612505_-
		1474	TGCCGCACTGGCCCAACTGT	chr17:42609757-42609780_-
TYK2	ENST00000525621.5	1475	CGGCATCGCTCCTCAGGCAC	chr17:42609720-42609743_-
		1476	TACTTCAAGGAATATCACGT	chr9:110250837-110250860_+
		1477	TTTATCACCTGCAGCGTCCA	chr9:110251423-110251446_+
		1478	TCAGACTCCAGCAGCCAAGA	chr9:110256431-110256454_-
TYMS	ENST00000323274.14	1479	TTTGCAAGGCCACACCACG	chr9:110251378-110251401_+
		1480	TAGTTGACTTCTCAGCCACG	chr9:110251393-110251416_-
		1481	TCTCCGCCATGGCATCCCC	chr19:10366438-10366461_-
		1482	CGAAGGACAGCGCCGAGCC	chr19:10364731-10364754_+
VDR	ENST00000395324.6	1483	CCCCAGCGTTCGGGAACTTG	chr19:10362341-10362364_-
		1484	GGGCTGGGCTCCATCCCCAA	chr19:10378343-10378366_+
		1485	CTCTGGGGATCTCTAGGATG	chr19:10368325-10368348_+
		1486	AGCCGGCCACAGGCATGGCG	chr18:657735-657758_-
VEGFA	ENST00000372055.8	1487	CTTCCAGTGAGGCATTTTG	chr18:662273-662296_+
		1488	CTGCCCCAAAATGCCTCCAC	chr18:662276-662299_-
		1489	CACGTTTGGTTGTCAGCAGA	chr18:659647-659670_-
		1490	CGGCCACAGGCATGGCGCGG	chr18:657732-657755_-
VEGFB	ENST00000309422.6	1491	GGAACGTGCCCCGATCTGT	chr12:47879038-47879061_-
		1492	CCCCGGATCTGTGGGGTGTG	chr12:47879030-47879053_-
		1493	CTGACCCTGGAGACTTTGAC	chr12:47879059-47879082_-
		1494	CAGGCGAAGCATGAAGCGGA	chr12:47865157-47865180_-
WEE1	ENST00000450114.6	1495	ACTTTGACCGGAACGTGCCC	chr12:47879047-47879070_-
		1496	GAGAAGTGCTAGCTCGGGCC	chr6:43770945-43770968_+
		1497	AGTAGCTCGCCGAGGCGCCG	chr6:43771149-43771172_+
		1498	GGCTTCCCCCGCGCGACCA	chr6:43770905-43770928_-
XIAP	ENST00000434753.7	1499	GCCGCGAGAAGTGCTAGCTC	chr6:43770940-43770963_+
		1500	CCTCTCCGGCTCGGGCTGTG	chr6:43771183-43771206_-
		1501	CCCCAGTGGGCACACACTCC	chr11:64235966-64235989_-
		1502	TGCGTGACTGTGCAGCGCTG	chr11:64235922-64235945_+
XPO1	ENST00000401558.6	1503	AGGGCTCATGGTGCCCGCCG	chr11:64234819-64234842_-
		1504	ACAGTGCTGTGAAGCCAGAC	chr11:64237200-64237223_+
		1505	CGGACTTGGTGCTGCCAGT	chr11:64235979-64236002_-
		1506	TTGCGGAAGGTCTTGTGTGG	chr11:9574452-9574475_-
XPO1	ENST00000401558.6	1507	ACTCGCCGCTGCCGCCCGCG	chr11:9574108-9574131_+
		1508	TCCTCCTCACAGTCGCTGCA	chr11:9574017-9574040_-
		1509	GAGGAGGACCTGTTGCTGCC	chr11:9574200-9574223_+
		1510	CGATCAAAAAAGCCATTGGC	chr11:9576624-9576647_+
XPO1	ENST00000401558.6	1511	CTATCTTTTGAGAACTGGGC	chrX:123886075-123886098_+
		1512	GCTTCATAATCTGCCATGGA	chrX:123886439-123886462_-
		1513	CCAAATTGCAGATTTATCAA	chrX:123885923-123885946_+
		1514	CTTCTTCACTATACATGGCA	chrX:123886132-123886155_-
XPO1	ENST00000401558.6	1515	ATAGTCTGGCCAGTTCTGAA	chrX:123886167-123886190_-
		1516	TAAAGGAGCATCCTGATGCT	chr2:61526467-61526490_-

YES1	ENST00000584307.5	1517	AACAAGAATGGCCCAAACAT	chr2:61499864-61499887_-
		1518	TTAAATGCTTAGATTTGACT	chr2:61499719-61499742_+
		1519	GGCAAATATAGCTGTCTCCT	chr2:61493906-61493929_+
		1520	TGGTCTCAAAAATATATCCC	chr2:61498698-61498721_+
		1521	GAAGCAAGATCAATCGCTAC	chr18:747979-748002_-
		1522	GGATCCTCCAAATGGTGTCA	chr18:756632-756655_+
		1523	TTGAATCCTGGAAATCAACG	chr18:745982-746005_-
		1524	ATGTTTCGGCGAAGTGTGGA	chr18:743259-743282_-
		1525	CAGAGTATCAAATTGTGCTC	chr18:745732-745755_+

Table 6B. Library of gene modulatory reagents.

Target gene	SEQ ID NO	gRNA #	gRNA Seq
ANPEP	1526	1	CGTTCAGGGCATAATCGCCG
ANPEP	1527	2	TCACGGTGGATACCAGCACG
ANPEP	1528	3	CATCACGCTTATCCACCCCA
ANPEP	1529	4	CCTTGGACCAAAGTAAAGCG
HDAC11	1530	1	GGCGAGCGTGATGTCCGCAT
HDAC11	1531	2	CGAGGCTGGGCCATCAACGT
HDAC11	1532	3	GCAACAGCAAAGGACCACTG
HDAC11	1533	4	ACAACCGCCACATCTACCCA
ROCK1	1534	1	GCAAAGTCTGTGGCAATGTG
ROCK1	1535	2	AGTCATACCTGAACAACCCA
ROCK1	1536	3	TTACATATTATAGCAATCGT
ROCK1	1537	4	CATGGTACGATGTGATACAG
BRAF	1538	1	ATACCCAATAGAGTCCGAGG
BRAF	1539	2	TCATAATTAACACACATCAG
BRAF	1540	3	ACAAATGATTAAGTTGACAC
BRAF	1541	4	GGGGGTAGCAGACAAACCTG
NRAS	1542	1	CCATGAGAGACCAATACATG
NRAS	1543	2	TGAATATGATCCCACCATAG
NRAS	1544	3	TGATGTACCTATGGTGCTAG
NRAS	1545	4	TTGCGGATATTAACCTCTAC
PPARG	1546	1	CACGACATTCAATTGCCATG
PPARG	1547	2	AGTGAAGGGCTTGATATCAA
PPARG	1548	3	TGGCATCTCTGTGTCAACCA
PPARG	1549	4	ACAGATGTGATCTTAACTGT
INHBB	1550	1	GCATACCTTCCCACTCACGG
INHBB	1551	2	CAGGACACCTGTACGTCGTG
INHBB	1552	3	GAAGAAGTATAGGCGACCC
INHBB	1553	4	TCGCCTGGGTCCACGAACAC
TOP2A	1554	1	TCCCGTCAGAACATGGACCC
TOP2A	1555	2	AGCATTGTAAAGATGTATCG
TOP2A	1556	3	TGTACGCTTATCCTGACTGA
TOP2A	1557	4	ATTCAGTACCAAATTTACTG

ADA	1558	1	TCACCGTACTGTCCACGCCG
ADA	1559	2	TGGACATACTCAAGACAGAG
ADA	1560	3	CACAGACTGGTCCCCCAAGG
ADA	1561	4	TCCCAGCTAACACAGCAGAG
SRC	1562	1	GACCTGGAACGGTACCACCA
SRC	1563	2	TCAATGCAGAGAACCCGAGA
SRC	1564	3	TGTCCTTCAAGAAAGGCGAG
SRC	1565	4	GTCACGGAGTACATGAGCAA
PIM1	1566	1	GGCGAGTCGGAGGACAACTG
PIM1	1567	2	GTCCAGGAGCCTAATGACGC
PIM1	1568	3	AAGGACCGGATTTCCGACTG
PIM1	1569	4	TCTTCGACTTCATCACGGAA
RPTOR	1570	1	GATCTGGCAGAACTTCGACT
RPTOR	1571	2	CTTACGTCGCAACGCCAAGG
RPTOR	1572	3	TGGTGTGGACCCTCCCGATG
RPTOR	1573	4	CACATGGCGTGCATGTACGT
PTK6	1574	1	CGCACCCGACAGGACGTAGT
PTK6	1575	2	CGTGGAAGACGTCCCCCGCG
PTK6	1576	3	CTCTCCCAGTCATCCCAATG
PTK6	1577	4	GCCGACGCACAGCTTCCGAG
CDK7	1578	1	AGCTCCAAATAGTAACTCGG
CDK7	1579	2	ATCTCTGGCCTTGTAACGG
CDK7	1580	3	TTTCCATAAAATCAAAGACA
CDK7	1581	4	TTAAAAACCTTACCCTATGT
PSMB10	1582	1	CGATCAGCGATGCACCCACG
PSMB10	1583	2	CACTAACGATTTCGGTCGTGG
PSMB10	1584	3	GAGCTACACGCGTTATCTAC
PSMB10	1585	4	TCTCCTTCGAGAACTGCCAA
MAP2K1	1586	1	CATCCTAGTCAACTCCCGTG
MAP2K1	1587	2	GCAGCAGCGAAAGCGCCTTG
MAP2K1	1588	3	GGGCACAAGGTCCTACATGT
MAP2K1	1589	4	TATGGTGC GTTCTACAGCGA
VEGFB	1590	1	CACACTCCAGGCCATCGTCA
VEGFB	1591	2	CATCTATCCATGACACCACT
VEGFB	1592	3	GCAGCACCAAGTCCGGATGC
VEGFB	1593	4	CGGTACCCGAGCAGTCAGCT
SLC2A2	1594	1	GTGCCACTAGAATAGGCTGT
SLC2A2	1595	2	CCTTTACATCAAGTTAGATG
SLC2A2	1596	3	CACCGATATACATAGGAACC
SLC2A2	1597	4	TAGTTGGAGCTCTCTTGATG
EHMT1	1598	1	GGGCCGGTGCACAAACAGCG
EHMT1	1599	2	TTCGGCTGCTTCCATCAACG
EHMT1	1600	3	ACTTATACGACTCAGAACCT
EHMT1	1601	4	CAACACACTAACTCGGATAG

CDK5	1602	1	TAGCCGCAATGTGCTACACA
CDK5	1603	2	CCTTTACAATCTCAGGATCG
CDK5	1604	3	CGTCCGCTGTTACTCAGCTG
CDK5	1605	4	CCGGGAGACTCATGAGATCG
CXCR2	1606	1	GGCGGCATCTAGTAGAAAAG
CXCR2	1607	2	TAAGATGACCAGCATCACGA
CXCR2	1608	3	CAGTGGCACGATGAAGCCAA
CXCR2	1609	4	CCAGCCTGCTATGAGGACAT
IFNAR1	1610	1	GTACATTGTATAAAGACCAC
IFNAR1	1611	2	ATAATTGGATAAAATTGTCT
IFNAR1	1612	3	CTCCGCGTACAAGCATCTGA
IFNAR1	1613	4	TAGATGACAACCTTTATCCTG
EHMT2	1614	1	CAAGAGGTGACCATCCCCCG
EHMT2	1615	2	CTCCAGGTGGTTGTTACCA
EHMT2	1616	3	CGGACAGGTACAACCTGCCGA
EHMT2	1617	4	CTCTCCGTCCCACTCTCAG
DHX9	1618	1	CAAAACATTATACTGGCATG
DHX9	1619	2	TCAATCACAGCATCCAAAGG
DHX9	1620	3	TGGATGTGGGAAAACACAC
DHX9	1621	4	GGAGATTTACCAACAACCAT
RAC1	1622	1	TCACATCTAGTGGTATCCTG
RAC1	1623	2	CTGTTTGGCGATAGGATAGG
RAC1	1624	3	ATTTAAGATACTTACACAGT
RAC1	1625	4	CTGGGCTTATGGGATACAGC
KIF11	1626	1	TCTTGTGTAGGAGTATACGG
KIF11	1627	2	GACTGAATTACCTTGTTACG
KIF11	1628	3	GAAGTTAGTGACGAACTGG
KIF11	1629	4	ACCTAATGAAGAGTATACCT
TUBD1	1630	1	AATGAATTCTCAGACATGTG
TUBD1	1631	2	ATAGAGGGACAAATACCTAG
TUBD1	1632	3	AGTGACTCACACAGTTCCCA
TUBD1	1633	4	GCATGCTTCTGTCAAAAACA
PSMD1	1634	1	CCTTAGATCGTTAGACACGG
PSMD1	1635	2	TGAATCTCTCTGTCGTGACA
PSMD1	1636	3	GTTAGCCAGAGCCACTAACT
PSMD1	1637	4	TCCTACACCAAACAATGTG
HDAC9	1638	1	AGCTTTGATCCAATGATGTG
HDAC9	1639	2	AACAGCATGAGAACTTGACA
HDAC9	1640	3	TTTCCCTCTAAAGTAACATG
HDAC9	1641	4	GAGAGCGCACGTGTGTGCGT
PIGF	1642	1	GGTCCTAACAACATAAGCA
PIGF	1643	2	TTTCAAACCTTACTCTATCAG
PIGF	1644	3	AAGAAGTTCATTATCACACA
PIGF	1645	4	TATTGGAAACACACTTGACA

TUBA4A	1646	1	GCTCGATGTCTAGGTTGCGG
TUBA4A	1647	2	TTCCTCTCACCAATGACCGT
TUBA4A	1648	3	GAGCCGCTCCATCAGGAGTG
TUBA4A	1649	4	GTGACAAGACCATTGGTGGA
TOP1MT	1650	1	GCTCCGATAACACCGTCACG
TOP1MT	1651	2	TCATGAATACACAACAAAGG
TOP1MT	1652	3	CCATACGAGCCCCCTCCCGA
TOP1MT	1653	4	GTGGCGACCATCCCAAGATG
NTRK3	1654	1	TCTTCACACGCTCAACGCCG
NTRK3	1655	2	CGTCAACCTGACCGTACGAG
NTRK3	1656	3	CATGTGGAATACTACCAAGA
NTRK3	1657	4	TCATGCCATCAACTTGACGC
RXRA	1658	1	CCTACGTGGAGGCAAACATG
RXRA	1659	2	AGGACTGCCTGATTGACAAG
RXRA	1660	3	AGGAAGCCATGTTTCCTGAG
RXRA	1661	4	CAAGGACCGGAACGAGAATG
MCL1	1662	1	AGGCGCTGGAGACCTTACGA
MCL1	1663	2	GTAATAACACCAGTACGGAC
MCL1	1664	3	AGTCGCTGGAGATTATCTCT
MCL1	1665	4	CCAAAAGTCGCCCTCCCGGG
MTOR	1666	1	TCAGGAAATGATCCGCACAG
MTOR	1667	2	GGTGATGGCCTGGACAACCA
MTOR	1668	3	CAGCATCGGATGCTTAGGAG
MTOR	1669	4	GTGAAGGGGGTAATGTGACG
HDAC7	1670	1	TGCAGTCGGTCCACTCTGAG
HDAC7	1671	2	GTTACCTGTAGGGAATGCCG
HDAC7	1672	3	AAGGACTGGGCAAAGTGGAA
HDAC7	1673	4	GACCTGGAGACAGATGGCGG
CHEK1	1674	1	ACACCACCTGAAGTGACTCG
CHEK1	1675	2	TGGTATTGGAATAACTCACA
CHEK1	1676	3	CTTACTGCAATGCTCGCTGG
CHEK1	1677	4	TTTCTGGAGTACTGTAGTGG
PSEN1	1678	1	GCCACGCAGTCCATTACAGG
PSEN1	1679	2	TAAAACCTATAACGTTGCTG
PSEN1	1680	3	ACCTGCCGGGAGTTACCCTG
PSEN1	1681	4	TGTATTTATACAGAACCACC
FOLH1	1682	1	TTATAGGCGTGGAATTGCAG
FOLH1	1683	2	GGAGAGAAAGCACTGAAAGG
FOLH1	1684	3	GAGGCGCCCCCTACCGAAG
FOLH1	1685	4	AAGATTCCAACCATCTGGAT
FKBP1A	1686	1	GGGCGCACCTTCCCCAAGCG
FKBP1A	1687	2	ACCGGTGTAGTGACCCACGC
FKBP1A	1688	3	GGCAAGCAGGAGGTGATCCG
FKBP1A	1689	4	GAAACCATCTCCCCAGGAGA

TUBG1	1690	1	GACATGATGGTAGACACCTG
TUBG1	1691	2	CGTGGAGGAGTTCGCCACCG
TUBG1	1692	3	AGATGGTAGTGACAGTCTAG
TUBG1	1693	4	TGACTGGTCCGTAGTGAGAG
GNRHR	1694	1	GTCCTGCAAAGACACTACTG
GNRHR	1695	2	GGAAGAAAGTAACCGTCACT
GNRHR	1696	3	TGTGGAACATTACAGTCCAA
GNRHR	1697	4	AGTCTCCAACAGGTTGGCTA
PLK2	1698	1	ATCACCACCATTTCGCACTCG
PLK2	1699	2	AGCCATGGAATAAAAGTTG
PLK2	1700	3	TATGTTGTCCAAAAACCCAG
PLK2	1701	4	GTCCTCAACAAACAAGGACA
PDGFRB	1702	1	TGTGGTAAGGCATATCCAAG
PDGFRB	1703	2	GACTAACGTGACGTACTGGG
PDGFRB	1704	3	GTCCCCTATGATCACCAACG
PDGFRB	1705	4	CTCCCGTGTCTAGCCCAGTG
FOLR1	1706	1	AGTTGGGGGAGCACTCGTAG
FOLR1	1707	2	CCATCCAGTGTCGACCCTGG
FOLR1	1708	3	CATGAACGCCAAGCACCACA
FOLR1	1709	4	GCTGCTCCTTCTAGTGTGGG
PLK3	1710	1	GCTGATAGGGAGTCGATCGG
PLK3	1711	2	GGTGCGAAAAACGCACGATG
PLK3	1712	3	GTGACCATACATCCGCCTCA
PLK3	1713	4	CTCAAGTACTTGCACCAGCG
MST1R	1714	1	CTGCCCACCTAAGCTTACTG
MST1R	1715	2	GTGGCATGTTAGTCACGGTG
MST1R	1716	3	GTGGGTATCAACGTGACCGT
MST1R	1717	4	CTCGGACCACATATTACAGGA
TUBA1A	1718	1	CTGTGATAAGTTGCTCAGGG
TUBA1A	1719	2	AGGTTGGACGCTCAATATCG
TUBA1A	1720	3	CTGGAGACCCGTGCACTGGT
TUBA1A	1721	4	TACAGAAAGCTGTTCATGGT
POLA1	1722	1	CATGACACAACAGCTCACAT
POLA1	1723	2	CAACAAGAACTCGTTACGCT
POLA1	1724	3	AAGCACGCAATAAAGACAAG
POLA1	1725	4	CTCTACACACTTTACCGTGG
DYRK1A	1726	1	TTCAACCAAAATACACCCGA
DYRK1A	1727	2	TCAGCAACCTCTAACTAACC
DYRK1A	1728	3	TGAGAAACACCAATTTCCGA
DYRK1A	1729	4	TTACAGGAGTACAAACCACC
ERBB4	1730	1	CTGGTGTGTCCAGATAGCTA
ERBB4	1731	2	AGCGGCGACACGACAGACAT
ERBB4	1732	3	ATGTCCAGATGGCTTACAGG
ERBB4	1733	4	ATAGAGTACTCTCCACCAA

NCSTN	1734	1	TAAAGCCTATAAATACAACCT
NCSTN	1735	2	CCAGCAGAACCATGTAAGGG
NCSTN	1736	3	ATGGTCTACGATATGGAGAA
NCSTN	1737	4	CAGTGCCCAAATGATGGGTT
ANGPT2	1738	1	ACCGAGTCATCGTATTCGAG
ANGPT2	1739	2	ACCAAACAGCGGAGCAAACG
ANGPT2	1740	3	TAACGTGTAGATGCCATTCTG
ANGPT2	1741	4	AAGAACTGAATTATTCACCG
AR	1742	1	AGGGTACCACACATCAGGTG
AR	1743	2	CCTTAAAGACATCCTGAGCG
AR	1744	3	GGACGCAACCTCTCTCGGGG
AR	1745	4	TCCAGCTTGATGCGAGCGTG
SLAMF7	1746	1	TCAGGGAGTAGCCTCCATCT
SLAMF7	1747	2	ACTCAGGGATCTACTATGTG
SLAMF7	1748	3	GACCAATCTGACATGCTGCA
SLAMF7	1749	4	TGGCTGTATGGTGACAAGAG
DHFR	1750	1	CGGCCCCGGCAGATACCTGAG
DHFR	1751	2	AACCTTAGGGAACCTCCACA
DHFR	1752	3	GTCGCTGTGTCCAGAACAT
DHFR	1753	4	GACATGGTCTGGATAGTTGG
PDGFRA	1754	1	TAAGTCAGGGGAAACGATTG
PDGFRA	1755	2	CCTGCGTTCTGAACTCACGG
PDGFRA	1756	3	GACTTGGTCGATGATCACCA
PDGFRA	1757	4	AAATAATCCGTCATTCTAG
TUBB3	1758	1	CTGGCCCCGGAAGCGCAAGG
TUBB3	1759	2	CATGGACAGTGTCCTCAG
TUBB3	1760	3	CAGCTGGTGGATGGACAGCG
TUBB3	1761	4	CTGGGCCAAGGGTCACTACA
IGF1R	1762	1	GGAGAACGACCATATCCGTG
IGF1R	1763	2	TTCCGAAATTTACCGCATGG
IGF1R	1764	3	GGTACAATGTGAAAGGCCGA
IGF1R	1765	4	TGTGGGGAATAAGCCCCCAA
RAF1	1766	1	GACCATGTGGACATTAGGTG
RAF1	1767	2	AGACTTCTCCACGAACACAA
RAF1	1768	3	GCCGAACAAGCAAAGAACAG
RAF1	1769	4	TGTTGCAGTAAAGATCCTAA
SYK	1770	1	GGTGTACGAGAGCCCCTACG
SYK	1771	2	CACACCACTACACCATCGAG
SYK	1772	3	ATCCGAGCCAGAGACAACAA
SYK	1773	4	TAATAACTCATCTTTAAGAG
MAP2	1774	1	TTTGTCAACAGAGATATGCG
MAP2	1775	2	CCTGATAAAAAGGACATGCA
MAP2	1776	3	CATGCCAAGTCCCTTTCAAG
MAP2	1777	4	GATTGCCGTCAAATTGTCAG

FOLR2	1778	1	AACTTTAACTGGGACCACTG
FOLR2	1779	2	AGAGGACTGTCAGCGCTGGT
FOLR2	1780	3	ACTGGCACAGAGGATGGGAC
FOLR2	1781	4	AAGCACCACAAGACAAAGCC
CDK9	1782	1	CCAGAGTGTACCCACACGGT
CDK9	1783	2	TCTCCCGCAAGGCTGTAATG
CDK9	1784	3	GCGGTTATAGGGGGAAGCTG
CDK9	1785	4	GCTGACTGATGAGGGCGAGT
PRKCG	1786	1	ACTCGAAGGTCACAAATTCG
PRKCG	1787	2	ATTCCACACAGGGTTTAGCG
PRKCG	1788	3	CGAGTATTACAATGTGCCGG
PRKCG	1789	4	CTCTACGGGCTTGTGCACCA
MS4A1	1790	1	TGGGTGCATAGATCCCTGCT
MS4A1	1791	2	TCATGAAGAAGCTTTGCGTG
MS4A1	1792	3	GTAACAGTATTGGGTAGATG
MS4A1	1793	4	TATTATTTCCGGATCACTCC
INHA	1794	1	TGCCCCGAAGACATGCCCTG
INHA	1795	2	GAGGACAAGTCAGCTGCCAG
INHA	1796	3	CGGACCAGACCACCCAGTGG
INHA	1797	4	CAGCAGCACCAGGACGGGGT
F2R	1798	1	GGAGCTGGTCAAATATCCGG
F2R	1799	2	AAATGACCGGGGATCTAAGG
F2R	1800	3	TGGCCATGATGTTTAGTGGG
F2R	1801	4	CACAAACAGCACATCTGCCG
MAPK11	1802	1	GCTTCTGGACGTCTTCACGC
MAPK11	1803	2	CTGCGGTTCGCACCTACCCGG
MAPK11	1804	3	TGCGCGCGTGGATCAGCGAC
MAPK11	1805	4	CCAGACGGAGCCGTAGGCGC
PLK1	1806	1	AACCAAAGTCGAATATGACG
PLK1	1807	2	CCTGCCTGACCATTCCACCA
PLK1	1808	3	AGCCAAGCACAAATTTGCCGT
PLK1	1809	4	CGTTGTCCTCGAAAAAGCCG
TUBB	1810	1	GCTGACCACACCAACCTACG
TUBB	1811	2	CCCCACCGGCACCTACCACG
TUBB	1812	3	AGATCCACCAGGATGGCACG
TUBB	1813	4	CTGCATTCCAGGTCAGTCTG
HDAC8	1814	1	ATTTGAGCGTATTCTCTACG
HDAC8	1815	2	ATAGTCAAATATCCCTTCAG
HDAC8	1816	3	GTAAATGTGCCCATTCAGGA
HDAC8	1817	4	GCTGCAGATAAGCATCAGTG
PTCH1	1818	1	TGATGTTCGATGGGCTTATCG
PTCH1	1819	2	AGCGGGAATTGGGATTAACG
PTCH1	1820	3	AAATGTACGAGCACTTCAAG
PTCH1	1821	4	AAGGTGTAATAATCAAACAA

PARP3	1822	1	GTGGACATGTTGGATCCACG
PARP3	1823	2	AGCAAGCAACAGATTGCACG
PARP3	1824	3	ACTTATCGAAGTACAGGCAG
PARP3	1825	4	GATGACGGTGTA AAAAGTGTG
HDAC2	1826	1	GATGTATCAACCTAGTGCTG
HDAC2	1827	2	TACAACAGATCGTGTAATGA
HDAC2	1828	3	CCTCCTCCAAGCATCAGTAA
HDAC2	1829	4	TCAAAGAGTCCATCAAACAC
APH1A	1830	1	GACACCACTGATGATACCGA
APH1A	1831	2	GCGTTATCATCCTGGTCGCA
APH1A	1832	3	AGTGATCAAGAAAAGCGCGA
APH1A	1833	4	GCTCACCATAGGCCATCTGG
PSMB1	1834	1	ATAATAAGGCCATGACTACG
PSMB1	1835	2	GTATACAGCTTTGATCCAGT
PSMB1	1836	3	TCTGATACTCGATTGAGTGA
PSMB1	1837	4	TTACCCTCCGTTGAAAACGT
DYRK3	1838	1	CCACGGGCGCAGTTCAACCA
DYRK3	1839	2	TTGGTGGTCCCAATAATGGA
DYRK3	1840	3	GGCATCCAAAGATTGCAAGA
DYRK3	1841	4	TGCAGAGTACATTTGAACAG
JAK3	1842	1	TGACGCGGAGGCGTATTCGG
JAK3	1843	2	ACTCTCCAGGCTTAACACAG
JAK3	1844	3	GTGTACAAATTCCTGCACCA
JAK3	1845	4	AGCTCTCGAAGACTGCTGTG
ATR	1846	1	TGACGTGCGAAAAACAAGATG
ATR	1847	2	GCCCAGGTCACCAATTGTGG
ATR	1848	3	CTGTGTGAGATGGTCAAGCA
ATR	1849	4	GATGCTTTGATTTATATGCA
FGFR4	1850	1	GAGGTAGATCTAGACTCACG
FGFR4	1851	2	TTGCACATAGGGGAAAACCGT
FGFR4	1852	3	GGTAACTGTGCCTATTCGAG
FGFR4	1853	4	TGGTGGCCACTGGTACAAGG
MAPK1	1854	1	ATCCAGACCATGATCACACA
MAPK1	1855	2	CAACCTCTCGTACATCGGCG
MAPK1	1856	3	GCTGACCTTGAGATCACAGG
MAPK1	1857	4	CCTACTGCCAGAGAACCCTG
HPSE	1858	1	TGGCAATCTCAAGTCAACCA
HPSE	1859	2	TGGTGACGGACAGGAACGAG
HPSE	1860	3	CCACCAAACCTCAGGTACGC
HPSE	1861	4	TAAAAATGTCCAATACATCA
IL2RB	1862	1	GCTGGGAAAAAGAACTTCGAG
IL2RB	1863	2	CCACAGATGCAACATAAGCT
IL2RB	1864	3	TTGGGAAGGACACCATTCCG
IL2RB	1865	4	CAGGGTGACGATGTCAACTG

BTK	1866	1	TATGAGTATGACTTTGAACG
BTK	1867	2	GATGGTAGTTAATGAGCTCA
BTK	1868	3	ATAAGGAGTTACCGTATCCC
BTK	1869	4	CTGTGTTTGCTAAATCCACA
IHH	1870	1	CTTGACGGAGCAATGCACGT
IHH	1871	2	CCAGCAGTCCATACTTATTG
IHH	1872	3	GATGTCTGGATTGTAATTGG
IHH	1873	4	GCGAGCGGCACGAGTTTGCG
RARG	1874	1	TGGGCAAGTATACCACGGTG
RARG	1875	2	GGGCTCAGCATCTCGAAAGG
RARG	1876	3	AAGCATGGCTTGTAGACCCG
RARG	1877	4	GCTACAGAAGTGCTTCGAAG
EDNRA	1878	1	TGTCAACACTAAGAGCGCAG
EDNRA	1879	2	CACATAGATAAGGTCTCCAA
EDNRA	1880	3	TGAAGCGATTGGCTTCGTCA
EDNRA	1881	4	CAACATCTCACAAGTCATGA
HSPA1B	1882	1	TCCATCCTGACGATCGACGA
HSPA1B	1883	2	GAGCTACAAGGGGAGACCA
HSPA1B	1884	3	ACACCGTGTTTGACGCGAAG
HSPA1B	1885	4	AGGATGCGGGTGTGATCGCG
BIRC5	1886	1	ATGCGGTGGTCCTTGAGAAA
BIRC5	1887	2	GAACATAAAAAAGCATTGTC
BIRC5	1888	3	GCTGCGCCTGCACCCCGGAG
BIRC5	1889	4	CAAGTCTGGCTCGTTCTCAG
PDE5A	1890	1	TGTTGCTGAAGGTTCAACAC
PDE5A	1891	2	GGGGCACTGTTATCTGCACG
PDE5A	1892	3	AAGAGAGCTACAGTCGTTAG
PDE5A	1893	4	AATTAAGAATCATAGGGAAG
MAP3K7	1894	1	ACCCAAAGCGCTAATTCACA
MAP3K7	1895	2	AATATTAGGATGGTTCACAC
MAP3K7	1896	3	CCCAGCTTCCGAATCATGT
MAP3K7	1897	4	CACACATGACCAATAACAAG
JAK1	1898	1	CCGGAAGTAGCCATCTACCA
JAK1	1899	2	GCCTAGACAGCACCGTAATG
JAK1	1900	3	TGGTTTCATTCTGAATGACGG
JAK1	1901	4	CACACTTACTCTCCACGTCG
PARP1	1902	1	CGATGCCTATTACTGCACTG
PARP1	1903	2	TACCGATCACCGTACCCACA
PARP1	1904	3	AGCTAGGCATGATTGACCGC
PARP1	1905	4	GGCCATGATTGAGAACTCG
NR3C1	1906	1	TAGAAAAAACTGTTTCGACCA
NR3C1	1907	2	CATCGAACTCTGCACCCCTG
NR3C1	1908	3	ATCAACAGGTCTGATCTCCA
NR3C1	1909	4	CTTTAAGTCTGTTCCCCCG

IL6	1910	1	CAAATTCGGTACATCCTCGA
IL6	1911	2	TGCCTGGTGAAAATCATCAC
IL6	1912	3	TTTGTCAATTCGTTCTGAAG
IL6	1913	4	TACTCTCAAATCTGTTCTGG
MSLN	1914	1	GCCCCGCAGAGCGTCCATCG
MSLN	1915	2	GGTGCTGGATCACAGACTCG
MSLN	1916	3	ACCCACCTAACATTTCCAGG
MSLN	1917	4	CAGCCGGGGTAGCAGCACTT
IKBKB	1918	1	GCTGGTTCATATCTTGAACA
IKBKB	1919	2	GCCATGGAGTACTGCCAAGG
IKBKB	1920	3	TTTGCAGGCATTCAAAAGTG
IKBKB	1921	4	TGAGGGCCACACATTGGACA
LIMK1	1922	1	GTGAAGAATTCCATCCACGT
LIMK1	1923	2	TCCGGCTTATACTCCCAGCG
LIMK1	1924	3	CGATAAAGGTCCCACACGTG
LIMK1	1925	4	GGTGTGGCCGGCAGACTACG
AURKC	1926	1	CTAGGAGGAAGACAATGTGT
AURKC	1927	2	AGATGAACAGCGCACAGCCA
AURKC	1928	3	ATTCTGGAATATGCTCCAAG
AURKC	1929	4	GGAAATAGTTATACAGGCGC
BRD2	1930	1	CCAGCTGCAATACCTACACA
BRD2	1931	2	ACCACTCTCTCTACGCATAG
BRD2	1932	3	ACAGTGGTAGGTATCTCAGG
BRD2	1933	4	CTTGTTGTAAATGTAACAGT
ROS1	1934	1	TACACCCCAGTCTACCGCAG
ROS1	1935	2	CTGGGCTGGAAAGACATATG
ROS1	1936	3	TGGTGATGCCATACCATGTG
ROS1	1937	4	GTGCACACCATACTCCATG
PIK3CD	1938	1	CAAGATGTGCCAATTCTGCG
PIK3CD	1939	2	TGTGCGCAGTAACCCCAACA
PIK3CD	1940	3	CAGCGGCTGCCGGAACACTG
PIK3CD	1941	4	TGATGGCGAAGGAGCCTACG
TLR5	1942	1	TATACAAGCTATTAGCTGCG
TLR5	1943	2	TTTGTTCATATAACCTTCTGG
TLR5	1944	3	GACACCTGGATCTTTCACAT
TLR5	1945	4	TACCCCTTGACTATTGACA
TNKS	1946	1	CCTACATTAGTCAACTGCCA
TNKS	1947	2	GGTACTCTACAACAGACACG
TNKS	1948	3	TGGTGCTGTGCTGCTAACTC
TNKS	1949	4	GATATTCAGGACTTACTGAG
BCL2	1950	1	TGTCGCAGAGGGGCTACGAG
BCL2	1951	2	CTGACGCCCTTACCGCGCG
BCL2	1952	3	GGCCTTCTTTGAGTTCGGTG
BCL2	1953	4	TGGACATCTCGGCGAAGTCG

ITK	1954	1	ATACTTTGAAGATCGTCATG
ITK	1955	2	AACTATCACCAACATAATGG
ITK	1956	3	ATCCTCAGGAAGTCGCACTG
ITK	1957	4	GGAAGGGGCTATGTCAGAAG
CDK1	1958	1	GACAAAACACAATCCCCTGT
CDK1	1959	2	GTATTCCAAAAGCTCTGGCA
CDK1	1960	3	ACCCTTATACACAACCTCCAT
CDK1	1961	4	GATCTCCAGAAGTATTGCTG
MET	1962	1	CCGATCGCACACATTTGTCTG
MET	1963	2	AGCTGTGGCAGCGTCAACAG
MET	1964	3	CTCACTGATATCGAATGCAA
MET	1965	4	TACTGTATTGTGTTGTCCCG
PIM2	1966	1	ATCCTGATAGACCTACGCCG
PIM2	1967	2	ATAGCAGTGCAGCTTCGAGT
PIM2	1968	3	CAAGCAGGCGGATCACGCCA
PIM2	1969	4	TGTCACGATGGACAACTCCA
TBK1	1970	1	TCCACGTTATGATTTAGACG
TBK1	1971	2	ACAGTGTATAAACTCCCACA
TBK1	1972	3	AATCAAGAACTTATCTACGA
TBK1	1973	4	AGTTGATCTTTGGAGCATTG
CDK2	1974	1	CATGGGTGTAAGTACGAACA
CDK2	1975	2	CAAATATTATTCCACAGCTG
CDK2	1976	3	TCTGAGGTTTAAGGTCTCGG
CDK2	1977	4	AAGCAGAGAGATCTCTCGGA
TLR8	1978	1	CATCGTTAAAAATGCCCCAG
TLR8	1979	2	ATTTAAGCGGGAAGTGTCCG
TLR8	1980	3	TCTTACTGAATTGTCCGACT
TLR8	1981	4	AACTTATCGACTATCAACTT
CPT1A	1982	1	CACATCGTCGTGTACCATCG
CPT1A	1983	2	GCTCAGTGAACATCCACCCG
CPT1A	1984	3	TACGCCAAATCTCTACTACA
CPT1A	1985	4	ACATCTACCTCCGAGGACGA
HSPA1A	1986	1	GACCAAGGCATTCTACCCCG
HSPA1A	1987	2	CCGCAAGTTCGGCGACCCGG
HSPA1A	1988	3	GCCGTCGTCGATCGTCAGGA
HSPA1A	1989	4	CTGCTGCAGGACTTCTTCAA
MGMT	1990	1	CGCAAACGGTGCGCACCGCG
MGMT	1991	2	GGTACTTGGAATAATGGACA
MGMT	1992	3	CTGCACGAAATAAAGCTCCT
MGMT	1993	4	ACTCTTCGATAGCCTCGGGC
VEGFA	1994	1	TGGTTTCGGAGGCCCGACCG
VEGFA	1995	2	GGAGGGCAGAATCATCACGA
VEGFA	1996	3	GGAGGAAGAGTAGCTCGCCG
VEGFA	1997	4	AGATGTACTCGATCTCATCA

PIK3CA	1998	1	GTTCGAACAGGTATCTACCA
PIK3CA	1999	2	AACCTCGAACCATAGGATCT
PIK3CA	2000	3	GGATTTAGCTATTCCCACGC
PIK3CA	2001	4	GAAGCTGTATAATGCTTGGG
PTGS2	2002	1	GGGCTCTAGTATAATAGGAG
PTGS2	2003	2	GTGGCATAACATCATCAGACC
PTGS2	2004	3	TCAAGACAGATCATAAGCGA
PTGS2	2005	4	AGTATAAGTGCGATTGTACC
IL2RG	2006	1	CATACCAATAATGCAGAGTG
IL2RG	2007	2	CTGCCCATCCACACTAGGCA
IL2RG	2008	3	GGTGCAGTACCGGACTGACT
IL2RG	2009	4	CATATCTCCAGTGATCCCCT
INHBA	2010	1	CGAGGAAGTGGGCTTAAAGG
INHBA	2011	2	ACAGGCAATCCGAACGTCCA
INHBA	2012	3	GCTGCACTTCGAGATTTCCTA
INHBA	2013	4	GCGATCAGAAAGCTTCATGT
JAK2	2014	1	CTGCCACTGCAATACCAACG
JAK2	2015	2	AATGAAGAGTACAACCTCAG
JAK2	2016	3	AGAAAACGATCAAACCCAC
JAK2	2017	4	TCTTCAGGAGAGAATACCAT
NEK11	2018	1	CATTATCACGGAGTACTGTG
NEK11	2019	2	CCAAGGCTATGACACAAAAGT
NEK11	2020	3	GAGTTGACTACATGCATGAG
NEK11	2021	4	TCAGACAAGAAAGCCAAACG
GART	2022	1	GTCTTCGGGAAGTACCTGAG
GART	2023	2	GCAGAGCAGTCCATCTAAGG
GART	2024	3	TGGCCTTCACAACCAAAGCA
GART	2025	4	AGCTAGGTCATACTCTCCAG
PSENEN	2026	1	CTGTGCCGGAAGTACTACCT
PSENEN	2027	2	CCTGGAGCGAGTGTCCAATG
PSENEN	2028	3	ACAGAACAGAGCCAAATCAA
PSENEN	2029	4	TGAGCACTATCACCCAGAAG
PRKDC	2030	1	GTTCTCAGAAACGATCAACA
PRKDC	2031	2	CTCCATAATCCGGACCACAA
PRKDC	2032	3	GCACATCATCATGCACCGTG
PRKDC	2033	4	GCAACATCAGAATACTATGG
LDLR	2034	1	CTTAAGGTCATTGCAGACGT
LDLR	2035	2	CAGAGCACTGGAATTTCGTCA
LDLR	2036	3	GACAACGGCTCAGACGAGCA
LDLR	2037	4	ATGAACAGGATCCACCACGA
FGR	2038	1	CGAGTTGAACTGAACCCGTG
FGR	2039	2	AGGGGACTTCAGAAGCTACG
FGR	2040	3	AGCTTGATTGAGTCAACAG
FGR	2041	4	GTGACCGAGTTCATGTGTCA

DOT1L	2042	1	GGGAGCGAATCGCCAACACG
DOT1L	2043	2	GCTGGAGGACTCATCCAAGG
DOT1L	2044	3	GCAGCAGGTCTACAACCACT
DOT1L	2045	4	TCAGACCGTGTCTCAGACGG
DRD2	2046	1	TAGCGCGTATTGTACAGCAT
DRD2	2047	2	CCTGATCGTCAGCCTCGCAG
DRD2	2048	3	CTCTTCGGACTCAATAACGC
DRD2	2049	4	GTGGCATAGTAGTTGTAGTG
PRKCA	2050	1	GCTCCACACTAAATCCGCAG
PRKCA	2051	2	CCTTGACCGAGTGAAACTCA
PRKCA	2052	3	AGGAAGGAAACATGGAATC
PRKCA	2053	4	AGGTGGGGCTTCCGTAAGTG
LHCGR	2054	1	GTGGCTGGGGTAAGTCAACG
LHCGR	2055	2	GCACAATGGAGCCTTCCGTG
LHCGR	2056	3	CTTGTTTGGGAATCAACTG
LHCGR	2057	4	TAGCCCATAATATCTTCACA
ADORA3	2058	1	GATGCCCAGGCTGACAACAA
ADORA3	2059	2	ATGGCGCACATGACAACCAG
ADORA3	2060	3	GACATTTCTGTGGTACTCTG
ADORA3	2061	4	ATTGGACTCTGCGCCATAGT
TERT	2062	1	CACACGCTAGTGGACCCCGA
TERT	2063	2	GTGACACCACACAGAAACCA
TERT	2064	3	CTCACGCAGACGGTGCTCTG
TERT	2065	4	GGCCCGCACACGCAGCACGA
HDAC10	2066	1	AGTCAGATGCAGACGCAGTG
HDAC10	2067	2	AGGATTTGACTCAGCCATCG
HDAC10	2068	3	CCGCAGCCCTGGATCGCCTG
HDAC10	2069	4	GACAACGCCGGATATCACAT
PRKCB	2070	1	TGACGTGGAGTGCACATATGG
PRKCB	2071	2	CAGAGGGCCAAGATCAGTCA
PRKCB	2072	3	CTTGCTGGATGTGATACATG
PRKCB	2073	4	CCACAGTGGTCACAAAACGT
GNRH1	2074	1	GCAGTCCATAGGACCAAGTGC
GNRH1	2075	2	CCAATTCAAAACTCCTAGC
GNRH1	2076	3	GCGTGGTGCATTCTGAAGCGT
GNRH1	2077	4	CTACTGACTTGGTGCGTGGA
STAT3	2078	1	ACGCCGGTCTTGATGACGAG
STAT3	2079	2	GAGACCGAGGTGTATCACCA
STAT3	2080	3	AACATGGAAGAATCCAACAA
STAT3	2081	4	TCGGCCGGTGCTGTACAATG
FGFR2	2082	1	CTTAGTCCAAGTATCACGG
FGFR2	2083	2	TGTGTCTGTTCTAGCACTCG
FGFR2	2084	3	GCCGGCAAATGCCTCCACAG
FGFR2	2085	4	GATAGCCATTTACTGCATAG

LCK	2086	1	GACCCACTGGTTACCTACGA
LCK	2087	2	GCCGGGAAAAGTGATTCGAG
LCK	2088	3	CTACAACGGGCACACGAAGG
LCK	2089	4	GCTGGTTCGGCTCTACGCTG
FOLR3	2090	1	GAAGAAGAATGCCTGCTGCA
FOLR3	2091	2	TGGCTTTGGTGACTGCTGCG
FOLR3	2092	3	ACTCATACCTGCCGGATCCA
FOLR3	2093	4	AACTTTAACTGGGATCACTG
PORCN	2094	1	TGCCGACATTCTCCCATCG
PORCN	2095	2	GTGACATGGCACAAGATGCG
PORCN	2096	3	GGAGCTGCCTCGGTCAATGG
PORCN	2097	4	TAGCTGTGGAAGGATATCCA
APH1B	2098	1	GGTTTGAAGAGTATAAACCC
APH1B	2099	2	TCTTGCCATGAACCAAACAA
APH1B	2100	3	GAAGATGATACGCAACGGCT
APH1B	2101	4	TTGGGCTTTGGAATCATGAG
PARP2	2102	1	CATGCAATGAATTCTACACC
PARP2	2103	2	AATACCAAGAAAGCCCCACT
PARP2	2104	3	GGGGGCGCAAGGCACAATGT
PARP2	2105	4	TTGTTCAAGCAATCTCAACA
BCL2L2	2106	1	GTGTGCTGAGAGTGTCAACA
BCL2L2	2107	2	AGCCCAACAACGCTTCACCC
BCL2L2	2108	3	ACTTTGTAGGTTATAAGCTG
BCL2L2	2109	4	AGACAAAGAAGGCTACAAGG
CYP17A1	2110	1	CCATACGAACCGAATAGATG
CYP17A1	2111	2	ATCGCGTCCAACAACCGTAA
CYP17A1	2112	3	TATGGACTGTCCGTTGTGGG
CYP17A1	2113	4	CAATACCTCCTACAAGAATG
EIF4E	2114	1	AAAGCTTACCTGTTCTGTAG
EIF4E	2115	2	GAAGATGAGAAAAACAAACG
EIF4E	2116	3	TTCTCCTCTTCTGTAGTCGG
EIF4E	2117	4	AAACTTGGCAAGCAAACCTG
ESR1	2118	1	TCAGATAATCGACGCCAGGG
ESR1	2119	2	CTGACCGTAGACCTGCGCGT
ESR1	2120	3	TACTCGGAATAGAGTATCGG
ESR1	2121	4	TCCAGGTACACCTCGCCCAG
IDH2	2122	1	GTCCTTGAAACGCCCATCGT
IDH2	2123	2	CTTTAGCTGGATGTCCACGT
IDH2	2124	3	GGGCATGTACAACACCGACG
IDH2	2125	4	ACTTCGACAAGAATAAGATC
IDO1	2126	1	ATCCCAGAACTAGACGTGCA
IDO1	2127	2	ACCAGACCGTCTGATAGCTG
IDO1	2128	3	GATACTTACTCATAAGTCAG
IDO1	2129	4	AGAACGGGACACTTTGCTAA

NOTCH3	2130	1	CACGCTGTGTGATCGCAACG
NOTCH3	2131	2	GACACCGATGTCTCAATGGG
NOTCH3	2132	3	GGTTGGTGCAGATACCATGA
NOTCH3	2133	4	GACAGGACAGTCTGACAGCG
AKT2	2134	1	TCTCGTCTGGAGAATCCACG
AKT2	2135	2	GACCCCATGGACTACAAGTG
AKT2	2136	3	GGGGGGTAGAGTCTGATCAG
AKT2	2137	4	CTCTTGAGTACTTGCACTCG
AURKA	2138	1	CTTCGAATGACAGTAAGACA
AURKA	2139	2	CCATATAGAAAATAATCCTG
AURKA	2140	3	CCTGAAAACCTACCGAAGGT
AURKA	2141	4	TGCTTGCAAAGGAATGCGCT
PPP2CA	2142	1	AACGCATCACCATTCTTCGA
PPP2CA	2143	2	AAAAGAATCCAACGTGCAAG
PPP2CA	2144	3	AATAAAAGTCATACCTCATG
PPP2CA	2145	4	CTCGCCATCTATAGATACAC
DNMT1	2146	1	GATTTCTGATGAAAAAGACG
DNMT1	2147	2	GCTCTACTGGAGCGACGAGG
DNMT1	2148	3	GAGGCAAAAAGAAATCCCCA
DNMT1	2149	4	TCACCCAAAAAATGCACCA
NTRK1	2150	1	CCCTTTCGAGTTCAACCCCG
NTRK1	2151	2	GCGCAGACACCCGTGCCGCA
NTRK1	2152	3	AGGGCACAAGAACAGTGCAG
NTRK1	2153	4	CTGGAGCTCCGTGATCTGAG
IFNAR2	2154	1	TGAAAGTGATAGCGATACTG
IFNAR2	2155	2	TGAGTGGAGAAGCACACACG
IFNAR2	2156	3	CGTCATTGAAGAACAGTCAG
IFNAR2	2157	4	ATATCCATGGCTTCCAACGG
MAPK8	2158	1	TAGTGGATTTATGGTCTGTG
MAPK8	2159	2	AGAATCAGACTCATGCCAAG
MAPK8	2160	3	TGATATTAGATATTGATCAG
MAPK8	2161	4	AGAAACTGCAACCAACAGTA
SMO	2162	1	CAAGAACTACCGATACCGTG
SMO	2163	2	GATTCTTGATCTCACAGTCA
SMO	2164	3	CCACATTTCGTGGCTGACTGG
SMO	2165	4	CAAGTGTGAGAATGACCGGG
MAP3K8	2166	1	ATCAGTCAGATATGGAACTG
MAP3K8	2167	2	CTTCGGTCATTTGAACACTT
MAP3K8	2168	3	CCAGGGGATCAGGAGAACAT
MAP3K8	2169	4	TGACACATGGTCATTAGACT
TXN	2170	1	TACTTCAAGGAATATCACGT
TXN	2171	2	CACACTCTGAAGCAACATCC
TXN	2172	3	TAGTTGACTTCTCAGCCACG
TXN	2173	4	GGTGAAGCAGATCGAGAGCA

IDH1	2174	1	ATGTAGATCCAATTCCACGT
IDH1	2175	2	CCCATCCACTCACAAGCCGG
IDH1	2176	3	CAAGCTATGAAATCAGAGGG
IDH1	2177	4	TACCTTCAAAGTTATGTACC
GSK3A	2178	1	CCTCCCATAACTCTGACCGA
GSK3A	2179	2	GCCCCGAGACAGTGTACCGGG
GSK3A	2180	3	TCAGCCTCACAATATTGCAG
GSK3A	2181	4	AGGAGACATTGGGCTCCCCT
PSMB9	2182	1	GTAGATGCGCTCGTGCAGCG
PSMB9	2183	2	CCAGACCCATTACCCCGGTG
PSMB9	2184	3	TATCAGCTATAAATATCGAG
PSMB9	2185	4	TCCCAGGGTTCCATATACCT
CD19	2186	1	CTAGGTCCGAAACATTCCAC
CD19	2187	2	GGAAAGTATTATTGTCACCG
CD19	2188	3	ATGAAAAGCCAGATGGCCAG
CD19	2189	4	AAGATGAAGAATGCCACAA
ESR2	2190	1	CCAGTTATCACATCTGTATG
ESR2	2191	2	TCAGCCTGTTGACCAAGTG
ESR2	2192	3	CCCCAGTGCGCCCTTCACCG
ESR2	2193	4	AGCAGGGCTATAGAATGTCA
FLT3	2194	1	AAAGCTGTTTCATGTGAACCA
FLT3	2195	2	GGTGCTTTGCGATTACAGG
FLT3	2196	3	GTAACCAAAGCTGATTGACT
FLT3	2197	4	GGGGTCTCAACGCACACCCG
MAP2K2	2198	1	AAGCACCAGATCATGCACCG
MAP2K2	2199	2	ACGGCGAGTTGCATTTCGTGC
MAP2K2	2200	3	GGCCCATCCCCTACCAGCGA
MAP2K2	2201	4	GGATTCCCAGAGGAGATCCTG
PGF	2202	1	CGTGTCCGAGTACCCCAGCG
PGF	2203	2	CCAGCGCCCGGCAGTAGCTG
PGF	2204	3	TGGGAACGGCTCGTCAGAGG
PGF	2205	4	GCTCCTAAAGATCCGTTCTG
ADORA2A	2206	1	GCGGCGGCCGACATCGCAGT
ADORA2A	2207	2	TGGCTTGGTGACCGGCACGA
ADORA2A	2208	3	ATGCTAGGTTGGAACAACCTG
ADORA2A	2209	4	AAGCAGTTGATGATGTGTAG
CXCR1	2210	1	CAGAACAGCATGACAAACAG
CXCR1	2211	2	GAAATGACACAGCAAAATGG
CXCR1	2212	3	CAGGCTCAGCAGGAACACTA
CXCR1	2213	4	ACTGACCCAGAAGCGTCACT
AKT3	2214	1	CTGCACCATAGAAACGTGTG
AKT3	2215	2	ATTTTCATGTAGATACTCCAG
AKT3	2216	3	ACAAATTGATAATATAGGAG
AKT3	2217	4	TATTTGAAACTACTAGGTAA

DPP4	2218	1	GGATTCCAAACAACACACAG
DPP4	2219	2	CTGCTGTGTAGAGTATAGAG
DPP4	2220	3	CTACTTGTGTGATGTGACAT
DPP4	2221	4	GAATATAAAGGAATGCCAGG
RET	2222	1	CGGCACAGCTCGTCGCACAG
RET	2223	2	CTAGATCGGGAAAGTCTGTG
RET	2224	3	TGCCGAACTTCACTACATGG
RET	2225	4	CCCGGTGACCGTGTACGACG
CHEK2	2226	1	GGGCCCATATCGAGCCCAG
CHEK2	2227	2	AGGTAAAGCTGGCTTTTCGAG
CHEK2	2228	3	GCATACATAGAAGATCACAG
CHEK2	2229	4	AGAGCTGTTTGACAAAGTGG
NAE1	2230	1	TCAAAGAAGCAGTATCGGCA
NAE1	2231	2	TAGCTAAATATTTAGCACAG
NAE1	2232	3	CACAGCACTAAATACAACCTC
NAE1	2233	4	ATCATTATAAAGAACATCC
HSP90AA1	2234	1	GATCTGTCAAGCTTTCATAC
HSP90AA1	2235	2	TCTCACGGGATATGTTTAGA
HSP90AA1	2236	3	CAGTGAGGACAGACACAGGT
HSP90AA1	2237	4	GATCAAAAGGAGCACGTCGT
TYK2	2238	1	TGAATGACGTGGCATCACTG
TYK2	2239	2	CAGGCGGCCCTCATACACGT
TYK2	2240	3	AATACCTAGCCACACTCGAG
TYK2	2241	4	TTGGGCCTGAGCATCGAAGA
ABL2	2242	1	AACCTCTGTAATGACGACGG
ABL2	2243	2	TGTACACCATCACTCCACAG
ABL2	2244	3	TATCGAATGGAACAGCCTGA
ABL2	2245	4	GGTTCAACATCACAACCATA
FGF1	2246	1	TGAGCCGTATAAAGCCCGT
FGF1	2247	2	CTCCTCTACTGTAGCAACGG
FGF1	2248	3	TTCCTGAGGATCCTTCCGGA
FGF1	2249	4	AGAAGTTTAATCTGCCTCCA
ERBB3	2250	1	ATGAGGCGATACTTGGAACG
ERBB3	2251	2	TGTCGAAATTATAGCCGAGG
ERBB3	2252	3	ATCATGTGAGACAACACCGG
ERBB3	2253	4	ACCATTGCCCAACCTCCGCG
NTRK2	2254	1	TGAATGGAATGCACCAGTGG
NTRK2	2255	2	ACGTCACTGATAAAACCGGT
NTRK2	2256	3	AACCTGCAGATACCCAATTG
NTRK2	2257	4	TTGGTGATGCCAAAGTACTG
HDAC3	2258	1	TCATCAATGCCATCCCGCAG
HDAC3	2259	2	ACCTGGAGCACAATGCACGT
HDAC3	2260	3	TGGGTCAATGCCAGGCGATG
HDAC3	2261	4	GTCAGCCCCACCAATATGCA

B4GALNT1	2262	1	CCCGTAGCCGATCATAACGG
B4GALNT1	2263	2	GGATCAAGGAGCAAGTAGTG
B4GALNT1	2264	3	TGGAGTTACTCTCACTGGAG
B4GALNT1	2265	4	GCGCGTTAGTGGCCCCTACG
RBM39	2266	1	TGGCGGCAAGAATTCGACCA
RBM39	2267	2	TTGGCACGCCTAAACTCGT
RBM39	2268	3	GGACCTATGAGGCTTTATGT
RBM39	2269	4	AAATTTAACAGTGCCATCCG
HDAC1	2270	1	CATCCGTCCAGATAACATGT
HDAC1	2271	2	TGAGTCATGCGGATTCGGTG
HDAC1	2272	3	GCACCGGGCAACGTTACGAA
HDAC1	2273	4	GGAGATGTTCCAGCCTAGTG
IL6R	2274	1	TGGAAACTATTCATGCTACC
IL6R	2275	2	ACTCACAAACAACATTGCTG
IL6R	2276	3	CCGTGGCCAGAAACCCCCGC
IL6R	2277	4	CCTGAGCACCCAGTGAACAG
BAX	2278	1	TCGGAAAAAGACCTCTCGGG
BAX	2279	2	GTTTCATCCAGGATCGAGCA
BAX	2280	3	AGTAGAAAAGGGCGACAACC
BAX	2281	4	GGACGAACTGGACAGTAACA
TOP1	2282	1	CGACCATGAATATACTACCA
TOP1	2283	2	TGGAAGAGGCTCATATGGTG
TOP1	2284	3	ACTCACTCATCCTCATCTCG
TOP1	2285	4	CAAACATAAAGACAGAGACA
EGFR	2286	1	TGTCACCACATAATTACCTG
EGFR	2287	2	GTGGAGCCTCTTACACCCAG
EGFR	2288	3	GTCTGCGTACTTCCAGACCA
EGFR	2289	4	TCTTGCCGGAATGTCAGCCG
RAD50	2290	1	CTAGGAACGTGAGTTAAGCA
RAD50	2291	2	AAGCGGCGTGATGAAATGCT
RAD50	2292	3	AAACAGCACAAGTTAGACAC
RAD50	2293	4	AAAACTGCCAACCAACTGA
BLK	2294	1	CAGGTCCCAGTATTTCATAG
BLK	2295	2	GCTGGTCCGACTCTACGCAG
BLK	2296	3	GCTTCTTGCTCCAATCAACA
BLK	2297	4	ACTCGGGCCACAAAGTTACT
GSK3B	2298	1	ATACCTTGACATAAATCACA
GSK3B	2299	2	CAGTATCAGGATCCAACAAG
GSK3B	2300	3	GTGGCTCCAAAGATCAACTC
GSK3B	2301	4	AGGTCCTGGGAACCTCCAACA
MAPK3	2302	1	GCAGTTGCAGTACATCGGCG
MAPK3	2303	2	AGTAGGTCTGATGTTTCAAG
MAPK3	2304	3	TTCCGCCATGAGAATGTCAT
MAPK3	2305	4	TGGAGGGCTTTAGATCTCGG

MUC5AC	2306	1	GAAGCCGGGAACCTACTACT
MUC5AC	2307	2	CAAGATGTGCCTCAACTACG
MUC5AC	2308	3	CCGTTAATGACTTTGCCACG
MUC5AC	2309	4	GAGGTGAGCATTGAACACCT
NBN	2310	1	TTCCCGAACTTTGAAGTCGG
NBN	2311	2	AGAATGCACTCACCTTGTCA
NBN	2312	3	CCAGGACCAAGCCTTTCACA
NBN	2313	4	AGCAGCCTCCACAAATTGAA
DDR2	2314	1	CCGTGACAAACCGAGCACTG
DDR2	2315	2	GGGCTAGGCCAATTGACCGA
DDR2	2316	3	GTAATTGATCTTGTACATGG
DDR2	2317	4	AAGTTGATGACAGCAACACT
NOTCH2	2318	1	TTGATGTCCATCTCACAACG
NOTCH2	2319	2	CTGGGGACACACATCGACGA
NOTCH2	2320	3	TTGTTGATATAATCCCAGCA
NOTCH2	2321	4	CATTGGTGGATACAGATGCG
VDR	2322	1	ACAGCTCTAGGGTCACAGAA
VDR	2323	2	CCACACACCCACAGATCCG
VDR	2324	3	CTGCCGGCTCAAACGCTGTG
VDR	2325	4	CCATCATTACACGAACTGG
BMX	2326	1	GGTTAGAAATTCGAGCCAAG
BMX	2327	2	GGGAAGACTTCCCTGACTGG
BMX	2328	3	TGTTGGCCTTTGTTGACACA
BMX	2329	4	GGGGTTACCCCTTATCTCTG
ABL1	2330	1	TCAGTGATGATATAGAACGG
ABL1	2331	2	GGTTCATCATCATTCAACGG
ABL1	2332	3	TTGCTCCCTCGAAAAGAGCG
ABL1	2333	4	CTTAGGCTATAATCACAATG
ANGPT1	2334	1	TTGCAATATGGATGTCAATG
ANGPT1	2335	2	GCAGCTTGAGAATTACATTG
ANGPT1	2336	3	AGATATAACCGGATTCAACA
ANGPT1	2337	4	GCAGAGAGATGCTCCACACG
CRTC2	2338	1	AGGGCCACTTACCCCCACGT
CRTC2	2339	2	CTTCGCCAGCTAGACTCTGG
CRTC2	2340	3	GAGGTTGGGATTGCTTAGGG
CRTC2	2341	4	CCACCTGCCATGAACACGGG
CRBN	2342	1	ACCAATGTTTCATATAAATGG
CRBN	2343	2	CTGACTGTGTTCTTAGCTCA
CRBN	2344	3	TGTATGTGATGTCGGCAGAC
CRBN	2345	4	TGAAGAGGTAATGTCTGTCC
IL1B	2346	1	CTTCGACACATGGGATAACG
IL1B	2347	2	GGTGGTCGGAGATTCGTAGC
IL1B	2348	3	CATGGCCACAACAACCTGACG
IL1B	2349	4	CTGAAAGCTCTCCACCTCCA

TNFSF11	2350	1	ACCCCGATCATGGTACCAAG
TNFSF11	2351	2	ATTCTATTAGGATCCATCTG
TNFSF11	2352	3	CATGAGCCATCCACCATCGC
TNFSF11	2353	4	GGAGGGCCACGAACATGGAG
FZD8	2354	1	CGGCGGTGGTTAGGTCGGTG
FZD8	2355	2	GGCCTGCTACCTCTTCGTGT
FZD8	2356	3	TAGCCGATGCCCTTACACAG
FZD8	2357	4	ACACGCTCACCATAGGCGCG
TGFBR1	2358	1	AGAACGTTCTGTGGTTCCGTG
TGFBR1	2359	2	TAAAAGGGCGATCTAATGAA
TGFBR1	2360	3	GTTGTGTATAACTTTGTCTG
TGFBR1	2361	4	ATGGGCAAGACCGCTCGCCG
FGF2	2362	1	TCTCCCGGACCCCGTCAACT
FGF2	2363	2	GCCACTTCAAGGACCCCAAG
FGF2	2364	3	GGGTGCCAGATTAGCGGACG
FGF2	2365	4	TTCACGGATGGGTGTCTCCG
DYRK4	2366	1	TTGGATGTACGTGTATACTG
DYRK4	2367	2	CAAAGACAACACCTACAATG
DYRK4	2368	3	CTCCAGAACTTCATAGCGGT
DYRK4	2369	4	TGAAGCCAAGAAGCTCGACA
IL2RA	2370	1	GGATACAGGGCTCTACACAG
IL2RA	2371	2	TGGCTTTGAATGTGGCGTGT
IL2RA	2372	3	TTGTTTCGTTGTGTTCCGAG
IL2RA	2373	4	CTGCAGGGAACCTCCACCAT
ARAF	2374	1	GCCCAACAAGCAACGCACGG
ARAF	2375	2	GTAGTGATGGAACCCCCCGG
ARAF	2376	3	TGGTCTACCGACTCATCAAG
ARAF	2377	4	AGTGTCCAGGATTTGTCCGG
MAPK14	2378	1	TGATGAAATGACAGGCTACG
MAPK14	2379	2	CACAAAAACGGGGTTACGTG
MAPK14	2380	3	AAGTAACCGCAGTTCTCTGT
MAPK14	2381	4	CAAGGCGAGTAATACCTGTC
CSF1R	2382	1	ACGCTACCTTCCAAAACACG
CSF1R	2383	2	GTTGGAAATCTACTTGATCG
CSF1R	2384	3	GCTGCCTTACAACGAGAAGT
CSF1R	2385	4	GCTTGCTAATGCTACCACCA
ROCK2	2386	1	TGTTTAGGGAGGTACGACTT
ROCK2	2387	2	ACCGGATTATATATCACCTG
ROCK2	2388	3	AGCTGAACATAAGGCCACAA
ROCK2	2389	4	TAGTAGGTAAATCCGATGAA
PRMT5	2390	1	GGAGAAAAACCCAAATGCCG
PRMT5	2391	2	GGTACTGAGAGTATTTGATG
PRMT5	2392	3	GAAGATTTCGAGGAACTCCG
PRMT5	2393	4	TGCACCAACTACACACACAG

FGFR3	2394	1	CATCCGGCAGACGTACACGC
FGFR3	2395	2	GGTGCTGAATGCCTCCCACG
FGFR3	2396	3	AAGAACGGCAGGGAGTTCCG
FGFR3	2397	4	CCCGAGACAGCTCCCATTG
CSNK2A2	2398	1	AGTTTACCTGATAGTCCACG
CSNK2A2	2399	2	TGATATTTGTTCCACCACGA
CSNK2A2	2400	3	TAGCAAGCATGATCTTTCGA
CSNK2A2	2401	4	TGTGCATGATTCCCTTGCTG
SIRT1	2402	1	CTCTGAGCCATACCTATCCG
SIRT1	2403	2	GCGGCGGCGATTGGGTACCG
SIRT1	2404	3	TCTGGTTTCATGATAGCAAG
SIRT1	2405	4	ATAGCCTTGTCAGATAAGGA
FGFR1	2406	1	GTTGCCCCGCCAACAAAACAG
FGFR1	2407	2	CTGGTCTTAGGCAAACCCCT
FGFR1	2408	3	AGTTCAAATGCCCTTCCAGT
FGFR1	2409	4	ACAGTGTGTACCTTCCAGAA
FRK	2410	1	CTATATTCCTTCTAACTACG
FRK	2411	2	AGTTGCGGTCTATCTCCCAT
FRK	2412	3	GCAGTGAAAACATTAACC
FRK	2413	4	CACTACACCAAGACAAGTGA
NAMPT	2414	1	GGGATGGAACATCTTCTTG
NAMPT	2415	2	CTGTTCCAGCAGCAGAACAC
NAMPT	2416	3	AATAGTATCAAGAAGTACAC
NAMPT	2417	4	CAGAGGAGTCTCTTCCAAG
ERBB2	2418	1	AACTACCTTTCTACGGACGT
ERBB2	2419	2	TTGGGATCCTCATCAAGCGA
ERBB2	2420	3	TCATCGCTCACAACCAAGTG
ERBB2	2421	4	GTTACCTATACATCTCAGCA
CHD1	2422	1	TTAATTCGCCTAAGAGAACG
CHD1	2423	2	TTCCGATGACTCATCAAGTG
CHD1	2424	3	AAGCAGCCATCCTATATTGG
CHD1	2425	4	ATGCCCAATTTAGACCTCCA
CD38	2426	1	TCTGGCCCATCAGTTCACAC
CD38	2427	2	TCAGACCGTACCTTGCAACA
CD38	2428	3	CTTGACGCATCGCGCCAGGA
CD38	2429	4	TCGCGGTGGTCGTCCCAGAG
EPHA2	2430	1	GAAGCCCCTGAAGACATACG
EPHA2	2431	2	CACACACCCGTATGGCAAAG
EPHA2	2432	3	TCACGGAGAAACCCTCGGTG
EPHA2	2433	4	CTGGTGCGGGTCAGTCCGTG
TLR7	2434	1	AATGGGGCATTATAACAACG
TLR7	2435	2	CAGCTACTAGAGATACCGCA
TLR7	2436	3	CAGTCTGTGAAAGGACGCTG
TLR7	2437	4	GAAGATTATGTAATGGCGAG

PRKCE	2438	1	GCACCGCTTGTGGACCACGC
PRKCE	2439	2	GCCTTGTCATTGACAACCG
PRKCE	2440	3	CCACGTTGGTCTCACATCGA
PRKCE	2441	4	ATGTGATCATCGATCTCTCA
EPHB4	2442	1	GTGCCCCGGAAGTACCCGACG
EPHB4	2443	2	CTTCCGGGTGAGATGCTCCG
EPHB4	2444	3	CTGCACGTCACACACTTCGT
EPHB4	2445	4	TGTCTGACATCCGGGTGACG
TNFSF13B	2446	1	GCTGTCTTGCTGCCTCACGG
TNFSF13B	2447	2	CAAACCTCACTTTCAGTCCCG
TNFSF13B	2448	3	TGTTTCCATCCTCCCACGGA
TNFSF13B	2449	4	TGGCTTCTCAGCTTTAAAAG
PSMB5	2450	1	TTTGTACTGATACACCATGT
PSMB5	2451	2	GCTTCATGGAACAACCACCC
PSMB5	2452	3	CCGCTACCGGTGAACCAGCG
PSMB5	2453	4	ATCTGTGGCTGGGATAAGAG
TNF	2454	1	TTGGAGTGATCGGCCCCCAG
TNF	2455	2	AGAGCTCTTACCTACAACAT
TNF	2456	3	GGAGCTGAGAGATAACCAGC
TNF	2457	4	GAGACACTTACTGACTGCCT
NOTCH4	2458	1	ACACCCCTCCATTAACACAT
NOTCH4	2459	2	GCTGCCATTGTATAGGCATG
NOTCH4	2460	3	TGTGTCAGCCTGGCTATTCG
NOTCH4	2461	4	GGAGGCCTCTGTGTCGACAG
FCGR1A	2462	1	CTGGGAGCAGCTCTACACAG
FCGR1A	2463	2	ATGGGCAGCAAGACCCTGCG
FCGR1A	2464	3	TGTGACATCCCCACTCCTGG
FCGR1A	2465	4	TCCAGCAGAGTCTTCACGGA
TUBB1	2466	1	GCTGATCGAGAATGTCCTAG
TUBB1	2467	2	GCTGACGACACCCACCTATG
TUBB1	2468	3	TGTGGTGGAGCCCTACAACG
TUBB1	2469	4	GCTCATGAACAAGATTAGAG
CCND3	2470	1	CACTGGAAGTAGGAGGCGCG
CCND3	2471	2	ACCAAGGCCTGTCGGTCACG
CCND3	2472	3	ACACACGCACCCGCAACTGG
CCND3	2473	4	CATGTGCAATCACAGCAGCC
SIK1	2474	1	ATGGTCGTGACAGTACTCCA
SIK1	2475	2	GCATCGAGTCACCAAAACGC
SIK1	2476	3	CCGGGGACACTTACATGGCG
SIK1	2477	4	CCCCTCAAAGACTTCCGGGG
PIK3CB	2478	1	AAAAATGCGCAAATTCAGCG
PIK3CB	2479	2	TGTAGCGTGGGTAAATACGA
PIK3CB	2480	3	AAAGAGCACTTGGAATCGG
PIK3CB	2481	4	TAAAACCATCGTAAGCTCAG

HDAC5	2482	1	ACGTTACACCCGTCAGTAGTG
HDAC5	2483	2	TATGCCCTGTACTTACAGTG
HDAC5	2484	3	GCCGGGTGCGCTGTTACACA
HDAC5	2485	4	AGGCCTGCTTAGCAAGTGCG
S1PR1	2486	1	GTCCGGCATTACAACACTACAC
S1PR1	2487	2	ACAAGCTCACTCCCGCCCAG
S1PR1	2488	3	TCTGCAGTACAGAATGACGA
S1PR1	2489	4	CAATAAAATAGTACATGGGT
PRKCI	2490	1	TCAGAATCCATCTACCGTAG
PRKCI	2491	2	TGTCTCGAACCTCATTGCAA
PRKCI	2492	3	ATCTGCACAGACCGAATATG
PRKCI	2493	4	AGCAAGAATGCAGCCCAACA
RPL3	2494	1	GGCTACGTGGAACCCCTCG
RPL3	2495	2	TGAGATGATCGACGTCATCG
RPL3	2496	3	CCGTGTCATTGCCCACACCC
RPL3	2497	4	CCACCGAGGCCTGCGCAAGG
PSMD2	2498	1	AGCCCACTAGCCGATACTTG
PSMD2	2499	2	GATGCTCGTGGAACGACTAG
PSMD2	2500	3	GGAAATCGTCCCCTATAACA
PSMD2	2501	4	CCTGTGGAATGATAGCAGTA
HDAC6	2502	1	TGTGCTGAGTTCCATTACCG
HDAC6	2503	2	AGGACACGCAGCGATCTAGG
HDAC6	2504	3	GCTTCCAGTGCTGAGTACGT
HDAC6	2505	4	CCTCTAGGATAAGGATAATG
RRM1	2506	1	CTTGTACCCCAATTCCAATG
RRM1	2507	2	CCTACCTAGAAAGTTGTGGG
RRM1	2508	3	TGGCAAACACTCTCCCATGG
RRM1	2509	4	GGATCTCTTCATGAAACGAG
CSNK2A1	2510	1	CTAGTTGGTGAGGATAGCCA
CSNK2A1	2511	2	AGTCACATGTGGTGGAATGG
CSNK2A1	2512	3	AGACATTGTAAAAGACCCTG
CSNK2A1	2513	4	GATTGATCATGAGCACAGAA
HCK	2514	1	ATCCGGACCCTGGACAACGG
HCK	2515	2	AATGGCCTCGTAATCATACA
HCK	2516	3	ATGTATTGCCTCCGACCTGG
HCK	2517	4	CCAGCTTGAGGGATTCCCGA
HDAC4	2518	1	CTTACCCGTACCAGTAGCGA
HDAC4	2519	2	GCATCAGCGTGTATACACG
HDAC4	2520	3	GGGGCTGACTTACCGCAGAG
HDAC4	2521	4	GGAGCCCATTGAGAGCGATG
RXRG	2522	1	TGTGTTTAACCAGAGATCCG
RXRG	2523	2	GAGGCAGAATGTGCTACCAG
RXRG	2524	3	TACGCTTGCCCATTC AACG
RXRG	2525	4	CTTCAAGAGGACGATAAGGA

RARB	2526	1	AAGCAGGGTTTGTACACTCG
RARB	2527	2	GTGGATTGACCCAAACCGAA
RARB	2528	3	AAGGCCGTCTGAGAAAGTCA
RARB	2529	4	GTGTTATTAATAAAGTCACC
KRAS	2530	1	AAGAGGAGTACAGTGCAATG
KRAS	2531	2	AGATATTCACCATTATAGGT
KRAS	2532	3	CTGAATTAGCTGTATCGTCA
KRAS	2533	4	GATGTACCTATGGTCCTAGT
TGFB1	2534	1	GGTTTCCACCATTAGCACGC
TGFB1	2535	2	TTGATGTCACCGGAGTTGTG
TGFB1	2536	3	GGTGAAGCGGAAGCGCATCG
TGFB1	2537	4	GAATGGTGGCCAGGTCACCT
INHBC	2538	1	TCTCACTTTCAAGGTCCAAG
INHBC	2539	2	CAGAGCTCAGTCATCCTGGG
INHBC	2540	3	AAGACGAGTCTGGTTGATGG
INHBC	2541	4	ACCTCCACGGGGTCCCACAG
CD274	2542	1	GGTTCCCAAGGACCTATATG
CD274	2543	2	ACTGCTTGTCCAGATGACTT
CD274	2544	3	ACATGTCAGTTCATGTTTCA
CD274	2545	4	CACCACCAATTCCAAGAGAG
KDM1A	2546	1	TGGAATAGCAGAGACTCCGG
KDM1A	2547	2	CTAAATAACTGTGAACTCGG
KDM1A	2548	3	TTTCTGAAACAGGATCGTGT
KDM1A	2549	4	TGAGAAGTCATCCGGTCATG
XPO1	2550	1	AGTGAGCTCTCAAAAAACGT
XPO1	2551	2	TAGTCGAATGGCTAAACCAG
XPO1	2552	3	TCTCAGGGAAACTCTTATGG
XPO1	2553	4	TCACACCAGCAATCTCAGTG
PIK3CG	2554	1	ACTTAACCCTCTCACAGCAG
PIK3CG	2555	2	TGGCGGCGGACTTCTACCAC
PIK3CG	2556	3	GAGAATACGTCCTCCACATG
PIK3CG	2557	4	TTGCCTCTACAAAAACTGTG
IL6ST	2558	1	TGAGTTGCATTGTGAACGAG
IL6ST	2559	2	TCTTAAATAGGTGCGATGCA
IL6ST	2560	3	AAACGAAGCTGTCTTAGAGT
IL6ST	2561	4	GATCTGATGTAACCTTCCCA
TYMS	2562	1	ATGTGCGCTTGGAATCCAAG
TYMS	2563	2	TCTACAGATTATTCAGGACA
TYMS	2564	3	TTCCAAGGGAGTGAAAATCT
TYMS	2565	4	ACCAAACGTGTGTTCTGGAA
ACPP (ACP3)	2566	1	ACTCCTTGGCTAGTACACTT
ACPP (ACP3)	2567	2	AAAGGCAGGTATAGCAACTG
ACPP (ACP3)	2568	3	CTACGACCCTTTATATTGTG
ACPP (ACP3)	2569	4	GCCATGAGGATTCTTTATG

PIM3	2570	1	GCTCCGTGATAAAGTCGAAG
PIM3	2571	2	GGCTTCGGCACGGTCTACGC
PIM3	2572	3	GACTGGTTCGAGCGGCCGA
PIM3	2573	4	ACGGTCTACACCGACTTCGA
MAP1A	2574	1	CAGGCTGCTTAGGAATAACG
MAP1A	2575	2	TGGAACAGGACACATACTGG
MAP1A	2576	3	ACACAAAGACCGTTGGCCAG
MAP1A	2577	4	TGTTGAACATAAGGCTCCGG
DYRK1B	2578	1	AGGCTCGCAAGTACTTTGAA
DYRK1B	2579	2	GATGAAGTACTATATAGGTG
DYRK1B	2580	3	CACAGAGAGCTTACGCAGCG
DYRK1B	2581	4	CATGACTACATCGTGCGCAG
BCL2L1	2582	1	CAGGCGACGAGTTTGAAGT
BCL2L1	2583	2	GACCCAGTTTACCCCATCC
BCL2L1	2584	3	CAGTGGCTCCATTCACCGCG
BCL2L1	2585	4	CTCCGATTCAAGTCCCTTCTG
FLT1	2586	1	ACAGCCACAGTCCGGCACGT
FLT1	2587	2	AGGTTGAGGGATACCATATG
FLT1	2588	3	CTTACCATATATATGCACTG
FLT1	2589	4	TGGCCACTGTGTGATCACTG
PSMB2	2590	1	GAGGAGGTTACATGATATG
PSMB2	2591	2	TTTATAAGATGCGAAATGGT
PSMB2	2592	3	AAGATATTACTCCTGTGTGT
PSMB2	2593	4	AGGGCCAGCGCTGTATTACA
CCND2	2594	1	ATGTGCTCAATGAAGTCATG
CCND2	2595	2	TGAAGGTCTGAGCATGCTTG
CCND2	2596	3	ACTCCATTATAGGTCTGTG
CCND2	2597	4	CACTTGAAGTAGGAGCACTG
CDK6	2598	1	GCCCCGCACTTGAAGAACGG
CDK6	2599	2	AACACTCCAGAGATCCACGG
CDK6	2600	3	TGGCTCACCTGACCACGTTG
CDK6	2601	4	CATTGCAGGTCGTCACGCTG
KDR	2602	1	TAATGTACACGACTCCATGT
KDR	2603	2	CCAATCACACAATTAAAGCG
KDR	2604	3	CAGCCTCTGCCAATCCATGT
KDR	2605	4	CAAGAACTGAATAAATGTG
BRD4	2606	1	AGTCGATTTCAATCTCGTCG
BRD4	2607	2	AGTCGAAGTGTCACTGTCCG
BRD4	2608	3	CCAGACCCCTGTCATGACAG
BRD4	2609	4	CACCAAACCTCTGAGCATCA
CCND1	2610	1	GTGTTCAATGAAATCGTGCG
CCND1	2611	2	GGTTGGCATCGGGGTACGCG
CCND1	2612	3	CGTGCCTCCGTAGGTCTGCG
CCND1	2613	4	AGAGGCCACGAACATGCAAG

LAP3	2614	1	CTCCACCGCAGACATGACGA
LAP3	2615	2	AAGTGCTAGTAGTAAAACCG
LAP3	2616	3	TGTCGGCAAAGCTCTATGGA
LAP3	2617	4	GACCTCATGAGGGCTGACAT
PSMB8	2618	1	CCAGAGCTCGCTTTACCCCG
PSMB8	2619	2	AAGGAACGTTTCAAGTTGAGA
PSMB8	2620	3	ACTAATGTAGGACCCAGCTG
PSMB8	2621	4	TGGAGAACGTATTTCAAGTGT
EZH2	2622	1	ATGTTGGGGGTACATTCAGG
EZH2	2623	2	TTATCAGAAGGAAATTTCCG
EZH2	2624	3	TTATGATGGGAAAGTACACG
EZH2	2625	4	CTTCTGTGAGCTCATTGCGC
HPRT1	2626	1	AATAAATCAAGGTCATAACC
HPRT1	2627	2	CTGTCCATAATTAGTCCATG
HPRT1	2628	3	ACTAGAATGACCAGTCAACA
HPRT1	2629	4	CACAGAGGGCTACAATGTGA
NPEPPS	2630	1	GTGATAGGGACCATCCACTG
NPEPPS	2631	2	GTCCGTGTTTACACTCCTGT
NPEPPS	2632	3	GAAAGTTTAGAAAATGCTAG
NPEPPS	2633	4	GCAAAGGCTGTAGTTGATGG
CDK4	2634	1	CCAGATGGCACTTACACCCG
CDK4	2635	2	AGTGTGAGAGTCCCCAATGG
CDK4	2636	3	GTCCACATATGCAACACCTG
CDK4	2637	4	GTCTACATGCTCAAACACCA
FYN	2638	1	ACGGGGACCTTGCGTACGAG
FYN	2639	2	TGGATACTACATTACCACCC
FYN	2640	3	GTCCCCCGAATCATTCTTG
FYN	2641	4	TTGTCCTTTGGAAACCCAAG
RPS6KB1	2642	1	CTCTTAGCCCCCATTCACTG
RPS6KB1	2643	2	AATGAAAGCATGGACCATGG
RPS6KB1	2644	3	CTTCGGGTACTTGGTAAAGG
RPS6KB1	2645	4	AGCAGAACGGAATATTCTGG
CRTC1	2646	1	TGTCAGTGGACAAACACGGA
CRTC1	2647	2	AAATCCCAGTACCTGCAACT
CRTC1	2648	3	GGTACCGTGACTGCAAGCGG
CRTC1	2649	4	GCGGCCAACCTGACGCACCT
PTK2	2650	1	TCTGATGATAAATGACTGCG
PTK2	2651	2	ATGTGGGAGATACTGATGCA
PTK2	2652	3	ACTTAAAGCTCAGCTCAGGT
PTK2	2653	4	AGAGCAAAAGATTTGTACAC
FNTA	2654	1	TCACAAACCCGTCGTCCATG
FNTA	2655	2	ATGCAGCCAATTATACAGTG
FNTA	2656	3	ATAGGCGAGTATTAGTGGA
FNTA	2657	4	TGTGGACCAACTTCTGAAAG

RARA	2658	1	GTGTAGCTCTCAGAGCACTC
RARA	2659	2	CTTCAAAGCACTTCTGCAGT
RARA	2660	3	AGAGTCCACCCAGCATAGGG
RARA	2661	4	AAGCAAGGCTTGTAGATGCG
PRLR	2662	1	CCATGAATGATACAACCGTG
PRLR	2663	2	TGTCCAGACTACATAACCGG
PRLR	2664	3	AAGACAGAAAACCTACCTG
PRLR	2665	4	AATGGACTGACATTAGATGC
ALK	2666	1	CCATACCTTAAATACGTAGG
ALK	2667	2	CTGTAGCACTTTCAGAAGCG
ALK	2668	3	TCCAGACAACCCATTTCGAG
ALK	2669	4	CTCTATTGCAGTTAGCGGAG
CXCR4	2670	1	TGACATGGACTGCCTTGCAT
CXCR4	2671	2	TCTTCTGGTAACCCATGACC
CXCR4	2672	3	CATCTTTGCCAACGTCAGTG
CXCR4	2673	4	ACACCGAGGAAATGGGCTCA
RICTOR	2674	1	GGCATAGTCGCAACATCTG
RICTOR	2675	2	TCTCCAAGGTGGGATAACGC
RICTOR	2676	3	GTGCCAAATAATTATCCATG
RICTOR	2677	4	TGTATAGGCAGGTAGACGTG
MDM2	2678	1	GAGAACATTACCGGATTCTGA
MDM2	2679	2	TACCATGATCTACAGGAACT
MDM2	2680	3	AGACACTTATACTATGAAAG
MDM2	2681	4	CAACATCTGTTGCAATGTGA
SHH	2682	1	CTCACCCGCAGAGAACTCGG
SHH	2683	2	AGTGGCCAGGAGTGAAACTG
SHH	2684	3	GCGCCAGCGGAAGGTATGAA
SHH	2685	4	TGTGGCGCCGCACAACGACT
SSTR5	2686	1	AGGCGGTGACAACAGGACGC
SSTR5	2687	2	ACGTCCGCGAACACCAGGAG
SSTR5	2688	3	GAAGGACGCGCGTTCTGCG
SSTR5	2689	4	GAGAATGTAGATGTTGGTGA
TUBE1	2690	1	ATTTGCTCCTCAACCTAACG
TUBE1	2691	2	ACTTTCCAGAATTCACCATG
TUBE1	2692	3	ACATCTGTCAAGTGTATACAG
TUBE1	2693	4	TTTATAATACATTCCATGGG
KIT	2694	1	TCAGACTTAATAGTCCGCGT
KIT	2695	2	GAAAGAAGACAACGACACGC
KIT	2696	3	GAATGGCATGCTCCAATGTG
KIT	2697	4	TCTAGTGCATTCAAGCACAA
AGXT	2698	1	GCTGCTGTTCTTAACCCACG
AGXT	2699	2	CCCCTTTACATGGACCGGCA
AGXT	2700	3	CCGATGACCAAGGACCCTGG
AGXT	2701	4	GTCAGTGAAGGAGATGAGCG

NOTCH1	2702	1	TGCAGGTCAGTACTGTACCG
NOTCH1	2703	2	TCCTGCCAGAACACCCACGG
NOTCH1	2704	3	TCGCACGCCTCCTCGATCAG
NOTCH1	2705	4	TTGACGTCGATCTCGCATCG
YES1	2706	1	CTAGTCGCAAAGATTCTCGA
YES1	2707	2	TCCAAAAGGCGTTACCCCTG
YES1	2708	3	AAATTGGTGAAACACTACAC
YES1	2709	4	AGAGAGAGTGAAACAATAA
CYP19A1	2710	1	TGATAGCAGAAAAAAGACGC
CYP19A1	2711	2	CAGCATGACACGACGCAGAA
CYP19A1	2712	3	GAGGGCACATCCTCAATACC
CYP19A1	2713	4	GCATGAATTCTCCATATACC
TEK	2714	1	TGGCACAGGAACACCCATAG
TEK	2715	2	AGACCACTCTAAATTTGACC
TEK	2716	3	GCCTGAAACAGCATAACCAGG
TEK	2717	4	TACTCGGCCAGGTATATAGG
TNFRSF8	2718	1	GTGTCCCTTAGACGACCTCG
TNFRSF8	2719	2	AGCTGCTTCTAACTGACGA
TNFRSF8	2720	3	ATCCAGAACGGGCTTCCCCG
TNFRSF8	2721	4	GATGTGGCACAGATCATGCC
HSPB1	2722	1	TGCCGGAGGAGTGGTCGCAG
HSPB1	2723	2	CTCGGAGATCCGGCACACTG
HSPB1	2724	3	TGGTCGAAGAGGCGGCTATG
HSPB1	2725	4	CACTGCGGGGCTCTCGATGG
WEE1	2726	1	TCATCAACAGAGCCCGCAA
WEE1	2727	2	CCATGAAGAGAGAACTACCC
WEE1	2728	3	CCAGGAGATGCGTCGCCGCG
WEE1	2729	4	TCTACGACGACACTGTCCTG
RXRB	2730	1	GGACAACAAAGACTGCACAG
RXRB	2731	2	ACGGCTATGTGCAATCTGCG
RXRB	2732	3	GCCCTGGCTGGATCCCGCAG
RXRB	2733	4	GTGGCTTCACATCTTCAGGG
INHBE	2734	1	GCACAGTTACTGGACAACCG
INHBE	2735	2	CTCACCCCTCAAGCCACTAG
INHBE	2736	3	GGGCACTGGTGCGAGCACAG
INHBE	2737	4	CCCTCCGGAGACTACAGCCA
AURKB	2738	1	ATTCTAGAGTATGCCCCCG
AURKB	2739	2	TCTTTCCGGAGGACTCGCTG
AURKB	2740	3	CATCAACCCATACTGCAGGT
AURKB	2741	4	TGACGAGCAGCGAACAGCCA
AKT1	2742	1	GAAGGTGCGTTCGATGACAG
AKT1	2743	2	CCTGCACTCGGAGAAGAACG
AKT1	2744	3	TGTTGAGGGGAGCCTCACGT
AKT1	2745	4	TGTCATGGAGTACGCCAACG

LYN	2746	1	TGAAAGACAAGTCGTCCGGG
LYN	2747	2	GCTCGTGAGGCTCTACGCTG
LYN	2748	3	TTACTATAACAACAGTACCA
LYN	2749	4	TAATAACATCACCATGCACA
SSTR2	2750	1	GGAGCCCACTCGGATTCCAG
SSTR2	2751	2	CATCGACCGATACCTGGCTG
SSTR2	2752	3	TGGTCTTCATCTTGGCATAG
SSTR2	2753	4	AGCCCAGCATATATCATGAT
MAPK9	2754	1	AGTACCGTGTCAACACGTAA
MAPK9	2755	2	CCGGGAACAGGACTTTATGG
MAPK9	2756	3	AGAAACTTCAGCCAAGTGTG
MAPK9	2757	4	CTTATGTCAGGTTATTACA
AXL	2758	1	CTGAGAACATTAGTGCTACG
AXL	2759	2	CGAAGCCCATAACGCCAAGG
AXL	2760	3	CCTAGCAGTACATACCACCA
AXL	2761	4	CCCGAAGCCAATGTACCTCG
XIAP	2762	1	ATGACAACTAAAGCACCGCA
XIAP	2763	2	ATGGATATACTCAGTTAACA
XIAP	2764	3	TCTGACCAGGCACGATCACA
XIAP	2765	4	TATCAGACACCATATACCCG
BRD3	2766	1	CATCACTGCAAACGTCACGT
BRD3	2767	2	GATGCTATCCAAGAAGCACG
BRD3	2768	3	ATACAATCCCCAGACCACG
BRD3	2769	4	TGAAGGTACACAGCAAGTGG
TOP2B	2770	1	TAGGCTACATGGCTTACCAG
TOP2B	2771	2	GTGTACACTGATATTAACAG
TOP2B	2772	3	ATGATTATGACCGATCAGGT
TOP2B	2773	4	ATCAACGTGTAGAGCCTGAG
SH2B3	2774	1	ACTACCGGGACACAGGCCGT
SH2B3	2775	2	GGAGCTCTTCGACCCACCCA
SH2B3	2776	3	TGAGTTGCACGCCGTAGCGG
SH2B3	2777	4	GCAGCAGCTGAATTCATGGA
DHH	2778	1	CCGCAACCACGTCCACGTGT
DHH	2779	2	CAGGATTCACTCCACTACGA
DHH	2780	3	AGGAAGAGCAGCACCGGCGT
DHH	2781	4	GAAATGCAACTGTGCGCCTG
DYRK2	2782	1	TTGAGGATAACAGTAACAAG
DYRK2	2783	2	CTAAATGCTAAGAAGCGCCA
DYRK2	2784	3	ACAGCATTCATAGACGGCAG
DYRK2	2785	4	CAAGCACTGCAGAATCGAGT
FLT4	2786	1	GCCCTCCAGTCACGGCACTG
FLT4	2787	2	CTCACCTCTCACGAACACGT
FLT4	2788	3	CATCGAATCCAAGCCATCCG
FLT4	2789	4	CATACCATGCACAATGACCT

Table 6C. Library of gene modulatory reagents.

Target gene	SEQ ID NO	gRNA #	gRNA Seq
CTRL-non-1	2790	1	CCCGATGGACTATACCGAAC
CTRL-non-2	2791	1	TCAATTCTCACTCACGACCA
CTRL-non-3	2792	1	GTTGATCGAAAATGGGAGAA
CTRL-non-4	2793	1	CGTCCCTTCGTCTCTGCTTA
CTRL-non-5	2794	1	AATCGACTCGAACTTCGTGT
CTRL-non-6	2795	1	AGCTCGCCATGTCGGTTC
CTRL-non-7	2796	1	CAGAGACAATGACATGTAGA
CTRL-non-8	2797	1	AACCACGGCATTGAGAGGTG
CTRL-non-9	2798	1	CAAATACAATTACTTATAGC
CTRL-non-10	2799	1	CGACTAACCGGAACTTTTT
CTRL-non-11	2800	1	CAAAAGTCTCGCTTGGTCCT
CTRL-non-12	2801	1	CAGTAGCGATCGAATGTCAA
CTRL-non-13	2802	1	AGTATTAGGTACCTGCCCTA
CTRL-non-14	2803	1	CTGGCTTATTAGCTATAAAG
CTRL-non-15	2804	1	AATATTTGGCTCGGCTGCGC
CTRL-non-16	2805	1	GCTTTCAATTGCAAAAATAC
CTRL-non-17	2806	1	ATACTCTCACAGGTACATAA
CTRL-non-18	2807	1	GCAAATTCAGACAGCTAATT
CTRL-non-19	2808	1	TCGCGCTTGGGTTATACGCT
CTRL-non-20	2809	1	CCTACGCGGTAGGGAACCTT
CTRL-non-21	2810	1	GACCGCAAAGTGGTCCGAAG
CTRL-non-22	2811	1	GCTGTTCCGAAGTTGAGAAT
CTRL-non-23	2812	1	CGCGTGTAGCTGGAGACAAG
CTRL-non-24	2813	1	CGCGGCCCCACGCGTCATCGC
CTRL-non-25	2814	1	TCCTGCCAAGAAACACCCTT
CTRL-non-26	2815	1	AAATTGGCTTTCGTTTCGTGC
CTRL-non-27	2816	1	TAAGGCGACCTGCGCTTGTG
CTRL-non-28	2817	1	TCGCGGACATAGGGCTCTAA
CTRL-non-29	2818	1	CGGTTTACATCTGCCCATCG
CTRL-non-30	2819	1	CGATGGATCCCTAGTTCCTG
CTRL-non-31	2820	1	CGAACTTAATCCCGTGGCAA
CTRL-non-32	2821	1	GTTCAATTCCAAGTCCGCTG
CTRL-non-33	2822	1	GTTTTCAAGTTGCCCAACAGC
CTRL-non-34	2823	1	CCTGCGGTGCACGGCTAGCC
CTRL-non-35	2824	1	GGGCGCTAAGATATATGCCC
CTRL-non-36	2825	1	CAAACAGTCTAAGGCGACGA
CTRL-non-37	2826	1	TGCCCCACTTAGCAACACTCT
CTRL-non-38	2827	1	AACGCTGTCTGACGTGTATA
CTRL-non-39	2828	1	GCCGCCGATTCATAAGTAA
CTRL-non-40	2829	1	ACGCATGCTTCCCAAAGCGT

CTRL-non-41	2830	1	AAGCACTAGTCCGTATGATG
CTRL-non-42	2831	1	TAGTCTCACCTGATGGCGTG
CTRL-non-43	2832	1	AGAAGAAAAAATGTCTACG
CTRL-non-44	2833	1	TCTGGCTTGACACGACCGTT
CTRL-non-45	2834	1	TCTATTTGTCTGCGCAGAA
CTRL-non-46	2835	1	CGAGCAAAGATTGTTGGATA
CTRL-non-47	2836	1	TTCTTAGAAGTTGCTCCACG
CTRL-non-48	2837	1	TAATCACATTGCTTAACCGG
CTRL-non-49	2838	1	GGAGAGGGCCCGCGAACTCA
CTRL-non-50	2839	1	ACCCATATATGCTGCCGCAC
CTRL-non-51	2840	1	CGGGATGCAGCTGGAGAGGA
CTRL-non-52	2841	1	GTCCTCATCCGGTCAGGCTG
CTRL-non-53	2842	1	AAATACAAGCTATAGCGATA
CTRL-non-54	2843	1	GCGATCGGAGTGCCACGATA
CTRL-non-55	2844	1	AGCGATTACGTATTAGATG
CTRL-non-56	2845	1	GAGTAATTTGGAACGTATTG
CTRL-non-57	2846	1	TTCTTCGGCCTACACCCGGT
CTRL-non-58	2847	1	GTACCCCTATGGCCGTTCTA
CTRL-non-59	2848	1	ATAGCGGATGTCCTTGAAA
CTRL-non-60	2849	1	CGTGTTTGGAAATTGCCGCG
CTRL-non-61	2850	1	GCCACACGAATCATAAAGAG
CTRL-non-62	2851	1	ACTTACGGCACTCGCATGCC
CTRL-non-63	2852	1	GAGACCACTTTCGTGCAAGC
CTRL-non-64	2853	1	TGCCGCTATACTAAAACCTT
CTRL-non-65	2854	1	ATCTCTATACTGTCACTCGC
CTRL-non-66	2855	1	TCATCTTACATCTGGGAGAC
CTRL-non-67	2856	1	TGAACGGTGAAGAGATAGGG
CTRL-non-68	2857	1	CTTCCTGCGTGGCTTTAAAC
CTRL-non-69	2858	1	AAACGAGATCGAGAAAGGTA
CTRL-non-70	2859	1	GAGCAGCTGTCAGGTCTTGT
CTRL-non-71	2860	1	GGTACTGGAAGTCCGAAACC
CTRL-non-72	2861	1	AGGCCACAAATTGTATACAG
CTRL-non-73	2862	1	CCCTTCTGGCGGGCCAAACA
CTRL-non-74	2863	1	TCAACCCAGCGCACCGTTG
CTRL-non-75	2864	1	TCGAGAGGAAAAACACACTG
CTRL-non-76	2865	1	GGCGCATTAAAGTCGAGAGC
CTRL-non-77	2866	1	GGAGATGCGGCCTTCTCAAA
CTRL-non-78	2867	1	CCGCTGTCTCACTAATCTCA
CTRL-non-79	2868	1	AGCATTCTACCAAGACCGA
CTRL-non-80	2869	1	GACTTCTAGAATATAAAAGA
CTRL-non-81	2870	1	CTGGTGACCGACAATTACAC
CTRL-non-82	2871	1	ATAGCCGCGCTCATTACTT
CTRL-non-83	2872	1	TACCCCTCCGGATACGGACTG
CTRL-non-84	2873	1	CTGCCCCAGGCGTAATCCTC

CTRL-non-85	2874	1	TACGTAAGTGACGACAGGAA
CTRL-non-86	2875	1	CAGCGCCGAAACTCTTTCCG
CTRL-non-87	2876	1	CGCTTCCGCGGCCCGTTCAA
CTRL-non-88	2877	1	TAAGCCTCATGAAGGAGGGG
CTRL-non-89	2878	1	ACAGCGCTCTCGTGTACTAT
CTRL-non-90	2879	1	AGTCTTAAAGACCCTAAGCT
CTRL-non-91	2880	1	CTTAAGTCATGAGCAAAGAT
CTRL-non-92	2881	1	GTTACGTACCCTCCAAC TTC
CTRL-non-93	2882	1	GGATATTGAGTAAACCCGAT
CTRL-non-94	2883	1	CGACGCTAGGTAACGTAGAG
CTRL-non-95	2884	1	GAGAAGGATGGAAATTAGAA
CTRL-non-96	2885	1	CTCCGTTATGTGGCATGAGA
CTRL-non-97	2886	1	GGGCCTACGATCAGAGGTGT
CTRL-non-98	2887	1	TCTAAAGCCGTCCTGATGTT
CTRL-non-99	2888	1	AAGGCGCGCAATGTGGCAG
CTRL-non-100	2889	1	GAACGTAGAAATTCCCATT
Ctrl-hg38-1	2890	1	GCCCAGTGGGTCCTCGTGAC
Ctrl-hg38-2	2891	1	TTGACATCAGAAACAGACGT
Ctrl-hg38-3	2892	1	TGTCATGGTTTGACTGTCCC
Ctrl-hg38-4	2893	1	GGCTCGGGATCCCTAGCAGG
Ctrl-hg38-5	2894	1	GTGTTGGATAAGTAATGGGG
Ctrl-hg38-6	2895	1	GGATATTTGAGCTCATCTCT
Ctrl-hg38-7	2896	1	GATACATTATAAGGAGCATT
Ctrl-hg38-8	2897	1	ATAATTAGTTTTGAGAATAG
Ctrl-hg38-9	2898	1	TGAGGGACATTCATCCGGCC
Ctrl-hg38-10	2899	1	GAGAACCAAGGATGGCTTAT
Ctrl-hg38-11	2900	1	TGCACTATTTTCATGGTGATA
Ctrl-hg38-12	2901	1	CGTTTTAAACTTGCAAGGTA
Ctrl-hg38-13	2902	1	ACCGGCTTCAACTCCTTCAG
Ctrl-hg38-14	2903	1	CATAGACCAATCAGCACTTT
Ctrl-hg38-15	2904	1	CTTGGGCATTTATGTCTCCA
Ctrl-hg38-16	2905	1	AATAATATTTCCCTGCACTC
Ctrl-hg38-17	2906	1	CTGGAAGTTTAGCAATCA
Ctrl-hg38-18	2907	1	TTAGTCACAGTCCCCTACCT
Ctrl-hg38-19	2908	1	ACTTATACCACATGGTAACC
Ctrl-hg38-20	2909	1	CTGCTATGGGGGAGTTATT
Ctrl-hg38-21	2910	1	AAGTCAACATGTCTAACTCA
Ctrl-hg38-22	2911	1	CCTAGCTCACTTAAGTTTGC
Ctrl-hg38-23	2912	1	GGGAGGTATTATTGGATTCT
Ctrl-hg38-24	2913	1	TTTATCAATTTACTGAAGTA
Ctrl-hg38-25	2914	1	CTTACCCTATAGGGGATATT
Ctrl-hg38-26	2915	1	CATGAGCCCCAAGGGATCTT
Ctrl-hg38-27	2916	1	AGGCCTGAGACTCACATTTT
Ctrl-hg38-28	2917	1	TCAATCTCAGCCCAGGACCT

Ctrl-hg38-29	2918	1	AGATACGTTTTAGACCTCAA
Ctrl-hg38-30	2919	1	TAGAGCCTCAACCATGTTTT
Ctrl-hg38-31	2920	1	CCAGGGGACCTGAACGCGTG
Ctrl-hg38-32	2921	1	ACACAGAGACATCTCCTGTC
Ctrl-hg38-33	2922	1	GGTAAGAATGAATAGTTCCC
Ctrl-hg38-34	2923	1	TGTCCTCATTCCAATTCTTG
Ctrl-hg38-35	2924	1	ATACGACTTAGCAGCCTTGT
Ctrl-hg38-36	2925	1	AAGGCCAATGATTGAAGTCA
Ctrl-hg38-37	2926	1	AGCACTTTAACTAGACAATA
Ctrl-hg38-38	2927	1	AGCAACACCAGCATCATGGC
Ctrl-hg38-39	2928	1	TAATTAAACACTTGCAACAT
Ctrl-hg38-40	2929	1	GAAGCACACGTGGTGTATTT
Ctrl-hg38-41	2930	1	GGAGCTTGAAGTTCTAAATG
Ctrl-hg38-42	2931	1	AATCAGCATTAACAGAAAGG
Ctrl-hg38-43	2932	1	CATGCTTAAGAGTTTCCTAT
Ctrl-hg38-44	2933	1	ATCATACCCCATGAGACTTT
Ctrl-hg38-45	2934	1	ATACTCACATCATGTTAAGA
Ctrl-hg38-46	2935	1	CGCCCATGTTGGCCATAAAC
Ctrl-hg38-47	2936	1	ATCAGTCTGTCTTGTAGGCA
Ctrl-hg38-48	2937	1	TTGCTGGGCTGACCCAAGCT
Ctrl-hg38-49	2938	1	GTTTAGGTAAAAATACCTTG
Ctrl-hg38-50	2939	1	TTCTACCCCACCACATCCCA
Ctrl-hg38-51	2940	1	TCGTGAAAACATACAAGTCT
Ctrl-hg38-52	2941	1	TCATGGTCGGATGAGTTGGG
Ctrl-hg38-53	2942	1	AAGCATTTCATCCAGACAA
Ctrl-hg38-54	2943	1	CCTGCTTCAGCCACTAAGCA
Ctrl-hg38-55	2944	1	TGGTCTAGCGTGTCTCGCTC
Ctrl-hg38-56	2945	1	CCAGCCAAACTACACCCCAG
Ctrl-hg38-57	2946	1	CAACGACTGCATTAGGGCAA
Ctrl-hg38-58	2947	1	TTCCCTGGGATAGCTGATAT
Ctrl-hg38-59	2948	1	TGTTGTGTGCATACCCTAGT
Ctrl-hg38-60	2949	1	GATGAATATGAATGTATGAC
Ctrl-hg38-61	2950	1	TAAGTGCATTTCTATGTCCCT
Ctrl-hg38-62	2951	1	GATTATCTATCCTGGTTCCC
Ctrl-hg38-63	2952	1	AATAAATAGCATGACTTATG
Ctrl-hg38-64	2953	1	TTTGCAATCCCCGAGGTGAC
Ctrl-hg38-65	2954	1	GCTGCCACAAAGGTTGTCAA
Ctrl-hg38-66	2955	1	GCAATAATTAGGACCACCCA
Ctrl-hg38-67	2956	1	AGATGACTGGAGTGCTACAA
Ctrl-hg38-68	2957	1	CTCATTGACCCACATAAAAT
Ctrl-hg38-69	2958	1	AACTCTTCTGTCTGATGAGCA
Ctrl-hg38-70	2959	1	GGGTAAACAGTCATGCTGCA
CTRL-non	2960	1	AAACTGTGCGACGGTAAGCG
CTRL-non	2961	2	AAAGATTACCTCGCTACGG

CTRL-non	2962	3	AACATGTCATCGTTACGCC
CTRL-non	2963	4	AACCGATTTCATCGCGTGG
CTRL-non	2964	5	AACGAAAGCTCGTTAACTCG
CTRL-non	2965	6	AACGATGCGGGCGACGTGCT
CTRL-non	2966	7	AACTCCCCGACTCCGTTCG
CTRL-non	2967	8	AAGCGATGGTCCGTATACTA
CTRL-non	2968	9	AATATTTGGCTCGGCTGCGC
CTRL-non	2969	10	AATCCGGAGTAATCCGACCC
CTRL-non	2970	11	AATCGACTCGAACTTCGTGT
CTRL-non	2971	12	ACACCATATCGGCGGGACGC
B2M	2972	1	GGCCGAGATGTCTCGCTCCG
B2M	2973	1	GGCCGAGATGTCTCGCTCCG
B2M	2974	2	GGCCACGGAGCGAGACATCT
B2M	2975	2	GGCCACGGAGCGAGACATCT
B2M	2976	1	GGCCGAGATGTCTCGCTCCG
B2M	2977	1	GGCCGAGATGTCTCGCTCCG
B2M	2978	2	GGCCACGGAGCGAGACATCT
B2M	2979	2	GGCCACGGAGCGAGACATCT

Table 6D. Library of gene modulatory reagents.

Target gene	SEQ ID NO	gRNA #	gRNA Seq
BIRC5	2980	1	AGTTCTTGAATGTAGAGATG
BIRC5	2981	2	GGGCAGTCTCACCCGCTCCG
BIRC5	2982	3	TCTTGAATGTAGAGATGCGG
BIRC5	2983	4	CAAGTCTGGCTCGTTCTCAG
BRAF	2984	1	GGGCCAGGCTCTGTTCAACG
BRAF	2985	2	ATACCCAATAGAGTCCGAGG
BRAF	2986	3	GCCCAACAAACAGAGGACAG
BRAF	2987	4	TCATAATTAACACACATCAG
CDK4	2988	1	AAGGCCCCGTGATCCCCACAG
CDK4	2989	2	GTCTACATGCTCAAACACCA
CDK4	2990	3	CCAGTGGCTGAAATTGGTGT
CDK4	2991	4	AGCCACTGGCTCATATCGAG
CDK6	2992	1	GCCCGCGACTTGAAGAACGG
CDK6	2993	2	CCAGCAGTACGAATGCGTGG
CDK6	2994	3	GACCTTCGAGCACCCCAACG
CDK6	2995	4	AATGAAGAAAGTCCAGACCT
CYP11B1	2996	1	CACTGTCCTGGGGACCCGGG
CYP11B1	2997	2	AATGGGCCCTAGTTCCTGGA
CYP11B1	2998	3	CAAAGGGCAGCACTGTCCTG
CYP11B1	2999	4	CCCCACAGGTACGACTTGGG
CYP11B2	3000	1	CATCGGGAGGAACCTCTGCA
CYP11B2	3001	2	AAACGGCAGCACCGTCCTAG

CYP11B2	3002	3	CCCCACAGGTACAACCTTGGG
CYP11B2	3003	4	CAACTTGGGAGGACCACGCA
EGFR	3004	1	GAGAACCTAGAAATCATACG
EGFR	3005	2	TGTCACCACATAATTACCTG
EGFR	3006	3	CCAGATGGATGTGAACCCCG
EGFR	3007	4	ATGGACTTCCAGAACCACCT
FLT3	3008	1	AGATACATCCACTTCCACAG
FLT3	3009	2	GAGACAGGAAATGTTCCCTG
FLT3	3010	3	AGAACAATGATTCATCAGTG
FLT3	3011	4	AAAGCTGTTTCATGTGAACCA
GART	3012	1	TTATCCTGGAGACTACACCA
GART	3013	2	AGAATTGAGCAAGGGCAGTG
GART	3014	3	TATCCTGGAGACTACACCAA
GART	3015	4	GTCTTCGGGAAGTACCTGAG
JAK1	3016	1	ACAAAGAGGAGAGATACCTG
JAK1	3017	2	GAGGAGCTCCAAGAAGACTG
JAK1	3018	3	CAAAGGACAAGGCCTCCTCG
JAK1	3019	4	GAAGACTGAGGTGAACCTGG
JAK2	3020	1	AGAGTTATAGATGGCCAGTG
JAK2	3021	2	CTGCCACTGCAATACCAACG
JAK2	3022	3	CAACCTCACCAACATTACAG
JAK2	3023	4	AATGAAGAGTACAACCTCAG
KIF11	3024	1	TCTTGTGTAGGAGTATACGG
KIF11	3025	2	GAAGGGGAAGAACATCCAGG
KIF11	3026	3	GCCCTCCAAGAGAATCCTGG
KIF11	3027	4	TTCGTCTGCGAAGAAGAAAG
KIT	3028	1	CTGGGTCTGTGAGAGGACAG
KIT	3029	2	GCCTAATCTCGTCGCCACG
KIT	3030	3	TCAACCATCTGTGAGTCCAG
KIT	3031	4	ACCACTAGCTTTCCAAACGG
MAP2K1	3032	1	AAGCACAAGATCATGCACAG
MAP2K1	3033	2	GCAGCAGCGAAAGCGCCTTG
MAP2K1	3034	3	GAGTTGACTAGGATGTTGGA
MAP2K1	3035	4	CTTACCCAGAAGCAGAAGGT
MAP2K2	3036	1	AAGCACCAGATCATGCACCG
MAP2K2	3037	2	CCTGGGGAAAGTCAGCATCG
MAP2K2	3038	3	AGGTGCTGAAAGAGGCCAAG
MAP2K2	3039	4	GGATTCCCAGGAGATCCTG
MDM2	3040	1	TTCCGAAGCTGGAATCTGTG
MDM2	3041	2	CGAAGCTGGAATCTGTGAGG
MDM2	3042	3	ACAGGTGTCACCTTGAAGGT
MDM2	3043	4	GTGGTTACAGCACCATCAGT
MET	3044	1	TCAGCTTCCCAACTTCACCG
MET	3045	2	CTTGGTGCAGAGGAGCAATG

MET	3046	3	ACTCTGTTCGATATTCATCA
MET	3047	4	ATGTCAGCAGTATGATTGTG
MTOR	3048	1	GCTGATGCAAGTGAAGACTG
MTOR	3049	2	TCAGGAAATGATCCGCACAG
MTOR	3050	3	AATAGGGTGAATGATCCGGG
MTOR	3051	4	CGTGCTGGACATCATCCGAG
PIK3CA	3052	1	TTATTAATGTAGCCTCACGG
PIK3CA	3053	2	CCATCATCAGGTGAACTGTG
PIK3CA	3054	3	GTTTGACTGGTTCAGCAGTG
PIK3CA	3055	4	AGCAAATCTTCTAATCCATG
PSMB5	3056	1	CTGCAACTATGACTCCATGG
PSMB5	3057	2	CGTGTGGAGAGACCGCTAC
PSMB5	3058	3	CCGCTACCGGTGAACCAGCG
PSMB5	3059	4	GAGATCAACCCATACCTGCT
RPL3	3060	1	GGCTACGTGGAAACCCCTCG
RPL3	3061	2	CATTGTAGAGACACCACCCA
RPL3	3062	3	TGTAGAGACACCACCCATGG
RPL3	3063	4	TGTGGGCATTGTGGGCTACG
TOP2A	3064	1	ATATAATGACTTCATCAACA
TOP2A	3065	2	TGTTGTGAAGAAGAAGAACA
TOP2A	3066	3	GTGTACGCTTATCCTGACTG
TOP2A	3067	4	AACCAATGTAGGTGTCTGGG
TUBG1	3068	1	CCAGGACGAGATGAGCGATG
TUBG1	3069	2	TGTGTCACTCCATTGCTGGG
TUBG1	3070	3	TTTTGACATCATAGACCGGG
TUBG1	3071	4	TGTAGGGTGATGATTCCCT

EXAMPLES

Example 1: Genetic Pharmacopeia

[00284] A drug library comprising molecularly targeted oncology drugs of Table 2B was generated. The drug library is updated periodically to include additional targeted oncology drugs as they are identified. A genetic pharmacopeia was generated to represent the genetic targets of the drug library (Table 5B).

[00285] A library of gene modulatory reagents comprising guide RNA (gRNA) sequences associated with each gene target was designed. As shown in Table 6A, five potential gRNA sequences were designed for each oncology drug target to generate gRNA sequences having SEQ ID NOS: 1-1525. The library of gene modulatory reagents is constructed to comprise at least one gRNA sequence selected from SEQ ID NOS: 1-1525. The library is constructed in a format compatible with use in primary cancer cells using a viral delivery method (adenovirus for Cas nuclease delivery, lentivirus for gRNA delivery).

Example 2: Cancer Functional Susceptibility Profiling

[00286] A method is performed to determine the functional susceptibility of a patient's cancer cells to one or more perturbagens which model the action of the targeted oncology drugs identified in Example 1. The library comprising at least one gRNA sequence selected from SEQ ID NOS: 1-1525 and associated

gene editing agent(s) (*e.g.*, RNA-guided nuclease) are delivered to primary cancer cells derived from the patient in order to genetically modify the cancer cells. The Cas nuclease and gRNA are delivered by lentivirus. In this example, genetic modification occurs via gene editing using a CRISPR-based method. The modified cancer cells are propagated *in vivo*, however, the method may be employed in *in vitro* environments that mimic the *in vivo* context. The effect of each gene edit is evaluated by screening the modified cancer cells in a pooled or array format. Next-generation sequencing is performed to determine the effect of the individual perturbations on the viability of the patient's cancer cells. Oncology drug(s) associated with the perturbagens that reduce viability of the cancer cells are selected as a putative therapeutic for the patient.

Example 3: CRISPR-based Method for Personalized Functional Genomics

[00287] Methods for the identification of patient-specific tumor therapeutic vulnerabilities were performed utilizing function genomics as outlined in FIG. 2. Patient-derived samples, obtained directly from the patient or after passage in mice (PDX), were dissociated and infected with a gRNA library corresponding to the desired therapeutic drug collection. Cells were viably maintained *in vitro*, using 3D and/or organoid approaches, allowing gRNA which target essential tumor regulators to be gradually depleted from the population ("drop-out). This approach leveraged the insight that the effect of each clinically used targeted oncology drug can be modeled by CRISPR-mediated mutation of the corresponding gene encoding the drug target (FIG. 3).

[00288] Guide-RNA library cloning

[00289] A library of guide RNAs (gRNA) with 1685 elements having 1585 gRNAs directed against drug target genes and 100 control gRNAs was designed (FIG. 4). The library comprises the target gRNAs of Table 6B and control gRNAs having SEQ ID NOS: 2790-2959 of Table 6C. Guide RNAs targeting the ubiquitously expressed but not essential cell surface molecule beta-2 microglobulin (B2M) were also included. The 20 nt gRNA sequence was flanked on either side by a sequence containing a recognition site for the Type-IIIS restriction enzyme Bbs-I, and outside of the Bbs-I elements flanked by primer binding sites that could be used for PCR amplification of the library. The upstream and downstream Bbs-I elements were designed such that Bbs-I digestion of the PCR product releases the 20 bp gRNA encoding sequence flanked with 4 bp overhangs compatible with the corresponding overhangs in the destination vector for gRNA expression. Using primers complementary to the primer binding sites in the library oligonucleotide pool, the library was amplified by PCR for 10 cycles using Q5 DNA polymerase. PCR products were purified using Zymo Clean&Concentrate kit and then included in a GoldenGate cloning reaction using 20 cycles of 37°C digestion with Bbs-I followed by 16°C ligation with T4-DNA ligase to introduce the library into the destination vector for gRNA expression. The GoldenGate cloning reaction was further cleaned using Zymo Clean&Concentrate kit and then used in multiple reactions for electroporation into electrocompetent Stbl-4 bacteria. The entire transformation reaction from 3-5 electroporations was inoculated into 600 ml of LB with appropriate antibiotic selection and grown for 18 hours at 30°C to avoid recombination. Bacterial cells were harvested and DNA isolated using Zymo Maxiprep kit. Barcode readcount distribution was measured by next generation sequencing of the pooled

plasmid DNA or transduced cells (FIG. 5), demonstrating near-complete barcode representation and broadly equal readcount distribution.

[00290] Another library of gRNAs directed against drug target genes was prepared comprising the gRNAs of Table 6D. The library also includes gRNAs having SEQ ID NOS: 2972-2979 directed to B2M, and control gRNAs having SEQ ID NOS: 2890-2905 and 2960-2971.

[00291] *Virus production*

[00292] Lentiviral particles containing viral genome encoding expression units for the gRNA library and Cas9 were generated by transfecting 293FT cells with transfer vector and 2nd generation lentiviral packaging plasmids (DR8.9 and pCMV-VSVG) in a ratio of 4:3:1 using Lipofectamine-3000 (Thermo) according to the manufacturer's instructions. Six hours after transfection, medium was changed to DMEM harvest medium containing 10% FCS. Virus containing supernatant was harvested at 30 and 54 hours after transfection, centrifuged for 5 minutes at 2500 rpm to remove debris and filtered through a 45 µm filter before pooling. Virus was precipitated from culture supernatants by incubation with PEG-8000 at 10% final concentration for >4 hours. PEG-precipitate was centrifuged for 1 hour at 4000 rpm and the pellet resuspended in ~1/100 the original volume. Aliquots were stored at -80°C until use.

[00293] *Tumor processing*

[00294] Tumor pieces were finely chopped using sterile razor blades in 0.5 ml digestion mix (DMEM/F12 with 1 mg/ml collagenase IV, 10 uM Y27632 and 20 µg/ml DNase). These were digested for 30 min at 37C, triturated with a 10 ml pipette, then digested for an additional 15 min at 37C. The mixture was strained through a 100 µm strainer. Cells were washed once with FACS buffer (PBS with 0.0% BSA, 1 mM EDTA) and resuspended in organoid medium (Advanced DMEM/F12 with 10 uM SB202190, 1X HEPES, 1.25 mM N-acetylcysteine, 10 mM nicotinamide, 1X Glutamax, 1X Primocin, 5% Knockout Serum Replacement, 1X B27 supplement, 0.1 nM cholera toxin, 0.5 uM A83-01, 10 uM Y27632, 1 uM PGE2, 10 nM [Leu15]-Gastrin I, 10 ng/ml rhFGF10, 10 ng/ml rhFGF2, 50 ng/ml EGF, 0.3 µg/ml hydrocortisone). For FACS analysis, 10 µl of cell sample was diluted with 190 µl FACS buffer containing 5 nM ToPro-3.

[00295] *Tumor cell infection and culture*

[00296] Cells were mixed in organoid medium with lentivirus at a target MOI of <1 in the presence 4 µg/ml polybrene, and incubated for 1 hour at room temperature. The suspension was then spun, the pellet resuspended in a minimal volume of organoid medium, and then plated onto collagen sponges (Ethicon) for 3D culture (FIG. 6A). Cells were grown at 37C with 5% CO₂. Medium was changed every 2 days.

[00297] *Sponge harvest*

[00298] Sponges were digested for 15 min at 37C with 1mg/ml Collagenase IV in DMEM-F12. Analysis of the re-isolated cells demonstrated the outgrowth of the small tumor-derived tumoroids/organoids (FIG. 6B). A small sample was retained for FACS (as described above), and the remainder was spun at 1200 rpm for 5 min. The supernatant was discarded and the pellet frozen at -80C for DNA isolation. Expression of beta-2 microglobulin protein was analyzed using directly conjugated

anti-B2M antibodies (FIG. 7), demonstrating loss of B2M protein expression at the precise frequency expected based on the relative abundance of B2M-targeting gRNAs in the gRNA library.

[00299] Cancer cell line culture

[00300] A549 lung carcinoma cells (American Type Culture Collection) were grown in Dulbecco's Modified Eagle Medium (Gibco) supplemented with 10% (v/v) fetal bovine serum, 1X Glutamax, and 1X antibiotic/antimycotic.

[00301] DNA preparation, PCR, and next-generation sequencing (NGS)

[00302] Genomic DNA was isolated using the Zymo Quick-DNA Miniprep Plus kit. 5ug of purified genomic DNA was used as input for first round PCR amplification using the Q5 2X Master Mix and primers specific to the lentiviral vector. 10% of the resulting first round reaction products was then used as input for the second round of PCR amplification, utilizing barcoding primers to allow multiplex NGS readout. Samples were analyzed on the Illumina MiSeq using standard Illumina sequencing primers (Admera).

[00303] Sequence Analysis

[00304] Read1 sequences corresponding to the PCR barcodes were used for de-multiplexing, generating single-sample FASTA files containing gRNA readcounts. Sequencing data was analyzed using the CRISPRCloud2 platform, generating both CPM-normalized readcounts as well as statistical analysis of gRNA abundance based beta-binomial modeling. Data were visualized as 'volcano' plots (DataGraph), describing the relationship between statistical significance and fold-change in gRNA abundance. Typically, comparison was made between gRNA abundance immediately following lentiviral transduction and at the end of the *in vitro* culture period.

[00305] Analysis of dropout frequency using library screening in the A549 lung cancer cell line demonstrated clear loss of gRNAs corresponding to known essential genes (e.g. TOP2A, TUBG1 and others), while non-targeting control gRNAs demonstrated no corresponding decrease in abundance (FIG. 8). The library utilized in this experiment comprised the gRNAs of Tables 6B-6C (SEQ ID NOS: 1526-2959) as described above.

[00306] Analysis of dropout frequency using library screening in primary human melanoma tumor sample demonstrated clear loss of gRNAs corresponding to a known melanoma therapeutic vulnerability (e.g. BRAF), while non-targeting control gRNAs demonstrated no corresponding decrease in abundance (FIG. 9). Additional hits corresponding to presumptive cancer therapeutic vulnerabilities were also identified. The library utilized in this experiment comprised the gRNAs of Table 6D (SEQ ID NOS: 2980-3071) and SEQ ID NOS: 2890-2905 and 2960-2979 of Table 6C, as described above.

Example 4: In vivo Validation of Personalized Genomic Profiling

[00307] Oncology drugs targeting presumptive cancer therapeutic vulnerabilities identified in Example 3, are tested in an *in vivo* animal model of the patient's cancer. Drugs that show efficacy for treating the cancer in the animal model are selected for treating the patient's cancer.

[00308] While preferred embodiments have been shown and described herein, it will be obvious to those skilled in the art that such embodiments are provided by way of example only. Numerous variations,

changes, and substitutions will occur to those skilled in the art without departing from the scope of this application. Various alternatives to the embodiments described herein may be employed in practicing the scope of this application.

CLAIMS

WHAT IS CLAIMED IS:

1. A method of treating cancer in a subject in need thereof, the method comprising administering to the subject a therapeutic molecule selected from a library of therapeutic molecules; wherein the therapeutic molecule has been selected by a method comprising: modifying cancer cells from the subject to knock down or knock out the function of a plurality of genes, each gene in the plurality of genes encoding for a protein target of a therapeutic molecule in the library of therapeutic molecules, whereby the therapeutic molecule has been selected if knocking down or knocking out the function of the gene that encodes for the protein target of the selected therapeutic molecule impairs cancer cell viability.
2. The method of claim 1, wherein the library of therapeutic molecules comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 therapeutic agents of Tables 2-3.
3. The method of claim 1 or claim 2, wherein one or more of the plurality of genes encode for a protein of Tables 3-5D.
4. A method of treating cancer in a subject in need thereof, the method comprising administering to the subject a therapeutic molecule selected from a library of therapeutic molecules; wherein the cancer of the subject has been determined to be susceptible to the selected therapeutic molecule by a method comprising:
 - (a) contacting a sample of cancer cells from the subject with a library of gene modulatory reagents to generate a plurality of modified cancer cells, wherein each modified cancer cell harbors one or more of the gene modulatory reagents, and each gene modulatory reagent is capable of knocking down or knocking out the function of a gene that encodes a protein target of a therapeutic molecule in the library of therapeutic molecules, and
 - (b) sequencing the plurality of modified cancer cells, wherein a gene modulatory reagent that impairs cell viability will have fewer sequence reads than a gene modulatory reagent that does not impair cell viability, and the gene that is knocked down or knocked out by the gene modulatory reagent that impairs cell viability encodes for the protein targeted by the selected therapeutic molecule.
5. The method of claim 4, wherein prior to sequencing, one or more of the plurality of modified cancer cells have been propagated.
6. The method of claim 4 or claim 5, wherein the cancer cells are primary cancer cells.
7. The method of any one of claims 4-6, wherein contacting comprises introducing the one or more gene modulatory reagents into each cancer cell by a viral or non-viral delivery method.
8. The method of claim 7, wherein one or more of the gene modulatory reagents in the library are encoded on a viral vector.
9. The method of any one of claims 4-8, wherein the library comprises from about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, from about 50 to about 2,000, from about 100 to about 2,000, or from about 500 to about 2,000 different gene modulatory reagents.

10. The method of any one of claims 4-9, wherein one or more gene modulatory reagents from the library of gene modulatory reagents comprises a nucleic acid sequence homologous to at least about 15 contiguous nucleotides of a gene encoding a protein of Tables 3-5D.
11. The method of any one of claims 4-10, wherein the library of therapeutic molecules comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 therapeutic agents of Tables 2-3.
12. The method of any one of claims 4-11, wherein one or more of the gene modulatory reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 1-2789, 2980-3071.
13. The method of any one of claims 4-12, wherein one or more of the gene modulatory reagents comprise a guide RNA (gRNA) sequence comprising homology to at least a portion of the gene that encodes a protein target of a therapeutic molecule in the library of therapeutic molecules.
14. The method of any one of claims 4-13, wherein the sample of cancer cells is contacted with an endonuclease.
15. The method of claim 14, wherein the endonuclease comprises a Cas9 or Cas12a endonuclease.
16. The method of any one of claims 13-15, wherein the gRNA is positioned within a viral vector.
17. A method of generating a plurality of modified cancer cells from a subject having cancer, the method comprising delivering a library of gene modulatory reagents to a sample of cancer cells from the subject to generate the plurality of modified cancer cells; wherein each modified cancer cell harbors one or more of the gene modulatory reagents, and each gene modulatory reagent is capable of knocking down or knocking out the function of a gene that encodes a protein target from a library of protein targets.
18. The method of claim 17, wherein one or more of the gene modulatory reagents comprises a guide RNA (gRNA) sequence comprising homology to at least a portion of the gene whose function is knocked down or knocked out in the modified cancer cell.
19. The method of claim 17, wherein one or more of the gene modulatory reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 1-2789, 2980-3071.
20. The method of any one of claims 17-19, wherein the sample of cancer cells is contacted with an endonuclease.
21. The method of claim 20, wherein the endonuclease comprises a Cas9 or Cas12a endonuclease.
22. The method of any one of claims 18-21, wherein the gRNA is positioned within a viral vector.
23. The method of any one of claims 17-22, wherein the sample of cancer cells comprises primary cancer cells.
24. The method of any one of claims 17-23, wherein the library comprises from about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, from about 50 to about 2,000, from about 100 to about 2,000, or from about 500 to about 2,000 different gene modulatory reagents.

25. The method of any one of claims 17-24, wherein the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Tables 3-5D.
26. The method of any one of claims 17-25, further comprising propagating the modified cancer cells.
27. A compilation comprising a plurality of modified cancer cells, wherein each modified cancer cell harbors one or more gene modulatory reagents, and each gene modulatory reagent is capable of knocking down or knocking out the function of a gene that encodes a protein target from a library of protein targets.
28. The compilation of claim 27, wherein at least one of the one or more of gene modulatory reagents comprises a sequence at least about 90% homologous to a sequence selected from SEQ ID NOS: 1-2789, 2980-3071.
29. The compilation of claim 27 or claim 28, wherein the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Tables 3-5D.
30. The compilation of any of claims 27-29, wherein one or more of the gene modulatory reagents comprise a guide RNA (gRNA) sequence comprising homology to at least a portion of the gene whose function is knocked down or knocked out in the modified cancer cell.
31. The compilation of claim 30, wherein the gRNA comprises homology to about 10 to about 50 contiguous nucleotides of the gene.
32. The compilation of claim 30 or claim 31, further comprising an endonuclease.
33. The compilation of claim 32, wherein the endonuclease comprises a Cas9 or Cas12a endonuclease.
34. The compilation of any one of claims 30-33, wherein the gRNA is positioned within a viral vector.
35. The compilation of any one of claims 27-34, wherein the modified cancer cells are modified primary cancer cells.
36. The compilation of any one of claims 27-35, comprising from about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, from about 50 to about 2,000, from about 100 to about 2,000, or from about 500 to about 2,000 different gene modulatory reagents.
37. The compilation of any one of claims 27-36, comprising from about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, from about 50 to about 2,000, from about 100 to about 2,000, or from about 500 to about 2,000 different populations of modified cancer cells.
38. A method of evaluating the functional effect of genetically modifying cancer cells from a subject, the method comprising: sequencing a plurality of modified cancer cells, wherein each modified cancer cell harbors one or more gene modulatory reagents, each gene modulatory reagent capable of knocking down or knocking out the function of a gene that encodes a protein target in a library of protein targets; and wherein a gene modulatory reagent that impairs cell viability will have fewer sequence reads than a gene modulatory reagent that does not impair cell viability.
39. The method of claim 38, further comprising determining which gene modulatory reagents have fewer than a threshold number of sequence reads.

40. The method of claim 39, wherein the threshold number of sequence reads is an expected number of sequence reads if the gene modulatory reagent did not impair cell viability.
41. The method of claim 39, wherein the threshold number of sequence reads is an average number of sequence reads for each gene modulatory reagent in the plurality of modified cancer cells.
42. The method of any one of claims 38-41, further comprising correlating each gene modulatory reagent that has fewer than the threshold number of sequence reads to its corresponding protein target in the library of protein targets.
43. The method of claim 42, further comprising correlating the corresponding protein target to a therapeutic molecule.
44. The method of any one of claims 38-43, wherein the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Tables 3-5D.
45. The method of any one of claims 38-44, wherein one or more of the gene modulatory reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 1-2789, 2980-3071.
46. A library comprising a plurality of gene modulatory reagents, each gene modulatory reagent capable of knocking down or knocking out the function of a gene that encodes a protein target from a library of protein targets.
47. The library of claim 46, wherein the plurality of gene modulatory reagents is capable of knocking down or knocking out the function of at least about 50% of the genes that encode for the protein targets in the library.
48. The library of claim 46 or claim 47, wherein the library of protein targets comprises at least 1, at least 2, at least 3, at least 4, at least 5, at least 10, or at least 20 protein targets of Tables 3-5D.
49. The library of any one of claims 46-48, wherein one or more of the plurality of gene modulatory reagents each comprise a guide RNA (gRNA) sequence comprising at least about 90% homology to a sequence selected from SEQ ID NOS: 1-2789, 2980-3071.
50. The library of any one of claims 46-49, wherein the plurality of gene modulatory reagents is capable of knocking down or knocking out the function of about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, about 50 to about 2,000, or about 100 to about 2,000 genes.
51. The library of any one of claims 46-50, wherein the library comprises about 10 to about 2,000, from about 10 to about 500, from about 10 to about 200, from about 10 to about 150, from about 50 to about 500, from about 50 to about 200, about 50 to about 2,000, or about 100 to about 2,000 gene modulatory reagents.
52. The library of any one of claims 46-51, wherein at least one of the gene modulatory reagents is capable of knocking out the function of a gene.
53. The library of claim 52, wherein at least one of the gene modulatory reagents comprise a gRNA sequence having homology to at least a portion of the gene whose function is knocked out by the gene modulatory reagent.

54. The library of any one of claims 46-53, wherein at least one of the gene modulatory reagents is positioned within a viral vector.