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(54) Title: SHARED NEOANTIGENS

(57) Abstract: Disclosed herein in one aspect is a pharmaceutical composition comprising a plurality of neoantigenic peptides and a pharmaceutically acceptable carrier, each neoantigenic peptide comprising a tumor-specific neoepitope capable of binding to an HLA protein in a subject, each tumor-specific neoepitope comprising a tumor-specific mutation present in a tumor, wherein (a) the composition comprises neoantigenic peptides comprising tumor-specific mutations present in at least 1% of subjects in a population of subjects suffering from cancer; (b) the composition comprises neoantigenic peptides comprising tumor-specific neoepitopes which bind to HLA proteins present in at least 5% of subjects in the population; and (c) the composition comprises at least one neoantigenic peptide capable of eliciting an immune response against a tumor present in at least 5% of the subjects in the population of subjects suffering from cancer.

SHARED NEOANTIGENS

RELATED APPLICATIONS AND INCORPORATION BY REFERENCE

[0001] This application claims priority and benefit of U.S. Provisional application serial number 62/179,877 filed May 20, 2015 and U.S. Provisional application serial number 62/389,377 filed February 23, 2016.

[0002] The foregoing applications, and all documents cited therein or during their prosecution ("appln cited documents") and all documents cited or referenced in the appln cited documents, and all documents cited or referenced herein ("herein cited documents"), and all documents cited or referenced in herein cited documents, together with any manufacturer's instructions, descriptions, product specifications, and product sheets for any products mentioned herein or in any document incorporated by reference herein, are hereby incorporated herein by reference, and may be employed in the practice of the invention. More specifically, all referenced documents are incorporated by reference to the same extent as if each individual document was specifically and individually indicated to be incorporated by reference.

FIELD OF THE INVENTION

[0003] The present invention relates to methods and compositions for treating neoplasias, e.g. tumors, particularly using at least one neoantigenic peptide which is suitable for treating a significant proportion of subjects in a population suffering from cancer.

BACKGROUND OF THE INVENTION

[0004] Approximately 1.6 million Americans are diagnosed with neoplasia every year, and approximately 580,000 people in the United States are expected to die of the disease in 2013. Over the past few decades there been significant improvements in the detection, diagnosis, and treatment of neoplasia, which have significantly increased the survival rate for many types of neoplasia. However, only about 60% of people diagnosed with neoplasia are still alive 5 years after the onset of treatment, which makes neoplasia the second leading cause of death in the United States.

[0005] Currently, there are a number of different existing cancer therapies, including ablation techniques (e.g., surgical procedures, cryogenic/heat treatment, ultrasound, radiofrequency, and radiation) and chemical techniques (e.g., pharmaceutical agents, cytotoxic/chemotherapeutic

agents, monoclonal antibodies, and various combinations thereof). Unfortunately, such therapies are frequently associated with serious risk, toxic side effects, and extremely high costs, as well as uncertain efficacy.

[0006] There is a growing interest in cancer therapies that seek to target cancerous cells with a patient's own immune system (e.g., cancer vaccines) because such therapies may mitigate/eliminate some of the herein-described disadvantages. Cancer vaccines are typically composed of tumor antigens and immunostimulatory molecules (e.g., cytokines or TLR ligands) that work together to induce antigen-specific cytotoxic T cells that target and destroy tumor cells. Current cancer vaccines may contain shared tumor antigens, which are native proteins (i.e. – proteins encoded by the DNA of all the normal cells in the individual) that are selectively expressed or over-expressed in tumors found in many individuals. While such shared tumor antigens are useful in identifying particular types of tumors, they are not ideal as immunogens for targeting a T-cell response to a particular tumor type because they are subject to the immune dampening effects of self-tolerance. Vaccines containing tumor-specific and patient-specific neoantigens can overcome some of the disadvantages of vaccines containing shared tumor antigens. However, the use of patient-specific neoantigens requires sequencing of individual subject's genomes, as well as the production of personalized compositions comprising a combination of neoantigens present in that individual subject. Accordingly, there is still a need for improved methods and compositions for delivering cancer vaccines.

[0007] Citation or identification of any document in this application is not an admission that such document is available as prior art to the present invention.

SUMMARY OF THE INVENTION

[0008] Preferred statements (features) and embodiments of this invention are set herein below. Each statements and embodiments of the invention so defined may be combined with any other statement and/or embodiments unless clearly indicated to the contrary. In particular, any feature indicated as being preferred or advantageous may be combined with any other feature or features or statements indicated as being preferred or advantageous. Hereto, the present invention is in particular captured by any one or any combination of one or more of the below statements and embodiments, with any other statement and/or embodiments.

[0009] It is an objective of the invention to provide methods and compositions for the treatment of a population of cancer patients by eliciting an immune response targeting the cancer. In one aspect, the present invention relates to a pharmaceutical composition comprising at least one neoantigenic peptide and a pharmaceutically acceptable carrier, each at least one neoantigenic peptide comprising a tumor-specific neoepitope capable of binding to an HLA protein in a subject, each tumor-specific neoepitope comprising a tumor-specific mutation present in a tumor. The composition may include one neoantigenic peptide. In other embodiments, the composition may include more than 100 neoantigenic peptides. Preferably, the composition includes about 20 neoantigenic peptides. The at least one neoantigenic peptide may include a tumor-specific mutation. The mutation may be recurrent. Preferably, the mutation is present in a large proportion of a population. A recurrent mutation may be based on the mutation being present in a tumor in at least 1% of subjects in a population of subjects suffering from cancer. The composition may include at least one neoantigenic peptide containing a tumor-specific neoepitope which binds to an HLA protein present in at least 5% of subjects in the population of subjects suffering from cancer. Additionally, the composition may contain at least one neoantigenic peptide capable of eliciting an immune response against a tumor present in at least 5% of the subjects in the population of subjects suffering from cancer. The ability to elicit an immune response refers to the ability of the immune system to present an antigen to a lymphocyte. In order for the immune system to present an antigen, the antigen needs to be presented by a subjects HLA proteins. In order to elicit an immune response against a tumor, the tumor needs to contain the mutations leading to expression of the antigen. In order for the composition to provide a benefit to a population in need thereof, the population has to include subjects that express an HLA allele capable of binding the at least one neoantigenic peptide present in the composition and the population has to include subjects containing tumors with mutations that lead to neoantigenic epitopes present in the neoantigenic peptides.

[0010] The composition may be specific to a population of subjects suffering from cancer that share a characteristic. The population may have cancer or may have a specific cancer. The population may share a common set of HLA subtypes. They may share HLA subtypes based on ethnicity. Not being bound by a theory the percentage of HLA types in a population can be predicted based on ethnicity without testing. Not being bound by a theory, different populations express different HLA types capable of binding different neoantigenic peptides. Therefore a

composition can be formulated to provide a benefit to a large proportion of that population, whereas the composition would not provide a benefit to another population. Not being bound by a theory, different cancers contain different mutations and thus compositions tailored to specific cancers can be used to provide a greater benefit to a population with one type of cancer as compared to a population that includes more than one type. In one embodiment, the population is suffering from adrenocortical carcinoma (ACC), bladder urothelial carcinoma (BLCA), breast invasive carcinoma (BRCA), cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC), colon adenocarcinoma (COAD), Chronic lymphocytic Leukaemia (CLL), colorectal cancer (CRC), Diffuse large B-cell lymphoma (DLBCL), glioblastoma multiforme (GBM), head and neck squamous cell carcinoma (HNSC), kidney chromophobe (KICH), kidney renal clear cell carcinoma (KIRC), kidney renal papillary cell carcinoma (KIRP), acute myeloid leukemia (LAML), liver hepatocellular carcinoma (LIHC), lung adenocarcinoma (LUAD), lung squamous cell carcinoma (LUSC), multiple myeloma (MM), ovarian serous cystadenocarcinoma (OV), pancreatic adenocarcinoma (PAAD), prostate adenocarcinoma (PRAD), rectum adenocarcinoma (READ), skin cutaneous melanoma (SKCM), stomach adenocarcinoma (STAD), testicular germ cell tumors (TGCT), thyroid adenocarcinoma (THCA), uterine corpus endometrioid carcinoma (UCEC), or uterine carcinosarcoma (UCS).

[0011] In one embodiment, the population of subjects is suffering from CLL; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of "CLL"; and at least one of a set of six of the at least one tumor-specific mutation will be found in 17.49% of subjects in the CLL population. The population of subjects may be suffering from BLCA, the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"BLCA"; and at least one of a set of six of the at least one tumor-specific mutation will be found in 26.92% of subjects in the population. The population of subjects may be suffering from BRCA; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"BRCA"; and at least one of a set of 18 of the at least one tumor-specific mutation will be found in 36.04% of subjects in the population. The population of subjects may be suffering from COAD; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"COAD"; and at least one of a set of three of the at least one tumor-specific mutation will be found in 27.14% of subjects in the population. The population of subjects may

be suffering from GBM; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"GBM"; and at least one of a set of 14 of the at least one tumor-specific mutation will be found in 34.36% of subjects in the population. The population of subjects may be suffering from HNSC; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"HNSC"; and at least one of a set of 10 of the at least one tumor-specific mutation will be found in 21.61% of subjects in the population. The population of subjects may be suffering from KIRC; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"KIRC"; and at least one of a set of four of the at least one tumor-specific mutation will be found in 6% of subjects in the population. The population of subjects may be suffering from LAML; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"LAML"; and at least one of a set of 11 of the at least one tumor-specific mutation will be found in 47.45% of subjects in the population. The population of subjects may be suffering from LUAD; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"LUAD"; and at least one of a set of 11 of the at least one tumor-specific mutation will be found in 33.42% of subjects in the population. The population of subjects may be suffering from LUSC; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"LUSC"; and at least one of a set of two of the at least one tumor-specific mutation will be found in 7.87% of subjects in the population. The population of subjects may be suffering from OV; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"OV"; and at least one of a set of ten of the at least one tumor-specific mutation will be found in 22.78% of subjects in the population. The population of subjects may be suffering from READ; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"READ"; and at least one of a set of two of the at least one tumor-specific mutation will be found in 20.51% of subjects in the population. The population of subjects may be suffering from SKCM; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"SKCM"; and at least one of a set 64 of the at least one tumor-specific mutation will be found in 90.91% of subjects in the population. The population of subjects may be suffering from UCEC; the at least one tumor-specific mutation comprises any combination of

mutations in Table 8 with an exemplary disease of"UCEC"; and at least one of a set of 30 of the at least one tumor-specific mutation will be found in 67.74% of subjects in the population. The population of subjects may be suffering from ACC; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"ACC"; and at least one of a set of 161 of the at least one tumor-specific mutation will be found in 50% of subjects in the population. The population of subjects may be suffering from CESC; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"CESC"; and at least one of a set of four of the at least one tumor-specific mutation will be found in 23.71% of subjects in the population. The population of subjects may be suffering from CRC; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"CRC"; and at least one of a set of 15 of the at least one tumor-specific mutation will be found in 56.65% of subjects in the population. The population of subjects may be suffering from DLBCL; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"DLBCL"; and at least one of a set of 2 of the at least one tumor-specific mutation will be found in 13.79% of subjects in the population. The population of subjects may be suffering from KICH; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"KICH"; and at least one of a set of 24 of the at least one tumor-specific mutation will be found in 50% of subjects in the population. The population of subjects may be suffering from KIRP; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"KIRP"; and at least one of a set of nine of the at least one tumor-specific mutation will be found in 42.24% of subjects in the population. The population of subjects may be suffering from LIHC; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"LIHC"; and at least one of a set of 2 of the at least one tumor-specific mutation will be found in 6.57% of subjects in the population. The population of subjects may be suffering from MM; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"MM"; and at least one of a set of 6 of the at least one tumor-specific mutation will be found in 23.9% of subjects in the population. The population of subjects may be suffering from PRAD; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"PRAD"; and at least one of a set of 24 of the

at least one tumor-specific mutation will be found in 39.85% of subjects in the population. The population of subjects may be suffering from STAD; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"STAD"; and at least one of a set of 150 of the at least one tumor-specific mutation will be found in 48.79% of subjects in the population. The population of subjects may be suffering from TGCT; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"TGCT"; and at least one of a set of 14 of the at least one tumor-specific mutation will be found in 51.61% of subjects in the population. The population of subjects may be suffering from THCA; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"THCA"; and at least one of a set of five of the at least one tumor-specific mutation will be found in 69.88% of subjects in the population. The population of subjects may be suffering from UCS; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"UCS"; and at least one of a set of two of the at least one tumor-specific mutation will be found in 16.07% of subjects in the population. The population of subjects may be suffering from PAAD; the at least one tumor-specific mutation comprises any combination of mutations in Table 8 with an exemplary disease of"PAAD"; and at least one of a set of 53 of the at least one tumor-specific mutation will be found in 50% of subjects in the population. The population of subjects may also be suffering from a solid tumor. The solid tumor may be clear cell Renal Cell Carcinoma (ccRCC), melanoma, sarcoma, or a cancer of the bladder, colon, brain, breast, head and neck, endometrium, lung, ovary, pancreas or prostate. The population of subjects may be suffering from a liquid tumor. The liquid tumor may be Non-Hodgkin's lymphoma or leukemia.

[0012] In another embodiment, the at least one tumor-specific mutation has an incidence of at least 500 patients a year in the population of subjects suffering from cancer, and wherein the at least one mutation may be a mutation listed for the population in Table 9. The at least one neoantigenic peptide may be at least one peptide listed in Table 9.

[0013] In another embodiment, the population suffering from cancer is being treated with a drug or therapy. The population suffering from cancer may have been previously treated with, is currently being treated with, or is selected to treated with ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK or antiestrogen therapy.

[0014] In another embodiment, the composition comprises at least one neoantigenic peptide capable of eliciting an immune response against a tumor present in at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% of subjects in a population of subjects suffering from cancer.

[0015] In another embodiment, at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% of subjects in the population has at least one tumor-specific mutation present in the composition; and at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% of subjects in the population has at least one HLA protein which binds to a tumor-specific neoepitope present in the composition.

[0016] In one embodiment, the tumor-specific mutations comprise splice-variant mutations, point mutations, and/or frameshift mutations. In another embodiment, the tumor-specific mutations comprise drug resistance mutations. In one embodiment, the neoantigenic peptides include not only the resulting mutated neoantigen protein sequence, but a long peptide region surrounding and including the mutation and includes all contiguous segments within it (see Tables 1-4). In one embodiment, the tumor-specific mutations are present in one or more genes encoding a protein selected from the group consisting of Programmed Death-Ligand 1 (PD-L1), androgen receptor (AR), Bruton's Tyrosine Kinase (BTK), Epidermal Growth Factor Receptor (EGFR), BCR-Abl, c-kit, PIK3CA, HER2, EML4-ALK, KRAS, ALK, ROS1, AKT1, BRAF, MEK1, MEK2, NRAS, RAC1, and ESR1. In one embodiment, the tumor-specific mutations are present in one or more genes listed in any of the Tables presented herein. In one embodiment, the at least one tumor-specific mutation is derived from alternative splicing of PD-L1 or AR. In one embodiment, the at least one tumor-specific mutation is derived from splice variant sPD-L1, AR-V1 or AR-V7. In one embodiment, the least one tumor-specific mutation is a drug resistance mutation selected from the group consisting of BTK/C481S, EGFR/T790M, BCR-Abl/T315I, BCR-Abl/Y253H, BCR-Abl/E255K, BCR-Abl/E255V, c-kit/T670I, PIK3CA/E545K, PIK3CA/E542K, HER2/G776(YVMA), HER2/E545K, EML4-ALK/G1269A, KRAS/G12V/D, ALK/L1196M, ALK/G1202R, ALK/S1206Y, ALK/1151T(ins), ALK/F1174C, ROS1/G2032R, AKT1/E17K, BRAF/V600E, MEK1/Q56P, MEK1/E203K, MEK1/C121S, MEK1/V60E, MEK1/G128V, MEK1/V154I, MEK1/P124S, MEK1/P124L, NRAS/Q61K/L/R, NRAS/T58I, MEK2/C125S, RAC1/P29S, ESR1/S463P, AR/V534E, AR/P535H, AR/L536Q, AR/L536R, AR/Y537C, AR/Y537S, AR/Y537N, AR/D538G and AR/F876L. In one embodiment, the drug

resistance mutation is induced by treatment with ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK or antiestrogen therapy. In another embodiment, a subject has a drug resistance mutation before treatment.

[0017] In another embodiment, the composition comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 neoantigenic peptides. The composition may include 15 to 20 neoantigenic peptides. The composition may include greater than 100, 200, or 300 neoantigenic peptides. Each neoantigenic peptide may be from about 5 to about 50 amino acids in length.

[0018] In another embodiment, the pharmaceutical composition is an immunogenic or vaccine composition. The pharmaceutical composition may further comprise an immunomodulator or adjuvant. The immunodulator or adjuvant may be selected from the group consisting of poly-ICLC, 1018 ISS, aluminum salts, Amplivax, AS15, BCG, CP-870,893, CpG7909, CyaA, cyclic di-nucleotides such as STING, dSLIM, GM-CSF, IC30, IC31, Imiquimod, ImuFact IMP321, IS Patch, ISS, ISCOMATRIX, Juvlmmune, LipoVac, MF59, monophosphoryllipid A, Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, OK-432, OM-174, OM-197-MP-EC, ONTAK, PepTel®, vector system, PLGA microparticles, resiquimod, SRL172, Virosomes and other Virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, and Aquila's QS21 stimulon.

[0019] In another embodiment, the pharmaceutical composition comprises one or more neoantigenic peptides as defined in Table 1, 2, 3 or 4.

[0020] In one embodiment, each tumor-specific neoepitope binds to HLA-A, -B or –C or to HLADRB, HLADBM XXXXX with a K_D of less than 500 nM.

[0021] In another aspect, the present invention relates to a method of treating or preventing a tumor in a subject in need thereof by administering to the subject any pharmaceutical composition as described herein.

[0022] In one embodiment, a method of treating or preventing a tumor in a patient in need thereof is provided, comprising administering to a patient a composition comprising at least one neoantigenic peptide and a pharmaceutically acceptable carrier, each at least one neoantigenic peptide comprising a tumor-specific neoepitope capable of binding to an HLA protein in a subject, each tumor-specific neoepitope comprising a tumor-specific mutation present in a tumor, wherein the composition comprises at least one neoantigenic peptide comprising a tumor-

specific mutation present in a tumor in at least 1% of subjects in a population of subjects suffering from cancer; the composition comprises at least one neoantigenic peptide comprising a tumor-specific neoepitope which binds to an HLA protein present in at least 5% of subjects in the population of subjects suffering from cancer; and the composition comprises at least one neoantigenic peptide capable of eliciting an immune response against a tumor present in at least 5% of the subjects in the population of subjects suffering from cancer.

[0023] In one embodiment, the population of subjects is suffering from adrenocortical carcinoma (ACC), bladder urothelial carcinoma (BLCA), breast invasive carcinoma (BRCA), cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC), colon adenocarcinoma (COAD), Chronic lymphocytic Leukaemia (CLL), colorectal cancer (CRC), Diffuse large B-cell lymphoma (DLBCL), glioblastoma multiforme (GBM), head and neck squamous cell carcinoma (HNSC), kidney chromophobe (KICH), kidney renal clear cell carcinoma (KIRC), kidney renal papillary cell carcinoma (KIRP), acute myeloid leukemia (LAML), liver hepatocellular carcinoma (LIHC), lung adenocarcinoma (LUAD), lung squamous cell carcinoma (LUSC), multiple myeloma (MM), ovarian serous cystadenocarcinoma (OV), pancreatic adenocarcinoma (PAAD), prostate adenocarcinoma (PRAD), rectum adenocarcinoma (READ), skin cutaneous melanoma (SKCM), stomach adenocarcinoma (STAD), testicular germ cell tumors (TGCT), thyroid adenocarcinoma (THCA), uterine corpus endometrioid carcinoma (UCEC), or uterine carcinosarcoma (UCS). In one embodiment, the population of subjects is suffering from a solid tumor. The solid tumor may be clear cell Renal Cell Carcinoma (ccRCC), melanoma, sarcoma, or a cancer of the bladder, colon, brain, breast, head and neck, endometrium, lung, ovary, pancreas or prostate. In one embodiment, the population of subjects is suffering from a liquid tumor. The liquid tumor may be Non-Hodgkin's lymphoma or leukemia.

[0024] In one embodiment, the population suffering from cancer was treated with, is being treated with, or is selected to treated with ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK or antiestrogen therapy.

[0025] In one embodiment, the at least one neoantigenic peptide is capable of eliciting an immune response against a tumor present in at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% of subjects in the population of subjects suffering from cancer. In one embodiment, at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% of subjects in the population has at least one tumor-specific mutation present in the composition

and, at least 5%, 10%, 20%, 30%, 40%, 50%, 60%, 70%, 80%, 90%, 95% or 99% of subjects in the population has at least one HLA protein which binds to a tumor-specific neoepitope present in the composition.

[0026] In another embodiment, the tumor-specific mutations comprise splice-variant mutations, point mutations, and/or frameshift mutations. The tumor-specific mutations may be drug resistance mutations. The tumor-specific mutations may be present in one or more genes encoding a protein selected from the group consisting of Programmed Death-Ligand 1 (PD-L1), androgen receptor (AR), Bruton's Tyrosine Kinase (BTK), Epidermal Growth Factor Receptor (EGFR), BCR-Abl, c-kit, PIK3CA, HER2, EML4-ALK, KRAS, ALK, ROS1, AKT1, BRAF, MEK1, MEK2, NRAS, RAC1, and ESR1. The tumor-specific mutations may be present in one or more genes listed in any of the Tables. The at least one tumor-specific mutation may be derived from alternative splicing of PD-L1 or AR. The at least one tumor-specific mutation may be derived from splice variant sPD-L1, AR-V1 or AR-V7.

[0027] In one embodiment, the at least one tumor-specific mutation is a drug resistance mutation selected from the group consisting of BTK/C481S, EGFR/T790M, BCR-Abl/T315I, BCR-Abl/Y253H, BCR-Abl/E255K, BCR-Abl/E255V, c-kit/T670I, PIK3CA/E545K, PIK3CA/E542K, HER2/G776(YVMA), HER2/E545K, EML4-ALK/G1269A, KRAS/G12V/D, ALK/L1196M, ALK/G1202R, ALK/S1206Y, ALK/1151T(ins), ALK/F1174C, ROS1/G2032R, AKT1/E17K, BRAF/V600E, MEK1/Q56P, MEK1/E203K, MEK1/C121S, MEK1/V60E, MEK1/G128V, MEK1/V154I, MEK1/P124S, MEK1/P124L, NRAS/Q61K/L/R, NRAS/T58I, MEK2/C125S, RAC1/P29S, ESR1/S463P, AR/V534E, AR/P535H, AR/L536Q, AR/L536R, AR/Y537C, AR/Y537S, AR/Y537N, AR/D538G and AR/F876L. The drug resistance mutation may be induced by treatment with ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK or antiestrogen therapy.

[0028] In another embodiment, the composition comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 neoantigenic peptides. In a preferred embodiment, the composition comprises 15 to 20 neoantigenic peptides.

[0029] In another embodiment, each neoantigenic peptide is from about 5 to about 50 amino acids in length.

[0030] In another embodiment, the composition is an immunogenic or vaccine composition. For instance, the immunogenic or vaccine composition may comprise an immunomodulator or

adjuvant. The immunodulator or adjuvant may be selected from the group consisting of poly-ICLC, 1018 ISS, aluminum salts, Amplivax, AS15, BCG, CP-870,893, CpG7909, CyaA, cyclic di-nucleotides such as STING, dSLIM, GM-CSF, IC30, IC31, Imiquimod, ImuFact IMP321, IS Patch, ISS, ISCOMATRIX, Juvlmmune, LipoVac, MF59, monophosphoryllipid A, Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, OK-432, OM-174, OM-197-MP-EC, ONTAK, PepTel®, vector system, PLGA microparticles, resiquimod, SRL172, Virosomes and other Virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, and Aquila's QS21 stimulon.

[0031] In one embodiment, the composition comprises one or more neoantigenic peptides as defined in Table 1, 2, 3 or 4.

[0032] In one embodiment, each tumor-specific neoepitope binds to HLA-A, -B or –C or to HLADRB, HLADBM XXXXX with a K_D of less than 500 nM.

[0033] In another aspect, the present invention provides a method of prophylactic cancer treatment comprising selecting a cancer drug for a patient in need thereof, the drug selected from the group consisting of ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK and antiestrogen therapy; and administering prophylactically to the subject, before drug resistant mutations can be detected, a pharmaceutical composition comprising neoantigenic peptides derived from drug resistant mutations associated with the selected cancer drug.

[0034] The shared neoantigen immunogenic composition can be administered via subcompositions, each containing a portion of the neoantigens, and sub-compositions can be administered to different places on the subject or patient; for instance, a composition comprising 20 different neoantigens, can be administered in four (4) subcompositions, each containing 5 of the 20 different neoantigens, and the four (4) subcompositions can be administered so as to endeavor to deliver each subcomposition to a separate set of draining lymph nodes of the patient, e.g., to each of the arms and legs (e.g., thigh or upper thigh or near buttocks or lower back on each side of the patient) so as to endeavor to deliver fewer neoantigens to each set of draining lymph nodes of the patient or subject and thereby limit competition between neoantigens. Of course, the number of locations and hence number of subcompositions can vary, e.g., the skilled practitioner could consider administration at or near the spleen to have a fifth point of administration, and the skilled practitioner can vary the locations such that only one, two

or three are used (e.g., each arm and a leg, each of legs and one arm, each of the legs and no arms, or only both arms). The shared neoantigen immunogenic composition administered at the aforementioned various intervals can be different formulations, and the subcompositions administered at different places on the subject or patient during a single administration can be different compositions. For instance, a first administration can be of a whole shared neoantigen immunogenic composition and a next or later administration can be of a vector (e.g., viral vector or plasmid) that has expression of antigen(s) in vivo. Likewise, in the administration of different subcompositions to different locations on the patient or subject, some of the subcompositions can comprise a whole antigen and some of the subcompositions can comprise a vector (e.g., viral vector or plasmid) that has expression of antigen(s) in vivo. And some compositions and subcompositions can comprise both vector(s) (e.g., viral vector or plasmid) that has / have expression of antigen(s) in vivo and whole antigens. Some vectors (e.g., poxvirus) that have expression of antigen(s) in vivo can have an immunostimulatory or adjuvanting effect, and hence compositions or subcompositions that contain such vectors can be self-adjuvanting. Also, by changing up the nature of how the antigens are presented to the immune system, the administrations can "prime" and then "boost" the immune system. And in this text, when there is mention of a "vaccine" it is intended that the invention comprehends immunogenic compositions, and when there is mention of a patient or subject it is intended that such an individual is a patient or subject in need of the herein disclosed treatments, administrations, compositions, and generally the subject invention.

[0035] Moreover, the invention applies to the use of any type of expression vector, such as a viral expression vector, e.g., poxvirus (e.g., orthopoxvirus or avipoxvirus such as vaccinia virus, including Modified Vaccinia Ankara or MVA, MVA-BN, NYVAC according to WO-A-92/15672, fowlpox, e.g., TROVAX, canarypox, e.g., ALVAC (WO-A-95/27780 and WO-A-92/15672) pigeonpox, swinepox and the like), adenovirus, AAV, herpesvirus, and lentivirus; or a plasmid or DNA or nucleic acid molecule vector. Some vectors that are cytoplasmic, such as poxvirus vectors, may be advantageous. However adenovirus, AAV and lentivirus can also be advantageous to use in the practice of the invention.

[0036] In a ready-for-use, especially reconstituted, shared neoantigen immunogenic composition, the vector, e.g., viral vector, is present in the quantities within the ambit of the

skilled person from this disclosure and the knowledge in the art (such as in patent and scientific literature cited herein).

[0037] Whole antigen or vector, e.g., recombinant live vaccines may exist in a freeze-dried form allowing their storage and are reconstituted immediately before use in a solvent or excipient, which can include an adjuvant as herein discussed.

[0038] The subject of the invention is therefore also a vaccination or immunization set or kit comprising, packaged separately, freeze-dried vaccine and a solution, advantageously including an adjuvant compound as herein discussed for the reconstitution of the freeze-dried vaccine.

[0039] The subject of the invention is also a method of vaccination or immunization comprising or consisting essentially of or consisting of administering, e.g., by the parenteral, preferably subcutaneous, intramuscular or intradermal, route or by the mucosal route a vaccine or immunogenic composition in accordance with the invention at the rate of one or more administrations. Optionally this method includes a preliminary step of reconstituting the freeze-dried shared neoantigen immunogenic composition (e.g., if lyophilized whole antigen or vector) in a solution, advantageously also including an adjuvant.

[0040] In one embodiment, the shared neoantigen immunogenic composition is administered at a dose of about 10 μg to 1 mg per 70 kg individual as to each neoantigenic peptide. In another embodiment, the shared neoantigen immunogenic composition is administered at an average weekly dose level of about 10 μg to 2000 μg per 70 kg individual as to each neoantigenic peptide. In another related embodiment, the administration is intravenous. In one embodiment, the shared neoantigen immunogenic composition is administered intravenously or subcutaneously.

[0041] In another embodiment, the method further comprises (a) obtaining a sample of tumor tissue from each subject; (b) detecting one or more of the tumor-specific mutations in the sample; and (c) selecting a subject from the population of subjects for treatment with the at least one neoantigenic peptides if at least one of the tumor-specific mutations are detected in the sample from the subject.

[0042] In another embodiment, the method further comprises (a) determining HLA allotypes present in each subject; and (b) selecting a subject from the population of subjects for treatment with the at least one neoantigenic peptides if one or more HLA allotypes present in the subject

binds to one or more of the tumor-specific neoepitopes present in the at least one neoantigenic peptides.

[0043] Embodiments of the present invention relate to compositions and methods using shared neoantigens, which (unlike shared native (non-mutated) antigens derived from genes differentially expressed in tumors) have desirable properties such as not being subject to the immune-dampening effects of central tolerance and high tumor specificity. This is because the neoantigens are expressed only in tumor tissue, e.g. are generated by tumor-specific mutations or splicing defects. Such splice variants or mutations may generate immunogenic epitopes across a variety of HLA alleles, thus covering a significant proportion of the population. Moreover, because these mutations may be present in a significant proportion of subjects suffering from cancer, the compositions described herein do not require sequencing of whole genomes of subjects and may be used as an "off-the-shelf" product to treat multiple subjects. For instance, the method may simply involve detecting in a tumor sample from the subject one or more of the specific mutations present in the composition, and administering the composition to subjects in which at least one mutation is present. This is in contrast to methods using patient-specific neoantigen mixtures, which require whole genome or whole exome sequencing of each subject and the production of personalized treatment compositions.

[0044] Other embodiments relate to a combination therapy wherein the methods of treatment using a shared neoantigen composition of the present invention are used in concert with a current drug regimen. The shared neoantigen composition may be administered prophylactically. In one embodiment, a patient in need thereof is treated with chemotherapy and/or a targeted therapy in combination with a shared neoantigen immunogenic composition before a drug resistance mutation can be detected. The shared neoantigen immunogenic composition can be tailored to include neoantigen peptides specific to the resistance mutations associated with a chosen therapy. In another embodiment, the shared neoantigen composition is administered before the subject is treated with a chemotherapy and/or a targeted therapy, to generate an immune response to cells harboring a drug resistance mutation before such cells develop. The administering can be serially or sequentially or at substantially the same time or substantially simultaneously. For example, the administering of the shared neoantigen immunogenic composition and the administering of a cancer therapy can be at about the same time or substantially simultaneously. Alternatively, the administering of the shared neoantigen immunogenic composition can be on

one time schedule, e.g., weekly, biweekly, every three weeks, monthly, bimonthly, every quarter year (every three months), every third of a year (every four months), every five months, twice yearly (every six months), every seven months, every eight months, every nine months, every ten months, every eleven months, annually or the like, and the administering of the cancer therapy can be on a different schedule that is typical for the therapy such that the subject or patient has two different treatment schedules running concomitantly and the administering of the shared neoantigen immunogenic composition and the administering of the cancer therapy can be sequentially or serially. In preferred embodiments the subject may be treated with ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK or antiestrogen therapy.

[0045] In another aspect the present invention provides a diagnostic method for early detection and tracking of cancer progression by determining the presence of at least one neoantigenic peptide of the present invention in a patient sample. The patient sample may be derived from blood, sputum, saliva, urine, tumor tissue, lymphatic fluid, semen or feces.

[0046] In one embodiment, the diagnostic method is used before administering the shared neoantigen composition as described herein. The diagnostic method may include comparing the amount of shared neoantigen mutations in a series of at least two samples taken during treatment with a cancer therapy and/or shared neoantigen composition. Not being bound by a theory, an increase or decrease in shared neoantigen mutations can be used to determine treatment efficacy.

[0047] In one embodiment, the mutated genes can be detected using PCR based methods or sequencing. Reverse transcription PCR (RT-PCR) can be used to detect mutations in transcribed neoantigen genes. Additionally, any sequencing technique can be used to determine the presence of a mutation. In a preferred embodiment, pyrosequencing is used. The present invention also provides for a kit that includes primers that are specific to sequences encompassing the neoantigen mutations.

[0048] In another embodiment the mutated genes are detected by immunological detection methods. Antibodies specific to the shared neoantigen mutations can be used to detect the muations. The antibodies may be bound to an array. The array may include antibodies to detect more than one of the shared neoantigen mutations of the present invention. The antibodies can be configured for use in an ELISA assay. Therefore, a composition or kit may be provided that includes antibodies specifically recognizing the shared neoantigens of the present invention.

[0049] In another aspect the present invention provides a method of treating or preventing a tumor in a population of subjects in need thereof, comprising administering to a subject an agent comprising an extracellular ligand-binding domain recognizing a tumor-specific neoepitope comprising a tumor-specific mutation having an incidence of at least 1% of subjects in the population. The agent may be an antibody, antibody fragment, antibody drug conjugate, aptamer, CAR, or T cell receptor. The antibody or antibody fragment may be humanized, fully humanized, or chimeric. The antibody fragment may be a nanobody, Fab, Fab', (Fab')2, Fv, ScFv, diabody, triabody, tetrabody, Bis-scFv, minibody, Fab2, or Fab3 fragment. The tumor-specific mutation may be a mutation listed for any population in Table 9. The tumor-specific mutation may be within a gene containing an extracellular domain. The tumor-specific mutation may be FGFR3 S249C, ERBB3 V104M, EGFR L858R, MUC4 H4205Q, PDGFRA R483fs, TMEM52 23_26LLPL>L, or PODXL 28_30PSP>P. The tumor-specific mutation may be within the extracellular domain. The tumor-specific mutation comprises FGFR3 S249C or ERBB3 V104M. Not being bound by a theory, the presence of a neoepitope in a protein with an extracellular domain allows the neoepitope to be presented on the surface of a cell. Not being bound by a theory, the presence of a neoepitope in the extracellular domain allows the neoepitope to be presented on the surface of a cell.

[0050] The invention is further described by the following numbered paragraphs:

1. An isolated neoantigenic peptide comprising a tumor-specific neoepitope defined in Tables 1-9, wherein the isolated neoantigenic peptide is not a native polypeptide.

2. An isolated neoantigenic peptide 100 amino acids or less in length which comprises a tumor-specific neoepitope defined in Tables 1-9.

3. The isolated neoantigenic peptide of paragraph 1 or 2, which is between about 5 to about 50 amino acids in length.

4. The isolated neoantigenic peptide of any of paragraphs 1-3, which is between about 15 to about 35 amino acids in length.

5. The isolated neoantigenic peptide of paragraph 4, which is about 15 amino acids or less in length.

6. The isolated neoantigenic peptide of paragraph 5, which is between about 8 and about 11 amino acids in length.

7. The isolated neoantigenic peptide of paragraph 6, which is 9 or 10 amino acids in length.

8. The isolated neoantigenic peptide of any of paragraphs 1-7, which binds major histocompatibility complex (MHC) class I.

9. The isolated neoantigenic peptide of paragraph 8, which binds MHC class I with a binding affinity of less than about 500 nM.

10. The isolated neoantigenic peptide of any of paragraphs 1-3, which is about 30 amino acids or less in length.

11. The isolated neoantigenic peptide of paragraph 10, which is between about 6 and about 25 amino acids in length.

12. The isolated neoantigenic peptide of paragraph 11, which is between about 15 and about 24 amino acids in length.

13. The isolated neoantigenic peptide of paragraph 11, which is between about 9 and about 15 amino acids in length.

14. The isolated neoantigenic peptide of any of paragraphs 1-3 and 10-13, which binds MHC class II.

15. The isolated neoantigenic peptide of paragraph 14, which binds MHC class II with a binding affinity of less than about 1000 nM.

16. The isolated neoantigenic peptide of any of paragraphs 1-15, further comprising flanking amino acids.

17. The isolated neoantigenic peptide of paragraph 16, wherein the flanking amino acids are not native flanking amino acids.

18. The isolated neoantigenic peptide of any of paragraphs 1-17, which is linked to at least a second neoantigenic peptide.

19. The isolated neoantigenic peptide of paragraph 18, wherein peptides are linked using a poly-glycine or poly-serine linker.

20. The isolated neoantigenic peptide of paragraph 18 or 19, wherein the second neoantigenic peptide binds MHC class I or class II with a binding affinity of less than about 1000 nM.

21. The isolated neoantigenic peptide of paragraph 20, wherein the second neoantigenic peptide binds MHC class I or class II with a binding affinity of less than about 500 nM.

22. The isolated neoantigenic peptide of paragraph 20 or 21, wherein both of the neoepitopes bind to human leukocyte antigen (HLA) -A, -B, -C, -DP, -DQ, or -DR.

23. The isolated neoantigenic peptide of any of paragraphs 20-22, wherein the isolated neoantigenic peptide and the second neoantigenic peptide binds a class I HLA or the isolated neoantigenic peptide and the second neoantigenic peptide binds a class II HLA.

24. The isolated neoantigenic peptide of any of paragraphs 20-22, wherein the isolated neoantigenic peptide binds a class II HLA and the second neoantigenic peptide binds a class I HLA or the isolated neoantigenic peptide binds a class I HLA and the second neoantigenic peptide binds a class II HLA.

25. The isolated neoantigenic peptide of any of paragraphs 1-24, further comprising modifications which increase in vivo half-life, cellular targeting, antigen uptake, antigen processing, MHC affinity, MHC stability, or antigen presentation.

26. The isolated neoantigenic peptide of paragraph 25, wherein the modification is conjugation to a carrier protein, conjugation to a ligand, conjugation to an antibody, PEGylation, polysialylation HESylation, recombinant PEG mimetics, Fc fusion, albumin fusion, nanoparticle attachment, nanoparticulate encapsulation, cholesterol fusion, iron fusion, acylation, amidation, glycosylation, side chain oxidation, phosphorylation, biotinylation, the addition of a surface active material, the addition of amino acid mimetics, or the addition of unnatural amino acids.

27. The isolated neoantigenic peptide of paragraph 25, wherein the cells that are targeted are antigen presenting cells.

28. The isolated neoantigenic peptide of paragraph 27, wherein the antigen presenting cells are dendritic cells.

29. The isolated neoantigenic peptide of paragraph 29, wherein the dendritic cells are targeted using the CD141, DEC205, or XCR1 marker.

30. A pharmaceutical composition comprising at least one neoantigenic peptide and a pharmaceutically acceptable carrier, each at least one neoantigenic peptide comprising a tumor-specific neoepitope capable of binding to an HLA protein in a subject, each tumor-specific neoepitope comprising a tumor-specific mutation present in a tumor, wherein:

(a) the composition comprises at least one neoantigenic peptide comprising a tumor-specific mutation present in a tumor in at least 1% of subjects in a population of subjects suffering from cancer;

(b) the composition comprises at least one neoantigenic peptide comprising a tumor-specific neoepitope which binds to an HLA protein present in at least 5% of subjects in the population of subjects suffering from cancer; or

(c) the composition comprises at least one neoantigenic peptide capable of eliciting an immune response against a tumor present in at least 5% of the subjects in the population of subjects suffering from cancer.

31. The pharmaceutical composition of paragraph 30, wherein the population of subjects is suffering from adrenocortical carcinoma (ACC), bladder urothelial carcinoma (BLCA), breast invasive carcinoma (BRCA), cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC), colon adenocarcinoma (COAD), Chronic lymphocytic Leukaemia (CLL), colorectal cancer (CRC), Diffuse large B-cell lymphoma (DLBCL), glioblastoma multiforme (GBM), head and neck squamous cell carcinoma (HNSC), kidney chromophobe (KICH), kidney renal clear cell carcinoma (KIRC), kidney renal papillary cell carcinoma (KIRP), acute myeloid leukemia (LAML), liver hepatocellular carcinoma (LIHC), lung adenocarcinoma (LUAD), lung squamous cell carcinoma (LUSC), multiple myeloma (MM), ovarian serous cystadenocarcinoma (OV), pancreatic adenocarcinoma (PAAD), prostate adenocarcinoma (PRAD), rectum adenocarcinoma (READ), skin cutaneous melanoma (SKCM), stomach adenocarcinoma (STAD), testicular germ cell tumors (TGCT), thyroid adenocarcinoma (THCA), uterine corpus endometrioid carcinoma (UCEC), or uterine carcinosarcoma (UCS).

32. The pharmaceutical composition of paragraph 30 or 31, wherein the population suffering from cancer was treated with, is being treated with, or is selected to be treated with a cancer therapeutic, optionally ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK inhibitor or antiestrogen therapy..

33. The pharmaceutical composition of any of paragraphs 30-33, wherein the tumor-specific mutations comprise splice-variant mutations, point mutations, and/or frameshift mutations.

34. The pharmaceutical composition of any of paragraphs 30-33, wherein the at least one neoantigenic peptide comprises at least one neoantigenic peptide derived from a long peptide

region flanking and including the tumor specific mutation, and wherein all contiguous segments within the long peptide are included.

35. The pharmaceutical composition of any of paragraphs 30-34, wherein the tumor-specific mutations are present in one or more genes listed in Tables 1-9.

36. The pharmaceutical composition of any of paragraphs 30-35, wherein the composition comprises at least one neoantigenic peptide as defined in any of Tables 1-9.

37. The pharmaceutical composition of any of paragraphs 30-36, wherein the tumor-specific mutations are present in one or more genes encoding a protein selected from the group consisting of Programmed Death-Ligand 1 (PD-L1), androgen receptor (AR), Bruton's Tyrosine Kinase (BTK), Epidermal Growth Factor Receptor (EGFR), BCR-Abl, c-kit, PIK3CA, HER2, EML4-ALK, KRAS, ALK, ROS1, AKT1, BRAF, MEK1, MEK2, NRAS, RAC1, and ESR1.

38. The pharmaceutical composition of paragraph 37, wherein at least one tumor-specific mutation is derived from alternative splicing of PD-L1 or AR.

39. The pharmaceutical composition of paragraph 38, wherein at least one tumor-specific mutation is derived from splice variant sPD-L1, AR-V1 or AR-V7.

40. The pharmaceutical composition of any of paragraphs 30-39, wherein the tumor-specific mutations comprise drug resistance mutations.

41. The pharmaceutical composition of paragraph 40, wherein at least one tumor-specific mutation is a drug resistance mutation selected from the group consisting of BTK/C481S, EGFR/T790M, BCR-Abl/T315I, BCR-Abl/Y253H, BCR-Abl/E255K, BCR-Abl/E255V, c-kit/T670I, PIK3CA/E545K, PIK3CA/E542K, HER2/G776(YVMA), HER2/E545K, EML4-ALK/G1269A, KRAS/G12V/D, ALK/L1196M, ALK/G1202R, ALK/S1206Y, ALK/1151T(ins), ALK/F1174C, ROS1/G2032R, AKT1/E17K, BRAF/V600E, MEK1/Q56P, MEK1/E203K, MEK1/C121S, MEK1/V60E, MEK1/G128V, MEK1/V154I, MEK1/P124S, MEK1/P124L, NRAS/Q61K/L/R, NRAS/T58I, MEK2/C125S, RAC1/P29S, ESR1/S463P, AR/V534E, AR/P535H, AR/L536Q, AR/L536R, AR/Y537C, AR/Y537S, AR/Y537N, AR/D538G and AR/F876L.

42. The pharmaceutical composition of any of paragraphs 30-41, wherein the at least one tumor-specific mutation has an incidence of at least 500 patients a year in the population of subjects suffering from cancer, and wherein the at least one mutation comprises a mutation listed for the population in Table 9.

43. The pharmaceutical composition of paragraph 42, wherein the at least one neoantigenic peptide comprises at least one peptide listed in Table 9.

44. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from CLL; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of SF3B1:p.K700E, MYD88:p.L273P, NOTCH1:p.P2514fs, ABCA11P:p.E901D, AHNAK:p.D3823E, ZNF814:p.E348D, AHNAK:p.V1220I, AHNAK:p.H1203N, ANKRD30A:p.A232V, APOOL:p.I138L, EGR2:p.H397N, MKI67:p.H2213D, NRAS:p.Q61R, PLIN4:p.M691V, XPO1:p.E571K, ZCRB1:p.L76F, ZNF700:p.N652H, ZNF700:p.Q654R, ZNF844:p.D458H, AHNAK:p.A4046V, ANKRD36:p.P337R, C1orf170:p.T203I, CAST:p.D639E, EGR2:p.E369K, GPR123:p.L630P, IKZF3:p.L162R, MUC4:p.P4224R, OR9Q1:p.M34L, PKD2:p.Y486F, PRAMEF11:p.R104Q, SYNJ1:p.I681F, TP53:p.R248Q, TP53:p.R248W, TRPV2:p.L627del, ZNF254:p.S498A, ZNF732:p.A459T, ZNF749:p.E530Q, ZNF845:p.M423I, ABCA11P:p.G900E, ACRC:p.E243D, ACRC:p.A244V, ACSL3:p.T188S, ADAMTS2:p.D948N, AGAP6:p.S127I, AHNAK:p.A2114G, ANKRD36:p.D1014Y, ARID3A:p.G550fs, ARID4A:p.D1154E, ATP2B4:p.R183H, ATRNL1:p.L1244F, BNC1:p.Y937N, BRAF:p.K601N, BTLA:p.Q86K, C14orf177:p.G90V, C2orf44:p.N456K, C3orf15:p.R552Q, CACNA2D1:p.Y376N, CALD1:p.E340K, CCDC15:p.P488H, CCDC79:p.N440T, CCNB3:p.A932T, CD109:p.L470Q, CD209:p.Q189L, CKAP2:p.*684K, CMA1:p.I81K, CMIP:p.A230T, CNTNAP4:p.I12F, CRYM:p.*315K, DICER1:p.E1705K, DPCR1:p.L716P, EIF3A:p.M1093L, EIF4G3:p.R8H, ETFDH:p.I281F, EWSR1:p.Y656C, F5:p.L1332P, F5:p.L1253F, FAM50A:p.H317R, FBXL13:p.S102R, FBXW7:p.R465H, FHL1:p.D184E, FILIP1:p.I522K, FRG1B:p.Q39K, GNB1:p.I80T, GPR110:p.R443G, GPR98:p.Y6152F, HDGFL1:p.188_189insA, IGF2BP2:p.T186S, IL1R2:p.L364fs, KIAA1109:p.L4680P, KRAS:p.G13D, KRTAP19-1:p.G61S, MAF:p.G53fs, MAGEC1:p.L609H, MAP2K1:p.K57N, MED12:p.L36R, MED12:p.G44S, METAP2:p.Y137N, METTL9:p.Y57F, MGP:p.V15L, MKI67:p.R2222K, MUC16:p.T11005I, MUC4:p.S3941N, MUC4:p.S3941G, MUC4:p.V3091L, MUC4:p.S2951Y, MUC4:p.A2841S, MUC4:p.S2760A, MUC4:p.T2335M, MUC4:p.T1627K, MUC4:p.T1547S, MUC4:p.H1133Q, MYD88:p.M240T, NEDD4L:p.P194del, NEFH:p.S704T, NRG4:p.G21fs, OR2A25:p.S105C, OR4C16:p.Y63F, OR4N4:p.L150fs, PABPC1:p.K254fs, PIWIL1:p.P372fs,

PLCD3:p.E499fs, PLEKHB1:p.S146P, PPIL4:p.S382R, PRDM4:p.*802K, PRG4:p.N675H, PRKAB1:p.P104H, R3HDM2:p.S592G, R3HDM2:p.S588N, R3HDM2:p.R206W, RPS2:p.R200G, RPTN:p.G364S, SF3B1:p.K666E, SF3B1:p.N626Y, SF3B1:p.Y623C, SIX3:p.I27L, SLC39A7:p.L456fs, SLC6A9:p.R94K, TFG:p.A382V, TGOLN2:p.K83R, TGOLN2:p.T80S, TLR2:p.D327V, TNKS2:p.T619fs, TP53:p.R273H, TP53:p.C242F, TP53:p.R175H, TWISTNB:p.H306Q, UBXN7:p.A276V, WDR78:p.N110K, XIRP2:p.V3008E, ZNF382:p.H186Q, ZNF578:p.R306H, ZNF578:p.G311S, ZNF578:p.H334R, ZNF700:p.S649C, ZNF705A:p.D298N, ZNF836:p.K608Q, and ZNF836:p.I571N; and

45. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from BLCA; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of PIK3CA:p.E545K, FGFR3:p.S249C, TP53:p.R248Q, PIK3CA:p.E542K, RXRA:p.S427F, ZNF814:p.D404E, FBXW7:p.R505G, NOTCH2:p.P6fs, TP53:p.E285K, ANKRD30A:p.A353P, C3orf70:p.S6L, EFCAB6:p.R379K, ERCC2:p.N238S, FAM47C:p.Q225E, FOXQ1:p.S135L, HLA-A:p.Q78R, MUC4:p.H4205Q, OTUD4:p.T909I, SLAMF1:p.S277fs, SPRED3:p.S128del, TMCO2:p.S15fs, TP53:p.R280T, TP53:p.E271K, TP53:p.A159V, ZNF706:p.I8N, ZNF706:p.R3P, ACACB:p.E2318Q, ACPP:p.E321K, ACRC:p.A264V, ADAMTS2:p.23_24insL, AFF3:p.E919K, AHNAK:p.S4150F, AHNAK:p.D2889H, AHNAK:p.V1940A, ALX4:p.R126Q, ANKRD12:p.E627K, ANKRD32:p.T999N, ARID1A:p.S614L, ASXL2:p.117_118SS>S, ATP12A:p.R858C, ATP9A:p.R519Q, BCAS3:p.T214M, BPI:p.M255I, CACNG8:p.V146G, CAMSAP1:p.T466fs, CDC27:p.I91fs, CDKN1A:p.E44fs, CEP192:p.S2058L, CGB8:p.T18A, CHRNA3:p.L23del, CHST4:p.D352N, CLIP1:p.S1018fs, COX6A1:p.S8L, CREBBP:p.D1435H, CRIPAK:p.M48fs, CSPG5:p.D119N, CUL1:p.E485K, DLC1:p.S741T, DLL3:p.D318H, DOPEY2:p.E1196K, ECM1:p.E266K, EEF1A2:p.Y418S, EEF2K:p.E673K, EMILIN1:p.R27G, ERBB2:p.S310F, ERBB3:p.M91I, ERBB3:p.V104L, ERBB3:p.D297Y, ERCC2:p.Y14C, FAM155A:p.Q86del, FAM43B:p.E272del, FASTKD3:p.Q625E, FBXW7:p.S546L, FGFR3:p.R248C, FGFR3:p.G380R, FGFRL1:p.H479fs, GBE1:p.M587I, GIMAP1-GIMAP5:p.S311C, GNA13:p.R200G, H1FOO:p.A214fs, HEATR7B2:p.E1109K, HIST1H1D:p.I81M, HRAS:p.G12D, HRCT1:p.H92P, ILF3:p.E484K, KCNK2:p.S6W, KIAA0907:p.Q446P, KIF23:p.E350K, KLF5:p.S118L, KLHL15:p.D185G, LAMA4:p.E639K,

LILRA1:p.H410Y, LILRB1:p.L479del, LLGL2:p.P955fs, LPIN1:p.S974L, LRRC16A:p.D227N, LRTM2:p.S139L, LURAP1L:p.55_56insGGG, MAGEC1:p.P553del, MCL1:p.E171del, MN1:p.S472L, MUC7:p.A191V, MVP:p.E412K, NBPF10:p.E3455K, NFE2L2:p.E79K, NFE2L2:p.R34G, NOS1AP:p.Q306del, OR2T35:p.V319fs, OR4N2:p.L150fs, PABPC3:p.K333fs, PAX3:p.S197L, PBX2:p.E70K, PBXIP1:p.H729del, PCDP1:p.E537K, PEX1:p.I370fs, PHLDA3:p.E82K, PLEKHM2:p.S459L, PLVAP:p.A321V, POLR3B:p.L372F, POTEC:p.R477Q, PPL:p.H326Y, PPP1R15A:p.E196K, PRDM16:p.E271Q, PRIC285:p.E1289Q, PRMT8:p.S31P, PUF60:p.S396L, RAB11FIP4:p.S596L, RAD51C:p.D167N, RAD51C:p.Y224H, RALGPS1:p.R381Q, RARS2:p.R6C, RBM26:p.P644A, RERE:p.K176N, RXRA:p.S427Y, SERPINA12:p.R211G, SF3B1:p.E902K, SLC6A9:p.R243W, SLC9A5:p.L447F, SPESP1:p.F121L, SRPRB:p.G14S, SYN2:p.A34del, SYTL2:p.I440M, TAB3:p.R211T, TAF1B:p.R292C, TAOK2:p.L981del, TAS1R3:p.E525K, TAS2R9:p.E163Q, TBC1D1:p.S71F, TBC1D2B:p.R920Q, TFPI2:p.R222C, TM6SF1:p.S15W, TMEM131:p.K640fs, TMEM19:p.G331fs, TP53:p.R273C, TP53:p.R248W, TP53:p.R175H, TP53:p.K132N, TRAM1:p.E41Q, TSKS:p.E513K, TTN:p.C20935G, UBOX5:p.S417L, UGP2:p.D262H, VGF:p.E433K, XAB2:p.E782K, XYLB:p.S87F, ZC3H4:p.E798K, ZNF208:p.K852E, ZNF208:p.I647S, ZNF626:p.G198E, ZNF749:p.Q457E, ZNF761:p.H373R, ZNF799:p.T43A, ZNF799:p.W41G, ZNF799:p.E589G, ZNF844:p.P503R, ZNF845:p.M423T, ZNF845:p.T479M, ZNF860:p.H464R, ZNF878:p.S181R, ZNF91:p.R333H, and ZNF91:p.H305R.

46. The pharmaceutical composition of any of paragraphs 30-43, wherein:

(a) the population of subjects is suffering from BRCA; and

(b) the at least one tumor-specific mutation comprises any combination of frameshift mutations selected from the group consisting of GATA3:p.L328fs, GATA3:p.N334fs, GATA3:p.L344fs, GATA3:p.H400fs, GATA3:p.S408fs, GATA3:p.S430fs, GATA3:p.H434fs, GATA3:p.H435fs, and GATA3:p.S408fs.

47. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from BRCA; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of PIK3CA:p.H1047R, PIK3CA:p.E545K, PIK3CA:p.E542K, AKT1:p.E17K, TP53:p.R175H, PIK3CA:p.N345K, PIK3CA:p.H1047L,

SF3B1:p.K700E, GATA3:p.S408fs, PIK3CA:p.E726K, TP53:p.Y220C, TP53:p.H193R, PIK3CA:p.Q546R, TP53:p.R273C, TP53:p.R248W, TP53:p.R273H, TP53:p.I195T, TP53:p.H179R, FGFR2:p.N549K, NUP93:p.E14K, PIK3CA:p.C420R, PIK3CA:p.E453K, PIK3CA:p.Q546K, TP53:p.V216M, TP53:p.C176F, CDH1:p.E243K, ERBB2:p.L755S, KRAS:p.G12V, PIK3CA:p.E545A, TBL1XR1:p.I141fs, TP53:p.G266E, TP53:p.R248Q, TP53:p.Y163C, TP53:p.C141Y, TP53:p.G108fs, ACPP:p.R43W, AKT2:p.I289M, ARHGAP9:p.R137C, C9orf174:p.R136W, CDC42BPA:p.P675T, COL12A1:p.S395L, CRISPLD1:p.R222W, CT47B1:p.234_243EKLTEEATEE>E, CYP1A2:p.V483M, DAB2IP:p.E161K, DGKB:p.S13L, DMD:p.K1772N, DPEP1:p.V11L, ERBB2:p.S310F, ERBB2:p.D769Y, ERBB3:p.E928G, ESYT1:p.R816W, FAM179A:p.A831T, FAM58BP:p.A70T, FMN2:p.S751F, GALNTL6:p.K567del, GATA3:p.L328fs, GATA3:p.N334fs, GATA3:p.L344fs, GATA3:p.H400fs, GATA3:p.S408fs, GATA3:p.S430fs, GATA3:p.H434fs, GATA3:p.H435fs, GDAP1:p.T307A, GRB14:p.A300T, GUCY2C:p.G549C, IL17B:p.R34W, KCNB2:p.R231H, KIF1B:p.R1320W, KIF26B:p.V1113M, KLF4:p.K434Q, LY9:p.I69L, MAP2K4:p.S184L, MAP2K4:p.S251I, MAP2K4:p.T261fs, MAP3K1:p.L318fs, MAP3K1:p.I761fs, MAP3K1:p.V1346del, MAP3K1:p.L1384fs, MAPK13:p.E315K, MAPK4:p.V100M, MARCH5:p.R170C, MBP:p.E120K, MEFV:p.R377H, METTL15:p.Q53E, MS4A4A:p.V99M, MUC17:p.R4415H, MYH6:p.T847M, MYO5B:p.A405V, NARS2:p.P240R, NLGN4X:p.D382N, NLRC4:p.R288W, OR13G1:p.R258H, OR2AK2:p.V45I, OTOF:p.T388M, PACSIN2:p.Q331H, PALM2-AKAP2:p.A299T, PCDH19:p.R286C, PCDHGC5:p.D664N, PIK3CA:p.R88Q, PIK3CA:p.E110del, PIK3CA:p.K111del, PIK3CA:p.PVPHGLEDL447del, PIK3CA:p.L455fs, PIK3CA:p.M1004I, PIK3CA:p.M1043I, PIK3CA:p.N1044Y, PIK3R1:p.KPDL567del, PREX2:p.R363Q, PRRX1:p.A196V, PTEN:p.V317fs, RGSL1:p.V222I, RUNX1:p.R142fs, RUNX1:p.D96fs, SCN2A:p.R36K, SLC25A32:p.Q83E, SLC25A45:p.G106C, STRA6:p.Q68R, STX6:p.H153D, TBX3:p.H187Y, TFPT:p.S252C, TINAG:p.R332W, TMEM71:p.R63Q, TP53:p.E286K, TP53:p.R282W, TP53:p.V272M, TP53:p.S241fs, TP53:p.C238fs, TP53:p.C238F, TP53:p.C238Y, TP53:p.Y234C, TP53:p.Y220S, TP53:p.R209fs, TP53:p.G199V, TP53:p.L194R, TP53:p.H193L, TP53:p.H193Y, TP53:p.V173L, TP53:p.V173M, TP53:p.K132N, TP53:p.R110fs, TUBD1:p.A200V, VLDLR:p.R231H, VWA3A:p.V955I, VWF:p.K1720N, XPO1:p.E571K, and ZNF268:p.F901del.

48. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from COAD; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting ofKRAS:p.G12D, BRAF:p.V600E, KRAS:p.G12V, ACVR2A:p.K435fs, GRB14:p.KKK295del, SEC63:p.L532fs, TGFBR2:p.E125fs, ATR:p.K771fs, ICA1:p.N204fs, KRAS:p.G12C, TP53:p.R175H, ABCA8:p.R842Q, ACTL7B:p.R354H, ACVR2A:p.K435fs, AIM2:p.K340fs, ALG2:p.S302Y, ANKIB1:p.K144fs, ARSG:p.V131I, ATP10D:p.R311H, AXIN2:p.W663fs, C5orf30:p.D4N, CACNG3:p.V134I, CASP5:p.K78fs, CC2D2A:p.R1284C, CDH10:p.E349K, DNMT1:p.E432K, DOCK2:p.G170R, DOCK5:p.E177K, EGR2:p.R390H, ERBB3:p.V104M, FAM135B:p.R884H, FBXW7:p.R505C, FBXW7:p.R465H, FHDC1:p.R254W, FOXL1:p.N89K, HCN4:p.R525H, HLA-DMA:p.E84K, HTR3B:p.R236C, ITGA4:p.T673M, KIF18A:p.R17C, KIF20B:p.E991K, KLHL5:p.R326C, KRAS:p.A146T, KRAS:p.G13D, LPHN3:p.R1183Q, MAP2K4:p.R287H, MAPK8IP1:p.L217fs, MFSD5:p.R280Q, MUC16:p.R8606H, MYO6:p.D1180N, NAA25:p.S807Y, NBPF14:p.V44L, NRAS:p.Q61K, NRAS:p.G13R, PAX3:p.T424M, PGAM1:p.R240H, PHF3:p.R1410I, PIK3CA:p.R88Q, PIK3CA:p.E545K, PIK3CA:p.H1047R, PLXNA3:p.V14fs, POSTN:p.R508C, PTPRU:p.D1434N, PYGO2:p.Q150fs, RBBP7:p.E274K, SFPQ:p.R611Q, SGSM1:p.F1117L, SLC25A40:p.R96Q, SLC8A1:p.R431H, SLITRK3:p.S298L, SPATA22:p.S150L, SUN3:p.E128K, TGFBR1:p.S241L, TP53:p.R273H, TP53:p.R273C, TP53:p.R248W, TRPV5:p.R492H, USP40:p.S851L, VPS13C:p.D1359Y, ZBTB24:p.L607I, ZNF434:p.R306C, ZNF443:p.R301I, ZNF484:p.R138C, and ZNF770:p.S441P.

49. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from GBM; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of HSD17B7P2:p.N175S, IDH1:p.R132H, EGFR:p.A289V, EGFR:p.G598V, WASH3P:p.G175S, ZNF814:p.D404E, RPSA:p.Q111E, NBPF10:p.E3455K, TP53:p.R248Q, BRAF:p.V600E, EGFR:p.A289T, PRB2:p.N230del, RGPD5:p.P1760A, TP53:p.R175H, CHEK2:p.K373E, EGFR:p.R108K, EGFR:p.R222C, PIK3CA:p.E545K, PIK3R1:p.G376R, POTEC:p.K507E, SDHAP2:p.V195E, SLC6A10P:p.K88N, TP53:p.R282W, TP53:p.R273H, CD3EAP:p.K219del, DST:p.R146C,

EGFR:p.A289D, EGFR:p.H304Y, FRG1B:p.S71N, GOLGA8DP:p.A116E, KRTAP4-11:p.R121K, KRTAP4-11:p.S48R, MAP3K1:p.P324L, OGDH:p.I78fs, PODXL:p.S162fs, PSPH:p.V145I, SPINT1:p.A316V, TP53:p.R248W, TP53:p.G245S, TP53:p.Y220C, TP53:p.R158H, TSHZ2:p.A222T, UBC:p.L149R, ZDHHC4:p.R300H, ZNF844:p.R447P, AASS:p.T878fs, ABCC10:p.R570W, ADAM29:p.V205I, ADAMTS8:p.V524M, AGAP3:p.R766W, AICDA:p.Y144F, AK7:p.A159V, AK8:p.D243A, ANO2:p.R334C, AOX1:p.A507V, ARHGAP5:p.M691L, CALN1:p.V231I, CARM1:p.A202V, CD163L1:p.V721M, CD1D:p.L25fs, CD209:p.A283T, CDH18:p.A195T, CILP2:p.V553M, CIZ1:p.L89P, CLOCK:p.L123fs, COL6A5:p.T2224M, CSF2RB:p.G298S, CSMD3:p.E171K, CYP2D6:p.H352R, DCAF12L1:p.R335H, DCAF12L2:p.R246H, DPP10:p.V183I, DPY19L2P1:p.R378Q, DQX1:p.R505H, DRD5:p.S275R, DVL2:p.V66G, EFCAB6:p.R379K, EGFR:p.L62R, EGFR:p.R252C, EGFR:p.P596S, EGFR:p.P596L, EGFR:p.G598A, EGFR:p.E709K, EPHA1:p.A184T, ERC2:p.R20H, ESPNP:p.R627Q, FAM126B:p.R382H, FBN3:p.V886I, FGF14:p.T229M, FLG2:p.H1901fs, FLG:p.R2886H, FLNA:p.V1240M, FOXG1:p.H57del, FPR2:p.R54Q, FRG1B:p.K13N, FRG1B:p.A53T, GABRA6:p.V314I, GJB3:p.R160H, GLT8D2:p.A178V, GRM3:p.R183C, HERC1:p.R2330H, HNF1B:p.T417M, HTRA3:p.Q403R, IDH1:p.R132G, IFNA10:p.L80F, IFNA10:p.V79A, JHDM1D:p.R313H, JPH1:p.A395T, KEL:p.V411M, KIAA0907:p.R516fs, KIAA1704:p.D88del, KLK6:p.R120H, KRAS:p.G12D, KRTAP4-7:p.L121V, KRTAP4-7:p.L148V, KRTAP5-4:p.S131C, LAT2:p.L18W, LIMK2:p.R203H, LUM:p.R330C, MCOLN3:p.V141I, MGAT4B:p.T444P, MUC17:p.V77M, MUC17:p.3204_3205insP, MYO1D:p.T109M, MYO6:p.Q914fs, NAP1L5:p.140_141EE>E, NF1:p.F1658fs, NHP2L1:p.R84C, NLRP5:p.R737W, NPTX1:p.A263T, NUFIP2:p.Q29del, ODF4:p.R61C, OR11H12:p.H154P, OR2A7:p.V18I, OR2H1:p.V287I, OR2T12:p.R184H, OR5D13:p.R236C, OR5P2:p.A100V, OR6N2:p.R293C, PASD1:p.A236del, PCDH11X:p.T486M, PCDHB13:p.P221L, PDGFRA:p.E229K, PDGFRB:p.S650L, PHC3:p.T35del, PIK3C2B:p.R287fs, PIK3CA:p.M1V, PIK3CA:p.R88Q, PIK3CA:p.M1043V, PIK3CA:p.H1047R, PIK3R1:p.K379N, PODNL1:p.A150V, POTEE:p.V166M, POTEG:p.R136H, PRKCD:p.G432fs, PROKR2:p.V297I, PTEN:p.C136Y, PTEN:p.S170N, PTEN:p.R173H, PTEN:p.T277I, PTEN:p.V317fs, PTPN14:p.E716del, R3HDM2:p.412_413QQ>Q, RAB11FIP5:p.R170H, RASAL3:p.R82H, RB1:p.N316fs, RDH8:p.A198V, REN:p.15_16LL>L, RIMBP2:p.R830H, SCAF11:p.E926fs,

SCN7A:p.R1358H, SCNN1G:p.R564H, SDHAP2:p.R31C, SDHAP3:p.A66T, SEMG2:p.R292C, SH3RF2:p.R318C, SHB:p.A460T, SIGLEC10:p.T250M, SLC13A5:p.Q273P, SLC17A9:p.V324I, SLC22A9:p.R407Q, SLC26A3:p.V88I, SLC5A3:p.A302fs, SLC9A4:p.R631H, SPAM1:p.R346Q, SPEN:p.E803fs, SPTA1:p.A2011V, SUSD5:p.T513M, SYNE1:p.R8468H, TARSL2:p.G366D, TAS2R41:p.A255T, TAT:p.R367H, TFPI2:p.R206C, THSD7B:p.R90C, TMEM147:p.A92V, TMEM156:p.R81C, TMPRSS6:p.V302I, TNFSF9:p.A232T, TP53:p.C238F, TP53:p.C238Y, TP53:p.Y234C, TP53:p.V216M, TP53:p.H179R, TP53:p.T155N, TRAPPC10:p.K133fs, TTN:p.R21402W, TTN:p.V16403M, TUBBP5:p.V102M, TYRP1:p.T352fs, UBC:p.R73L, UGT2B28:p.P289H, USH2A:p.R3719H, WASH6P:p.L211V, ZFP42:p.V227I, ZFP42:p.T264M, ZNF181:p.V305G, ZNF280B:p.E400K, ZNF534:p.N583K, ZNF563:p.W208fs, ZNF844:p.F487L, and ZPBP:p.R154C.

50. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from HNSC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting ofPIK3CA:p.E545K, PIK3CA:p.E542K, TP53:p.R175H, PIK3CA:p.H1047R, TP53:p.R282W, TP53:p.R248Q, TP53:p.R273H, TP53:p.R248W, TP53:p.G245S, RHOA:p.E40Q, EP300:p.D1399N, HRAS:p.G13V, MB21D2:p.Q311E, NFE2L2:p.E79Q, TP53:p.H179Y, FBXW7:p.R505G, HIST1H2BF:p.E77K, HRAS:p.G12D, MAPK1:p.E322K, NFE2L2:p.D29H, TP53:p.P278S, TP53:p.C242F, TP53:p.Y220C, TP53:p.H193L, TP53:p.H179R, TP53:p.V157F, TP53:p.R110L, AKNAD1:p.K620R, ANXA6:p.R231Q, AP1G2:p.D243N, ATAD5:p.D441N, ATP6AP2:p.E119Q, B2M:p.M1I, BCL11A:p.E579K, C1orf172:p.Y30fs, C7orf57:p.E30K, CCDC135:p.E313K, CDH12:p.P706T, CDH7:p.Q225K, CDK11B:p.E79del, CDKN2A:p.H83Y, CHCHD4:p.T79M, CIRH1A:p.S250I, CLSTN2:p.P759L, CRB1:p.L628fs, DENND5B:p.G1023E, DNAH5:p.Q1797E, DSP:p.R160G, EDA:p.L58F, EFCAB6:p.E1002K, ELF4:p.S415L, EP300:p.C1164Y, EPHA3:p.T802R, EPHA6:p.D952H, ERBB2:p.M916I, ESRRA:p.D219N, FAM101A:p.I89del, FBXO24:p.M553V, FCAR:p.V233M, GPANK1:p.Y351fs, GPR20:p.V300I, GPRASP1:p.S706L, GPRIN3:p.R633fs, GRID2:p.T649fs, GRM3:p.F682L, GUCY2F:p.S404L, HCRTR2:p.D100Y, HIST1H3C:p.K37M, HIST1H4C:p.R68P, HLX:p.S12T, HOXD10:p.Y151C, HPS3:p.K812N, HRAS:p.G12A, HRAS:p.G12S, IFT140:p.E664K, INPPL1:p.T493M, ITGA10:p.R669Q, ITGB1:p.D158N,

KIAA1429:p.D1526N, KIAA1429:p.S138F, KPRP:p.E553fs, KSR2:p.T555M, LINGO2:p.P410T, LPCAT1:p.V187del, MAGEB3:p.V75A, MAP3K7:p.E524Q, MAP4K3:p.P657fs, MAP9:p.K485N, MARS2:p.R481Q, MBOAT7:p.R424W, MUC16:p.R12774H, MUC5B:p.T4388M, MYH11:p.E993K, MYOCD:p.T493M, MYOM1:p.R63Q, NANOS3:p.S183L, NCOR1:p.R1561Q, NCOR1:p.Q169E, NCR1:p.D213N, NFE2L2:p.E79K, ODZ1:p.R366M, OPN1MW:p.A285T, OR2M2:p.A95fs, OR2M3:p.M273I, OR2T33:p.R120S, OR6V1:p.I248fs, PABPC5:p.P58L, PACSIN1:p.E359K, PIK3CA:p.M1043V, PIK3CA:p.H1047L, PIWIL1:p.V699M, PLIN5:p.430_431insNG, PLXNA3:p.P58S, PRB1:p.R274fs, PRSS1:p.D107N, RAC1:p.A159V, RGS7:p.L21fs, RPA1:p.R31H, RPL18:p.R178fs, SFI1:p.R821Q, SLC35D3:p.*417S, SLC5A7:p.G336C, SMARCA4:p.P913L, STAT3:p.D661V, SYCP2:p.K474N, SYT6:p.R249H, TBX21:p.E494K, THSD7A:p.R1046C, THSD7A:p.C728F, TMC3:p.R934S, TMTC2:p.T409R, TP53:p.E285K, TP53:p.C275F, TP53:p.R273C, TP53:p.G266E, TP53:p.G262V, TP53:p.R249S, TP53:p.G245V, TP53:p.C238F, TP53:p.M237I, TP53:p.Y236C, TP53:p.Y236D, TP53:p.R196P, TP53:p.PHHERC177del, TP53:p.V173L, TP53:p.V173M, TP53:p.Y163C, TP53:p.P151T, TP53:p.V143M, TP53:p.P58fs, URI1:p.S13fs, ZNF177:p.K384N, ZNF750:p.S96fs, and ZZZ3:p.R5Q.

51. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from KIRC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of WASH3P:p.G175S, VHL:p.L89H, VHL:p.S111N, WDR52:p.V1227G, KRT1:p.552_559YGSGGSSY>Y, KRTAP1-1:p.S34C, PALM2-AKAP2:p.1075_1076insEA, ZNF814:p.D404E, DOPEY2:p.Y2048S, KAT2B:p.W111fs, PABPC1:p.E156fs, PCDHGC5:p.G599V, PIK3CA:p.E545K, RRAD:p.A278E, SIRPA:p.D131del, UQCRFS1:p.I83V, VHL:p.P45L, VHL:p.V74D, VHL:p.R82P, VHL:p.L116fs, VHL:p.L158V, VHL:p.L169P, WDR73:p.DGTRSQ315del, ABCA3:p.E95D, ABCC5:p.L1090fs, ACADS:p.R330H, ACAN:p.G952E, ACSM2A:p.L402fs, ADAM23:p.K380M, ADH1A:p.D154V, AFF3:p.SA620del, AGAP6:p.D69fs, AGAP7:p.E71fs, AHNAK:p.5_6insE, AIDA:p.K247M, ALAS1:p.G302R, ANAPC16:p.R95fs, ANK2:p.N453S, ANKRD36:p.K378R, ARHGEF5:p.E487G, ARSD:p.AGV234del, ARSD:p.A234G, ATP2A1:p.G704C, ATP7A:p.Q990fs, AVIL:p.G299fs, AXDND1:p.EQ991del, BAP1:p.N78S,

BAP1:p.M1I, BLM:p.H660Q, BMPER:p.RIAL444del, BRK1:p.K70Q, BTRC:p.I416M, C16orf55:p.D118A, C19orf33:p.K102E, C20orf132:p.E382D, C2orf71:p.1225_1226insS, C6orf132:p.173_182PPPLLLEPPP>P, CASP5:p.R23fs, CATSPER4:p.T425M, CCDC120:p.I8V, CCR5:p.S185I, CCZ1:p.E214D, CD7:p.P174fs, CDAN1:p.L646fs, CDH23:p.F1132Y, CDK5RAP2:p.H1592Q, CENPB:p.E410V, CERCAM:p.A85fs, CHEK2:p.K373E, CHIT1:p.P284fs, CLCN2:p.645_645R>RR, CLUL1:p.G463R, CNTNAP4:p.Y436S, CUL9:p.D1726E, CWC25:p.K364E, CXorf51B:p.V43I, DDX39B:p.F149fs, DIRAS1:p.G79C, DISP2:p.F1021S, DNMBP:p.T78P, DOCK8:p.A177fs, DPCR1:p.H383N, DPCR1:p.L768del, EGFR:p.L838M, ENPEP:p.F289C, ESPNP:p.W122fs, FAM105A:p.H126N, FAM186A:p.IPPQAQELEIPL1556del, FAM194B:p.EEEEYL135del, FAM22F:p.S691del, FAM22F:p.P690fs, FAM47A:p.LRPEPPETGVSH235del, FAM47C:p.P388S, FAM78A:p.W192L, FBXO34:p.Q294fs, FGFR3:p.R571fs, FGFR3:p.P716H, FMN2:p.AIPPPPPLPGA956del, FOXD4L4:p.C405fs, FUT6:p.S140fs, GJA1:p.A311fs, GOLGA5:p.L492I, GPM6A:p.A50V, GPRIN1:p.231_239RKEDPGSLR>R, GRAMD1B:p.P356H, GREB1:p.S344Y, GRM6:p.A718fs, GUSB:p.L501V, GUSB:p.C500R, HBB:p.F86C, HDAC6:p.G977D, HEXDC:p.T482P, HNF1B:p.N302K, HNRPLL:p.M327V, HRC:p.P439fs, HSFX2:p.D92E, IL1RAP:p.F50C, IVL:p.EQQEGQLKHP167del, KANK4:p.S253P, KCNJ18:p.E378K, KIAA1751:p.K97N, KRT1:p.SSYGSGG557del, KRT2:p.L299W, KRT4:p.F154fs, KRTAP10-6:p.49_49P>PSCCAP, KRTAP5-7:p.C120Y, KRTAP9-2:p.CCQP140del, LARS:p.P185fs, LCP1:p.P445fs, LOC338651:p.PHRSHSPPWS102del, LRCH2:p.D717G, LTA4H:p.F107L, LYST:p.Q710H, MAFA:p.207_208HH>H, MAGEC1:p.P239del, MAP2K5:p.Q445R, MAPKAPK2:p.T214fs, MARCKS:p.K152fs, MED12L:p.P2071S, MEGF6:p.A582fs, MGST3:p.G143fs, MLXIPL:p.S790R, MOCOS:p.S849P, MST1R:p.M464V, MTOR:p.C1483F, MTOR:p.L1460P, MUC16:p.P11260A, MUC17:p.R1227fs, MUC17:p.H1228fs, MUC2:p.1480_1481insI, MUC6:p.P1569fs, MYO3A:p.N525S, NBPF3:p.D491V, NCOR1P1:p.L52P, NDUFA4L2:p.G3fs, NEFH:p.651_651K>KAKSPEK, NES:p.V611L, NFAT5:p.Q906E, NOXO1:p.G3fs, NR2C1:p.S270I, NSMCE2:p.Q31fs, NUDT21:p.W13fs, ODZ2:p.W628fs, ONECUT1:p.L424M, OR10A3:p.F73V, OR4F4:p.E15G, OR4N2:p.L150fs, OR51B5:p.A66fs, OR7C1:p.F104fs, PABPC1:p.Y408F, PABPC1:p.K333fs, PABPC1:p.A181T, PABPC3:p.P191T, PALLD:p.A996T, PALM2-AKAP2:p.G1118fs, PARD6A:p.G84fs,

PASK:p.T62I, PCDH15:p.C1713F, PCNT:p.G136S, PGM5:p.G426fs, PGPEP1L:p.R164fs, PIK3C2B:p.F1473L, PIK3CA:p.N1044K, PIK3R5:p.L371R, PITRM1:p.P816T, PLIN4:p.T347I, PODXL:p.28_30PSP>P, POLR1C:p.K332Q, POTED:p.I214V, PPM1E:p.R311W, PRKCE:p.Q157fs, PROX1:p.V225D, PRRC2C:p.P1883T, PRX:p.P549L, PSD3:p.T563P, PTCH1:p.P689H, RANBP3:p.L386W, RASGEF1C:p.A188T, RGPD6:p.F946L, RHEB:p.Y35N, RIMBP3:p.A396del, RIN3:p.L449V, RLIM:p.S501L, RNF17:p.S351C, RUNX2:p.P466H, SCAF1:p.P208fs, SDK1:p.K508fs, SECISBP2:p.D608E, SERPINB3:p.S209C, SESTD1:p.I306M, SFRP4:p.P325fs, SH3KBP1:p.P563fs, SIPA1L3:p.G777A, SLC13A2:p.L493fs, SLC16A9:p.CVLLGG470del, SLC25A5:p.A118T, SLC44A5:p.V70F, SLC4A8:p.N229K, SLC52A1:p.G370del, SLC52A2:p.G399fs, SLC6A10P:p.K88N, SLC6A14:p.A85fs, SLC9B1:p.V446fs, SON:p.VLESSAVT1359del, SP8:p.G165del, SPAG1:p.353_354insD, SPATA9:p.C189F, SPEG:p.A992fs, SPTB:p.T1864I, SRA1:p.V110L, STAT6:p.P354fs, STK11IP:p.A155E, STXBP3:p.E279G, SVIL:p.M93T, SYNE1:p.R8468S, SYNJ2:p.K832T, SYNPO:p.G619fs, TAOK2:p.Q899fs, TAS2R38:p.I311T, TBC1D12:p.F608Y, TBC1D1:p.H277R, TBC1D3:p.A556fs, TBC1D3C:p.A495fs, TBC1D3F:p.A556fs, TCF7:p.H140P, TDRD10:p.W276C, THRAP3:p.K551R, TMEM102:p.A110P, TMEM161B:p.L142P, TMEM230:p.D140G, TMEM47:p.G87S, TRDN:p.*730Y, TTBK1:p.T1065S, UBE2O:p.R1118fs, UBR5:p.T1306fs, UPK3A:p.G272fs, VHL:p.G39S, VHL:p.S65L, VHL:p.N78D, VHL:p.R79P, VHL:p.W88L, VHL:p.L89P, VHL:p.R107P, VHL:p.S111R, VHL:p.H115N, VHL:p.D121Y, VHL:p.G123fs, VHL:p.D126fs, VHL:p.L128H, VHL:p.L135F, VHL:p.I151T, VHL:p.L153P, VHL:p.L158P, VHL:p.Q164fs, VHL:p.L184P, VHL:p.L188P, WASH6P:p.315_316insAPP, WASH6P:p.T201M, WWP2:p.G458A, ZCCHC6:p.K937N, ZFAND2B:p.I149T, ZFR2:p.Y107N, ZNF273:p.N319K, ZNF462:p.S650T, ZNF516:p.A256D, ZNF519:p.H431Y, ZNF687:p.F858C, ZNF732:p.E227Q, ZNF880:p.Q406R, ZP3:p.V362fs, and ZRANB1:p.*735fs.

52. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from LAML; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of NPM1:p.W288fs, DNMT3A:p.R882H, NPM1:p.L287fs, IDH2:p.R140Q, IDH1:p.R132C, FLT3:p.D835Y, DNMT3A:p.R882C, FLT3:p.600_601insFREYEYD, IDH1:p.R132H, NRAS:p.G13D, U2AF1:p.S34F, KIT:p.D816V,

FLT3:p.D835E, IDH2:p.R172K, NRAS:p.G12D, WT1:p.S381fs, ABTB1:p.L249fs, DNMT3A:p.R736H, FLT3:p.D835H, KRAS:p.G12D, NPM1:p.L287fs, NRAS:p.Q61H, NRAS:p.Q61K, PHACTR1:p.V251fs, RBBP4:p.E330K, RUNX1:p.R135G, and U2AF1:p.S34Y.

53. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from LUAD; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of KRAS:p.G12C, KRAS:p.G12V, EGFR:p.L858R, U2AF1:p.S34F, KRAS:p.G12A, TP53:p.R158L, KRAS:p.G12D, PIK3CA:p.E545K, TP53:p.R273L, EGFR:p.ELREA746del, KRAS:p.G13D, A2ML1:p.S654fs, BRAF:p.G469V, CTNNB1:p.S37F, EGFR:p.G719A, KRAS:p.G13C, MYOF:p.G165fs, EGFR:p.S768I, FAM47C:p.G948W, KRAS:p.Q61L, MYH10:p.L1091fs, NRAS:p.Q61L, OR4C3:p.H130fs, PI15:p.V22F, RAD50:p.D69Y, RIT1:p.M90I, TP53:p.C275F, TP53:p.R249M, TP53:p.R249G, TP53:p.R248P, TP53:p.R175H, TP53:p.Y163C, TP53:p.A159P, TP53:p.V157F, TP53:p.G154V, ABCB1:p.R467L, ACBD3:p.R224L, ACTA1:p.G275C, ACTN2:p.D893Y, ADAM30:p.Q741H, ADAMTS14:p.G238C, ADAMTS20:p.R1251S, ADAMTS20:p.R541L, ADAMTS5:p.L549M, ADAMTS9:p.G659W, ADCY2:p.P1016T, ADCY5:p.G623C, AFP:p.A182G, AHDC1:p.P155Q, AKAP1:p.LDRNEEG317del, ALKBH1:p.K137E, ANK2:p.Q3076L, ANKRD44:p.G339C, ANO3:p.A41S, AP1G1:p.R723L, APBB2:p.T243fs, APOB:p.L973M, APOBR:p.R840L, AQP10:p.Q261L, ARAP3:p.R1226L, ARFIP2:p.R86L, ARHGAP36:p.P16H, ARL13B:p.R358L, ASCC2:p.R365L, ASPM:p.S240F, ASXL3:p.P1470Q, ATRN:p.P197Q, AVIL:p.G64W, AXDND1:p.W101R, B3GAT1:p.R125L, BARX2:p.R68P, BCL9L:p.G980C, BCOR:p.N1459S, BEND2:p.P536Q, BMS1:p.G455V, BRAF:p.V600E, BRAF:p.G466V, BRD9:p.G330W, BRF1:p.V469L, BRWD3:p.H160N, BTRC:p.G260W, C11orf68:p.V135L, C15orf2:p.V753F, C15orf2:p.G906W, C18orf8:p.M61I, C1GALT1:p.G299V, C1orf173:p.G1454S, C1orf173:p.S688Y, C1orf87:p.R541L, C2orf53:p.P272H, C3orf20:p.R740L, C7:p.R687S, C7orf58:p.G140W, C7orf58:p.R238L, CACNA1A:p.S772Y, CACNA1D:p.R1073L, CACNA1E:p.R2089Q, CACNA2D1:p.A352E, CACNG3:p.R232W, CADPS:p.R959S, CALB2:p.R258C, CAMK2B:p.G131V, CARD11:p.I1065M, CCDC111:p.R417L, CCDC141:p.E1204V, CCDC19:p.R279L, CCDC19:p.R207L, CCKAR:p.L271M, CD1B:p.W41L, CDH10:p.S577R, CDH10:p.R472C, CDH10:p.R128S,

CDH18:p.A721S, CDH20:p.P433H, CDH6:p.Q237K, CDK13:p.R880S, CDK4:p.R24L, CELF4:p.A309P, CFDP1:p.P129fs, CHN1:p.K264N, CHRNA4:p.S396R, CHRNA9:p.P361Q, CLCNKA:p.P124Q, CLEC12B:p.W217L, CLK4:p.R68L, CNTFR:p.D252Y, CNTN6:p.R807M, CNTNAP2:p.F395L, COL19A1:p.P538Q, COL5A2:p.G612W, COL5A2:p.G516W, COL9A1:p.P211Q, CPE:p.P290Q, CPNE8:p.Q127H, CPSF4:p.P219Q, CRIPAK:p.S180fs, CROT:p.Q580H, CRTC3:p.S363L, CSMD2:p.P1855Q, CSMD3:p.T2810N, CSMD3:p.P2727T, CSMD3:p.Q174H, CUBN:p.G596C, CUL4B:p.R91S, CUL7:p.L371F, CXCL9:p.K122N, CXCR4:p.E345Q, CXorf59:p.R198M, CYP11B1:p.R498G, CYP27A1:p.P112Q, CYP2B6:p.A444E, DACH2:p.R539L, DCC:p.R446H, DDX56:p.R329L, DEFA1:p.W90C, DENND2A:p.R688Q, DENND2A:p.R499L, DMBT1:p.R1521L, DNAH5:p.R3822L, DNAH9:p.S2993R, DNAI2:p.V231L, DPP6:p.L757F, DSG4:p.R128L, DST:p.A4410S, DZIP3:p.M322L, EBF3:p.R231S, EFCAB4B:p.E265Q, EHHADH:p.Q704H, ELAVL2:p.L263F, EMR1:p.R493H, ENAH:p.R514L, ENPP1:p.G738E, EPB41L3:p.A896S, EPG5:p.R2289L, EPHA1:p.G111V, EPHB6:p.R337H, EPRS:p.V1151L, ERBB2:p.S310Y, ERBB2:p.774_775insAYVM, ERBB2:p.776_776G>VC, ERN2:p.T295K, FAM120B:p.P467H, FAM127C:p.F52L, FAM135B:p.W240C, FAM210B:p.L112F, FAM47A:p.R690L, FAM47B:p.W163C, FAM47B:p.L567F, FAM5C:p.R457G, FAM70B:p.P277T, FAM71B:p.L583M, FAM75A6:p.R304S, FAM75A6:p.P54L, FAM75D1:p.R1265S, FARP1:p.R299L, FAT1:p.R4359L, FAT3:p.R1266H, FAT3:p.G1899V, FAT3:p.H3574N, FBXO18:p.M144I, FBXO31:p.G443fs, FCGBP:p.A1022S, FCRL2:p.V505L, FERD3L:p.P92H, FGB:p.E339Q, FGFR2:p.E116K, FGFRL1:p.R243L, FGFRL1:p.V274L, FKBPL:p.R320L, FLG2:p.G1545V, FLG2:p.L572F, FLG:p.P3254H, FLG:p.P2466Q, FMN2:p.P992T, FOLH1:p.A643S, FOXRED1:p.R136L, FRAS1:p.C382F, FRG2B:p.D142Y, FRMPD1:p.E1093Q, FSHB:p.T43N, GABRA5:p.Q224K, GADL1:p.L352I, GAL3ST3:p.A271S, GALNT14:p.D234E, GAS8:p.R313S, GATA3:p.M443I, GCDH:p.R82C, GEM:p.R268L, GFRAL:p.Q308K, GIT2:p.R123L, GJB4:p.R22S, GLB1L2:p.I407M, GLOD4:p.Q223fs, GNAO1:p.P283Q, GPNMB:p.I174M, GPR137B:p.G240C, GPR158:p.P762T, GPR98:p.G4307W, GRB7:p.R239L, GRHL1:p.G608W, GRID1:p.R683L, GRIK1:p.R368Q, GRM5:p.P895fs, GTF2E1:p.R192L, H3F3C:p.R131L, HAO2:p.H12N, HCN1:p.P231Q, HECW1:p.A183S, HGF:p.M686T, HIP1:p.R940L, HIST1H1E:p.R25P, HLA-DMA:p.A236fs, HOXA5:p.G11C, HS3ST3A1:p.G399W, HSD17B6:p.F209L,

HSPA13:p.V85L, HSPBAP1:p.R282L, HTR5A:p.W298C, IGHMBP2:p.R615S, IL2:p.R103M, IL2RA:p.G61W, IL32:p.P215T, ING1:p.A220S, INMT:p.G56V, ITGA8:p.G616C, ITGAD:p.L528fs, ITGAX:p.R283H, ITIH1:p.G254W, ITIH2:p.L842V, ITK:p.R29L, ITPR2:p.P358Q, JMJD1C:p.R1198S, KCNA1:p.G376C, KCNH8:p.M455I, KCNJ3:p.L430F, KCNK18:p.G23V, KCNK2:p.R166L, KEAP1:p.G603W, KEAP1:p.R260L, KEAP1:p.S144F, KHDRBS2:p.S203L, KIAA1211:p.P1203Q, KIAA1549:p.L1272F, KIAA1755:p.Q108H, KIF15:p.E252Q, KIF9:p.G480R, KIRREL:p.G604C, KLF5:p.E419Q, KRAS:p.Q61H, KRTAP10-12:p.R64P, KRTAP27-1:p.M124I, KRTAP4-5:p.C91F, KRTAP5-1:p.S193Y, L1CAM:p.R632S, L3MBTL4:p.W162L, LAMA1:p.D1030Y, LAMB1:p.T1610fs, LAMB4:p.G1239W, LAMB4:p.G588W, LEF1:p.I53V, LEKR1:p.Q450K, LIM2:p.S150T, LIPJ:p.P236Q, LPHN3:p.E740D, LPPR4:p.R527S, LRFN5:p.N132K, LRP1B:p.G3563C, LRP2:p.M4039I, LRRC4C:p.Q10L, LRRIQ1:p.W792L, LRRTM4:p.S243Y, MAGEA10:p.R7H, MAGEC2:p.W109C, MAGI1:p.G1156V, MAGI2:p.P1044T, MAK:p.P373Q, MAP2K1:p.K57N, MARCH11:p.R193L, MEPE:p.G142C, MKI67:p.R1081S, MKRN3:p.P448H, MLL3:p.N393K, MLL3:p.Q356K, MMRN1:p.A1013S, MOGAT2:p.Q66fs, MXRA5:p.D324Y, MYH4:p.T790M, MYH8:p.R1117C, MYH8:p.H1006N, MYO5B:p.R708L, MYO7B:p.P2040H, MYO9B:p.R94L, MYT1L:p.P351Q, NAA11:p.T184K, NAB1:p.L72F, NAV1:p.R938L, NBPF15:p.G665E, NCAM2:p.G698C, NCAPD2:p.R220L, NDST3:p.V427I, NEK2:p.R239S, NFIA:p.L294F, NLRP3:p.R157C, NOTCH2:p.R2105L, NR4A2:p.R314L, NRG1:p.V481L, NRXN1:p.R813S, NRXN1:p.A660S, NRXN3:p.P23H, NRXN3:p.R103C, NTM:p.G333C, NUAK1:p.G173C, NYAP2:p.P437L, ODZ3:p.P218Q, OIT3:p.R508S, OOEP:p.R101C, OPN1LW:p.P283H, OR10H4:p.M199I, OR10J1:p.L157Q, OR10X1:p.L298I, OR10Z1:p.L205F, OR14A16:p.G160C, OR2A25:p.M80I, OR2AG2:p.G249W, OR2AK2:p.W37C, OR2H2:p.L205F, OR2J2:p.G234W, OR2L13:p.M106I, OR2L13:p.T242A, OR2L3:p.M1I, OR2L3:p.L67I, OR2L8:p.R121C, OR2L8:p.R171S, OR2M2:p.F177L, OR2M2:p.F323L, OR2M5:p.V205L, OR2T12:p.M258L, OR2T27:p.D11Y, OR2T33:p.P165Q, OR2T34:p.C246F, OR2T6:p.V213L, OR4C12:p.D309Y, OR4C12:p.M279I, OR4C16:p.L162M, OR4M2:p.A119S, OR4M2:p.A161S, OR51V1:p.P298T, OR5AS1:p.M39I, OR5B12:p.S289C, OR5B17:p.M266I, OR5D14:p.H246N, OR5D16:p.P264T, OR5D18:p.R123H, OR5F1:p.G44V, OR5J2:p.A36S, OR5L1:p.T275N, OR6C65:p.I154fs, OR6C75:p.G94W, OR6K2:p.P79Q, OR8D2:p.R306M, OR9A2:p.R289W, OR9G9:p.R169L, P2RX7:p.P142Q, P2RY10:p.T10K,

P2RY10:p.V196L, PABPC5:p.R99S, PAPPA2:p.P917T, PAPPA2:p.P1706H, PBLD:p.P55Q, PCDH10:p.R587S, PCDH10:p.V986L, PCDH11X:p.R1010I, PCDHAC2:p.A742V, PCDHB5:p.P649S, PCDHGC5:p.K12N, PCDHGC5:p.P684H, PCLO:p.P3946T, PCMTD1:p.R271M, PDPR:p.G793W, PDYN:p.G191W, PDZD2:p.R565S, PDZD8:p.S980G, PFKM:p.R118S, PIGM:p.R225L, PIK3CA:p.E542K, PIK3CG:p.V165I, PILRA:p.S291fs, PLCE1:p.G564C, PLCL1:p.M564I, PLEKHA6:p.R110L, PNKP:p.G174W, POGZ:p.G75W, POLE:p.R573L, POM121L12:p.P231T, POM121L12:p.P242H, POTEE:p.V288M, POTEM:p.S78R, POU3F3:p.D321Y, PPT2:p.R265L, PRDM16:p.P1036L, PRELP:p.D201Y, PRPF40B:p.R160S, PRPF6:p.R763L, PTEN:p.R234L, PTPN11:p.G503V, PTPN13:p.E2067K, PTPRJ:p.G334W, PTPRT:p.R928L, PTPRU:p.P559S, PXDNL:p.P1456T, QSOX1:p.R401L, QSOX2:p.R683L, RAB13:p.R167L, RAB8A:p.G20W, RAPGEFL1:p.R356L, RBM19:p.G390W, RCL1:p.P112Q, REG1B:p.W57L, REG3A:p.S150L, REG4:p.G110V, RIMS2:p.R55L, RIT2:p.R85L, RLN2:p.S138C, RNF20:p.P529Q, RORB:p.G94W, RPL10L:p.K187T, RPRD2:p.R97S, RTN1:p.S103W, RUNX2:p.R337M, RYR2:p.K2413N, RYR2:p.M4334I, RYR3:p.P1670T, S100PBP:p.R5L, S1PR1:p.L104F, SAGE1:p.H298Q, SALL1:p.E965K, SALL1:p.R898W, SALL4:p.R187L, SBSPON:p.G133W, SCAF8:p.G740C, SCG2:p.P252Q, SCML4:p.L261F, SCN2A:p.T155K, SEC24D:p.A50fs, SEC61A2:p.G126V, SERPINA12:p.D253Y, SERPINA9:p.M414I, SERPINC1:p.R45L, SGIP1:p.R502L, SH3GL3:p.R174L, SH3PXD2A:p.S759L, SI:p.V1217F, SKOR1:p.Y883C, SLC1A2:p.F348fs, SLC24A5:p.R35S, SLC25A48:p.R101S, SLC35E2:p.R201L, SLC39A12:p.C628S, SLC39A6:p.R53L, SLC4A5:p.I533V, SLC5A1:p.G53W, SLC5A7:p.G442V, SLC6A11:p.W299L, SLC6A2:p.S354C, SLC8A1:p.G433C, SLIT1:p.R1460L, SLITRK5:p.R68L, SLITRK5:p.R468M, SLITRK6:p.N741K, SORL1:p.R205L, SOS1:p.N233Y, SOX9:p.E75K, SPAG16:p.V439L, SPIN4:p.Y171C, SPRR2D:p.P30fs, SPTA1:p.G2367C, SPTA1:p.D2243Y, SSX3:p.P127T, ST18:p.H778Q, STAC3:p.G117W, STOML3:p.D86Y, STX2:p.R107L, SUMF2:p.G110E, SUN3:p.P339Q, SV2C:p.P60Q, SYNDIG1:p.D135Y, SYNE1:p.K8632E, TARS2:p.E199K, TAS2R16:p.Q177H, TCOF1:p.K264R, TCTE1:p.S127I, TDO2:p.Q197H, THSD7A:p.G810W, THSD7A:p.R801L, TIFAB:p.D43E, TIGD4:p.S312F, TLL1:p.P53Q, TMPRSS11E:p.G259C, TMTC1:p.A864D, TMTC1:p.G212V, TMX3:p.R151C, TNNI1:p.R67L, TNR:p.L692I, TOP2A:p.R736L, TP53:p.R337L, TP53:p.E285K, TP53:p.R283P, TP53:p.D281N, TP53:p.C277F, TP53:p.V274F, TP53:p.R273H, TP53:p.I255F,

TP53:p.R249S, TP53:p.M237I, TP53:p.S215I, TP53:p.C176F, TP53:p.R110L, TP53:p.G105C, TP53:p.P72fs, TPO:p.E558K, TRAF6:p.R502S, TRIM42:p.Q127K, TRIM48:p.A93D, TRIM4:p.R398L, TRIM51:p.W131C, TRIM9:p.R337S, TRIML1:p.H399Q, TRPM3:p.G298W, TSC1:p.G378C, TSG101:p.R276S, TSHZ1:p.K501N, TSHZ3:p.G677V, TTF2:p.R761S, TUBA3C:p.Q176fs, UBAC1:p.K330N, UBE2J2:p.G193W, UBR1:p.G1647W, UGT2B7:p.M214I, VMP1:p.E369Q, VPS13B:p.G2575W, VSTM2A:p.G75V, VWA3B:p.R557L, WBP11:p.P227fs, WDR52:p.G612C, WDR59:p.R837S, WDR75:p.P287Q, WDR88:p.G100W, ZCCHC5:p.G335W, ZFHX4:p.L811F, ZFHX4:p.T1663N, ZFHX4:p.H2511Q, ZFP14:p.Q17L, ZIC1:p.A112E, ZNF154:p.T408N, ZNF223:p.G23W, ZNF295:p.S732C, ZNF322:p.K106N, ZNF385D:p.T226S, ZNF454:p.S190I, ZNF492:p.P392H, ZNF521:p.G640C, ZNF521:p.P270H, ZNF536:p.G186C, ZNF536:p.G663W, ZNF644:p.G21W, ZNF716:p.H263L, ZNF71:p.V411L, ZNF782:p.G484W, ZNF831:p.Q617K, ZNF98:p.C492F, and ZSWIM2:p.S214Y.

54. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from LUSC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of PIK3CA:p.E545K, TP53:p.R158L, KRTAP5-5:p.GCG47del, NFE2L2:p.E79Q, CDKN2A:p.D108Y, DHX9:p.V40G, MAFA:p.207_208HH>H, NFE2L2:p.R34Q, PBX2:p.Y262F, PIK3CA:p.E542K, TP53:p.R273L, TP53:p.C242F, TP53:p.R175G, TP53:p.Y163C, TP53:p.V157F, AICDA:p.R131G, ALPK2:p.D53N, ANKFN1:p.M280I, ARPC1A:p.F212L, ASXL2:p.S1081L, C1orf74:p.D254N, C3orf30:p.D227E, CCDC121:p.W397L, CHN2:p.I43M, CLEC4C:p.R179L, CLN3:p.G206S, CNTN5:p.T178N, COL12A1:p.G2753C, CPS1:p.T855K, CSMD3:p.T1094K, CSMD3:p.Q691K, DDX11:p.R167T, EGFR:p.L861Q, EME1:p.D570H, EP300:p.D1399N, ESYT3:p.S574F, FAM135B:p.L648M, FAM135B:p.Q285H, FAM47A:p.G372W, FBXW7:p.R505G, FGFR3:p.S249C, GALNT13:p.G358C, GNL3L:p.K20N, GPC5:p.R347L, HCN1:p.A714S, HCN1:p.R659L, HCN1:p.G499V, HCN1:p.P326T, HERC2P3:p.A803V, HEXDC:p.T482P, HIST1H3B:p.E74K, HIST2H2BE:p.G54D, IFNA10:p.V79A, IL7R:p.S54L, INADL:p.P1340A, ISX:p.C2F, ITGAX:p.R685H, ITPR1:p.E1883Q, KCNN3:p.80_81insQQ, KEAP1:p.G480W, KEAP1:p.R470C, KEAP1:p.V155F, KIAA1751:p.L63F, KIAA2022:p.C345F, KIR3DL2:p.K229E, KLF5:p.E419Q, LAMA4:p.M1293I,

LMLN:p.G199C, LRP2:p.A516V, LRRC66:p.F458L, LSG1:p.R517L, LUM:p.R310L, MB21D2:p.Q311E, MCHR1:p.S306F, MKRN3:p.G270V, MUC16:p.N11594K, NFE2L2:p.G81S, NFE2L2:p.G31A, NFE2L2:p.L30F, NFE2L2:p.D29H, OR2B11:p.G10V, OR2T2:p.F13V, OR4K2:p.C254F, OR51F2:p.R67P, OR51S1:p.R159Q, OR5D18:p.T271K, OR8H2:p.L166F, OR8J3:p.S160L, OR8K3:p.K235N, PCDHB1:p.N568K, PHIP:p.I1681M, PIK3CA:p.E726K, PIK3CA:p.H1047R, PLCE1:p.G439C, PRSS57:p.E39Q, PYHIN1:p.G148A, RANBP6:p.I984L, RBMXL1:p.G305C, REG1B:p.M67I, RGS6:p.W366L, RNF5:p.T136I, RP1:p.S1771L, RRP15:p.L214F, RYR2:p.E711K, SAMD3:p.Q206H, SLITRK3:p.R214L, SON:p.S908L, SP4:p.E11del, STK11:p.G279fs, TARBP1:p.L782V, TBCD:p.R476C, TMPRSS11F:p.R274Q, TP53:p.R337L, TP53:p.E271K, TP53:p.R267P, TP53:p.G245V, TP53:p.Y234C, TP53:p.Y220C, TP53:p.H214R, TP53:p.H193L, TP53:p.H179L, TPTE:p.M541I, TRIM7:p.L332I, TTN:p.T32425M, ZFP36L2:p.D240N, ZNF208:p.H883Q, ZNF48:p.R235H, ZNF626:p.K473R, ZNF676:p.P43T, ZZZ3:p.R162Q.

55. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from OV; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of TP53:p.R273H, TP53:p.Y220C, TP53:p.R248Q, TP53:p.R175H, TP53:p.R273C, TP53:p.I195T, TP53:p.R248W, TP53:p.R282W, TP53:p.C176Y, TP53:p.V157F, TP53:p.S241F, TP53:p.H179R, TP53:p.G245S, TP53:p.H193R, ADCY2:p.V888I, B2M:p.M1V, BAP1:p.R227C, CYP4A11:p.V185F, DNAH5:p.R3197Q, GART:p.K807fs, GRIN2B:p.R519Q, HRNR:p.M1fs, KLHL29:p.L716fs, KRAS:p.G12V, MGA:p.R2435Q, MYO3A:p.N525S, NPAS2:p.Q201R, NRAS:p.Q61R, PDAP1:p.K55fs, PGAP1:p.F565C, TP53:p.S315fs, TP53:p.C275Y, TP53:p.R273L, TP53:p.V272M, TP53:p.G266V, TP53:p.G266R, TP53:p.D259Y, TP53:p.P250L, TP53:p.G245D, TP53:p.G245V, TP53:p.G244C, TP53:p.C238fs, TP53:p.Y236C, TP53:p.Y234C, TP53:p.V216M, TP53:p.S215R, TP53:p.Y205C, TP53:p.L194R, TP53:p.P191del, TP53:p.Y163C, TP53:p.A159V, TP53:p.K132N, TRPC7:p.D210V, UXS1:p.V100L, WNT11:p.C344Y, and ZNF295:p.E885A.

56. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from READ; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of KRAS:p.G12V, TP53:p.R273H, KRAS:p.A146T, KRAS:p.G12D, TP53:p.R175H, AKAP9:p.L3482I, APBA1:p.E624K, BAG5:p.D439N, C17orf97:p.E230D, CDH23:p.F177L, CERS3:p.E95D, DNAH5:p.R982H, ERBB2:p.V842I, GABRB3:p.D500N, KRAS:p.G13D, KRAS:p.G12C, KRAS:p.G12S, LRP6:p.R675Q, MACF1:p.F722L, MBOAT2:p.R43Q, MYO1D:p.E246K, NLRC4:p.E409K, NRAP:p.E327K, NRAS:p.Q61K, PCDH15:p.R1552I, PIK3CA:p.N345K, PIK3CA:p.E545K, POLE:p.S459F, PPP2R2B:p.P326L, SMAD4:p.R361H, TP53:p.R248W, ZFP2:p.R150I, and ZNF563:p.K26N.

57. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from SKCM; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of BRAF:p.V600E, NRAS:p.Q61R, NRAS:p.Q61K, HSD17B7P2:p.N175S, BRAF:p.V600K, DISP1:p.G732L, IDH1:p.R132C, NRAS:p.Q61L, MUC16:p.P5119S, RAC1:p.P29S, WASH3P:p.G175S, AGAP9:p.M248V, C15orf23:p.S24F, DNAH5:p.D3236N, SPTLC3:p.R97K, TMC5:p.R276C, CFB:p.R314M, FRG1B:p.A50P, INMT:p.S212F, LOC649330:p.G93E, MAP2K1:p.P124S, RGS7:p.R44C, STK19:p.D89N, ADAM30:p.G97L, ARL16:p.G6R, ARMC4:p.E22K, BRAF:p.K601E, CAPN13:p.P405S, CD1C:p.R89C, CLCC1:p.P406Q, CNTN5:p.S379F, DNAH5:p.R742Q, EEF1B2:p.S43G, FRG1B:p.I59V, GABRG1:p.E205K, IARS2:p.R832C, IL32:p.D218fs, ISX:p.R86C, KLHDC7A:p.E635K, NAP1L4:p.P285Q, NBPF10:p.Q908E, OR2A5:p.S71L, OR4E2:p.R226Q, OR4M1:p.G41E, OR4M2:p.S268F, OR4N2:p.G41E, OR51B2:p.S163L, PCDHGC5:p.R293C, PCLO:p.R4133C, PHGDH:p.G173L, POTEG:p.D51N, PPP6C:p.R301C, PRAMEF11:p.C84S, PSG9:p.E404K, PTPRB:p.D1560N, RNF152:p.P95S, SPAG16:p.P488S, SPATA8:p.E18K, TAF1A:p.R172M, TCEB3C:p.E308K, THSD7B:p.E126K, TTN:p.E12129K, XIRP2:p.D2439N, and ZNF831:p.R1393Q.

58. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from UCEC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of RPL22:p.K15fs, PTEN:p.R130G, PTEN:p.R130Q, KRAS:p.G12D, KRAS:p.G12V, PIK3CA:p.H1047R, PIK3CA:p.R88Q,

PIK3CA:p.E545K, PTEN:p.V317fs, FGFR2:p.S252W, PIK3CA:p.E542K, CTNNB1:p.S37F, POLE:p.P286R, PPP2R1A:p.P179R, CTNNB1:p.S37C, KRAS:p.G13D, CTNNB1:p.D32N, CTNNB1:p.S33F, CTNNB1:p.G34R, KIAA2026:p.R574C, LIMCH1:p.R806fs, PIK3CA:p.H1047L, ALPK2:p.K523fs, CTNNB1:p.S33C, FBXW7:p.R505C, HPD:p.R284fs, KRAS:p.G12A, PIK3CA:p.R93Q, POLE:p.V411L, TP53:p.R248W, ABCA11P:p.R385I, ABI1:p.K445N, ACSM2B:p.K195N, APOB:p.F3102L, ASCC3:p.R136Q, C12orf4:p.R335Q, CCDC132:p.R838C, CHD4:p.R975H, CSDE1:p.R220C, CTNNB1:p.D32Y, CTNNB1:p.S33Y, CTNNB1:p.T41I, EXOC1:p.R588C, FBXW7:p.R465H, FGFR2:p.N549K, FUBP1:p.R430C, GEN1:p.S509L, IK:p.E90fs, KIF20B:p.E54K, MAX:p.H28R, MBOAT2:p.R43Q, METTL14:p.R298P, MFGE8:p.D170N, MS4A8B:p.S3L, NSMCE1:p.D244N, OXR1:p.E122K, PCDH19:p.E530K, PIK3CA:p.R108H, PIK3CA:p.N345K, PIK3CA:p.C420R, PIK3CA:p.Q546P, PIK3CA:p.Q546R, PTEN:p.R130L, RBL2:p.E127K, RXFP1:p.S223Y, SF3B1:p.R957Q, SLC20A1:p.P328fs, SOX17:p.S403I, TNS1:p.Q659del, TP53:p.R273H, TP53:p.R273C, TP53:p.R248Q, TTN:p.D16823N, TXNL1:p.R234C, ZFHX3:p.R1893fs, ZNF180:p.R625I, ZNF257:p.R392I, ZNF354B:p.D609N, ZNF43:p.R280C, ZNF709:p.R468I, ZNF765:p.S254L, ABCA5:p.R1476Q, ACVR1:p.R206H, ADAD1:p.S11L, ADAM9:p.R256Q, ADD3:p.E570K, ADGB:p.S1124L, AGXT2:p.R502C, AMBN:p.S225Y, ANKDD1A:p.R24H, ARHGEF33:p.R46I, ATP10B:p.L1304I, ATP2C1:p.E724K, ATP9A:p.R290Q, ATR:p.R1814fs, AVL9:p.F34L, BMPER:p.R241Q, BTN3A2:p.E153K, C14orf118:p.R279I, C14orf166B:p.F230L, C3orf23:p.R217C, C3orf62:p.R185Q, CACNA1C:p.S710L, CAGE1:p.E539K, CARD10:p.KE272del, CCDC144A:p.S1264L, CCDC168:p.D5020Y, CCDC36:p.R209I, CD55:p.E156K, CEP44:p.S253L, CIITA:p.E728K, CREBBP:p.P2094L, CTNNB1:p.S37A, CTTNBP2:p.S420L, DCT:p.R532Q, DIAPH2:p.E121K, DLG2:p.S624L, DNAH10:p.R1888Q, DNAH14:p.R1367C, DNAH7:p.R2961Q, DNAH8:p.R1347H, DNAJC13:p.E1248K, DNMT1:p.E51K, DST:p.S1767Y, DYNC2H1:p.E883D, EMR1:p.R631Q, EPHX4:p.R282Q, ERCC6L2:p.L445I, F10:p.E117K, FAM155B:p.E158K, FAM83B:p.R206Q, FARP1:p.S383L, FAT3:p.A4159T, FBXW7:p.R689W, FBXW7:p.R465C, FBXW7:p.G423V, FN1:p.R290C, FZD6:p.R416Q, GABRA3:p.R73H, GABRA4:p.R460Q, GALNTL2:p.E395K, GFAP:p.A233T, GGA2:p.A63V, GIGYF2:p.R227H, GNPTAB:p.R1189Q, GPR112:p.S1283Y, GPR98:p.R4142W, GRIA3:p.S646Y, GRM6:p.E363D, HMCN1:p.S133Y, HSPA4L:p.R483C, HTR2A:p.S219L, INTS7:p.R940C, INTS7:p.R106I, ITM2C:p.E167K, JAKMIP2:p.R283I,

KCND3:p.S438L, KCNS2:p.D211N, KDM1B:p.F361L, KIAA0556:p.L330I, KIAA1147:p.A149V, KIF23:p.R150Q, KIF27:p.K925N, KIF9:p.R594Q, KLHL13:p.E213K, KLHL28:p.E33K, LIN9:p.R183W, LRBA:p.E2103K, LRP2:p.R2432I, MAGI2:p.L450M, MC5R:p.A109T, MEGF10:p.S1053L, MKI67:p.T1664fs, MKLN1:p.F485L, MMRN1:p.F917L, MSH4:p.E730K, MTOR:p.S2215Y, MUC7:p.S336L, MYBPC2:p.R646H, N4BP2L2:p.R506C, NAPSA:p.R121Q, NCOA7:p.E369D, NCR1:p.R258W, NEK11:p.R374Q, NHEJ1:p.R109Q, NNMT:p.E233K, NOTCH4:p.15_16LL>L, NPY1R:p.A371T, NRAS:p.Q61R, OGDHL:p.R57C, OMA1:p.R445Q, OPRM1:p.R462C, OR4C12:p.F248L, OR5AK2:p.K89N, OSBPL6:p.R577Q, PCDHAC2:p.K138N, PCDHB12:p.R289C, PCDHGC5:p.A70T, PIK3CA:p.R38H, PIK3CA:p.E39K, PIK3CA:p.E110del, PIK3CA:p.K111E, PIK3CA:p.Q546K, PIK3CA:p.M1043V, PIK3CA:p.M1043I, PLA2G3:p.R201Q, PLXNA1:p.E1295K, PON1:p.R306Q, POTEE:p.R303I, POTEF:p.K674N, PPP2R1A:p.S256F, PPP2R3B:p.F310L, PRAM1:p.A268T, PREX1:p.E1246K, PRKCQ:p.A324V, PTEN:p.R130P, PVRL4:p.A358T, RAI2:p.S385Y, RBM39:p.T353I, RELN:p.F2722L, RFPL1:p.R148Q, ROBO2:p.D1018N, ROS1:p.R245I, RPS6KA6:p.S394Y, RSBN1:p.E572K, RYR1:p.A2576T, SACS:p.R2906Q, SCAPER:p.R366Q, SELP:p.R429W, SENP7:p.S673Y, SEPHS1:p.E13K, SFRP4:p.R232Q, SGK1:p.K367del, SIX1:p.E191K, SLC10A7:p.S261L, SLC12A2:p.R828Q, SLC16A14:p.R495Q, SLC7A2:p.R322W, SMCR8:p.E175K, SOS1:p.N233Y, SPOP:p.E50K, STRN3:p.K218N, STXBP6:p.D92N, SULT1E1:p.R77Q, SUN3:p.L124I, SUSD1:p.R343C, SYNM:p.R516Q, TAF1:p.R843W, TDRD3:p.R322Q, THADA:p.S1941L, TLN2:p.S208L, TMEM161B:p.R315Q, TMPRSS3:p.R16Q, TP53:p.Y220C, TPTE:p.S423L, TRANK1:p.E846K, TRPC5:p.S490L, TRPM3:p.R429W, TSSK1B:p.E301K, TTLL7:p.R751H, TTN:p.S20317L, TTN:p.E6404K, TTN:p.R4434Q, TTN:p.R2506Q, UGT8:p.E102K, USF1:p.R52Q, USP16:p.R455Q, USP25:p.R873H, USP33:p.R36Q, VPRBP:p.R802Q, VPS13B:p.R692Q, WDR65:p.F110C, YTHDC2:p.E185K, ZFYVE1:p.R266Q, ZKSCAN1:p.R541fs, ZNF117:p.R157I, ZNF180:p.R569I, ZNF195:p.R59Q, ZNF254:p.K179N, ZNF263:p.R510I, ZNF333:p.R554Q, ZNF354B:p.R402I, ZNF442:p.R309Q, ZNF454:p.R376I, ZNF485:p.R374I, ZNF488:p.R206Q, ZNF559:p.E284K, ZNF594:p.R287I, ZNF611:p.R390I, ZNF645:p.R154C, ZNF649:p.R338Q, ZNF649:p.R198I, ZNF674:p.R405I, ZNF675:p.R220I, ZNF678:p.R564I, ZNF732:p.R354I, ZNF780A:p.R466Q, ZNF823:p.R547I, ZNF836:p.R854I, ZNF836:p.R630I, ZNF841:p.R757I, and ZNF98:p.R370I.

59. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from ACC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of ZFPM1:p.EPL444del, GARS:p.P42A, ZNF517:p.V349A, LRIG1:p.L24V, CCDC102A:p.R96W, OPRD1:p.C27F, SOWAHA:p.R124P, LACTB:p.M5L, TOR3A:p.F13L, ZFPM1:p.E444fs, ZNF787:p.D367del, LRIG1:p.L26V, IRX3:p.L422P, TRIOBP:p.H1300R, TUBA1C:p.L146F, ZFPM1:p.P445fs, ZFPM1:p.446_447LA>P, TPO:p.S398T, USP42:p.R779P, ERCC2:p.D312N, GLTPD2:p.D209E, OTOP1:p.LLW104del, RINL:p.P402L, AMDHD1:p.S3G, ASPDH:p.Q266R, KCNK17:p.S21G, TMEM247:p.Q128E, MUC5B:p.D682G, OBSCN:p.R4516W, FAM184B:p.R784W, SEMA5B:p.V840D, ZNF598:p.E25G, ADAD2:p.G44E, C1orf106:p.R538C, ZAR1:p.Q42H, PANK2:p.G126A, PODXL:p.28_30PSP>P, SALL3:p.L593V, THEM4:p.L17R, C2orf81:p.T315P, CLDN23:p.V210M, FAM109A:p.GGG156del, FPGS:p.I22V, HHIPL1:p.V692A, MUC5B:p.M2869T, PLEC:p.R1386Q, SYT8:p.R373W, TAF5:p.S130A, TMEM189-UBE2V1:p.N6D, UQCRFS1:p.S6A, B3GNT6:p.L316fs, CCDC105:p.P499T, CLIC6:p.Q298E, IDUA:p.T374P, NOTCH2:p.C19W, RGS9BP:p.A96S, RREB1:p.G783V, SP8:p.G165del, WDR34:p.W60G, C19orf10:p.G12R, CELSR2:p.16_17insP, FAM75C1:p.71_71H>HLVSQRH, GPRIN2:p.R446H, KBTBD13:p.A81V, OGFR:p.S557T, PODXL:p.30_30P>PSP, BHLHE22:p.L62Q, C4orf32:p.G32E, C5orf65:p.Q245R, KNDC1:p.V806D, KRTAP10-6:p.49_49P>PSCCAP, LRP11:p.P92R, MAP1S:p.S411C, NOL9:p.S58A, RASIP1:p.R601C, RGMB:p.S63R, SARM1:p.R23P, TSC22D2:p.A419T, ZNF628:p.T230A, ZNF814:p.A337V, AATK:p.A541T, BTBD11:p.G265A, CRIPAK:p.C143R, KCTD3:p.F9V, KRT8:p.S59A, MUC5B:p.S681G, NCOR2:p.1846_1847insSSG, OGFR:p.E556K, APOE:p.C130R, C10orf95:p.A85S, C13orf33:p.R59G, CRIPAK:p.C174R, FAM18B2:p.C51Y, GLI3:p.P998L, GLTSCR2:p.Q389R, HECTD2:p.P19A, IRF2BPL:p.123_125QQQ>Q, MEX3C:p.179_182AAAA>A, NEFH:p.EE658del, RNF149:p.S9G, RNF222:p.A133T, SEZ6L2:p.R74P, TNIP2:p.R73G, ARRDC4:p.T79A, B3GNT6:p.P330fs, BAG1:p.G45R, C22orf26:p.P28L, CHDH:p.E40A, COQ2:p.V66L, CTGF:p.H83D, DLEU7:p.A83V, EPPK1:p.D2378H, FAM86C1:p.R30P, FZD1:p.93_94insP, GPRIN2:p.V241M, GPX1:p.11_13AAA>A, HES3:p.P96T, JMJD4:p.A11V, KANK3:p.R359H, LPPR2:p.A186S,

NEFH:p.665_666insEE, NOM1:p.R24G, RNF39:p.G263C, SCRT1:p.S133A, SNED1:p.L1228P, TTLL11:p.122_123insKA, ZCCHC3:p.A159del, ZNF219:p.QP233del, ASB16:p.T249A, ASB2:p.H515P, ATP9B:p.S39G, AVL9:p.G7fs, C17orf96:p.L63V, C19orf29:p.A499V, CRB2:p.T1110M, CRIPAK:p.P173R, CRIPAK:p.I190L, CSGALNACT2:p.L362F, CTBS:p.LAL31del, CTNNB1:p.S45P, DMRT1:p.S45T, DOK7:p.G461D, FBRSL1:p.A836V, FEZ2:p.P50L, FRG1:p.S169N, HSD17B1:p.G313S, IBA57:p.S130R, KIF1A:p.E917D, KRTAP9-1:p.160_160Q>QPSCGSSCCQ, LURAP1L:p.55_56insGGG, NMU:p.A19E, NMU:p.A18E, NOXA1:p.D6E, NPTX1:p.G100D, PLIN5:p.R306W, TBP:p.95_96insQ, TMEM200C:p.S498G, TNXB:p.V706fs, VARS:p.P51S, ZC3H12D:p.P405S, and ZZEF1:p.V30A.

60. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from CESC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of PIK3CA:p.E545K, PIK3CA:p.E542K, MAPK1:p.E322K, EP300:p.D1399N, ERBB2:p.S310F, ERBB3:p.V104M, KRAS:p.G12D, ANKRD12:p.E721Q, ANKRD36:p.M1144T, MICA:p.G318fs, PIK3CA:p.E726K, PTEN:p.R130Q, ABCD1:p.S606P, ACTL7B:p.E211K, ADAM21:p.F129C, ADAMTS12:p.P1053A, AKT1:p.E17K, ANKLE1:p.V643L, ANO3:p.M956I, AOAH:p.R326T, APOD:p.S115L, ASCC1:p.H207Y, ATM:p.S800F, AURKA:p.S387L, BAG5:p.M286I, C12orf43:p.E28Q, C16orf3:p.G65S, C3orf70:p.S6L, C4orf21:p.E800Q, CALB2:p.K60N, CALCB:p.R81T, CCDC152:p.E153Q, CCDC53:p.R58C, CDC27:p.P242S, CFHR5:p.R441H, CLOCK:p.L123fs, CMYA5:p.E2733K, CNTRL:p.P185S, CSHL1:p.R117Q, CSMD3:p.H952Y, CTNNB1:p.D32G, CTSH:p.E254Q, DHPS:p.F49L, DMPK:p.R44H, DNAH14:p.F622fs, DNAH3:p.E3367Q, DNAH8:p.E587D, DNASE1L1:p.D212N, ECE2:p.D254N, FAM71B:p.H445D, FAM73A:p.G23V, FAS:p.E261K, FBXW7:p.R505G, FBXW7:p.R465C, FEZF2:p.E82K, FKBPL:p.E161Q, FMNL1:p.E927Q, GPATCH3:p.E275Q, GPR142:p.R304T, GPRIN2:p.T100P, GRAMD2:p.I123M, HERC2:p.S329F, HGF:p.G229A, HIF3A:p.A72T, HIST1H1B:p.K188N, HIST1H2AL:p.R30P, HIST2H2AC:p.R30P, HLA-C:p.N104K, HLA-DPB1:p.G114fs, HRNR:p.G2539S, INVS:p.R799K, JPH3:p.Q433H, JUP:p.S627L, KIAA1211:p.R308fs, KIAA1211:p.E309fs, KLK2:p.E161K, KRAS:p.G13D, KRAS:p.G12V, LIN9:p.E231K, LOC151174:p.P90S, LRRC37A3:p.A406D, LRTM2:p.L176V, MEPE:p.S30T,

MUC12:p.R2634C, MUC4:p.S2936L, MYOM2:p.D988N, NFE2L2:p.D29H, NOTCH2:p.R2298W, NPIPL1:p.P250L, NR5A2:p.E80K, NYAP2:p.R197Q, OBSL1:p.E1642K, OR13C2:p.L9V, OSBP:p.Q721H, PAOX:p.H107Y, PDILT:p.E500K, PIAS3:p.D460N, PLEKHO2:p.E351Q, PNRC1:p.R73C, PPP4R1:p.L597F, PREP:p.F469L, PRKDC:p.Q3568E, PSME3:p.R231W, RANBP6:p.R915W, RCAN2:p.D440N, RNPC3:p.E116fs, SDHAP1:p.H66Y, SDHAP2:p.S37fs, SERPINA3:p.K158N, SERPINA4:p.R98C, SF1:p.R255W, SGSM1:p.E818K, SIM1:p.V213M, SLC10A4:p.F281L, SLC25A5:p.I79F, SLC35G2:p.K62fs, SLC4A9:p.R617C, SLCO2A1:p.M479I, SND1:p.Q38E, SPATA17:p.R72K, SRSF12:p.S150C, TADA2B:p.E67K, TCTEX1D2:p.S74L, TEDDM1:p.M166I, TEX15:p.E1652Q, TMC2:p.E92D, TMEM131:p.E1319Q, TNKS2:p.T619fs, TNS1:p.Q659del, TP53:p.E285K, TRAF3:p.S9F, TRIM61:p.K98N, TRPM1:p.M996I, TUFT1:p.L101F, U2AF1:p.S34F, UNC93B1:p.V498M, USP4:p.L259V, VCAN:p.S1308C, WDR17:p.P278S, ZBED4:p.S385L, ZEB2:p.E1094K, ZFYVE9:p.M1147I, ZNF16:p.R452W, ZNF677:p.R131T, and ZSWIM4:p.E407K.

61. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from CRC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of KRAS:p.G12D, KRAS:p.G12V, BRAF:p.V600E, KRAS:p.G13D, TP53:p.R175H, PIK3CA:p.E545K, FBXW7:p.R465H, KRAS:p.A146T, PIK3CA:p.H1047R, TP53:p.R248W, CDC27:p.D555E, SMAD4:p.R361H, TP53:p.R273H, KRAS:p.G12C, NRAS:p.Q61K, ERBB2:p.V842I, ERBB3:p.V104M, FBXW7:p.R465C, PIK3CA:p.R88Q, PIK3CA:p.E542K, TP53:p.R273C, TP53:p.G245S, AXIN2:p.G665fs, C16orf45:p.T106N, C20orf26:p.R1088Q, DNMT1:p.E432K, FBXW7:p.R505C, HLCS:p.E362K, HPSE2:p.K58N, KIF14:p.R598Q, KIF18A:p.R17C, KIF20B:p.E991K, KLHL5:p.R326C, KLK2:p.P57T, KRAS:p.G12A, KRAS:p.G12S, LPHN3:p.R1183Q, LRP6:p.R675Q, MYH8:p.R1048Q, NRAP:p.E327K, NRAS:p.G12C, PIK3CA:p.N345K, POSTN:p.R508C, PPP2R1A:p.R183W, PTEN:p.R130Q, RAF1:p.S257L, SDK1:p.T1181M, SGSM1:p.F1117L, TCF7L2:p.R482fs, TP53:p.R282W, TRIM23:p.R289Q, UGT8:p.E102K, ZNF491:p.R343Q, A2M:p.R732Q, AADACL4:p.A266T, ABCA8:p.E1158K, ABCA8:p.R842Q, ABCA8:p.A696T, ABCB8:p.R345H, ACACA:p.R1731C, ACADM:p.F48C, ACOT9:p.R50Q, ACPP:p.R105Q, ACTL7B:p.R354H, ACTL9:p.R331H, ACVR1:p.S290L, ADAM30:p.S314Y, ADAM32:p.R559Q, ADAMTS16:p.D817N, ADAMTS4:p.R156W,

ADCY5:p.R661H, AGMAT:p.V313M, AGPAT4:p.A212T, AKAP12:p.E1282K, AKAP9:p.L3482I, ALB:p.S294L, ALDH1L1:p.A870T, ALG2:p.S302Y, AMOTL1:p.R676Q, AMPD1:p.K502N, AMPH:p.R292W, ANKRD6:p.R479C, APBA1:p.K730N, APBA1:p.E624K, APC:p.E847fs, APC:p.F1354fs, APC:p.M1413fs, APOB:p.R3136C, APOB:p.A43V, APPL1:p.R668W, AQPEP:p.A309T, ARF4:p.R149H, ARFGEF1:p.D1632N, ARHGAP32:p.E1253K, ARHGAP36:p.R128C, ARHGAP36:p.A147V, ARHGAP5:p.D890fs, ARNTL:p.T395M, ARPP21:p.R338H, ARSG:p.V131I, ASCC3:p.R1197Q, ATP10D:p.R311H, ATP6V0A4:p.R191Q, ATP9B:p.R265Q, AXDND1:p.E930D, AXIN2:p.W663fs, B2M:p.L13fs, B3GALNT1:p.R145Q, BACH1:p.R538Q, BAG5:p.D439N, BBOX1:p.F176V, BCL2L11:p.R91Q, BCL7A:p.T52M, BCLAF1:p.R37fs, BEND5:p.R198C, BICD2:p.R162H, BLVRA:p.S44L, BMP3:p.R344W, BNC2:p.R512W, BRPF1:p.R66C, BRWD3:p.R787C, BTBD7:p.S436L, BUB1B:p.F996L, BZRAP1:p.V1627I, C11orf30:p.R1111C, C14orf101:p.E295K, C14orf102:p.D115N, C14orf105:p.R100I, C15orf2:p.V488I, C15orf33:p.D340N, C16orf87:p.R151I, C1RL:p.L351fs, C22orf40:p.P32fs, C3orf39:p.R333W, C5orf30:p.D4N, C5orf4:p.R114Q, C6orf170:p.K724T, C7orf63:p.A10T, CACHD1:p.S720Y, CACNA1A:p.T665M, CACNA2D3:p.A332T, CACNB2:p.R608H, CACNG3:p.V134I, CACNG3:p.A138V, CACNG5:p.G121R, CADM1:p.S190L, CADPS:p.A1073T, CAPRIN2:p.E13K, CARD11:p.R423Q, CASC1:p.R54Q, CASP14:p.R5W, CBFB:p.E152K, CC2D2A:p.R1284C, CCDC18:p.K615N, CCDC60:p.R230H, CCDC81:p.R259I, CCDC88C:p.P1851fs, CCKBR:p.V236M, CD101:p.D283Y, CD101:p.R594Q, CD180:p.N228T, CDC14B:p.R375C, CDCA7L:p.P405fs, CDH10:p.E349K, CDH12:p.D674N, CDH20:p.A134V, CDH23:p.F177L, CDH2:p.D547Y, CDH9:p.F523L, CDK16:p.R108C, CEACAM5:p.L640I, CEP152:p.E21K, CERS3:p.E95D, CHD4:p.R975H, CHD5:p.A801T, CIZ1:p.V668A, CLEC18A:p.R423H, CLTCL1:p.R481W, CMAS:p.R110Q, CNRIP1:p.R102W, COBLL1:p.K732N, COL14A1:p.R1082I, COL17A1:p.P1004L, COL4A6:p.L550I, COL6A3:p.D2792N, COPB1:p.R425C, CORO2A:p.*526R, COX15:p.L86I, CSMD1:p.S781Y, CTCFL:p.E423K, CTDNEP1:p.E126K, CTTNBP2:p.R164C, CYP4B1:p.E434D, DACH2:p.R539C, DBC1:p.V216I, DBF4B:p.S254Y, DCHS2:p.F2149L, DCLK2:p.S549Y, DDI1:p.R275Q, DENND4A:p.P357H, DENND4C:p.R1081Q, DHTKD1:p.R410Q, DISP1:p.R763C, DKK2:p.R230H, DKK4:p.R203Q, DLC1:p.A350V, DLC1:p.E222D, DMD:p.R3195H, DNAH5:p.R982H, DNAH5:p.R224Q, DNAH9:p.D1547N,

DNAJC24:p.E61K, DNM1:p.A251T, DNMT1:p.E1531Q, DNMT3B:p.R92W, DOCK10:p.A1830V, DOCK1:p.E864K, DOCK2:p.G170R, DOCK3:p.R1183C, DOCK5:p.E177K, DOK5:p.R274W, DPP8:p.G165R, DPY19L1:p.F378L, DUOX2:p.F880L, DVL2:p.A601fs, EBAG9:p.E187K, EBF3:p.G255fs, EDNRB:p.L450R, EGR2:p.R390H, EHD3:p.E44K, EIF2C1:p.R139Q, ELF3:p.F305fs, ELMOD2:p.T141M, EMR2:p.S75L, ENAM:p.R373H, ENOX2:p.R356W, ENTPD7:p.E327K, EPG5:p.D369N, EPHB2:p.R392H, ERCC6:p.V780I, ERCC6L:p.R505Q, ERRFI1:p.A421T, ESCO1:p.R300Q, ETV6:p.R369W, F8:p.S2269Y, FAM123B:p.F173fs, FAM135B:p.R884H, FAM169B:p.K165N, FAM170A:p.E56K, FAM171B:p.D459N, FAM181A:p.R109H, FAM5B:p.R402C, FBXO11:p.A432V, FBXW7:p.R689W, FBXW7:p.S582L, FBXW7:p.R14Q, FGF14:p.A236V, FHDC1:p.R254W, FHOD3:p.A225T, FHOD3:p.E813K, FMO3:p.F510L, FNDC1:p.R652H, FOXK1:p.R354W, FOXN3:p.P96fs, FPGT-TNNI3K:p.R455H, FZD3:p.D367N, GABRA4:p.R460Q, GABRA5:p.S126N, GABRB3:p.D500N, GALNTL5:p.R262I, GJA1:p.R362Q, GLRA3:p.L454I, GLRA3:p.F132L, GOLGA4:p.Q1536H, GP2:p.S41L, GPC6:p.A214T, GPLD1:p.R717Q, GPR125:p.R113Q, GPR156:p.F754L, GPR158:p.D566N, GPR21:p.R216H, GPR61:p.A62T, GPR98:p.R4142W, GPRC5A:p.V30I, GRAP2:p.E69D, GRIA1:p.R218C, GRIA2:p.R845Q, GRM7:p.R679Q, GTF3A:p.K306N, HAO1:p.R172C, HARS2:p.R168H, HBB:p.F42L, HCN4:p.R525H, HDAC5:p.A1044T, HGF:p.S467Y, HIPK4:p.R280H, HLA-DMA:p.E84K, HMG20A:p.E248D, HPS3:p.S468L, HRSP12:p.R120Q, HS3ST1:p.E287K, HTR3B:p.R236C, HTR5A:p.R152C, HTT:p.D1548N, HYDIN:p.R1187C, HYDIN:p.R939Q, HYDIN:p.R451Q, HYOU1:p.R158C, IFT172:p.A944V, IGJ:p.R77Q, IL17RA:p.Q803fs, IL1RAPL2:p.T647M, IL3:p.A90T, IL5RA:p.L47I, INPP5D:p.R523Q, INPP5K:p.R263C, IRAK3:p.R267Q, IREB2:p.R419Q, ITGA4:p.T673M, ITGA4:p.F900L, ITIH5:p.A912T, ITK:p.E196K, JAG1:p.A462T, JAK1:p.V310I, KAL1:p.V303I, KBTBD8:p.V549I, KCNA3:p.A415V, KCND3:p.S438L, KCNMB4:p.F209L, KCTD20:p.L314fs, KDELC1:p.L447I, KIAA0528:p.R181Q, KIAA0556:p.R1082W, KIAA1109:p.S4937Y, KIAA1804:p.V474M, KIAA1804:p.R477W, KIF16B:p.R145Q, KIF26B:p.A1114V, KPNA4:p.R29Q, KRAS:p.K117N, KRAS:p.Q61L, KRAS:p.Q61K, KRT6B:p.L197P, L1CAM:p.T186M, LALBA:p.A41T, LAMA4:p.A558V, LBX1:p.R176W, LPAR4:p.R145Q, LRP1B:p.K2623N, LRP2:p.R3043C, LRP2:p.S737L, LRRC18:p.R218W, LRRC31:p.K23T, LRRC7:p.R1389H, LZTS2:p.P100fs, MACF1:p.S292L, MACF1:p.F722L,

MAEL:p.R345C, MAGEE1:p.V380M, MAGI1:p.R1198C, MAP1B:p.E2046D, MAP2:p.K530N, MAP2K4:p.R287H, MAP3K4:p.R275Q, MAP7D2:p.R487C, MAPK8IP1:p.L217fs, MBOAT2:p.R43Q, MCF2L2:p.R926Q, MECOM:p.R969C, METTL16:p.R200Q, METTL21A:p.R174Q, METTL6:p.F56L, MFF:p.R162C, MFSD5:p.R280Q, MIA3:p.Q356H, MMAA:p.R326C, MORC1:p.D113Y, MORC2:p.R740H, MPDZ:p.L804I, MR1:p.S46L, MRPL47:p.L234I, MS4A8B:p.S3L, MSH4:p.K464N, MSH6:p.T1085fs, MSH6:p.R1095H, MUC16:p.R8606H, MYH13:p.D311N, MYH7:p.R1689C, MYO1D:p.E246K, MYO3A:p.N525H, MYO6:p.D1180N, MYO9A:p.R2179Q, MYO9A:p.R167Q, MYOZ2:p.E251K, MYT1:p.E226K, NAA25:p.S807Y, NCAM1:p.R474W, NCOA4:p.R562Q, NEB:p.D5434N, NEB:p.L1591I, NEB:p.E1214K, NEDD9:p.A798T, NEDD9:p.A316T, NEK1:p.R608C, NFASC:p.V256I, NINL:p.R1366C, NLRC4:p.D593N, NLRC4:p.E409K, NLRP4:p.V229I, NLRP5:p.R392H, NME9:p.E75K, NOLC1:p.T428M, NPC1:p.E451K, NPSR1:p.R235Q, NRAS:p.Q61L, NRAS:p.G13R, NRAS:p.G12D, NRG2:p.T246M, NTN4:p.E59K, NUB1:p.R373Q, NUDT15:p.S83Y, NUF2:p.S340L, NUP88:p.A302V, ODZ1:p.R2556W, OGDHL:p.A427T, OGFRL1:p.E427K, OLFM4:p.K132N, OPRM1:p.R353H, OR10A3:p.S93Y, OR2M3:p.R235H, OR52W1:p.R133C, OR5AU1:p.R312H, OR5B17:p.R163H, OR8S1:p.A99V, OSTN:p.R115Q, OTOL1:p.V431I, OTUD3:p.R277I, PAN3:p.S580N, PANK3:p.R260I, PAX3:p.T424M, PCBP1:p.L102Q, PCDH10:p.V477M, PCDH15:p.R1552I, PCDHAC2:p.A519T, PCDHAC2:p.E190K, PCDHAC2:p.A266T, PCDHAC2:p.A156V, PCDHAC2:p.E271K, PCDHAC2:p.A736V, PCDHB5:p.D51Y, PCDHB8:p.D235N, PCDHGC5:p.S289L, PCDHGC5:p.V662M, PCNXL2:p.R135Q, PCOLCE2:p.A348V, PCOLCE2:p.R87H, PDE4B:p.S417L, PGAM1:p.R240H, PHF3:p.R1410I, PIAS2:p.S519L, PIGR:p.A580T, PIK3CA:p.D350G, PIK3CA:p.E545A, PIK3CA:p.E545G, PIK3CA:p.Q546K, PIP4K2C:p.R204H, PKHD1L1:p.F1856L, PLA2G4A:p.E443K, PLCG2:p.E544K, PLCG2:p.D973N, PLEKHA6:p.V328fs, PLEKHG4B:p.E384K, PLK1:p.D233G, PLOD3:p.R297fs, PLSCR3:p.E77K, PLXNC1:p.S462L, PLXNC1:p.R819C, POLA1:p.E603D, POLE:p.S459F, POLE:p.V411L, POLQ:p.R860Q, PPP2R2B:p.P326L, PPP2R5C:p.S259Y, PRAMEF4:p.R248H, PREX1:p.V731I, PRKAA2:p.R407Q, PRKAR2B:p.S309L, PRKCI:p.R480C, PRKRA:p.K122N, PSG8:p.R397C, PSG8:p.R320C, PSMD12:p.R201Q, PTPDC1:p.R430W, PTPN12:p.R765Q, PTPN13:p.S887L, PTPRD:p.L1053I,

PTPRU:p.D1434N, PXDN:p.P856fs, PXDNL:p.T1312M, QRSL1:p.S226L, RAB7L1:p.R79W, RALGAPA1:p.R398C, RANBP2:p.R1231C, RBBP7:p.E313K, RBBP7:p.E274K, RBFOX2:p.A340T, RBMXL1:p.R331Q, RHOBTB1:p.T464M, RIMS2:p.R599Q, RIN3:p.S708L, RLBP1:p.D281N, RLBP1:p.A72V, RNASET2:p.A127V, RNF113B:p.A172V, RNF150:p.R236Q, RNF150:p.S208L, RNF43:p.S216L, ROR2:p.D672N, RPL6:p.F193C, RPS6KA5:p.E166K, RSPO2:p.R28C, RUVBL1:p.E431K, RUVBL1:p.R117C, RWDD2B:p.R254H, RXFP3:p.R113C, RYR3:p.R2705Q, SAGE1:p.R229C, SCFD2:p.R545W, SCML4:p.R194Q, SCN10A:p.T1570M, SCN11A:p.A1688T, SCN11A:p.V1289I, SCN11A:p.V566I, SCUBE2:p.V342M, SEMA3A:p.D81N, SEMA4D:p.R252Q, SEPHS1:p.R371Q, SEZ6L:p.S207L, SFPQ:p.R611Q, SFSWAP:p.S617Y, SGCG:p.A220V, SGCZ:p.I41M, SH3TC2:p.R89C, SIGLEC11:p.S363F, SIPA1L1:p.R1063Q, SIPA1L1:p.S1227Y, SLC12A1:p.S292L, SLC22A15:p.S201L, SLC24A2:p.A134V, SLC25A40:p.R96Q, SLC2A7:p.A65T, SLC30A9:p.R194H, SLC33A1:p.S542L, SLC35F3:p.A280T, SLC39A7:p.R382C, SLC43A1:p.P133L, SLC43A3:p.R216H, SLC44A5:p.R185H, SLC6A2:p.A562T, SLC8A1:p.R431H, SLFN12L:p.F232fs, SLITRK1:p.R52H, SLITRK3:p.S298L, SMAD2:p.R321Q, SMARCA4:p.R381Q, SOCS5:p.S464L, SORBS1:p.V1156M, SORBS1:p.F570L, SORCS2:p.R320W, SOX6:p.R719W, SPATA22:p.S150L, SPEG:p.A944V, SPTB:p.R86C, SPTBN4:p.A1993V, STIM2:p.R572Q, STT3B:p.D583Y, SULT1C4:p.R85Q, SUN3:p.E128K, SUPT6H:p.A957T, SYNE1:p.I1249L, SYNE1:p.R170W, SYNE2:p.K3103N, SYNGR4:p.R169Q, SYT7:p.T349M, TANK:p.S380L, TAS1R2:p.R270C, TAS2R1:p.F183L, TCF7L2:p.R488C, TDRD10:p.S322L, TECTB:p.L29I, TEKT5:p.R401H, TGFBR1:p.S241L, THAP5:p.S287Y, THSD7B:p.R90H, TLL1:p.T153M, TLL2:p.S872L, TM9SF2:p.R91H, TMCC3:p.R110H, TMEM132A:p.R481C, TMEM132D:p.R578W, TMEM55A:p.R189Q, TMEM74:p.R125Q, TMPRSS11A:p.S288L, TNIP2:p.A139T, TOP2B:p.R656H, TOX:p.S354L, TP53:p.G244D, TP53:p.R175C, TPO:p.A826T, TPR:p.S2155L, TPTE2:p.R258Q, TPTE:p.S423L, TRAK1:p.D627N, TRAPPC11:p.R568Q, TRIM23:p.R396Q, TRIM44:p.D331N, TRIO:p.R661W, TRPA1:p.K54N, TRPC5:p.S490L, TRPM6:p.R995H, TRPM7:p.R1862C, TRPM7:p.R843Q, TRPS1:p.R1125W, TRPV5:p.R492H, TRRAP:p.R3515W, TSHZ1:p.R881M, TTC21A:p.S270Y, TTN:p.R22795C, TTN:p.R3193Q, TTN:p.R328H, TUBA3D:p.R243Q, TUFT1:p.A340T, TXNDC15:p.R343Q, UBE2NL:p.R86I, UBIAD1:p.A97T, UGT2A1:p.N97fs, USH2A:p.F2369L, USP11:p.A286T,

USP25:p.R1119Q, USP26:p.R861Q, USP29:p.F81L, USP31:p.D391N, USP40:p.S851L, UTP14A:p.V148I, VAV3:p.E685K, VCAN:p.R1125H, VPS13C:p.D1359Y, WBSCR17:p.R228C, WDR3:p.E841K, WDR52:p.A157T, XKR6:p.R268Q, XPOT:p.R541W, YTHDC1:p.R267Q, YTHDC2:p.E634K, ZBBX:p.R596I, ZBTB24:p.L607I, ZC3H13:p.R103Q, ZCWPW2:p.D144N, ZEB2:p.R156H, ZFHX4:p.E237D, ZFP14:p.R386C, ZFP28:p.R525I, ZFP2:p.R150I, ZFP3:p.R273I, ZFP90:p.R330Q, ZHX2:p.V790I, ZIC4:p.S305L, ZIM3:p.D352N, ZKSCAN4:p.R319Q, ZMYM4:p.R1446Q, ZNF117:p.R185I, ZNF167:p.R683I, ZNF180:p.R401I, ZNF19:p.R349I, ZNF205:p.R384C, ZNF236:p.S1480L, ZNF248:p.R568I, ZNF259:p.R174I, ZNF266:p.R512Q, ZNF266:p.R344Q, ZNF280B:p.E363K, ZNF283:p.R392Q, ZNF32:p.S62L, ZNF345:p.R82Q, ZNF345:p.R334I, ZNF350:p.R310Q, ZNF434:p.R306C, ZNF439:p.E239D, ZNF439:p.R262I, ZNF443:p.R301I, ZNF445:p.L682M, ZNF470:p.R641I, ZNF471:p.R282I, ZNF484:p.R138C, ZNF528:p.R279Q, ZNF563:p.K26N, ZNF573:p.R350I, ZNF583:p.R344I, ZNF585A:p.E638K, ZNF585A:p.E491D, ZNF625:p.R235Q, ZNF652:p.K327N, ZNF677:p.R451I, ZNF678:p.R368I, ZNF699:p.R41I, ZNF70:p.R244I, ZNF770:p.S441P, ZNF774:p.R423Q, ZNF782:p.K247T, ZNF7:p.R337I, and ZNF831:p.E949D.

62. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from DLBCL; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of EZH2:p.Y641F, MYD88:p.L273P, BCL2:p.G33R, CARD11:p.E626K, ADCY2:p.A87V, BCL2:p.N172S, BCL2:p.H20Q, BRAF:p.K601E, BTG1:p.L31F, CACNA1E:p.R1458C, CARD11:p.E93D, CD79B:p.Y197D, CD79B:p.Y197H, CREBBP:p.R1446H, GRID1:p.E622K, HIST1H1C:p.A65V, HIST1H1E:p.G133A, HIST1H3B:p.A48S, KRAS:p.G13D, MYD88:p.S251N, PABPC1:p.R94C, PIM1:p.L164F, PIM1:p.L184F, POU2F2:p.T239A, POU2F2:p.T239S, RELN:p.R2971Q, SLC25A48:p.A67T, STAT6:p.D468H, TNF:p.L47F, and TRAF7:p.R11H.

63. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from KICH; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of ACR:p.W279C, AGRN:p.1284_1285VT>A, C7orf25:p.R384fs, CAMSAP1:p.T466fs, CBWD6:p.E102fs, DOCK8:p.L1111fs,

EBPL:p.Q196P, EBPL:p.L189V, GFM1:p.A17fs, GOLGA6L6:p.D570E, ITGA5:p.A48D, LUZP2:p.S154fs, MTMR9:p.K193fs, MUC16:p.P10452fs, MUC4:p.S2832P, ODF2L:p.K407fs, RHBDD3:p.G34fs, RILPL1:p.S358R, TAS2R30:p.L236fs, TRRAP:p.A973S, UBR5:p.K2120fs, URGCP:p.G639fs, ZNF98:p.A222T, and ZSWIM6:p.Q610fs.

64. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from KIRP; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of FAM18B2:p.C51Y, ZNF598:p.E25G, NEFH:p.E645K, EEF1B2:p.S43G, NEFH:p.AKSPEKEE652del, OBP2B:p.K61N, SKI:p.A62G, C14orf126:p.R6W, KRT8:p.S59A, ACSBG2:p.I250M, ASIC2:p.R46L, CSGALNACT2:p.L362F, FRG1B:p.A50P, IDUA:p.H33Q, KRTAP4-5:p.S74C, SCAF11:p.E926fs, SYN2:p.A34del, ZNF814:p.R322K, BMS1:p.E878D, JMY:p.P822T, KIF1A:p.E917D, KRTAP4-7:p.S57P, LAMA5:p.L2223R, LRP1:p.P1058T, MED16:p.H449Q, MUC2:p.T1488P, MUC5B:p.D682G, NACA2:p.R75K, NEFH:p.665_666insEE, OR2L8:p.S201fs, RGPD5:p.P1760A, RRN3:p.P11S, RRN3:p.R9C, STAG3L2:p.L81fs, ZNF814:p.G320E, ACP6:p.V29G, AHNAK2:p.S2166F, AHNAK2:p.P1215S, AP1G1:p.I782fs, AQP2:p.N68T, BAIAP2L2:p.V396M, BMP6:p.Q118L, BST1:p.G36A, CDR1:p.V31A, CLDN7:p.S172A, CLIP1:p.S1018fs, COL18A1:p.G884fs, CROCC:p.A355P, CTAGE15P:p.A364V, CUBN:p.I2816M, DMRT2:p.T106S, DPY19L1:p.V249L, DSPP:p.D1047N, EBPL:p.L189V, EIF4G1:p.E465del, EXOSC2:p.R11P, FAM216A:p.P36S, FCGR2A:p.V222G, FMOD:p.S331R, FOLR2:p.Q112R, FRG1B:p.L20P, GAGE2B:p.9_10insY, GDPD5:p.G593fs, GIMAP8:p.A544S, GLUD2:p.R300G, GLUD2:p.S496R, GPR135:p.Q5P, HOXD8:p.Q67H, IER5:p.R194G, IL25:p.C168fs, JSRP1:p.V92A, KRAS:p.G12D, KRTAP1-1:p.Y86C, KRTAP4-11:p.L161V, LTBP1:p.L163P, MAML2:p.Q591K, MAPK7:p.A501D, MEF2A:p.P99S, MET:p.H1094Y, MET:p.M1250T, MST1:p.N435fs, MUC2:p.T1582R, MUC2:p.T1722I, MUC4:p.A4222T, MUC4:p.T2335M, MUC4:p.P1138L, MUC5B:p.S1098A, MUC5B:p.S3431N, MYH7:p.A1487T, NBPF10:p.R39fs, NBPF10:p.Y638S, NEFH:p.654_654S>SPEKAKS, PARG:p.A584T, PBX2:p.Y262F, PIP4K2A:p.R219K, RLIM:p.S471P, RUNX2:p.Q71E, SGK223:p.R63S, SMARCB1:p.L365fs, SRCAP:p.Q1875fs, TBC1D2B:p.R920Q, TCF7L2:p.R482fs, TMEM131:p.K640fs, TMEM60:p.K77fs, TPPP:p.R30K, TRPV3:p.A218E, TTBK2:p.C83W, UBXN11:p.S510G, UGT1A1:p.T4A,

UTS2R:p.A289E, YBX1:p.P250L, ZNF514:p.V81G, ZNF516:p.A256D, ZNF681:p.K405Q, ZNF814:p.D404E, ZNF814:p.P323H, ZXDB:p.G206R.

65. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from LIHC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of TP53:p.R249S, CTNNB1:p.D32V, CTNNB1:p.D32G, CTNNB1:p.S33P, CTNNB1:p.K335I, CTNNB1:p.H36P, EEF1A1:p.T432L, GNAS:p.R844C, OR2T4:p.V137L, TP53:p.H193R, ATXN1:p.Q217H, CSMD3:p.F2383fs, CTNNB1:p.D32N, CTNNB1:p.S33C, CTNNB1:p.G34V, CTNNB1:p.S45P, CTNNB1:p.N387K, DHRS4:p.I218T, DNM2:p.E378D, F5:p.Q426L, GALNTL5:p.A45T, GPX1:p.P77R, GRM8:p.R852C, IDH1:p.R132C, KIF26B:p.A2033T, KRT8:p.S59A, LOC100132247:p.T532P, NEB:p.D3854H, PIK3CA:p.H1047R, SOLH:p.R714H, TP53:p.R158H, TP53:p.V157F, and ZNF638:p.D400N.

66. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from MM; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of NRAS:p.Q61R, KRAS:p.Q61H, KRAS:p.G13D, NRAS:p.Q61K, BRAF:p.V600E, NRAS:p.Q61H, NRAS:p.G13R, ZNF717:p.W315C, ATP13A4:p.V431G, DNAJC12:p.R135K, IRF4:p.K123R, KRAS:p.A146T, KRAS:p.Q61R, KRAS:p.G12A, KRAS:p.G12D, ZNF717:p.N594I, ACTG1:p.A22P, ARL6IP1:p.M75L, BEND2:p.E630K, BRAF:p.G469A, CDHR1:p.R218G, DIS3:p.R780K, DMXL2:p.D2412E, DNAJC10:p.I80K, EGR1:p.Q9H, FGFR3:p.*807S, IDH1:p.R132C, IL6ST:p.P216H, INTS12:p.M1V, KRAS:p.K117N, KRAS:p.A59G, KRAS:p.G12R, MAX:p.R36W, MLL5:p.G492E, NBPF1:p.E810K, NRAS:p.Q61L, NRAS:p.G12D, ODF2L:p.E294K, PADI2:p.T114P, PNLIP:p.T37M, PRDM1:p.S588C, PTPN11:p.E76K, PTPN14:p.E286K, RBM6:p.V675G, SCN10A:p.R1142H, SRGAP1:p.T61M, SUSD1:p.T168P, TAS2R16:p.V231I, TINAG:p.E403K, TRIP12:p.L1775P, and ZNF717:p.C844S.

67. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from PRAD; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of HSD17B7P2:p.N175S, RGPD5:p.P1760A,

FRG1B:p.L52S, EEF1B2:p.S43G, FRG1B:p.I10T, FRG1B:p.A53T, LRRC37A2:p.T102S, NBPF10:p.E3455K, PTH2:p.L22V, CYP2D7P1:p.S32A, FAM47C:p.N648D, MAP3K9:p.E38del, MUC4:p.H4205Q, CHEK2:p.K373E, FRG1B:p.A11T, FRG1B:p.A50P, HLA-J:p.R124W, KRTAP1-5:p.I88T, KRTAP4-9:p.D18V, NPIP:p.A271V, PDGFRA:p.R483fs, ZNF780A:p.Q600H, ZNF845:p.R925H, ZNF91:p.R333H, ARFGAP3:p.N299fs, BTN2A3P:p.P3S, FNBP4:p.TT58del, HLA-A:p.Q78R, LOC554223:p.RAPWMEQ147del, PODXL:p.28_30PSP>P, POLI:p.D17del, SPOP:p.F133L, SYN2:p.A34del, TMEM52:p.23_26LLPL>L, UBC:p.L149R, ZNF208:p.I647S, ZNF799:p.E589G, ZNF814:p.D404E, ASTN2:p.L221del, B4GALNT1:p.G88fs, C16orf74:p.S21del, CCDC15:p.H458P, CD209:p.R129W, CNTNAP1:p.S1029I, DBR1:p.541_542DD>D, FAM22F:p.S691del, FRG1B:p.D32V, FRG1B:p.I34T, FRG1B:p.N55D, FRG1B:p.I59V, FRG1B:p.S71N, KIF25:p.W3R, KRTAP4-11:p.L161V, KRTAP4-11:p.M93V, KRTAP4-11:p.R51K, KRTAP4-6:p.S153Y, LILRB5:p.S598P, LMOD2:p.E124del, LOC645752:p.L40P, LRP1:p.P1058T, LRRIQ3:p.K244fs, LURAP1L:p.55_56insGGG, MLLT10:p.V463E, MYOCD:p.Q310del, NBPF10:p.N1369D, OTUD4:p.T909I, PARG:p.A584T, PEX1:p.I370fs, POTEC:p.K507E, POTEC:p.R477Q, POU4F2:p.68_69insG, PRG4:p.T417P, SDHAP2:p.R31C, SPOP:p.F133C, SPOP:p.W131G, TIMD4:p.T152del, TMEM121:p.P299del, TP53:p.G245S, UBC:p.R73L, UBC:p.I191T, WASH3P:p.G175S, ZMIZ1:p.D1048fs, ZNF709:p.T413I, ACADS:p.R330H, ADAMTS7:p.K1357fs, AFF2:p.R597H, AGAP6:p.S127I, AK302238:p.A44T, AK302879:p.Q191R, ALDH1A2:p.R85C, ANAPC1:p.T537A, ANKRD36C:p.H438R, AP4B1:p.R276W, ARFGAP2:p.S38N, BBS9:p.F268fs, BC139719:p.L133R, BRAF:p.G469A, C22orf43:p.D171del, CANT1:p.K131R, CHD3:p.E35del, CLEC4A:p.R209H, CNOT3:p.E20K, CNPY3:p.17_18LL>L, CNTNAP3B:p.S317T, CNTNAP3B:p.M1247I, CTNNB1:p.T41A, DDX10:p.D788del, DLC1:p.S741T, DPY19L2:p.M210V, EDC4:p.S617del, EFCAB6:p.R379K, ERC2:p.927_928HH>H, FAM111B:p.S269fs, FEM1A:p.L620M, FHOD3:p.A632fs, FLJ43860:p.L850fs, FMN2:p.G59del, FNBP4:p.914_915PP>P, FRG1:p.E86del, FRG1B:p.K13N, FRG1B:p.P42Q, GABRB1:p.R416C, GABRR2:p.A368V, GAGE2B:p.9_10insY, GOLGA8DP:p.N84H, GOT2:p.R355W, GPATCH4:p.K210fs, HDGFL1:p.188_189insA, HLA-DQB2:p.G250S, HLA-DQB2:p.R247H, IDH1:p.R132H, IL27:p.E176del, IRF2BPL:p.123_125QQQ>Q, KANK3:p.DGDS489del, KIAA1462:p.858_859SS>S, KRTAP4-11:p.S48R, KRTAP4-7:p.S57P,

KRTAP4-8:p.C95S, LPHN3:p.R826H, LRP10:p.L11del, LRP5:p.S1609P, LRRC16B:p.R787W, MAS1L:p.R324G, MECOM:p.R915Q, MED12:p.L1224F, MED12L:p.Q2115del, MESP2:p.GQGQGQGQ195del, MGAT4C:p.T345M, MLEC:p.E238del, MSLNL:p.T68P, MUC7:p.S173P, MYC:p.Q37del, NBPF10:p.N440D, NLRP6:p.E611del, NOX3:p.C404fs, OR1M1:p.V69I, OR7E24:p.L7fs, OTUD4:p.A153del, PANK2:p.T417fs, PCLO:p.S496P, PCNT:p.S162G, PCSK9:p.23_24insL, PHOSPHO1:p.S32del, POU4F1:p.H108del, PRAMEF8:p.R319H, PRDM7:p.M387L, PRG4:p.T597P, PTPRD:p.R1323C, PTPRF:p.R1174Q, ROBO3:p.RS1367del, ROCK1:p.T518S, RPTN:p.G296S, RTL1:p.152_152E>EE, SIRPA:p.V233I, SLC2A6:p.A230D, SLC8A2:p.E710del, SMG7:p.E846fs, SNAPC4:p.S542del, SP8:p.G165del, SPOP:p.F133I, SPOP:p.F133V, SPOP:p.F102C, SPOP:p.F102V, SRSF11:p.G17fs, SRSF4:p.K396del, SSPO:p.S4198fs, STAG3L2:p.L81fs, STK19:p.R18fs, TBC1D2B:p.R920Q, TBC1D9:p.P1233T, TCHH:p.P1158R, TCOF1:p.K1366del, TNRC18:p.2664_2665SS>S, TP53:p.R248Q, TP53:p.R175H, TP53:p.C141G, TSPAN4:p.L92V, UBXN11:p.GPGPGPSP504del, UTP3:p.E81del, WASH3P:p.L187V, ZAN:p.P717L, ZAN:p.L878P, ZFP90:p.R591fs, ZNF761:p.H373R, and ZNF91:p.H305R.

68. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from STAD; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of RNF43:p.G659fs, BZRAP1:p.P1416fs, XYLT2:p.Y526fs, LARP4B:p.T163fs, PGM5:p.I98V, ZBTB20:p.P692fs, ARID1A:p.G1848fs, FHOD3:p.P334fs, KIAA0182:p.T120fs, ATP6V1B1:p.Y383fs, PIK3CA:p.H1047R, FRMD4A:p.P1005fs, PIK3CA:p.E545K, CDC14A:p.N123fs, KRAS:p.G13D, MLL2:p.T172fs, BCORL1:p.S1679fs, PLEKHA6:p.V328fs, C9orf131:p.P342fs, CD4:p.Q164fs, FBXW7:p.R465C, GNG12:p.T68fs, IRS4:p.G591fs, JARID2:p.V422fs, KIAA0195:p.I902fs, MBD6:p.P732fs, MVK:p.P138fs, PAMR1:p.G101fs, WNT16:p.W165fs, ZNF43:p.N251fs, ABCA6:p.L306fs, ADAM28:p.K73fs, AOC3:p.L79fs, ATP2A1:p.R819fs, B2M:p.L13fs, C6orf89:p.P58fs, CNTLN:p.K1305fs, CR2:p.V206fs, DYRK4:p.K468fs, ERBB3:p.V104M, GLI1:p.W272fs, KRAS:p.G12D, MLL2:p.T172fs, MSH6:p.T1085fs, NLK:p.C190fs, OR5M3:p.T89fs, PAX6:p.P375fs, PTEN:p.L265fs, RABGAP1:p.K928fs, RAD51AP2:p.T316fs, SVIL:p.G1862fs, TP53:p.R273H, WNK4:p.G606fs, ARID1A:p.P2139fs, AXIN2:p.G665fs,

C13orf33:p.R67fs, C1QTNF5:p.P308fs, CELSR1:p.G614fs, CRYGD:p.G159fs, DCHS1:p.R235fs, DDC:p.I433fs, EDNRB:p.Y383fs, EPHA2:p.P460fs, FOXN3:p.P96fs, HDAC4:p.P901fs, INF2:p.S527fs, KIRREL2:p.V649fs, KLF3:p.I104fs, KLHL14:p.P231fs, MAP7D3:p.Q308fs, OTX2:p.R44fs, PAFAH1B1:p.K302fs, PLAGL2:p.P10fs, POLM:p.P97fs, PRPF40B:p.I31fs, RALGAPB:p.T379fs, SBNO1:p.N1139fs, SERPINI1:p.L81fs, SH3KBP1:p.L574fs, SLC12A7:p.H686fs, SLC27A3:p.P643fs, TBX4:p.S370fs, TP53:p.R273C, TP53:p.R175H, TRAM1L1:p.R345fs, WBP1:p.P138fs, ABCC4:p.L883fs, AKAP13:p.K2785fs, ALDH3A1:p.P562fs, ALPK2:p.L356fs, ARFGEF1:p.P1552fs, ARID1A:p.G1848fs, AVPR1A:p.F351fs, BAX:p.M38fs, C14orf43:p.P313fs, C1QTNF5:p.G194fs, C7orf50:p.L179fs, CDC25C:p.K322fs, CETN3:p.K63fs, CHD3:p.P597fs, CTCF:p.K202fs, CTSC:p.F105fs, DDX17:p.G163fs, DLGAP3:p.G377fs, EBF3:p.G255fs, FHDC1:p.F100fs, FILIP1L:p.K749fs, FLNB:p.W529fs, GBP7:p.G431fs, GCC2:p.E700fs, GPR161:p.G517fs, IWS1:p.S802fs, KIAA0240:p.K895fs, KIAA1967:p.P415fs, LRRC43:p.D558fs, MACF1:p.R707fs, MBD6:p.G780fs, MLL3:p.F4496fs, MPRIP:p.A351fs, MUC6:p.2129_2130SS>S, NOX5:p.P467fs, OPTN:p.P24fs, OR4K5:p.F177fs, PIK3CA:p.N345K, PIK3CA:p.E542K, PLXNA1:p.P1016fs, PNPLA7:p.P1199fs, PODN:p.I301fs, PPP2R3B:p.T389fs, PRSS36:p.L680fs, RGL2:p.G203fs, RHOQ:p.V190fs, RNF111:p.R771fs, RTN2:p.P313fs, SALL4:p.V995fs, SBF1:p.P1076fs, SETDB2:p.R715fs, SNAPC2:p.T292fs, SPG20:p.F232fs, SRCAP:p.P1876fs, STAT2:p.P489fs, TCHP:p.E172fs, TP53:p.R282W, TP53:p.R248Q, USP21:p.K474fs, WDR7:p.G262fs, ZBTB7C:p.E157fs, ZFC3H1:p.K385fs, ZNF124:p.T339fs, ZNF626:p.K115fs, ADNP2:p.S322fs, AGAP1:p.G127fs, ALDH2:p.L286fs, ARHGAP5:p.D890fs, ARHGEF17:p.A615fs, ARID1A:p.Y1324fs, ART1:p.I243fs, ASCL4:p.D35fs, ATXN2L:p.G998fs, B3GNT5:p.F30fs, BCKDHA:p.H37fs, BCL9L:p.P1127fs, BEND3:p.D265fs, BNC2:p.S575R, BRD3:p.P24fs, C12orf51:p.P4235fs, C1R:p.P216fs, C7orf49:p.G130fs, CA2:p.I145fs, CABP5:p.R145fs, CASD1:p.F781fs, CASP8:p.R471fs, CCDC153:p.P200fs, CD93:p.D280fs, CROT:p.L32fs, CSF3R:p.P468fs, CTCF:p.K202fs, ERBB2:p.S310F, FAM46D:p.S69R, FBN3:p.G601fs, FBXO21:p.F144fs, GAS6:p.G150fs, GLYR1:p.G380fs, GXYLT1:p.L223fs, HAUS6:p.S530fs, IGF2R:p.T1314fs, ITGB1:p.L378I, KDM3B:p.P1316fs, KIF13A:p.K1115fs, KLF3:p.S224fs, LARP1:p.A223fs, LRP1:p.G1488fs, LRP1:p.G1488fs, MAGEE2:p.Q45fs, MAMSTR:p.P162fs, MAPK15:p.Q511fs, MLL2:p.P647fs, MOCS2:p.P22fs, MTG1:p.L105fs, MTG1:p.H327fs, MTIF2:p.N109fs,

NID2:p.R1035fs, PAX2:p.P395fs, PCCA:p.R230H, PDZD2:p.R101fs, PFKP:p.M593fs, PIK3CA:p.R88Q, PLA2G1B:p.L53fs, PLAU:p.R201fs, PMEPA1:p.P208fs, POP1:p.K750fs, PTCH1:p.P1307fs, PTPRT:p.P1075fs, RDBP:p.P6fs, RNMT:p.K392fs, ROBO2:p.P1080fs, RUNDC3B:p.L6fs, SDAD1:p.K275fs, SLC10A6:p.G109fs, SNAPC1:p.D211fs, SPATA5L1:p.C685fs, SPTA1:p.K1732T, STAT5B:p.P367fs, SYT4:p.M1fs, TAF1L:p.K851fs, TAP2:p.L75fs, TBL1XR1:p.N126fs, THEMIS:p.K406fs, TMEM79:p.P161fs, TP53:p.C176F, TP53BP2:p.K69fs, TP53RK:p.L174fs, UBQLN2:p.A523fs, UHRF1BP1:p.I1330fs, VPRBP:p.K939fs, VPS13B:p.T56fs, WASF3:p.P305fs, YLPM1:p.E1178fs, ZC3H13:p.K1006fs, ZC3H18:p.P825fs, ZC3H4:p.E779Q, ZNF48:p.P247fs, ZNF608:p.A465fs, ZNF878:p.S238fs, ZSCAN18:p.P225fs, ABCB1:p.R527fs, ABCB6:p.G318fs, ACACB:p.G255fs, ACP1:p.Q123fs, ACTL6A:p.L88fs, ADAMTSL4:p.G778fs, AGBL5:p.I420fs, AHI1:p.K303fs, AKAP9:p.M3743fs, AKD1:p.R1209fs, ANKRD40:p.D99E, ARHGEF5:p.S1512fs, ARID1A:p.K1071fs, ARID3A:p.S557G, ARPP21:p.I130fs, ASPN:p.F67fs, ASXL3:p.E873fs, ATP6V1C2:p.R312fs, BEST3:p.P444fs, BRAF:p.P403fs, BRMS1:p.G107fs, BTBD11:p.T451fs, BTBD11:p.A561V, C11orf9:p.S261fs, C14orf102:p.R90fs, C14orf43:p.Q36fs, C15orf52:p.G98fs, C19orf21:p.R262C, C19orf70:p.P50fs, C20orf160:p.P46fs, C3:p.P890fs, CADPS2:p.N468fs, CASC3:p.S232F, CASC3:p.P603L, CASC3:p.P645L, CASC3:p.S658L, CASKIN2:p.P727fs, CBLL1:p.E138fs, CBLN3:p.P69fs, CCDC108:p.P1164fs, CCDC148:p.K420fs, CCDC153:p.P200fs, CCDC169-SOHLH2:p.K162R, CCDC88A:p.K677fs, CD1E:p.F85V, CD3EAP:p.K218fs, CDH11:p.K357T, CDH1:p.D254Y, CDH23:p.V403I, CFI:p.K37fs, CHPF2:p.D645fs, CIC:p.R507fs, CIC:p.A1114fs, CIC:p.A1114fs, CLSTN1:p.T615M, CNBD1:p.L396P, CNGA4:p.K510T, CNOT6:p.S248fs, CNTROB:p.R920fs, COL9A1:p.P283fs, CPAMD8:p.P784fs, CR1L:p.L79fs, CRB1:p.F630V, CSMD1:p.L3410V, CTNNA3:p.K856fs, CTNND1:p.I447fs, CTSD:p.P89fs, CUX1:p.A439fs, CYP7B1:p.K332T, DAB2IP:p.D994fs, DNAH11:p.T871fs, DNAH8:p.K1688fs, DNAJC1:p.K193fs, DNM2:p.P791fs, DSTN:p.F101fs, DYRK1B:p.Q545fs, EAF2:p.V109fs, EDNRB:p.A104V, EEA1:p.N570fs, EFHA1:p.F290fs, EGR1:p.P332fs, EIF4G3:p.K563fs, ELK3:p.S173fs, ENTPD2:p.G204fs, EOMES:p.G332fs, EPHA10:p.P868fs, EPHB6:p.G54fs, EPHX1:p.P132fs, EPPK1:p.G2015fs, ERBB4:p.M1fs, ESF1:p.T99fs, EXOSC8:p.L160fs, FAM113B:p.R51fs, FAM116A:p.L441fs, FAM135B:p.S645R, FAM151A:p.P117fs, FAM193A:p.D428fs, FAM193A:p.D428fs, FAM214B:p.A42fs, FAM40B:p.R740C,

FAM70B:p.S19L, FASTKD1:p.K3fs, FBXW7:p.R479Q, FBXW9:p.G298fs, FER:p.L474fs, FERMT2:p.K152fs, FGGY:p.G138fs, FIGNL1:p.K309fs, FLG:p.K159fs, FLNB:p.W529fs, FOLH1:p.S501fs, FYB:p.G324fs, GABRD:p.Q412fs, GALNTL1:p.W317fs, GANAB:p.L23fs, GCDH:p.L389fs, GIMAP7:p.V276fs, GIPC3:p.G227fs, GLI3:p.P1033fs, GLIPR1L2:p.G92fs, GNPNAT1:p.F54fs, GON4L:p.M134fs, GPATCH4:p.K210fs, GRK4:p.K22fs, GTF3C1:p.S767fs, GTF3C4:p.E562fs, H2AFY2:p.K144fs, HCFC1R1:p.P83fs, HCRTR2:p.S9fs, HCRTR2:p.S9fs, HDLBP:p.G747fs, HECA:p.R333fs, HIVEP3:p.H554fs, HIVEP3:p.P534fs, HLA-C:p.P209fs, HOOK1:p.L361fs, HOXD8:p.P122fs, HTT:p.G697fs, IBTK:p.K1213fs, IDE:p.K37fs, IFT172:p.A837T, INPPL1:p.A974fs, INPPL1:p.P1154fs, INSM2:p.T533fs, INTS12:p.L14fs, INVS:p.R815fs, IPO11:p.S844fs, IRX6:p.A425V, ISG20L2:p.P288fs, ITGB8:p.A7fs, JARID2:p.G394fs, JHDM1D:p.R97fs, KBTBD6:p.G442fs, KCNC1:p.K455fs, KCNH2:p.G149A, KCNJ10:p.P102fs, KCNMB2:p.N151K, KCTD21:p.T6M, KIAA0586:p.A1592fs, KIAA1009:p.F406fs, KIAA1109:p.E1588fs, KIAA2026:p.K690fs, KIF26B:p.S1065fs, KIF6:p.L204fs, KIRREL:p.P335fs, KLC2:p.T568fs, KRAS:p.Q61H, KRAS:p.G12S, MAN1C1:p.G431fs, MAP1A:p.P2063fs, MAP2:p.K1472fs, MAP3K12:p.R449del, MAP7D1:p.A80fs, MGST2:p.K102fs, MKI67:p.T1664fs, MKL1:p.P307fs, MLL2:p.P2354fs, MLL2:p.L656fs, MLL2:p.P647fs, MLL2:p.L1877fs, MMP3:p.I64fs, MPDZ:p.K1582fs, MTUS2:p.R1005W, MUC16:p.A6156T, MYB:p.R481fs, MYEOV:p.L269fs, MYH11:p.K1263del, MYO18A:p.P209fs, MYO7A:p.I539fs, MYOCD:p.G226fs, NAA16:p.H514fs, NBEA:p.V2247fs, NCAPD3:p.Q909fs, NCAPH:p.T466fs, NCOR2:p.P1308fs, NEFM:p.A213V, NEK8:p.V690fs, NF1:p.T676fs, NHLRC1:p.F204fs, NKD1:p.P286fs, NPR3:p.Y138H, NT5M:p.P206fs, NUFIP2:p.R224fs, NUP210:p.L135fs, NYNRIN:p.G113fs, OBSCN:p.G997fs, OGDH:p.Y948fs, OR4C16:p.S135R, OR51A7:p.L124R, OR7C1:p.C179fs, OSBP2:p.H627fs, OTOF:p.E1304K, P2RX1:p.R20fs, PALB2:p.M296fs, PALB2:p.N280fs, PANK1:p.K400fs, PAPD4:p.C225fs, PAPPA2:p.I1683fs, PARP15:p.K461fs, PARP4:p.K847fs, PCDH10:p.N118fs, PCDH10:p.P225fs, PCGF3:p.H63fs, PELI2:p.G197fs, PHACTR1:p.V251fs, PHACTR2:p.S237fs, PHACTR4:p.S354fs, PHKB:p.K642fs, PIAS3:p.H116fs, PIGO:p.P787fs, PIGT:p.A346fs, PIK3R3:p.M341fs, PITPNM1:p.P295fs, PKN2:p.K76fs, PLA2G15:p.W230fs, PLAG1:p.K184fs, PLEKHO1:p.T254fs, PLOD3:p.R297fs, PLOD3:p.P296fs, PLXNA2:p.P464fs, POLQ:p.L1430fs, PPARGC1B:p.P135fs, PPL:p.P454fs, PPM1H:p.P226fs, PPP1R12C:p.P372fs,

PREX2:p.R562fs, PRICKLE4:p.Q109fs, PRKAR1B:p.P87fs, PRKCG:p.R345C, PRMT8:p.S28fs, PROX1:p.F592fs, PRRG3:p.R163fs, PSD2:p.G256fs, PTCHD3:p.F588fs, PTPN4:p.N319fs, PTPRC:p.Q895H, PWWP2B:p.S84fs, PYGO2:p.Q150fs, RABGAP1:p.K928fs, RB1CC1:p.N1171fs, RBM6:p.R96fs, RHOA:p.Y42C, RIMS1:p.R71G, RIMS2:p.V401fs, RING1:p.G171fs, RINT1:p.L107fs, RNF43:p.P116fs, ROBO2:p.K1293fs, RPS6KA6:p.K109fs, RRS1:p.N45fs, RSF1:p.K386fs, RUSC2:p.P486fs, RXFP3:p.A60V, SAFB:p.W798fs, SCARF1:p.R614Q, SCLT1:p.K109fs, SERPINB12:p.Q168fs, SGK3:p.L61fs, SGOL2:p.E407fs, SIGLEC1:p.P318fs, SIK1:p.Q678fs, SLC16A6:p.G98fs, SLC25A17:p.F28fs, SLC26A7:p.I629fs, SLC32A1:p.V494I, SLC4A3:p.L1061fs, SLC7A10:p.P157fs, SLC9A2:p.T746fs, SLITRK1:p.K45fs, SND1:p.H721fs, SOAT1:p.F64fs, SORBS2:p.E1158fs, SOX7:p.L309fs, SPAG17:p.Q1264fs, SPTY2D1:p.P485fs, SRCIN1:p.P865fs, SREBF2:p.H763fs, SRRT:p.G102fs, STAB1:p.P1120fs, STRADA:p.R333fs, STX2:p.K252fs, SV2A:p.E138fs, SYCP2:p.M176fs, SYNJ2:p.P1111fs, TAS2R10:p.L196fs, TBC1D22B:p.A175fs, TEAD2:p.P298fs, TFE3:p.G482fs, TGM6:p.T358fs, TIMM44:p.K83fs, TIMP3:p.A199fs, TLR4:p.L498V, TMEM132D:p.P206fs, TMEM41A:p.F156fs, TMEM41B:p.F230fs, TMTC4:p.R611C, TNK2:p.P632fs, TOPBP1:p.I1381fs, TP53:p.E286K, TP53:p.P152fs, TRIP11:p.K541fs, TRPA1:p.T673fs, TRPM8:p.H765fs, TTF1:p.K336fs, TTI1:p.R707H, TTN:p.E15192D, U2AF2:p.L175fs, UBC:p.G684fs, UBR4:p.P2802fs, UPF2:p.E1033D, UPK2:p.P49fs, USP13:p.I116fs, USP15:p.K782fs, VASH1:p.G3fs, VEZF1:p.355_356insN, VPS13A:p.F2883fs, WAPAL:p.R522fs, WDFY3:p.L1842fs, WDR59:p.N160fs, WDR5:p.N214fs, WDR60:p.Q412fs, WDTC1:p.M287fs, WHSC1L1:p.K418fs, WNT1:p.W167fs, XIRP2:p.E1007D, YBX2:p.P226fs, YIF1A:p.R131fs, ZBBX:p.E151del, ZBTB40:p.L262fs, ZBTB7C:p.G342fs, ZBTB7C:p.D154fs, ZC3H18:p.T701fs, ZDHHC5:p.E651del, ZDHHC7:p.P316fs, ZFHX3:p.R1893fs, ZFHX3:p.E763fs, ZFHX4:p.L408fs, ZHX3:p.N249K, ZIM3:p.I384fs, ZKSCAN5:p.D13fs, ZMYM4:p.K345fs, ZNF236:p.T1410M, ZNF23:p.F122fs, ZNF334:p.K426fs, ZNF358:p.T130fs, ZNF701:p.L296fs, ZNF711:p.L737fs, and ZNF831:p.A49fs.

69. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from TGCT; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of FAM18B2:p.C51Y, BTN2A3P:p.P3S,

MUC2:p.G1715S, NBPF10:p.L44V, SP8:p.G156S, DCP1B:p.Q252H, DEK:p.E41D, ERC1:p.K692R, FAM104B:p.D75H, FRG1B:p.M49V, KRTAP10-10:p.V234M, LRRCC1:p.A6V, NRAS:p.Q61R, PNPLA4:p.L223P, ANKLE1:p.C644fs, ANKLE1:p.C644fs, KIT:p.D816H, KIT:p.D816Y, MUC2:p.T1597I, PSMD11:p.A5V, RHPN2:p.V73M, RUNX2:p.Q71E, SP4:p.E7K, TUBA1C:p.L146F, ZNF814:p.Y324H, ADAMTS17:p.N572T, ATRX:p.K1936R, BCL11B:p.E535D, BMP2K:p.Q460H, BMP2K:p.H487Q, C12orf32:p.D60V, C22orf43:p.K19E, CDC27:p.N571I, CDC27:p.P242S, DDX11:p.K208fs, EBPL:p.L189V, EZH2:p.K510R, FAM86A:p.A141T, GAS2L2:p.D189A, GRID2IP:p.LS754del, HGC6.3:p.E171G, KIT:p.D816V, KIT:p.N822Y, KIT:p.N822K, KRAS:p.Q61R, KRAS:p.G12V, KRTAP1-1:p.I116V, LRRC37BP1:p.Y166D, MEF2A:p.R127Q, MFF:p.S7F, MST1:p.R347W, MUC4:p.S3048L, MUC6:p.H2000Q, MUC6:p.P1977H, NAT10:p.I393T, OPLAH:p.A900D, PIEZO1:p.Q749E, PRAMEF4:p.F300V, RBM10:p.E184D, SERINC2:p.T121P, SPIN2A:p.M150V, SRRM2:p.A2257S, SSBP3:p.K6R, ZNF680:p.R501W, ABCC8:p.Y512C, ABCC9:p.L466P, ABCD1:p.H169Q, ABL2:p.P19T, ACVR2B:p.R48C, AHDC1:p.P33fs, AHNAK2:p.L1640M, ALPPL2:p.W31S, AMMECR1:p.G77C, ANK3:p.D1322E, ANKHD1-EIF4EBP3:p.G60S, ANKRD11:p.Y2015S, ANKRD11:p.K369R, ANKRD50:p.V637M, APBB3:p.L450P, ARHGAP24:p.T35A, ARID4B:p.G1076A, ARMC3:p.A514T, ARRB2:p.T99P, ATAD5:p.I305V, ATXN3:p.305_306insQQQQQQQ, AVPR1B:p.G39R, AXDND1:p.E994Q, BAI2:p.A231G, BEST3:p.P383L, BIRC6:p.V414L, BIRC8:p.A225M, BRWD1:p.K1319R, BTN2A2:p.L15F, C12orf51:p.A2644T, C12orf65:p.K143T, C16orf62:p.L244I, C1QBP:p.T225I, C1orf167:p.S123G, C5orf25:p.Y4F, CACNA1E:p.G2080S, CAPNS1:p.LV303del, CCDC159:p.A332S, CDKAL1:p.P409L, CDYL:p.V48A, CDYL:p.A60G, CELSR2:p.L17P, CHD4:p.E138D, CKAP5:p.G576A, CLCC1:p.K52R, CMTM8:p.S26T, CNKSR2:p.P249L, CNTN5:p.I501T, COG5:p.H617R, COL15A1:p.K708R, COL6A3:p.A2378D, CRYGB:p.R143G, CSGALNACT2:p.L362F, CUL4A:p.I438F, CXXC1:p.Q156H, CYP19A1:p.F406L, DCLRE1B:p.F28I, DDX11:p.A376T, DDX11:p.E680D, DEPDC5:p.R1525Q, DLC1:p.S741T, DNMT1:p.R995Q, DOCK11:p.Q169E, DSPP:p.D1047N, E2F7:p.I91S, EBF1:p.D353G, ECI2:p.K55R, EEF1A2:p.Y418S, EIF3J:p.A8G, EML6:p.K805R, EPAS1:p.S474T, EPRS:p.L1335I, ERICH1:p.E327K, FAM101B:p.L5P, FAM104A:p.M1R, FAM110D:p.R71H, FAM155A:p.Q95R, FAM186A:p.G1492E, FAM194B:p.Y139H, FAM21B:p.P1231S, FAM32A:p.K9R,

FAM46B:p.H416R, FAM48B1:p.I499V, FAM48B1:p.A516P, FAM5C:p.S425W, FAM86C2P:p.C120Y, FBXL14:p.V48G, FRMPD3:p.Q832del, FRS2:p.L47S, GDF5:p.E105fs, GPNMB:p.C3fs, GPT2:p.R10P, H2AFV:p.Q125R, HDLBP:p.R503C, HERC2:p.R2129C, HIST1H2BJ:p.K13R, HLX:p.N231K, HMGB3:p.E198D, HSF4:p.R169W, HSF4:p.S491P, HYAL4:p.D222N, INO80E:p.P206fs, INTS4:p.S460A, IQCF6:p.R3H, ITPR1:p.M1569I, ITPR3:p.R1698G, KANSL3:p.G376E, KCNA4:p.E627del, KDM5A:p.P423S, KDM6A:p.Y362fs, KIAA0020:p.K63R, KIDINS220:p.N851S, KIT:p.W557G, KLHDC2:p.W321S, KRAS:p.A146T, KRAS:p.Q61H, KRAS:p.Q61L, KRAS:p.G12A, KRAS:p.G12R, KRBA1:p.R839G, KRTAP4-8:p.T63S, L2HGDH:p.P441del, LAMC3:p.P174Q, LHCGR:p.L16Q, LOC401296:p.L144M, LPHN2:p.F906I, LRP12:p.G310C, LTB4R:p.F73L, LTBP3:p.L35del, LUC7L3:p.S148T, LYPD4:p.T64K, MAMLD1:p.Q572L, MAP4K2:p.R341G, MAPK7:p.A501D, MAT2A:p.E166G, MED12L:p.C1292Y, MESP2:p.Q182E, MEX3C:p.R534S, MIER2:p.L131F, MLL5:p.Y66C, MLLT3:p.177_178SS>S, MMS19:p.D1005N, MRPS25:p.E119del, MSH6:p.D576A, MTIF3:p.G65E, MUC17:p.M1807T, MUC17:p.T2279N, MUC17:p.G2474S, MUC2:p.TTPSPP1475del, MUC2:p.T1568M, MUC2:p.T1580N, MUC2:p.T1704I, MUC2:p.T1706M, MUC4:p.H1117D, MUC5B:p.R1097H, MYEF2:p.K323E, MYEOV:p.L302H, MYH8:p.A785V, MYO1A:p.N584K, NAP1L3:p.P353R, NAV1:p.I1433M, NCAM1:p.E131G, NEB:p.D3107N, NEFH:p.V670E, NELL2:p.G170D, NHS:p.D1561N, NKD2:p.H447del, NSD1:p.T461R, NT5C3:p.A3P, NYAP1:p.P480S, OBSCN:p.A908T, OR10J1:p.R244Q, OR1S2:p.M298I, OR2L3:p.K294R, OR6K6:p.F311L, PABPC3:p.V325fs, PBX2:p.Y262F, PCDHB4:p.P255F, PCMTD1:p.V281A, PCP4L1:p.K64R, PDE3A:p.A98E, PDIA6:p.N56K, PDS5A:p.L1309F, PHLDA2:p.R28S, PIGR:p.V183G, PIK3CA:p.E545K, PIK3CD:p.C381R, PKD1:p.T938M, PLEKHM1:p.A895V, PLEKHN1:p.A600D, PLXND1:p.R367L, PMS2:p.K651R, PNMA3:p.E200G, POTEF:p.S112G, PRAMEF8:p.I448V, PRDM2:p.E278D, PRODH:p.L527V, PRPF31:p.R289W, PSME4:p.N495D, PTGR1:p.E40A, PTPRB:p.Q726H, RABGEF1:p.N207D, RAC1:p.P34R, RANBP17:p.M900I, REV3L:p.A30S, RFC3:p.I82N, RFC3:p.K296N, RIMBP3:p.Q1154R, RPL19:p.R151C, RPL5:p.R58fs, RPTN:p.M538I, RRAD:p.A278E, RYR1:p.D668Y, RYR2:p.L2023F, SAFB:p.G799V, SCRIB:p.G332V, SDK1:p.Y2146C, SEC16A:p.T443K, SEC31B:p.P905S, SELO:p.R565Q, SELP:p.A297T, SI:p.I1681K, SLC2A7:p.H268Q, SLC37A1:p.V528I, SLC38A1:p.G100R, SMARCA2:p.D1158A, SMARCA5:p.T156fs,

SMC3:p.E970Q, SMG1:p.P2696H, SNRNP200:p.A2129G, SPIN2B:p.M150V, ST6GALNAC1:p.S354N, STAMBPL1:p.Y143H, STARD8:p.G662A, STON1-GTF2A1L:p.N451S, SYMPK:p.A336G, TAS2R8:p.W98C, TCHH:p.W1016R, TET1:p.T1472S, TIAM1:p.G247M, TNS1:p.P183S, TOR1AIP2:p.G146R, TPRX1:p.S216P, TPRX1:p.S200P, TRMT61A:p.S244I, TSPAN4:p.L92V, TTF1:p.Q530R, UBE2M:p.G131D, UBR5:p.R2517S, UGT2B11:p.R447I, UMODL1:p.M559I, UNC93A:p.V445A, USP46:p.Q137R, VWA2:p.G317D, VWA7:p.V792G, WASH3P:p.L187V, WNT5B:p.K327E, WRN:p.E510D, XDH:p.P410S, ZAN:p.S755P, ZC3H11A:p.I777T, ZC3H7A:p.C575S, ZDHHC11:p.H250Q, ZFHX4:p.D3239N, ZKSCAN3:p.K200A, ZMYM4:p.T367I, ZNF174:p.P353T, ZNF322:p.Y353C, ZNF592:p.K324Q, ZNF592:p.P500T, ZNF782:p.C145F, ZNF799:p.C453R, ZNF804B:p.P644S, and ZNRF3:p.R889W.

70. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from THCA; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of BRAF:p.V600E, NRAS:p.Q61R, HRAS:p.Q61R, NRAS:p.Q61K, OTUD4:p.T909I, HRAS:p.Q61K, NLRP6:p.E611G, AKT1:p.E17K, ANKMY1:p.N302I, ATP6V1A:p.L237P, CYP19A1:p.S113I, DCUN1D4:p.L275P, DGCR8:p.E518K, DLC1:p.S741T, DNAH10:p.C1853F, EIF1AX:p.G9D, FAM75D5:p.L222P, FCGRT:p.P40A, KRAS:p.Q61K, LMX1B:p.Q285del, MAS1L:p.R324G, MED15:p.S35I, MEGF6:p.Y393C, ODZ2:p.A1529V, OR5L1:p.R122H, OR6K6:p.F311L, OTX1:p.D315N, POTEE:p.S75G, SCN5A:p.D1978H, TOP2A:p.K1199E, and TSG101:p.K265R.

71. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from UCS; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of TP53:p.R248Q, ZNF814:p.D404E, BTN2A3P:p.P3S, FBXW7:p.R465C, FRG1B:p.G65E, MUC4:p.H4205Q, NBPF10:p.V99F, PIK3CA:p.E545K, PIK3CA:p.H1047R, PPP2R1A:p.P179R, DDX11L2:p.*128Q, FBXW7:p.R479Q, FRG1B:p.K13N, FRG1B:p.L52S, HSD17B7P2:p.N175S, KRAS:p.G12V, LOC283788:p.S37G, TP53:p.R273H, TP53:p.S241Y, ADAMTS12:p.E359K, BCL2L11:p.L187fs, CDC27:p.L460fs, CHEK2:p.K373E, ESPNP:p.W122fs, FBXW7:p.R689W,

FBXW7:p.R505G, FBXW7:p.R465H, FCGBP:p.V4019M, FRG1B:p.I10T, FRG1B:p.D32V, FRG1B:p.R37K, KRAS:p.G12D, LOC100233156:p.R21C, LOC283788:p.I46M, LRP1B:p.L1392F, MAMLD1:p.Q572L, MST1P9:p.L319P, MUC4:p.A2390T, MUC4:p.G2172S, NBPF10:p.E3455K, PIK3CA:p.G106V, PODXL:p.28_30PSP>P, POTEC:p.R477Q, PPP2R1A:p.R183W, PPP2R1A:p.S219L, PTPN18:p.TG378del, RGPD3:p.N756D, RPL13AP20:p.G107R, SAMD4B:p.R477W, SMAP1:p.E169fs, TP53:p.H193R, TP53:p.H179R, TP53:p.R175H, TUBBP5:p.R119H, and U2AF1:p.S34F.

72. The pharmaceutical composition of any of paragraphs 30-36, wherein:

(a) the population of subjects is suffering from PAAD; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of RBM14:p.AAAAAAA286del, KRAS:p.G12D, JMY:p.PPPPPPPPPPPP811del, RIOK1:p.D69del, LCE2A:p.SSGGCCGSSSGGCC47del, KRAS:p.G12V, C1QB:p.GPKGPMGPKGGPGAPGAP90del, ZFHX3:p.V777del, DBR1:p.541_542DD>D, AEBP1:p.K1133del, KRAS:p.G12R, RBM47:p.495_502AAAAAAAA>A, AP3S1:p.K41fs, MLL2:p.AEGPHLSPQPEELHLSPQ792del, RFX1:p.386_401GGGGGGGGGGGGGGSG>G, AXDND1:p.EQ991del, HERC2P3:p.A803V, RGPD3:p.N756D, FNDC1:p.D1180del, ANAPC1:p.T537A, IRS4:p.21_22AA>A, GIGYF2:p.Q1005del, NCOA3:p.Q1253fs, SIK3:p.950_951QQ>Q, GPR6:p.AAAAATAAGGPDTGEWGPPA36del, NBPF12:p.D1323fs, SHROOM4:p.1156_1157EE>E, ZMIZ2:p.VAAAAATATATATAT153del, DGKK:p.PAPP41del, LZTS1:p.RTQDLEGALRTKGLEL432del, CASQ2:p.395_396DD>D, DCP1B:p.251_252insH, ESPNP:p.296_317PPPPSFPPPPPPPPGTQLPPPPP>P, KBTBD6:p.T403K, NBPF16:p.D449fs, ANKRD36C:p.H438R, ESPN:p.PPPPPPSFPPPPPPPPGTQLPP430del, FCGBP:p.A2493V, KRAS:p.Q61H, NCOA3:p.Q1276del, OR2T2:p.C203fs, TMCC1:p.Q565L, BCKDHA:p.G129fs, ESPNP:p.H64fs, GNAS:p.R844H, NBPF14:p.R25C, OGFOD1:p.G477fs, RBM12:p.P693S, SLC38A10:p.1071_1072II>I, SORBS2:p.P866S, TP53:p.R248W, TP53:p.R175H, and UBAC1:p.E269del.

73. The pharmaceutical composition of any of paragraphs 30-72, wherein the composition comprises 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 26, at least 27, at least 28, at least 29, or at least 30 neoantigenic peptides.

74. The pharmaceutical composition of paragraph 73, wherein the composition comprises 15 to 20 neoantigenic peptides.

75. The pharmaceutical composition of paragraphs 73 or 74, further comprising at least one additional neoantigenic peptide which is specific for an individual patient's tumor.

76. The pharmaceutical composition of paragraph 75, wherein the patient specific neoantigenic peptide is selected by identifying sequence differences between the genome, exome, and/or transcriptome of the patient's tumor sample and the genome, exome, and/or transcriptome of a non-tumor sample.

77. The pharmaceutical composition of paragraph 75, wherein the samples are fresh or formalin-fixed paraffin embedded tumor tissues, freshly isolated cells, or circulating tumor cells.

78. The pharmaceutical composition of paragraph 75, wherein the sequence differences are determined by Next Generation Sequencing.

79. The pharmaceutical composition of any of paragraphs 30-78, wherein each neoantigenic peptide is from about 5 to about 50 amino acids in length.

80. The pharmaceutical composition of paragraph 79, wherein each neoantigenic peptide is between about 15 to about 35 amino acids in length; is about 15 amino acids or less in length; is about 8 and about 11 amino acids in length; or is 9 or 10 amino acids in length.

81. The pharmaceutical composition of paragraph 79 or 80, wherein each neoantigenic peptide binds major histocompatibility complex (MHC) class I.

82. The pharmaceutical composition of any one of paragraphs 30-81, wherein each neoantigenic peptide binds to MHC class I with a binding affinity of less than about 500 nM, or optionally each neoantigenic peptide binds to HLA-A, -B or –C with a K_D of less than 500 nM.

83. The pharmaceutical composition of paragraph 79, wherein each neoantigenic peptide is about 30 amino acids or less in length; is between about 6 and about 25 amino acids in length; is between about 15 and about 24 amino acids in length; or is between about 9 and about 15 amino acids in length.

84. The pharmaceutical composition of paragraph 79, 82 or 83, wherein each neoantigenic peptide binds major histocompatibility complex (MHC) class II.

85. The pharmaceutical composition of paragraph 84, wherein each neoantigenic peptide binds to MHC class I with a binding affinity of less than about 500 nM, or optionally each neoantigenic peptide binds to HLA-A, -B or –C with a K_D of less than 500 nM.

86. The pharmaceutical composition of any of paragraphs 30-85, wherein at least one neoantigenic peptide further comprises flanking amino acids.

87. The pharmaceutical composition of paragraph 86, wherein the flanking amino acids are not native flanking amino acids.

88. The pharmaceutical composition of any of paragraphs 30-87, which at least one neoantigenic peptide is linked to at least a second neoantigenic peptide.

89. The pharmaceutical composition of paragraph 88, wherein peptides are linked using a poly-glycine or poly-serine linker.

90. The pharmaceutical composition of paragraph 88 or 89, wherein the second neoantigenic peptide binds MHC class I or class II with a binding affinity of less than about 1000 nM.

91. The pharmaceutical composition of any of paragraphs 88-90, wherein the second neoantigenic peptide binds MHC class I or class II with a binding affinity of less than about 500 nM.

92. The pharmaceutical composition of any of paragraphs 88-91, wherein both of the neoepitopes bind to human leukocyte antigen (HLA) -A, -B, -C, -DP, -DQ, or -DR.

93. The pharmaceutical composition of any of paragraphs 88-92, wherein the isolated neoantigenic peptide and the second neoantigenic peptide binds a class I HLA or the isolated neoantigenic peptide and the second neoantigenic peptide binds a class II HLA.

94. The pharmaceutical composition of any of paragraphs 88-92, wherein the isolated neoantigenic peptide binds a class II HLA and the second neoantigenic peptide binds a class I HLA or the isolated neoantigenic peptide binds a class I HLA and the second neoantigenic peptide binds a class II HLA.

95. The pharmaceutical composition of any of paragraphs 30-94, wherein at least one neoantigenic peptide further comprises modifications which increase in vivo half-life, cellular targeting, antigen uptake, antigen processing, MHC affinity, MHC stability, or antigen presentation.

96. The pharmaceutical composition of paragraph 95, wherein the modification is conjugation to a carrier protein, conjugation to a ligand, conjugation to an antibody, PEGylation, polysialylation HESylation, recombinant PEG mimetics, Fc fusion, albumin fusion, nanoparticle attachment, nanoparticulate encapsulation, cholesterol fusion, iron fusion, acylation, amidation, glycosylation, side chain oxidation, phosphorylation, biotinylation, the addition of a surface active material, the addition of amino acid mimetics, or the addition of unnatural amino acids.

97. The pharmaceutical composition of paragraph 95, wherein the cells that are targeted are antigen presenting cells.

98. The pharmaceutical composition of paragraph 97, wherein the antigen presenting cells are dendritic cells.

99. The pharmaceutical composition of paragraph 98, wherein the dendritic cells are targeted using DEC205, XCR1, CD197, CD80, CD86, CD123, CD209, CD273, CD283, CD289, CD184, CD85h, CD85j, CD85k, CD85d, CD85g, CD85a, CD141, CD11c, CD83, TSLP receptor, or CD1a marker.

100. The pharmaceutical composition of paragraph 99, wherein the dendritic cells are targeted using the CD141, DEC205, or XCR1 marker.

101. The pharmaceutical composition of any of paragraphs 30-100, which is an immunogenic or vaccine composition.

102. The pharmaceutical composition of paragraph 101, further comprising an immunomodulator or adjuvant.

103. The pharmaceutical composition of paragraph 102, wherein the immunodulator or adjuvant is selected from the group consisting of Poly(I:C), Poly-ICLC, STING agonist, 1018 ISS, aluminium salts, Amplivax, AS15, BCG, CP-870,893, CpG7909, CyaA, dSLIM, GM-CSF, IC30, IC31, Imiquimod, ImuFact IMP321, IS Patch, ISS, ISCOMATRIX, JuvImmune, LipoVac, MF59, monophosphoryl lipid A, Montanide IMS 1312 VG, Montanide ISA 206 VG, Montanide ISA 50 V2, Montanide ISA 51 VG, OK-432, OM-174, OM-197-MP-EC, ISA-TLR2 agonist, ONTAK, PepTel®. vector system, PLG microparticles, resiquimod, SRL172, virosomes and other virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, Pam3CSK4, acrylic or methacrylic polymers, copolymers of maleic anhydride, and QS21 stimulon.

104. An isolated polynucleotide encoding the isolated neoantigenic peptide of any of paragraphs 1-24.

105. The isolated polynucleotide of paragraph 104, which is RNA.

106. The isolated polynucleotide of paragraph 105, wherein the RNA is modified to increase stability, increase cellular targeting, increase translation efficiency, adjuvanticity, cytosol accessibility, and/or decrease cytotoxicity.

107. The isolated polynucleotide of paragraph 106, wherein the modification is conjugation to a carrier protein, conjugation to a ligand, conjugation to an antibody, codon optimization, increased GC-content, incorporation of modified nucleosides, incorporation of 5'-cap or cap analog, and/or incorporation of an unmasked poly-A sequence.

108. A cell comprising the polynucleotide of any of paragraphs 104-107.

109. A vector comprising the polynucleotide of any one of paragraphs 104-107.

110. The vector of paragraph 110, in which the polynucleotide is operably linked to a promoter.

111. The vector of paragraphs 109 or 110, which is a plasmid, phage, transposon, cosmid, virus, or virion.

112. The vector of paragraph 111, which is an adeno-associated virus, herpesvirus, lentivirus, or pseudotypes thereof.

113. An in vivo delivery system comprising the isolated polynucleotide of any of paragraphs 104-107.

114. The delivery system of paragraph 113, wherein the delivery system includes spherical nucleic acids, viruses, virus-like particles, plasmids, bacterial plasmids, or nanoparticles.

115. A cell comprising the vector or delivery system of any of paragraphs 109-114.

116. The cell of paragraph 115, which is an antigen presenting cell.

117. The cell of paragraph 116, which is a dendritic cell.

118. The cell of paragraph 117, which is an immature dendritic cell.

119. A composition comprising at least one polynucleotide of any of paragraphs 104-107.

120. The composition of paragraph 119, wherein the composition comprises 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 26, at least 27, at least 28, at least 29, or at least 30 of the isolated polynucleotides.

121. The composition of paragraph 120, wherein the composition comprises between about 2 and about 20 polynucleotides.

122. The composition of any one of paragraphs 119-121, wherein the composition further 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 26, at least 27, at least 28, at least 29, or at least 30 additional neoantigenic polynucleotides encoding for additional neoantigenic peptides.

123. The composition of paragraph 122, wherein the composition comprises between about 4 and about 20 additional neoantigenic polynucleotides.

124. The composition of paragraph 122, wherein the isolated polynucleotides and the additional neoantigenic polynucleotides are linked.

125. The composition of paragraph 124, wherein the polynucleotides are linked using nucleic acids that encode a poly-glycine or poly-serine linker.

126. The composition of any of paragraphs 122-125, wherein at least one of the additional neoantigenic peptide is specific for an individual patient's tumor.

127. The composition of paragraph 126, wherein the patient specific neoantigenic peptide is selected by identifying sequence differences between the genome, exome, and/or transcriptome of the patient's tumor sample and the genome, exome, and/or transcriptome of a non-tumor sample.

128. The composition of paragraph 127, wherein the samples are fresh or formalin-fixed paraffin embedded tumor tissues, freshly isolated cells, or circulating tumor cells.

129. The composition of paragraphs 127 or 128, wherein the sequence differences are determined by Next Generation Sequencing.

130. A T cell receptor (TCR) capable of binding at least one neoantigenic peptide listed in any of paragraphs 1-27, optionally a neoantigenic peptide comprising FGFR3 S249C, ERBB3 V104M, EGFR L858R, MUC4 H4205Q, PDGFRA R483fs, TMEM52 23_26LLPL>L, or PODXL 28_30PSP>P.

131. The TCR of paragraph 130, which is capable of binding the isolated neoantigenic peptide in the context of MHC class I or class II.

132. A chimeric antigen receptor comprising: (i) a T cell activation molecule; (ii) a transmembrane region; and (iii) an antigen recognition moiety capable of binding an isolated neoantigenic peptide of any one of paragraphs 1-27.

133. The chimeric antigen receptor of paragraph 132, wherein CD3-zeta is the T cell activation molecule.

134. The chimeric antigen receptor of paragraph 132 or 133, further comprising at least one costimulatory signaling domain.

135. The chimeric antigen receptor of any of paragraphs 132-134, wherein the signaling domain is CD28, 4-1BB, ICOS, OX40, ITAM, or Fc epsilon RI-gamma.

136. The chimeric antigen receptor of any of paragraphs 132-135, wherein the antigen recognition moiety is capable of binding the isolated neoantigenic peptide in the context of MHC class I or class II.

137. The chimeric antigen receptor of any of paragraphs 132-136, comprising the CD3-zeta, CD28, CTLA-4, ICOS, BTLA, KIR, LAG3, CD137, OX40, CD27, CD40L, Tim-3, A2aR, or PD-1 transmembrane region.

138. The chimeric antigen receptor of any of paragraphs 132-137, wherein the tumor-specific epitope is located in the extracellular domain of a tumor associated polypeptide, optionally the tumor-specific epitope comprises FGFR3 S249C, ERBB3 V104M, EGFR L858R, MUC4 H4205Q, PDGFRA R483fs, TMEM52 23_26LLPL>L, or PODXL 28_30PSP>P.

139. A T cell comprising the T cell receptor or chimeric antigen receptor of any of paragraphs 130-138.

140. The T cell of paragraph 139, which is a helper or cytotoxic T cell.

141. A nucleic acid comprising a promoter operably linked to a polynucleotide encoding the T cell receptor of paragraph 130 or 131.

142. The nucleic acid of paragraph 141, wherein the TCR is capable of binding the at least one neoantigenic peptide in the context of major histocompatibility complex (MHC) class I or class II.

143. A nucleic acid comprising a promoter operably linked to a polynucleotide encoding the chimeric antigen receptor of any of paragraphs 132-138.

144. The nucleic acid of paragraph 143, wherein the antigen recognition moiety is capable of binding the at least one neoantigenic peptide in the context of major histocompatibility complex (MHC) class I or class II.

145. The nucleic acid of paragraphs 143 or 144, wherein the tumor-specific epitope is located in the extracellular domain of a tumor associated polypeptide.

146. The nucleic acid of any of paragraphs 143-145, comprising the CD3-zeta, CD28, CTLA-4, ICOS, BTLA, KIR, LAG3, CD137, OX40, CD27, CD40L, Tim-3, A2aR, or PD-1 transmembrane region.

147. An antibody capable of binding at least one neoantigenic peptide listed in Tables 1-9.

148. A modified cell transfected or transduced with the nucleic acid of any one of paragraphs 141-146.

149. The modified cell of paragraph 148, wherein the modified cell is a T cell, tumor infiltrating lymphocyte, NK-T cell, TCR-expressing cell, CD4+ T cell, CD8+ T cell, or NK cell.

150. A composition comprising the T cell receptor or chimeric antigen receptor of any of paragraphs 130-138.

151. A composition comprising autologous patient T cells containing the T cell receptor or chimeric antigen receptor of any of paragraphs 130-138.

152. The composition of paragraph 150 or 151, further comprising an immune checkpoint inhibitor.

153. The composition of paragraph 150 of 151, further comprising at least two immune checkpoint inhibitors.

154. The composition of paragraph 152 or 153, wherein the immune checkpoint inhibitor inhibits a checkpoint protein selected from the group consisting of CTLA-4, PDL1, PDL2, PD1, B7-H3, B7-H4, BTLA, HVEM, TIM3, GAL9, LAG3, VISTA, KIR, 2B4, CD160, CGEN-15049, CHK 1, CHK2, A2aR, and B-7 family ligands or a combination thereof.

155. The composition of paragraph 154, wherein the immune checkpoint inhibitor interacts with a ligand of a checkpoint protein selected from the group consisting of CTLA-4, PDL1, PDL2, PD1, B7-H3, B7-H4, BTLA, HVEM, TIM3, GAL9, LAG3, VISTA, KIR, 2B4, CD160, CGEN-15049, CHK 1, CHK2, A2aR, and B-7 family ligands or a combination thereof.

156. The composition of any of paragraphs 119-129 or 150-156, further comprising an immune modulator or adjuvant.

157. The composition of paragraph 156, wherein the immune modulator is a co-stimulatory ligand, a TNF ligand, an Ig superfamily ligand, CD28, CD80, CD86, ICOS, CD40L, OX40, CD27, GITR, CD30, DR3, CD69, or 4-1BB.

158. The composition of paragraph 156, wherein the immune modulator is at least one cancer cell or cancer cell extract.

159. The composition of paragraph 158, wherein the cancer cell is autologous to the subject in need of the composition.

160. The composition of paragraph 159, wherein the cancer cell has undergone lysis or been exposed to UV radiation.

161. The composition of paragraph 156, wherein the composition further comprises an adjuvant.

162. The composition of paragraph 161, wherein the adjuvant is selected from the group consisting of: Poly(I:C), Poly-ICLC, STING agonist, 1018 ISS, aluminium salts, Amplivax, AS15, BCG, CP-870,893, CpG7909, CyaA, dSLIM, GM-CSF, IC30, IC31, Imiquimod, ImuFact IMP321, IS Patch, ISS, ISCOMATRIX, JuvImmune, LipoVac, MF59, monophosphoryl lipid A, Montanide IMS 1312 VG, Montanide ISA 206 VG, Montanide ISA 50 V2, Montanide ISA 51 VG, OK-432, OM-174, OM-197-MP-EC, ISA-TLR2 agonist, ONTAK, PepTel®. vector system, PLG microparticles, resiquimod, SRL172, virosomes and other virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, Pam3CSK4, acrylic or methacrylic polymers, copolymers of maleic anhydride, and QS21 stimulon.

163. The composition of paragraph 161 or 162, wherein the adjuvant induces a humoral immune response when administered to a subject.

164. The composition of paragraph 162, wherein the adjuvant induces a T helper cell type 1 response when administered to a subject.

165. An in vivo delivery system comprising the pharmaceutical composition of any of paragraphs 30-103.

166. The delivery system of paragraph 165, wherein the delivery system includes cell-penetrating peptides, nanoparticulate encapsulation, virus like particles, or liposomes.

167. The delivery system of paragraph 166, wherein the cell-penetrating peptide is TAT peptide, herpes simplex virus VP22, transportan, or Antp.

168. A cell comprising the isolated neoantigenic peptide of any of paragraphs 1-29.

169. The cell of paragraph 168, which is an antigen presenting cell.

170. The cell of paragraph 169, which is a dendritic cell.

171. A method of treating cancer or initiating, enhancing, or prolonging an anti-tumor responses in a subject in need thereof comprising administering to the subject the peptide, polynucleotide, vector, composition, antibody, or cells of any of paragraphs 1-164.

172. A method of prophylactic cancer treatment comprising:

(a) selecting a cancer drug for a patient in need thereof, the drug selected from the group consisting of ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK inhibitors, and antiestrogen therapy; and

(b) administering prophylactically to the subject, a pharmaceutical composition according to any of paragraphs 30-103 wherein the at least one neoantigenic peptide is derived from drug resistant mutations associated with the selected cancer drug.

173. A method of treating or preventing a tumor in a population of subjects in need thereof, comprising administering to a subject an agent comprising an extracellular ligand-binding domain recognizing a tumor-specific neoepitope comprising a tumor-specific mutation having an incidence of at least 1% of subjects in the population.

174. The method according to any of paragraphs 171-173, wherein the tumor-specific mutation comprises a mutation listed for any population in Table 9.

175. The method according to any of paragraphs 171-173, wherein the tumor-specific mutation is within a gene containing an extracellular domain.

176. The method according to paragraph 175, wherein the tumor-specific mutation comprises FGFR3 S249C, ERBB3 V104M, EGFR L858R, MUC4 H4205Q, PDGFRA R483fs, TMEM52 23_26LLPL>L, or PODXL 28_30PSP>P.

177. The method according to paragraph 176, wherein the tumor-specific mutation is within the extracellular domain.

178. The method according to paragraph 177, wherein the tumor-specific mutation comprises FGFR3 S249C or ERBB3 V104M.

179. The method of any of paragraph 171-178, wherein the subject is a human.

180. The method of paragraph 179, wherein the subject has cancer.

181. The method of paragraph 180, wherein the cancer is selected from the group consisting of urogenital, gynecological, lung, gastrointestinal , head and neck cancer, malignant glioblastoma, malignant mesothelioma, non-metastatic or metastatic breast cancer, malignant melanoma, Merkel Cell Carcinoma or bone and soft tissue sarcomas, haematologic neoplasias, multiple myeloma, acute myelogenous leukemia, chronic myelogenous leukemia, myelodysplastic syndrome and acute lymphoblastic leukemia, non-small cell lung cancer (NSCLC), breast cancer, metastatic colorectal cancers, hormone sensitive or hormone refractory prostate cancer, colorectal cancer, ovarian cancer, hepatocellular cancer, renal cell cancer, pancreatic cancer, gastric cancer, oesophageal cancers, hepatocellular cancers, cholangiocellular cancers, head and neck squamous cell cancer soft tissue sarcoma, and small cell lung cancer.

182. The method of any of paragraphs 171-181, wherein the subject has undergone surgical removal of the tumor.

183. The method of any of paragraphs 171-182, wherein the peptide, polynucleotide, vector, composition, or cells is administered via intravenous, intraperitoneal, intratumoral, intradermal, or subcutaneous administration.

184. The method of paragraph 183, wherein the peptide, polynucleotide, vector, composition, or cells is administered into an anatomic site that drains into a lymph node basin.

185. The method of paragraph 184, wherein administration is into multiple lymph node basins.

186. The method of any one of paragraphs 183-185, wherein administration is by a subcutaneous or intradermal route.

187. The method of paragraph 183, wherein peptide is administered.

188. The method of paragraph 187, wherein administration is intratumorally.

189. The method of paragraph 183, wherein polynucleotide, optionally RNA, is administered.

190. The method of paragraph 189, wherein the polynucleotide is administered intravenously.

191. The method of paragraph 183, wherein the cell is a T cell or dendritic cell.

192. The method of paragraph 191, wherein the peptide or polynucleotide comprises an antigen presenting cell targeting moiety.

193. The method of any of paragraphs 171-192, further comprising administering at least one immune checkpoint inhibitor to the subject.

194. The method of paragraph 193, wherein the checkpoint inhibitor is a biologic therapeutic or a small molecule.

195. The method of paragraph 193 or 194, wherein the checkpoint inhibitor is selected from the group consisting of a monoclonal antibody, a humanized antibody, a fully human antibody and a fusion protein or a combination thereof.

196. The method of any of paragraphs 193-195, wherein the checkpoint inhibitor inhibits a checkpoint protein selected from the group consisting of CTLA-4, PDL1, PDL2, PD1, B7-H3, B7-H4, BTLA, HVEM, TIM3, GAL9, LAG3, VISTA, KIR, 2B4, CD160, CGEN-15049, CHK 1, CHK2, A2aR, and B-7 family ligands or a combination thereof.

197. The method of any of paragraphs 193-196, wherein the checkpoint inhibitor interacts with a ligand of a checkpoint protein selected from the group consisting of CTLA-4, PDL1, PDL2, PD1, B7-H3, B7-H4, BTLA, HVEM, TIM3, GAL9, LAG3, VISTA, KIR, 2B4, CD160, CGEN-15049, CHK 1, CHK2, A2aR, and B-7 family ligands or a combination thereof.

198. The method of any of paragraphs 193-197, wherein two or more checkpoint inhibitors are administered.

199. The method of paragraph 198, wherein the checkpoint inhibitors are: (i) ipilimumab or tremelimumab, and (ii) nivolumab.

200. The method of any of paragraphs 193-199, wherein the checkpoint inhibitor and the composition are administered simultaneously or sequentially in any order.

201. The method of paragraph 200, wherein the peptide, polynucleotide, vector, composition, or cells is administered prior to the checkpoint inhibitor.

202. The method of paragraph 200, wherein the peptide, polynucleotide, vector, composition, or cells is administered after the checkpoint inhibitor.

203. The method of paragraph 200, wherein administration of the checkpoint inhibitor is continued throughout neoantigen peptide, polynucleotide, vector, composition, or cell therapy.

204. The method of any of paragraphs 193-203, wherein the neoantigen peptide, polynucleotide, vector, composition, or cell therapy is administered to subjects that only partially respond or do not respond to checkpoint inhibitor therapy.

205. The method of any one of paragraphs 193-204, wherein the checkpoint inhibitor is administered intravenously or subcutaneously.

206. The method of paragraph 205, wherein the checkpoint inhibitor is administered subcutaneously within about 2 cm of the site of administration of the composition.

207. The method of paragraph 206, wherein the composition is administered into the same draining lymph node as the checkpoint inhibitor.

208. The method of any of paragraphs 171-207, further comprising administering an additional therapeutic agent to the subject either prior to, simultaneously with, or after treatment with the peptide, polynucleotide, vector, composition, or cells.

209. The method of paragraph 208, wherein the additional agent is a chemotherapeutic agent, an immunomodulatory drug, an immune metabolism modifying drug, a targeted therapy, radiation an anti-angiogenesis agent, or an agent that reduces immune-suppression.

210. The method of paragraph 209, wherein the chemotherapeutic agent is an alkylating agent, a topoisomerase inhibitor, an anti-metabolite, or an anti-mitotic agent.

211. The method of paragraph 208, wherein the additional agent is an anti-glucocorticoid induced tumor necrosis factor family receptor (GITR) agonistic antibody or antibody fragment, ibrutinib, docetaxeol, cisplatin, or cyclophosphamide.

212. The method of any of paragraphs 171-211, which elicits a CD4+ T cell immune response.

213. The method of any of paragraphs 171-212, which elicits a CD4+ T cell immune response and a CD8+ T cell immune response.

214. A method for stimulating an immune response in a subject, comprising administering an effective amount of modified cells or composition of any of paragraphs 30-103, 108, 115-129, 139, 140, 148-164, and 168-170.

215. The method of paragraph 214, wherein the immune response is cytotoxic and/or humoral immune response.

216. The method of paragraph 214, wherein the method stimulates a T cell-mediated immune response in a subject.

217. The method of paragraph 216, wherein the T cell-mediated immune response is directed against a target cell.

218. The method of paragraph 217, wherein the target cell is a tumor cell.

219. The method of any of paragraphs 214-218, wherein the modified cells are transfected or transduced in vivo.

220. The method of any of paragraphs 214-219, wherein the modified cells are transfected or transduced ex vivo.

221. The method of any of paragraphs 214-220, wherein the modified cells are autologous patient T cells.

222. The method of paragraph 221, wherein the autologous patient T cells are obtained from a patient that has received a neoantigen peptide or nucleic acid vaccine.

223. The method of paragraph 222, wherein the neoantigen peptide or nucleic acid vaccine comprises at least one personalized neoantigen.

224. The method of paragraph 223, wherein the neoantigen peptide or nucleic acid vaccine comprises at least one additional neoantigenic peptide listed in Tables 1-9.

225. The method of paragraph 224, wherein the patient received a chemotherapeutic agent, an immunomodulatory drug, an immune metabolism modifying drug, targeted therapy or radiation prior to and/or during receipt of the neoantigen peptide or nucleic acid vaccine.

226. The method of any of paragraphs 222-225, wherein the patient receives treatment with at least one checkpoint inhibitor.

227. The method of any of paragraphs 222-226, wherein the autologous T cells are obtained from a patient that has already received at least one round of T cell therapy containing a neoantigen.

228. The method of any of paragraphs 222-227, wherein the method further comprises adoptive T cell therapy.

229. The method of paragraph 228, wherein the adoptive T cell therapy comprises autologous T-cells.

230. The method of paragraph 229, wherein the autologous T-cells are targeted against tumor antigens.

231. The method of paragraph 228 or 229 wherein the adoptive T cell therapy further comprises allogenic T-cells.

232. The method of paragraph 231, wherein the allogenic T-cells are targeted against tumor antigens.

233. The method of any of paragraphs 227-231, wherein the adoptive T cell therapy is administered before the checkpoint inhibitor.

234. A method for evaluating the efficacy of any of paragraphs 171-213, comprising: (i) measuring the number or concentration of target cells in a first sample obtained from the subject before administering the modified cell, (ii) measuring the number concentration of target cells in a second sample obtained from the subject after administration of the modified cell, and (iii) determining an increase or decrease of the number or concentration of target cells in the second sample compared to the number or concentration of target cells in the first sample.

235. The method of paragraph 234, wherein treatment efficacy is determined by monitoring a clinical outcome; an increase, enhancement or prolongation of anti-tumor activity by T cells; an increase in the number of anti-tumor T cells or activated T cells as compared with the number prior to treatment; B cell activity; CD4 T cell activity; or a combination thereof.

236. The method of paragraph 235, wherein treatment efficacy is determined by monitoring a biomarker.

237. The method of paragraph 236, wherein the biomarker is selected from the group consisting of CEA, Her-2/neu, bladder tumor antigen, thyroglobulin, alpha-fetoprotein, PSA, CA 125, CA19.9, CA 15.3, leptin, prolactin, osteopontin, IGF-II, CD98, fascin, sPIgR, 14-3-3 eta, troponin I, and b-type natriuretic peptide.

238. The method of paragraph 235, wherein clinical outcome is selected from the group consisting of tumor regression; tumor shrinkage; tumor necrosis; anti-tumor response by the immune system; tumor expansion, recurrence or spread; or a combination thereof.

239. The method of paragraph 235, wherein the treatment effect is predicted by presence of T cells or by presence of a gene signature indicating T cell inflammation or a combination thereof.

240. A kit comprising a neoantigen therapeutic of any of paragraphs 1-164.

[0051] Accordingly, it is an object of the invention not to encompass within the invention any previously known product, process of making the product, or method of using the product such that Applicants reserve the right and hereby disclose a disclaimer of any previously known product, process, or method. It is further noted that the invention does not intend to encompass within the scope of the invention any product, process, or making of the product or method of using the product, which does not meet the written description and enablement requirements of

the USPTO (35 U.S.C. §112, first paragraph) or the EPO (Article 83 of the EPC), such that Applicants reserve the right and hereby disclose a disclaimer of any previously described product, process of making the product, or method of using the product. It may be advantageous in the practice of the invention to be in compliance with Art. 53(c) EPC and Rule 28(b) and (c) EPC. All rights to explicitly disclaim any embodiments that are the subject of any granted patent(s) of applicant in the lineage of this application or in any other lineage or in any prior filed application of any third party is explicitly reserved Nothing herein is to be construed as a promise.

[0052] It is noted that in this disclosure and particularly in the claims and/or paragraphs, terms such as "comprises", "comprised", "comprising" and the like can have the meaning attributed to it in U.S. Patent law; e.g., they can mean "includes", "included", "including", and the like; and that terms such as "consisting essentially of" and "consists essentially of" have the meaning ascribed to them in U.S. Patent law, e.g., they allow for elements not explicitly recited, but exclude elements that are found in the prior art or that affect a basic or novel characteristic of the invention. Nothing herein is intended as a promise.

[0053] These and other embodiments are disclosed or are obvious from and encompassed by, the following Detailed Description.

DETAILED DESCRIPTION OF THE INVENTION

[0054] To facilitate an understanding of the present invention, a number of terms and phrases are defined herein:

[0055] Unless specifically stated or obvious from context, as used herein, the term "about" is understood as within a range of normal tolerance in the art, for example within 2 standard deviations of the mean. About can be understood as within 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, 0.5%, 0.1%, 0.05%, or 0.01% of the stated value. Unless otherwise clear from context, all numerical values provided herein are modified by the term about.

[0056] Unless specifically stated or obvious from context, as used herein, the term "or" is understood to be inclusive. Unless specifically stated or obvious from context, as used herein, the terms "a," "an," and "the" are understood to be singular or plural.

[0057] All gene name symbols refer to the gene as commonly known in the art. Gene symbols may be those refered to by the HUGO Gene Nomenclature Committee (HGNC). Any reference to the gene symbol is a reference made to the entire gene or variants of the gene. The HUGO Gene Nomenclature Committee is responsible for providing human gene naming guidelines and approving new, unique human gene names and symbols. All human gene names and symbols can be searched at www.genenames.org, the HGNC website, and the guidelines for their formation are available there (www.genenames.org/guidelines).

[0058] By "agent" is meant any small molecule chemical compound, antibody, nucleic acid molecule, or polypeptide, or fragments thereof.

[0059] By "ameliorate" is meant decrease, suppress, attenuate, diminish, arrest, or stabilize the development or progression of a disease (e.g., a neoplasia, tumor, etc.).

[0060] By "alteration" is meant a change (increase or decrease) in the expression levels oractivity of a gene or polypeptide as detected by standard art known methods such as those described herein. As used herein, an alteration includes a 10% change in expression levels, preferably a 25% change, more preferably a 40% change, and most preferably a 50% or greater change in expression levels.

[0061] By "analog" is meant a molecule that is not identical, but has analogous functional or structural features. For example, a tumor specific neo-antigen polypeptide analog retains the biological activity of a corresponding naturally-occurring tumor specific neo-antigen polypeptide, while having certain biochemical modifications that enhance the analog's function relative to a naturally-occurring polypeptide. Such biochemical modifications could increase the analog's protease resistance, membrane permeability, or half-life, without altering, for example, ligand binding. An analog may include an unnatural amino acid.

[0062] "Combination therapy" is intended to embrace administration of therapeutic agents (e.g. neoantigenic peptides described herein) in a sequential manner, that is, wherein each therapeutic agent is administered at a different time, as well as administration of these therapeutic agents, or at least two of the therapeutic agents, in a substantially simultaneous manner. Substantially simultaneous administration can be accomplished, for example, by administering to the subject a single capsule having a fixed ratio of each therapeutic agent or in multiple, single capsules for each of the therapeutic agents. For example, one combination of the present invention may comprise a pooled sample of neoantigenic peptides administered at the

same or different times, or they can be formulated as a single, co-formulated pharmaceutical composition comprising the peptides. As another example, a combination of the present invention (e.g., a pooled sample of tumor specific neoantigens) may be formulated as separate pharmaceutical compositions that can be administered at the same or different time. As used herein, the term "simultaneously" is meant to refer to administration of one or more agents at the same time. For example, in certain embodiments, the neoantigenic peptides are administered simultaneously. Simultaneously includes administration contemporaneously, that is during the same period of time. In certain embodiments, the one or more agents are administered simultaneously in the same hour, or simultaneously in the same day. Sequential or substantially simultaneous administration of each therapeutic agent can be effected by any appropriate route including, but not limited to, oral routes, intravenous routes, sub-cutaneous routes, intramuscular routes, direct absorption through mucous membrane tissues (e.g., nasal, mouth, vaginal, and rectal), and ocular routes (e.g., intravitreal, intraocular, etc.). The therapeutic agents can be administered by the same route or by different routes. For example, one component of a particular combination may be administered by intravenous injection while the other component(s) of the combination may be administered orally. The components may be administered in any therapeutically effective sequence. The phrase "combination" embraces groups of compounds or non-drug therapies useful as part of a combination therapy.

[0063] The term "neoantigen" or "neoantigenic" means a class of tumor antigens that arises from a tumor-specific mutation(s) which alters the amino acid sequence of genome encoded proteins.

[0064] By "neoplasia" is meant any disease that is caused by or results in inappropriately high levels of cell division, inappropriately low levels of apoptosis, or both. For example, cancer is an example of a neoplasia. Examples of cancers include, without limitation, leukemia (e.g., acute leukemia, acute lymphocytic leukemia, acute myelocytic leukemia, acute myeloblastic leukemia, acute promyelocytic leukemia, acute myelomonocytic leukemia, acute monocytic leukemia, acute erythroleukemia, chronic leukemia, chronic myelocytic leukemia, chronic lymphocytic leukemia), polycythemia vera, lymphoma (e.g., Hodgkin's disease, non-Hodgkin's disease), Waldenstrom's macroglobulinemia, heavy chain disease, and solid tumors such as sarcomas and carcinomas (e.g., fibrosarcoma, myxosarcoma, liposarcoma, chondrosarcoma, osteogenic sarcoma, chordoma, angiosarcoma, endotheliosarcoma, lymphangiosarcoma,

lymphangioendotheliosarcoma, synovioma, mesothelioma, Ewing's tumor, leiomyosarcoma, rhabdomyosarcoma, colon carcinoma, pancreatic cancer, breast cancer, ovarian cancer, prostate cancer, squamous cell carcinoma, basal cell carcinoma, adenocarcinoma, sweat gland carcinoma, sebaceous gland carcinoma, papillary carcinoma, papillary adenocarcinomas, cystadenocarcinoma, medullary carcinoma, bronchogenic carcinoma, renal cell carcinoma, hepatoma, nile duct carcinoma, choriocarcinoma, seminoma, embryonal carcinoma, Wilm's tumor, cervical cancer, uterine cancer, testicular cancer, lung carcinoma, small cell lung carcinoma, bladder carcinoma, epithelial carcinoma, glioma, astrocytoma, medulloblastoma, craniopharyngioma, ependymoma, pinealoma, hemangioblastoma, acoustic neuroma, oligodenroglioma, schwannoma, meningioma, melanoma, neuroblastoma, and retinoblastoma). Lymphoproliferative disorders are also considered to be proliferative diseases.

[0065] The term "vaccine" is meant to refer in the present context to a pooled sample of tumor-specific neoantigenic peptides, for example at least two, at least three, at least four, at least five, or more neoantigenic peptides. A "vaccine" is to be understood as meaning a composition for generating immunity for the prophylaxis and/or treatment of diseases (e.g., neoplasia/tumor). Accordingly, vaccines are medicaments which comprise antigens and are intended to be used in humans or animals for generating specific defense and protective substance by vaccination. A "vaccine composition " can include a pharmaceutically acceptable excipient, carrier or diluent.

[0066] The term "pharmaceutically acceptable" refers to approved or approvable by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopeia or other generally recognized pharmacopeia for use in animals, including humans.

[0067] A "pharmaceutically acceptable excipient, carrier or diluent" refers to an excipient, carrier or diluent that can be administered to a subject, together with an agent, and which does not destroy the pharmacological activity thereof and is nontoxic when administered in doses sufficient to deliver a therapeutic amount of the agent.

[0068] A "pharmaceutically acceptable salt" of pooled tumor specific neoantigens as recited herein may be an acid or base salt that is generally considered in the art to be suitable for use in contact with the tissues of human beings or animals without excessive toxicity, irritation, allergic response, or other problem or complication. Such salts include mineral and organic acid salts of basic residues such as amines, as well as alkali or organic salts of acidic residues such as carboxylic acids. Specific pharmaceutical salts include, but are not limited to, salts of acids such

as hydrochloric, phosphoric, hydrobromic, malic, glycolic, fumaric, sulfuric, sulfamic, sulfanilic, formic, toluenesulfonic, methanesulfonic, benzene sulfonic, ethane disulfonic, 2-hydroxyethylsulfonic, nitric, benzoic, 2-acetoxybenzoic, citric, tartaric, lactic, stearic, salicylic, glutamic, ascorbic, pamoic, succinic, fumaric, maleic, propionic, hydroxymaleic, hydroiodic, phenylacetic, alkanoic such as acetic, HOOC-(CH2)n-COOH where n is 0-4, and the like. Similarly, pharmaceutically acceptable cations include, but are not limited to sodium, potassium, calcium, aluminum, lithium and ammonium. Those of ordinary skill in the art will recognize from this disclosure and the knowledge in the art that further pharmaceutically acceptable salts for the pooled tumor specific neoantigens provided herein, including those listed by Remington's Pharmaceutical Sciences, 17th ed., Mack Publishing Company, Easton, PA, p. 1418 (1985). In general, a pharmaceutically acceptable acid or base salt can be synthesized from a parent compound that contains a basic or acidic moiety by any conventional chemical method. Briefly, such salts can be prepared by reacting the free acid or base forms of these compounds with a stoichiometric amount of the appropriate base or acid in an appropriate solvent.

[0069] By a "polypeptide" or "peptide" is meant a polypeptide that has been separated from components that naturally accompany it. Typically, the polypeptide is isolated when it is at least 60%, by weight, free from the proteins and naturally-occurring organic molecules with which it is naturally associated. Preferably, the preparation is at least 75%, more preferably at least 90%, and most preferably at least 99%, by weight, a polypeptide. An isolated polypeptide may be obtained, for example, by extraction from a natural source, by expression of a recombinant nucleic acid encoding such a polypeptide; or by chemically synthesizing the protein. Purity can be measured by any appropriate method, for example, column chromatography, polyacrylamide gel electrophoresis, or by HPLC analysis.

[0070] As used herein, the terms "prevent," "preventing," "prevention," "prophylactic treatment," and the like, refer to reducing the probability of developing a disease or condition in a subject, who does not have, but is at risk of or susceptible to developing a disease or condition.

[0071] The term "prime/ boost" or "prime/ boost dosing regimen" is meant to refer to the successive administrations of a vaccine or immunogenic or immunological compositions. The priming administration (priming) is the administration of a first vaccine or immunogenic or immunological composition type and may comprise one, two or more administrations. The boost administration is the second administration of a vaccine or immunogenic or immunological

composition type and may comprise one, two or more administrations, and, for instance, may comprise or consist essentially of annual administrations. In certain embodiments, administration of the neoplasia vaccine or immunogenic composition is in a prime/ boost dosing regimen.

[0072] Ranges provided herein are understood to be shorthand for all of the values within the range. For example, a range of 1 to 50 is understood to include any number, combination of numbers, or sub-range from the group consisting of 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, or 50, as well as all intervening decimal values between the aforementioned integers such as, for example, 1.1, 1.2, 1.3, 1.4, 1.5, 1.6, 1.7, 1.8, and 1.9. With respect to sub-ranges, "nested sub-ranges" that extend from either end point of the range are specifically contemplated. For example, a nested sub-range of an exemplary range of 1 to 50 may comprise 1 to 10, 1 to 20, 1 to 30, and 1 to 40 in one direction, or 50 to 40, 50 to 30, 50 to 20, and 50 to 10 in the other direction.

[0073] A "receptor" is to be understood as meaning a biological molecule or a molecule grouping capable of binding a ligand. A receptor may serve, to transmit information in a cell, a cell formation or an organism. The receptor comprises at least one receptor unit and frequently contains two or more receptor units, where each receptor unit may consist of a protein molecule, in particular a glycoprotein molecule. The receptor has a structure that complements the structure of a ligand and may complex the ligand as a binding partner. Signaling information may be transmitted by conformational changes of the receptor following binding with the ligand on the surface of a cell. According to the invention, a receptor may refer to particular proteins of MHC classes I and II capable of forming a receptor/ligand complex with a ligand, in particular a peptide or peptide fragment of suitable length.

[0074] The term "subject" refers to an animal which is the object of treatment, observation, or experiment. By way of example only, a subject includes, but is not limited to, a mammal, including, but not limited to, a human or a non-human mammal, such as a non-human primate, bovine, equine, canine, ovine, or feline.

[0075] The terms "treat," "treated," "treating," "treatment," and the like are meant to refer to reducing or ameliorating a disorder and/or symptoms associated therewith (e.g., a neoplasia or tumor). "Treating" may refer to administration of the therapy to a subject after the onset, or suspected onset, of a cancer. "Treating" includes the concepts of "alleviating", which refers to

lessening the frequency of occurrence or recurrence, or the severity, of any symptoms or other ill effects related to a cancer and/or the side effects associated with cancer therapy. The term "treating" also encompasses the concept of "managing" which refers to reducing the severity of a particular disease or disorder in a patient or delaying its recurrence, e.g., lengthening the period of remission in a patient who had suffered from the disease. It is appreciated that, although not precluded, treating a disorder or condition does not require that the disorder, condition, or symptoms associated therewith be completely eliminated.

[0076] The term "therapeutic effect" refers to some extent of relief of one or more of the symptoms of a disorder (e.g., a neoplasia or tumor) or its associated pathology. "Therapeutically effective amount" as used herein refers to an amount of an agent which is effective, upon single or multiple dose administration to the cell or subject, in prolonging the survivability of the patient with such a disorder, reducing one or more signs or symptoms of the disorder, preventing or delaying, and the like beyond that expected in the absence of such treatment. "Therapeutically effective amount" is intended to qualify the amount required to achieve a therapeutic effect. A physician or veterinarian having ordinary skill in the art can readily determine and prescribe the "therapeutically effective amount" (e.g., ED50) of the pharmaceutical composition required. For example, the physician or veterinarian could start doses of the compounds of the invention employed in a pharmaceutical composition at levels lower than that required in order to achieve the desired therapeutic effect and gradually increase the dosage until the desired effect is achieved.

[0077] The terms "spacer" or "linker" as used in reference to a fusion protein refers to a peptide that joins the proteins comprising a fusion protein. Generally, a spacer has no specific biological activity other than to join or to preserve some minimum distance or other spatial relationship between the proteins or RNA sequences. However, in certain embodiments, the constituent amino acids of a spacer may be selected to influence some property of the molecule such as the folding, net charge, or hydrophobicity of the molecule.

[0078] Suitable linkers for use in an embodiment of the present invention are well known to those of skill in the art and include, but are not limited to, straight or branched-chain carbon linkers, heterocyclic carbon linkers, or peptide linkers. The linker is used to separate two neoantigenic peptides by a distance sufficient to ensure that, in a preferred embodiment, each neoantigenic peptide properly folds. Preferred peptide linker sequences adopt a flexible extended

conformation and do not exhibit a propensity for developing an ordered secondary structure. Typical amino acids in flexible protein regions include Gly, Asn and Ser. Virtually any permutation of amino acid sequences containing Gly, Asn and Ser would be expected to satisfy the above criteria for a linker sequence. Other near neutral amino acids, such as Thr and Ala, also may be used in the linker sequence. Still other amino acid sequences that may be used as linkers are disclosed in Maratea et al. (1985), Gene 40: 39-46; Murphy et al. (1986) Proc. Nat'l. Acad. Sci. USA 83: 8258-62; U.S. Pat. No. 4,935,233; and U.S. Pat. No. 4,751,180.

[0079] The recitation of a listing of chemical groups in any definition of a variable herein includes definitions of that variable as any single group or combination of listed groups. The recitation of an embodiment for a variable or aspect herein includes that embodiment as any single embodiment or in combination with any other embodiments or portions thereof.

[0080] Any compositions or methods provided herein can be combined with one or more of any of the other compositions and methods provided herein.

[0081] The therapy disclosed herein constitutes a new method for treating various types of cancer. The therapy described herein also provides a method of therapy for achieving clinical benefit without an unacceptable level of side effects.

[0082] In one aspect the present invention relates to methods for the treatment of neoplasia, and more particularly tumors, by administering to a subject a vaccine or immunogenic composition comprising a plurality of tumor specific neoantigenic peptides. As described in more detail herein, in some embodiments the composition provides a specific, optimized subset of tumor-specific neoantigens suitable for the treatment of tumors in a high proportion of subjects suffering from cancer. In some embodiments, the tumor specific neoantigens may together bind to a high overall proportion of HLA allotypes present in the subject population.

[0083] The immune system can be classified into two functional subsystems: the innate and the acquired immune system. The innate immune system is the first line of defense against infections, and most potential pathogens are rapidly neutralized by this system before they can cause, for example, a noticeable infection. The acquired immune system reacts to molecular structures, referred to as antigens, of the intruding organism. There are two types of acquired immune reactions, which include the humoral immune reaction and the cell-mediated immune reaction. In the humoral immune reaction, antibodies secreted by B cells into bodily fluids bind to pathogen-derived antigens, leading to the elimination of the pathogen through a variety of

mechanisms, e.g. complement-mediated lysis. In the cell-mediated immune reaction, T-cells capable of destroying other cells are activated. For example, if proteins associated with a disease are present in a cell, they are fragmented proteolytically to peptides within the cell. Specific cell proteins then attach themselves to the antigen or peptide formed in this manner and transport them to the surface of the cell, where they are presented to the molecular defense mechanisms, in particular T-cells, of the body. Cytotoxic T cells recognize these antigens and kill the cells that harbor the antigens.

[0084] The molecules that transport and present peptides on the cell surface are referred to as proteins of the major histocompatibility complex (MHC). MHC proteins are classified into two types, referred to as MHC class I and MHC class II. The structures of the proteins of the two MHC classes are very similar; however, they have very different functions. Proteins of MHC class I are present on the surface of almost all cells of the body, including most tumor cells. MHC class I proteins are loaded with antigens that usually originate from endogenous proteins or from pathogens present inside cells, and are then presented to naïve or cytotoxic T-lymphocytes (CTLs). MHC class II proteins are present on dendritic cells, B- lymphocytes, macrophages and other antigen-presenting cells. They mainly present peptides, which are processed from external antigen sources, i.e. outside of the cells, to T-helper (Th) cells. Most of the peptides bound by the MHC class I proteins originate from cytoplasmic proteins produced in the healthy host cells of an organism itself, and do not normally stimulate an immune reaction. Accordingly, cytotoxic T-lymphocytes that recognize such self-peptide-presenting MHC molecules of class I are deleted in the thymus (central tolerance) or, after their release from the thymus, are deleted or inactivated, i.e. tolerized (peripheral tolerance). MHC molecules are capable of stimulating an immune reaction when they present peptides to non-tolerized T-lymphocytes. Cytotoxic T-lymphocytes have both T-cell receptors (TCR) and CD8 molecules on their surface. T-Cell receptors are capable of recognizing and binding peptides complexed with the molecules of MHC class I. Each cytotoxic T-lymphocyte expresses a unique T-cell receptor which is capable of binding specific MHC/peptide complexes.

[0085] The peptide antigens attach themselves to the molecules of MHC class I by competitive affinity binding within the endoplasmic reticulum, before they are presented on the cell surface. Here, the affinity of an individual peptide antigen is directly linked to its amino acid sequence and the presence of specific binding motifs in defined positions within the amino

acid sequence. If the sequence of such a peptide is known, it is possible to manipulate the immune system against diseased cells using, for example, peptide vaccines.

[0086] One of the critical barriers to developing curative and tumor-specific immunotherapy is the identification and selection of highly specific and restricted tumor antigens to avoid autoimmunity. Tumor neoantigens, which arise as a result of genetic change (e.g., inversions, translocations, deletions, missense mutations, splice site mutations, etc.) within malignant cells, represent the most tumor-specific class of antigens. Neoantigens have rarely been used in cancer vaccine or immunogenic compositions due to technical difficulties in identifying them, selecting optimized neoantigens, and producing neoantigens for use in a vaccine or immunogenic composition. These problems may be addressed by:

- identifying mutations in neoplasias/tumors which are present at the DNA level in tumor but not in matched germline samples from a high proportion of subjects having cancer;

- analyzing the identified mutations with one or more peptide-MHC binding prediction algorithms to generate a plurality of neoantigen T cell epitopes that are expressed within the neoplasia/tumor and that bind to a high proportion of patient HLA alleles; and

- synthesizing the plurality of neoantigenic peptides selected from the sets of all neoantigen peptides and predicted binding peptides for use in a cancer vaccine or immunogenic composition suitable for treating a high proportion of subjects having cancer.

[0087] For example, translating sequencing information into a therapeutic vaccine may include:

(1) *Prediction of mutated peptides that can bind to HLA molecules of a high proportion of individuals.* Efficiently choosing which particular mutations to utilize as immunogen requires the ability to predict which mutated peptides would efficiently bind to a high proportion of patient's HLA alleles. Recently, neural network based learning approaches with validated binding and non-binding peptides have advanced the accuracy of prediction algorithms for the major HLA-A and -B alleles.

(2) *Formulating the drug as a multi-epitope vaccine of long peptides.* Targeting as many mutated epitopes as practically possible takes advantage of the enormous capacity of the immune system, prevents the opportunity for immunological escape by down-modulation of a particular immune targeted gene product, and compensates for the known inaccuracy of epitope prediction approaches. Synthetic peptides provide a particularly useful means to prepare multiple immunogens efficiently and to rapidly translate identification of mutant epitopes to an effective vaccine. Peptides can be readily synthesized chemically and easily purified utilizing reagents free of contaminating bacteria or animal substances. The small size allows a clear focus on the mutated region of the protein and also reduces irrelevant antigenic competition from other components (unmutated protein or viral vector antigens).

(3) *Combination with a strong vaccine adjuvant.* Effective vaccines require a strong adjuvant to initiate an immune response. As described below, poly-ICLC, an agonist of TLR3 and the RNA helicase -domains of MDA5 and RIG3, has shown several desirable properties for a vaccine adjuvant. These properties include the induction of local and systemic activation of immune cells *in vivo,* production of stimulatory chemokines and cytokines, and stimulation of antigen-presentation by DCs. Furthermore, poly-ICLC can induce durable CD4+ and CD8+ responses in humans. Importantly, striking similarities in the upregulation of transcriptional and signal transduction pathways were seen in subjects vaccinated with poly-ICLC and in volunteers who had received the highly effective, replication-competent yellow fever vaccine. Furthermore, >90% of ovarian carcinoma patients immunized with poly-ICLC in combination with a NYES0-1 peptide vaccine (in addition to Montanide) showed induction of CD4+ and CD8+ T cell, as well as antibody responses to the peptide in a recent phase 1 study. At the same time, polyICLC has been extensively tested in more than 25 clinical trials to date and exhibited a relatively benign toxicity profile.

The above-described advantages of the invention are described further herein.

[0088] As described herein, there is a large body of evidence in both animals and humans that mutated epitopes are effective in inducing an immune response and that cases of spontaneous tumor regression or long term survival correlate with CD8+ T-cell responses to mutated epitopes (Buckwalter and Srivastava PK. "It is the antigen(s), stupid" and other lessons from over a decade of vaccitherapy of human cancer. Seminars in immunology 20:296-300 (2008); Karanikas et al, High frequency of cytolytic T lymphocytes directed against a tumor-

specific mutated antigen detectable with HLA tetramers in the blood of a lung carcinoma patient with long survival. Cancer Res. 61:3718-3724 (2001); Lennerz et al, The response of autologous T cells to a human melanoma is dominated by mutated neoantigens. Proc Natl Acad Sci U S A.102:16013 (2005)) and that "immunoediting" can be tracked to alterations in expression of dominant mutated antigens in mice and man (Matsushita et al, Cancer exome analysis reveals a T-cell-dependent mechanism of cancer immunoediting Nature 482:400 (2012); DuPage et al, Expression of tumor-specific antigens underlies cancer immunoediting Nature 482:405 (2012); and Sampson et al, Immunologic escape after prolonged progression-free survival with epidermal growth factor receptor variant III peptide vaccination in patients with newly diagnosed glioblastoma J Clin Oncol. 28:4722-4729 (2010)).

[0089] Sequencing technology has revealed that each tumor contains multiple, patient-specific mutations that alter the protein coding content of a gene. Such mutations create altered proteins, ranging from single amino acid changes (caused by missense mutations) to addition of long regions of novel amino acid sequence due to frame shifts, read-through of termination codons or translation of intron regions (novel open reading frame mutations; neoORFs). These mutated proteins are valuable targets for the host's immune response to the tumor as, unlike native proteins, they are not subject to the immune-dampening effects of self-tolerance. Therefore, mutated proteins are more likely to be immunogenic and are also more specific for the tumor cells compared to normal cells of the patient.

[0090] In one embodiment, the neoantigenic peptides in the composition together have affinity to a plurality of MHC molecules, e.g. which together cover a large proportion of the target population. Efficiently choosing which particular mutations to utilize as immunogen requires the ability to predict which mutated peptides would efficiently bind to the HLA alleles present in the patient population. Recently, neural network based learning approaches with validated binding and non-binding peptides have advanced the accuracy of prediction algorithms for the major HLA-A and -B alleles. Utilizing the recently improved algorithms for predicting which missense mutations create strong binding peptides to cognate MHC molecules, a set of peptides representative of optimal mutated epitopes (both neoORF and missense) for the patient population may be identified and prioritized (Zhang et al, Machine learning competition in immunology – Prediction of HLA class I binding peptides J Immunol Methods 374:1 (2011);

Lundegaard et al Prediction of epitopes using neural network based methods J Immunol Methods 374:26 (2011)).

[0091] Targeting as many mutated epitopes as practically possible takes advantage of the enormous capacity of the immune system, prevents the opportunity for immunological escape by down-modulation of a particular immune targeted gene product, and compensates for the known inaccuracy of epitope prediction approaches. Synthetic peptides provide a particularly useful means to prepare multiple immunogens efficiently and to rapidly translate identification of mutant epitopes to an effective vaccine or immunogenic composition. Peptides can be readily synthesized chemically and easily purified utilizing reagents free of contaminating bacteria or animal substances. The small size allows a clear focus on the mutated region of the protein and also reduces irrelevant antigenic competition from other components (unmutated protein or viral vector antigens).

[0092] In one embodiment the drug formulation is a multi-epitope vaccine or immunogenic composition of long peptides. Such "long" peptides undergo efficient internalization, processing and cross-presentation in professional antigen-presenting cells such as dendritic cells, and have been shown to induce CTLs in humans (Melief and van der Burg, Immunotherapy of established (pre) malignant disease by synthetic long peptide vaccines Nature Rev Cancer 8:351 (2008)). In one embodiment at least 2 peptides are prepared for immunization. In some embodiments 20 or more peptides are prepared for immunization. In one embodiment the neoantigenic peptide ranges from about 5 to about 50 amino acids in length. In another embodiment peptides from about 15 to about 35 amino acids in length is synthesized. In preferred embodiment the neoantigenic peptide ranges from about 20 to about 35 amino acids in length.

Production of Tumor Specific Neoantigens

[0093] The present invention is based, at least in part, on the ability to present the immune system of the patient with a pool of tumor specific neoantigens. One of skill in the art from this disclosure and the knowledge in the art will appreciate that there are a variety of ways in which to produce such tumor specific neoantigens. In general, such tumor specific neoantigens may be produced either in vitro or in vivo. Tumor specific neoantigens may be produced in vitro as peptides or polypeptides, which may then be formulated into a neoplasia vaccine or immunogenic composition and administered to a subject. As described in further detail herein,

such in vitro production may occur by a variety of methods known to one of skill in the art such as, for example, peptide synthesis or expression of a peptide/polypeptide from a DNA or RNA molecule in any of a variety of bacterial, eukaryotic, or viral recombinant expression systems, followed by purification of the expressed peptide/polypeptide. Alternatively, tumor specific neoantigens may be produced in vivo by introducing molecules (e.g., DNA, RNA, viral expression systems, and the like) that encode tumor specific neoantigens into a subject, whereupon the encoded tumor specific neoantigens are expressed. The methods of in vitro and in vivo production of neoantigens is also further described herein as it relates to pharmaceutical compositions and methods of delivery of the therapy.

[0094] In certain embodiments the present invention includes modified neoantigenic peptides. As used herein in reference to neoantigenic peptides, the terms "modified", "modification" and the like refer to one or more changes that enhance a desired property of the neoantigenic peptide, where the change does not alter the primary amino acid sequence of the neoantigenic peptide. "Modification" includes a covalent chemical modification that does not alter the primary amino acid sequence of the neoantigenic peptide itself. Such desired properties include, for example, prolonging the *in vivo* half-life, increasing the stability, reducing the clearance, altering the immunogenicity or allergenicity, enabling the raising of particular antibodies, cellular targeting, antigen uptake, antigen processing, MHC affinity, MHC stability, or antigen presentation. Changes to a neoantigenic peptide that may be carried out include, but are not limited to, conjugation to a carrier protein, conjugation to a ligand, conjugation to an antibody, PEGylation, polysialylation HESylation, recombinant PEG mimetics, Fc fusion, albumin fusion, nanoparticle attachment, nanoparticulate encapsulation, cholesterol fusion, iron fusion, acylation, amidation, glycosylation, side chain oxidation, phosphorylation, biotinylation, the addition of a surface active material, the addition of amino acid mimetics, or the addition of unnatural amino acids.

[0095] The clinical effectiveness of protein therapeutics is often limited by short plasma half-life and susceptibility to protease degradation. Studies of various therapeutic proteins (e.g., filgrastim) have shown that such difficulties may be overcome by various modifications, including conjugating or linking the polypeptide sequence to any of a variety of non-proteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes (see, for example, typically via a linking moiety covalently bound to both the

protein and the nonproteinaceous polymer, e.g., a PEG). Such PEG- conjugated biomolecules have been shown to possess clinically useful properties, including better physical and thermal stability, protection against susceptibility to enzymatic degradation, increased solubility, longer in vivo circulating half-life and decreased clearance, reduced immunogenicity and antigenicity, and reduced toxicity.

[0096] PEGs suitable for conjugation to a polypeptide sequence are generally soluble in water at room temperature, and have the general formula $R(O\text{-}CH_2\text{-}CH_2)_nO\text{-}R$, where R is hydrogen or a protective group such as an alkyl or an alkanol group, and where n is an integer from 1 to 1000. When R is a protective group, it generally has from 1 to 8 carbons. The PEG conjugated to the polypeptide sequence can be linear or branched. Branched PEG derivatives, "star-PEGs" and multi-armed PEGs are contemplated by the present disclosure. A molecular weight of the PEG used in the present disclosure is not restricted to any particular range, but certain embodiments have a molecular weight between 500 and 20,000 while other embodiments have a molecular weight between 4,000 and 10,000.

[0097] The present disclosure also contemplates compositions of conjugates wherein the PEGs have different n values and thus the various different PEGs are present in specific ratios. For example, some compositions comprise a mixture of conjugates where n=l, 2, 3 and 4. In some compositions, the percentage of conjugates where n=l is 18-25%, the percentage of conjugates where n=2 is 50-66%, the percentage of conjugates where n=3 is 12-16%, and the percentage of conjugates where n=4 is up to 5%. Such compositions can be produced by reaction conditions and purification methods know in the art. For example, cation exchange chromatography may be used to separate conjugates, and a fraction is then identified which contains the conjugate having, for example, the desired number of PEGs attached, purified free from unmodified protein sequences and from conjugates having other numbers of PEGs attached.

[0098] PEG may be bound to a polypeptide of the present disclosure via a terminal reactive group (a "spacer"). The spacer is, for example, a terminal reactive group which mediates a bond between the free amino or carboxyl groups of one or more of the polypeptide sequences and polyethylene glycol. The PEG having the spacer which may be bound to the free amino group includes N-hydroxysuccinylimide polyethylene glycol which may be prepared by activating succinic acid ester of polyethylene glycol with N- hydroxy succinylimide. Another activated

polyethylene glycol which may be bound to a free amino group is 2,4-bis(0-methoxypolyethyleneglycol)-6-chloro-s-triazine which may be prepared by reacting polyethylene glycol monomethyl ether with cyanuric chloride. The activated polyethylene glycol which is bound to the free carboxyl group includes polyoxyethylenediamine.

[0099] Conjugation of one or more of the polypeptide sequences of the present disclosure to PEG having a spacer may be carried out by various conventional methods. For example, the conjugation reaction can be carried out in solution at a pH of from 5 to 10, at temperature from 4°C to room temperature, for 30 minutes to 20 hours, utilizing a molar ratio of reagent to protein of from 4: 1 to 30: 1. Reaction conditions may be selected to direct the reaction towards producing predominantly a desired degree of substitution. In general, low temperature, low pH (e.g., pH=5), and short reaction time tend to decrease the number of PEGs attached, whereas high temperature, neutral to high pH (e.g., pH>7), and longer reaction time tend to increase the number of PEGs attached. Various means known in the art may be used to terminate the reaction. In some embodiments the reaction is terminated by acidifying the reaction mixture and freezing at, e.g., -20°C.

[00100] The present disclosure also contemplates the use of PEG Mimetics. Recombinant PEG mimetics have been developed that retain the attributes of PEG (e.g., enhanced serum half-life) while conferring several additional advantageous properties. By way of example, simple polypeptide chains (comprising, for example, Ala, Glu, Gly, Pro, Ser and Thr) capable of forming an extended conformation similar to PEG can be produced recombinantly already fused to the peptide or protein drug of interest (e.g., Amunix' XTEN technology; Mountain View, CA). This obviates the need for an additional conjugation step during the manufacturing process. Moreover, established molecular biology techniques enable control of the side chain composition of the polypeptide chains, allowing optimization of immunogenicity and manufacturing properties.

[00101] For purposes of the present disclosure, "glycosylation" is meant to broadly refer to the enzymatic process that attaches glycans to proteins, lipids or other organic molecules. The use of the term "glycosylation" in conjunction with the present disclosure is generally intended to mean adding or deleting one or more carbohydrate moieties (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that may or may not be present in the native sequence. In

addition, the phrase includes qualitative changes in the glycosylation of the native proteins involving a change in the nature and proportions of the various carbohydrate moieties present. Glycosylation can dramatically affect the physical properties of proteins and can also be important in protein stability, secretion, and subcellular localization. Proper glycosylation can be essential for biological activity. In fact, some genes from eucaryotic organisms, when expressed in bacteria (e.g., E. coli) which lack cellular processes for glycosylating proteins, yield proteins that are recovered with little or no activity by virtue of their lack of glycosylation.

[00102] Addition of glycosylation sites can be accomplished by altering the amino acid sequence. The alteration to the polypeptide may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues (for O-linked glycosylation sites) or asparagine residues (for N-linked glycosylation sites). The structures of N-linked and O- linked oligosaccharides and the sugar residues found in each type may be different. One type of sugar that is commonly found on both is N-acetylneuraminic acid (hereafter referred to as sialic acid). Sialic acid is usually the terminal residue of both N-linked and O-linked oligosaccharides and, by virtue of its negative charge, may confer acidic properties to the glycoprotein. A particular embodiment of the present disclosure comprises the generation and use of N-glycosylation variants.

[00103] The polypeptide sequences of the present disclosure may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding the polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids. Another means of increasing the number of carbohydrate moieties on the polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide.

[00104] Removal of carbohydrates may be accomplished chemically or enzymatically, or by substitution of codons encoding amino acid residues that are glycosylated. Chemical deglycosylation techniques are known, and enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases.

[00105] Dihydrofolate reductase (DHFR) - deficient Chinese Hamster Ovary (CHO) cells are a commonly used host cell for the production of recombinant glycoproteins. These cells do not express the enzyme beta-galactoside alpha-2,6-sialyltransferase and therefore do not add sialic acid in the alpha-2,6 linkage to N-linked oligosaccharides of glycoproteins produced in these cells.

[00106] The present disclosure also contemplates the use of polysialylation, the conjugation of peptides and proteins to the naturally occurring, biodegradable a-(2→8) linked polysialic acid ("PSA") in order to improve their stability and in vivo pharmacokinetics. PSA is a biodegradable, non-toxic natural polymer that is highly hydrophilic, giving it a high apparent molecular weight in the blood which increases its serum half-life. In addition, polysialylation of a range of peptide and protein therapeutics has led to markedly reduced proteolysis, retention of activity in vivo activity, and reduction in immunogenicity and antigenicity (see, e.g., G. Gregoriadis et al., Int. J. Pharmaceutics 300(1-2): 125-30). As with modifications with other conjugates (e.g., PEG), various techniques for site-specific polysialylation are available (see, e.g., T. Lindhout et al., PNAS 108(18)7397-7402 (2011)).

[00107] Additional suitable components and molecules for conjugation include, for example, thyroglobulin; albumins such as human serum albumin (HAS); tetanus toxoid; Diphtheria toxoid; polyamino acids such as poly(D-lysine:D-glutamic acid); VP6 polypeptides of rotaviruses; influenza virus hemaglutinin, influenza virus nucleoprotein; Keyhole Limpet Hemocyanin (KLH); and hepatitis B virus core protein and surface antigen; or any combination of the foregoing.

[00108] Fusion of albumin to one or more polypeptides of the present disclosure can, for example, be achieved by genetic manipulation, such that the DNA coding for HSA, or a fragment thereof, is joined to the DNA coding for the one or more polypeptide sequences. Thereafter, a suitable host can be transformed or transfected with the fused nucleotide sequences in the form of, for example, a suitable plasmid, so as to express a fusion polypeptide. The expression may be effected in vitro from, for example, prokaryotic or eukaryotic cells, or in vivo from, for example, a transgenic organism. In some embodiments of the present disclosure, the expression of the fusion protein is performed in mammalian cell lines, for example, CHO cell lines. Transformation is used broadly herein to refer to the genetic alteration of a cell resulting from the direct uptake, incorporation and expression of exogenous genetic material (exogenous DNA) from its surroundings and taken up through the cell membrane(s). Transformation occurs naturally in some species of bacteria, but it can also be effected by artificial means in other cells.

[00109] Furthermore, albumin itself may be modified to extend its circulating half-life. Fusion of the modified albumin to one or more Polypeptides can be attained by the genetic manipulation

techniques described above or by chemical conjugation; the resulting fusion molecule has a half-life that exceeds that of fusions with non-modified albumin. (See WO2011/051489).

[00110] Several albumin - binding strategies have been developed as alternatives for direct fusion, including albumin binding through a conjugated fatty acid chain (acylation). Because serum albumin is a transport protein for fatty acids, these natural ligands with albumin - binding activity have been used for half-life extension of small protein therapeutics. For example, insulin determir (LEVEMIR), an approved product for diabetes, comprises a myristyl chain conjugated to a genetically-modified insulin, resulting in a long- acting insulin analog.

[00111] Another type of modification is to conjugate (e.g., link) one or more additional components or molecules at the N- and/or C-terminus of a polypeptide sequence, such as another protein (e.g., a protein having an amino acid sequence heterologous to the subject protein), or a carrier molecule. Thus, an exemplary polypeptide sequence can be provided as a conjugate with another component or molecule.

[00112] A conjugate modification may result in a polypeptide sequence that retains activity with an additional or complementary function or activity of the second molecule. For example, a polypeptide sequence may be conjugated to a molecule, e.g., to facilitate solubility, storage, in vivo or shelf half-life or stability, reduction in immunogenicity, delayed or controlled release in vivo, etc. Other functions or activities include a conjugate that reduces toxicity relative to an unconjugated polypeptide sequence, a conjugate that targets a type of cell or organ more efficiently than an unconjugated polypeptide sequence, or a drug to further counter the causes or effects associated with a disorder or disease as set forth herein (e.g., diabetes).

[00113] A Polypeptide may also be conjugated to large, slowly metabolized macromolecules such as proteins; polysaccharides, such as sepharose, agarose, cellulose, cellulose beads; polymeric amino acids such as polyglutamic acid, polylysine; amino acid copolymers; inactivated virus particles; inactivated bacterial toxins such as toxoid from diphtheria, tetanus, cholera, leukotoxin molecules; inactivated bacteria; and dendritic cells.

[00114] Additional candidate components and molecules for conjugation include those suitable for isolation or purification. Particular non-limiting examples include binding molecules, such as biotin (biotin-avidin specific binding pair), an antibody, a receptor, a ligand, a lectin, or molecules that comprise a solid support, including, for example, plastic or polystyrene beads, plates or beads, magnetic beads, test strips, and membranes.

[00115] Purification methods such as cation exchange chromatography may be used to separate conjugates by charge difference, which effectively separates conjugates into their various molecular weights. For example, the cation exchange column can be loaded and then washed with ~20 mM sodium acetate, pH ~4, and then eluted with a linear (0 M to 0.5 M) NaCl gradient buffered at a pH from about 3 to 5.5, e.g., at pH ~4.5. The content of the fractions obtained by cation exchange chromatography may be identified by molecular weight using conventional methods, for example, mass spectroscopy, SDS-PAGE, or other known methods for separating molecular entities by molecular weight.

[00116] In certain embodiments, the amino- or carboxyl- terminus of a polypeptide sequence of the present disclosure can be fused with an immunoglobulin Fc region (e.g., human Fc) to form a fusion conjugate (or fusion molecule). Fc fusion conjugates have been shown to increase the systemic half-life of biopharmaceuticals, and thus the biopharmaceutical product may require less frequent administration.

[00117] Fc binds to the neonatal Fc receptor (FcRn) in endothelial cells that line the blood vessels, and, upon binding, the Fc fusion molecule is protected from degradation and re- released into the circulation, keeping the molecule in circulation longer. This Fc binding is believed to be the mechanism by which endogenous IgG retains its long plasma half-life. More recent Fc-fusion technology links a single copy of a biopharmaceutical to the Fc region of an antibody to optimize the pharmacokinetic and pharmacodynamic properties of the biopharmaceutical as compared to traditional Fc-fusion conjugates.

[00118] The present disclosure contemplates the use of other modifications, currently known or developed in the future, of the Polypeptides to improve one or more properties. One such method for prolonging the circulation half-life, increasing the stability, reducing the clearance, or altering the immunogenicity or allergenicity of a polypeptide of the present disclosure involves modification of the polypeptide sequences by hesylation, which utilizes hydroxyethyl starch derivatives linked to other molecules in order to modify the molecule's characteristics. Various aspects of hesylation are described in, for example, U.S. Patent Appln. Nos. 2007/0134197 and 2006/0258607.

In Vitro Peptide/Polypeptide Synthesis

[00119] Proteins or peptides may be made by any technique known to those of skill in the art, including the expression of proteins, polypeptides or peptides through standard molecular biological techniques, the isolation of proteins or peptides from natural sources, in vitro translation, or the chemical synthesis of proteins or peptides. The nucleotide and protein, polypeptide and peptide sequences corresponding to various genes have been previously disclosed, and may be found at computerized databases known to those of ordinary skill in the art. One such database is the National Center for Biotechnology Information's Genbank and GenPept databases located at the National Institutes of Health website. The coding regions for known genes may be amplified and/or expressed using the techniques disclosed herein or as would be known to those of ordinary skill in the art. Alternatively, various commercial preparations of proteins, polypeptides and peptides are known to those of skill in the art.

[00120] Peptides can be readily synthesized chemically utilizing reagents that are free of contaminating bacterial or animal substances (Merrifield RB: Solid phase peptide synthesis. I. The synthesis of a tetrapeptide. J. Am. Chem. Soc. 85:2149-54, 1963). In certain embodiments, neoantigenic peptides are prepared by (1) parallel solid-phase synthesis on multi-channel instruments using uniform synthesis and cleavage conditions; (2) purification over a RP-HPLC column with column stripping; and re-washing, but not replacement, between peptides; followed by (3) analysis with a limited set of the most informative assays. The Good Manufacturing Practices (GMP) footprint can be defined around the set of peptides for an individual patient, thus requiring suite changeover procedures only between syntheses of peptides for different patients.

[00121] Alternatively, a nucleic acid (e.g., a polynucleotide) encoding a neoantigenic peptide of the invention may be used to produce the neoantigenic peptide in vitro. The polynucleotide may be, e.g., DNA, cDNA, PNA, CNA, RNA, either single- and/or double-stranded, or native or stabilized forms of polynucleotides, such as e.g. polynucleotides with a phosphorothiate backbone, or combinations thereof and it may or may not contain introns so long as it codes for the peptide. In one embodiment in vitro translation is used to produce the peptide. Many exemplary systems exist that one skilled in the art could utilize (e.g., Retic Lysate IVT Kit, Life Technologies, Waltham, MA).

[00122] An expression vector capable of expressing a polypeptide can also be prepared. Expression vectors for different cell types are well known in the art and can be selected without undue experimentation. Generally, the DNA is inserted into an expression vector, such as a plasmid, in proper orientation and correct reading frame for expression. If necessary, the DNA may be linked to the appropriate transcriptional and translational regulatory control nucleotide sequences recognized by the desired host (e.g., bacteria), although such controls are generally available in the expression vector. The vector is then introduced into the host bacteria for cloning using standard techniques (see, e.g., Sambrook et al. (1989) Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory, Cold Spring Harbor, N.Y.).

[00123] Expression vectors comprising the isolated polynucleotides, as well as host cells containing the expression vectors, are also contemplated. The neoantigenic peptides may be provided in the form of RNA or cDNA molecules encoding the desired neoantigenic peptides. One or more neoantigenic peptides of the invention may be encoded by a single expression vector.

[00124] The term "polynucleotide encoding a polypeptide" encompasses a polynucleotide which includes only coding sequences for the polypeptide as well as a polynucleotide which includes additional coding and/or non-coding sequences. Polynucleotides can be in the form of RNA or in the form of DNA. DNA includes cDNA, genomic DNA, and synthetic DNA; and can be double-stranded or single-stranded, and if single stranded can be the coding strand or non-coding (anti-sense) strand.

[00125] In embodiments, the polynucleotides may comprise the coding sequence for the tumor specific neoantigenic peptide fused in the same reading frame to a polynucleotide which aids, for example, in expression and/or secretion of a polypeptide from a host cell (e.g., a leader sequence which functions as a secretory sequence for controlling transport of a polypeptide from the cell). The polypeptide having a leader sequence is a preprotein and can have the leader sequence cleaved by the host cell to form the mature form of the polypeptide.

[00126] In embodiments, the polynucleotides can comprise the coding sequence for the tumor specific neoantigenic peptide fused in the same reading frame to a marker sequence that allows, for example, for purification of the encoded polypeptide, which may then be incorporated into the personalized neoplasia vaccine or immunogenic composition. For example, the marker sequence can be a hexa-histidine tag supplied by a pQE-9 vector to provide for purification of

the mature polypeptide fused to the marker in the case of a bacterial host, or the marker sequence can be a hemagglutinin (HA) tag derived from the influenza hemagglutinin protein when a mammalian host (e.g., COS-7 cells) is used. Additional tags include, but are not limited to, Calmodulin tags, FLAG tags, Myc tags, S tags, SBP tags, Softag 1, Softag 3, V5 tag, Xpress tag, Isopeptag, SpyTag, Biotin Carboxyl Carrier Protein (BCCP) tags, GST tags, fluorescent protein tags (e.g., green fluorescent protein tags), maltose binding protein tags, Nus tags, Strep-tag, thioredoxin tag, TC tag, Ty tag, and the like.

[00127] In embodiments, the polynucleotides may comprise the coding sequence for one or more of the tumor specific neoantigenic peptides fused in the same reading frame to create a single concatamerized neoantigenic peptide construct capable of producing multiple neoantigenic peptides.

[00128] In certain embodiments, isolated nucleic acid molecules having a nucleotide sequence at least 60% identical, at least 65% identical, at least 70% identical, at least 75% identical, at least 80% identical, at least 85% identical, at least 90% identical, at least 95% identical, or at least 96%, 97%, 98% or 99% identical to a polynucleotide encoding a tumor specific neoantigenic peptide of the present invention, can be provided.

[00129] By a polynucleotide having a nucleotide sequence at least, for example, 95% "identical" to a reference nucleotide sequence is intended that the nucleotide sequence of the polynucleotide is identical to the reference sequence except that the polynucleotide sequence can include up to five point mutations per each 100 nucleotides of the reference nucleotide sequence. In other words, to obtain a polynucleotide having a nucleotide sequence at least 95% identical to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence can be deleted or substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence can be inserted into the reference sequence. These mutations of the reference sequence can occur at the amino- or carboxy-terminal positions of the reference nucleotide sequence or anywhere between those terminal positions, interspersed either individually among nucleotides in the reference sequence or in one or more contiguous groups within the reference sequence.

[00130] As a practical matter, whether any particular nucleic acid molecule is at least 80% identical, at least 85% identical, at least 90% identical, and in some embodiments, at least 95%, 96%, 97%, 98%, or 99% identical to a reference sequence can be determined conventionally

using known computer programs such as the Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, WI 53711). Bestfit uses the local homology algorithm of Smith and Waterman, Advances in Applied Mathematics 2:482-489 (1981), to find the best segment of homology between two sequences. When using Bestfit or any other sequence alignment program to determine whether a particular sequence is, for instance, 95% identical to a reference sequence according to the present invention, the parameters are set such that the percentage of identity is calculated over the full length of the reference nucleotide sequence and that gaps in homology of up to 5% of the total number of nucleotides in the reference sequence are allowed.

[00131] The isolated tumor specific neoantigenic peptides described herein can be produced in vitro (e.g., in the laboratory) by any suitable method known in the art. Such methods range from direct protein synthetic methods to constructing a DNA sequence encoding isolated polypeptide sequences and expressing those sequences in a suitable transformed host. In some embodiments, a DNA sequence is constructed using recombinant technology by isolating or synthesizing a DNA sequence encoding a wild-type protein of interest. Optionally, the sequence can be mutagenized by site-specific mutagenesis to provide functional analogs thereof. See, e.g. Zoeller et al., Proc. Nat'l. Acad. Sci. USA 81:5662-5066 (1984) and U.S. Pat. No. 4,588,585.

[00132] In embodiments, a DNA sequence encoding a polypeptide of interest would be constructed by chemical synthesis using an oligonucleotide synthesizer. Such oligonucleotides can be designed based on the amino acid sequence of the desired polypeptide and selecting those codons that are favored in the host cell in which the recombinant polypeptide of interest is produced. Standard methods can be applied to synthesize an isolated polynucleotide sequence encoding an isolated polypeptide of interest. For example, a complete amino acid sequence can be used to construct a back-translated gene. Further, a DNA oligomer containing a nucleotide sequence coding for the particular isolated polypeptide can be synthesized. For example, several small oligonucleotides coding for portions of the desired polypeptide can be synthesized and then ligated. The individual oligonucleotides typically contain 5' or 3' overhangs for complementary assembly.

[00133] Once assembled (e.g., by synthesis, site-directed mutagenesis, or another method), the polynucleotide sequences encoding a particular isolated polypeptide of interest is inserted into an expression vector and optionally operatively linked to an expression control sequence

appropriate for expression of the protein in a desired host. Proper assembly can be confirmed by nucleotide sequencing, restriction mapping, and expression of a biologically active polypeptide in a suitable host. As well known in the art, in order to obtain high expression levels of a transfected gene in a host, the gene can be operatively linked to transcriptional and translational expression control sequences that are functional in the chosen expression host.

[00134] Recombinant expression vectors may be used to amplify and express DNA encoding the tumor specific neoantigenic peptides. Recombinant expression vectors are replicable DNA constructs which have synthetic or cDNA-derived DNA fragments encoding a tumor specific neoantigenic peptide or a bioequivalent analog operatively linked to suitable transcriptional or translational regulatory elements derived from mammalian, microbial, viral or insect genes. A transcriptional unit generally comprises an assembly of (1) a genetic element or elements having a regulatory role in gene expression, for example, transcriptional promoters or enhancers, (2) a structural or coding sequence which is transcribed into mRNA and translated into protein, and (3) appropriate transcription and translation initiation and termination sequences, as described in detail herein. Such regulatory elements can include an operator sequence to control transcription. The ability to replicate in a host, usually conferred by an origin of replication, and a selection gene to facilitate recognition of transformants can additionally be incorporated. DNA regions are operatively linked when they are functionally related to each other. For example, DNA for a signal peptide (secretory leader) is operatively linked to DNA for a polypeptide if it is expressed as a precursor which participates in the secretion of the polypeptide; a promoter is operatively linked to a coding sequence if it controls the transcription of the sequence; or a ribosome binding site is operatively linked to a coding sequence if it is positioned so as to permit translation. Generally, operatively linked means contiguous, and in the case of secretory leaders, means contiguous and in reading frame. Structural elements intended for use in yeast expression systems include a leader sequence enabling extracellular secretion of translated protein by a host cell. Alternatively, where recombinant protein is expressed without a leader or transport sequence, it can include an N-terminal methionine residue. This residue can optionally be subsequently cleaved from the expressed recombinant protein to provide a final product.

[00135] Useful expression vectors for eukaryotic hosts, especially mammals or humans include, for example, vectors comprising expression control sequences from SV40, bovine papilloma virus, adenovirus and cytomegalovirus. Useful expression vectors for bacterial hosts

include known bacterial plasmids, such as plasmids from Escherichia coli, including pCR 1, pBR322, pMB9 and their derivatives, wider host range plasmids, such as M13 and filamentous single-stranded DNA phages.

[00136] Suitable host cells for expression of a polypeptide include prokaryotes, yeast, insect or higher eukaryotic cells under the control of appropriate promoters. Prokaryotes include gram negative or gram positive organisms, for example E. coli or bacilli. Higher eukaryotic cells include established cell lines of mammalian origin. Cell-free translation systems could also be employed. Appropriate cloning and expression vectors for use with bacterial, fungal, yeast, and mammalian cellular hosts are well known in the art (see Pouwels et al., Cloning Vectors: A Laboratory Manual, Elsevier, N.Y., 1985).

[00137] Various mammalian or insect cell culture systems are also advantageously employed to express recombinant protein. Expression of recombinant proteins in mammalian cells can be performed because such proteins are generally correctly folded, appropriately modified and completely functional. Examples of suitable mammalian host cell lines include the COS-7 lines of monkey kidney cells, described by Gluzman (Cell 23:175, 1981), and other cell lines capable of expressing an appropriate vector including, for example, L cells, C127, 3T3, Chinese hamster ovary (CHO), 293, HeLa and BHK cell lines. Mammalian expression vectors can comprise nontranscribed elements such as an origin of replication, a suitable promoter and enhancer linked to the gene to be expressed, and other 5' or 3' flanking nontranscribed sequences, and 5' or 3' nontranslated sequences, such as necessary ribosome binding sites, a polyadenylation site, splice donor and acceptor sites, and transcriptional termination sequences. Baculovirus systems for production of heterologous proteins in insect cells are reviewed by Luckow and Summers, Bio/Technology 6:47 (1988).

[00138] The proteins produced by a transformed host can be purified according to any suitable method. Such standard methods include chromatography (e.g., ion exchange, affinity and sizing column chromatography, and the like), centrifugation, differential solubility, or by any other standard technique for protein purification. Affinity tags such as hexahistidine, maltose binding domain, influenza coat sequence, glutathione-S-transferase, and the like can be attached to the protein to allow easy purification by passage over an appropriate affinity column. Isolated proteins can also be physically characterized using such techniques as proteolysis, nuclear magnetic resonance and x-ray crystallography.

[00139] For example, supernatants from systems which secrete recombinant protein into culture media can be first concentrated using a commercially available protein concentration filter, for example, an Amicon or Millipore Pellicon ultrafiltration unit. Following the concentration step, the concentrate can be applied to a suitable purification matrix. Alternatively, an anion exchange resin can be employed, for example, a matrix or substrate having pendant diethylaminoethyl (DEAE) groups. The matrices can be acrylamide, agarose, dextran, cellulose or other types commonly employed in protein purification. Alternatively, a cation exchange step can be employed. Suitable cation exchangers include various insoluble matrices comprising sulfopropyl or carboxymethyl groups. Finally, one or more reversed-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify a cancer stem cell protein-Fc composition. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a homogeneous recombinant protein.

[00140] Recombinant protein produced in bacterial culture can be isolated, for example, by initial extraction from cell pellets, followed by one or more concentration, salting-out, aqueous ion exchange or size exclusion chromatography steps. High performance liquid chromatography (HPLC) can be employed for final purification steps. Microbial cells employed in expression of a recombinant protein can be disrupted by any convenient method, including freeze-thaw cycling, sonication, mechanical disruption, or use of cell lysing agents.

In Vivo Peptide/Polypeptide Synthesis

[00141] The present invention also contemplates the use of nucleic acid molecules as vehicles for delivering neoantigenic peptides/polypeptides to the subject in need thereof, in vivo, in the form of, e.g., DNA/RNA vaccines (see, e.g., WO2012/159643, and WO2012/159754, hereby incorporated by reference in their entirety).

[00142] In one embodiment neoantigens may be administered to a patient in need thereof by use of a plasmid. These are plasmids which usually consist of a strong viral promoter to drive the in vivo transcription and translation of the gene (or complementary DNA) of interest (Mor, et al., (1995). The Journal of Immunology 155 (4): 2039–2046). Intron A may sometimes be included to improve mRNA stability and hence increase protein expression (Leitner et al.

(1997).The Journal of Immunology 159 (12): 6112–6119). Plasmids also include a strong polyadenylation/transcriptional termination signal, such as bovine growth hormone or rabbit beta-globulin polyadenylation sequences (Alarcon et al., (1999). Adv. Parasitol. Advances in Parasitology 42: 343–410; Robinson et al., (2000). Adv. Virus Res. Advances in Virus Research 55: 1–74; Böhmet al., (1996). Journal of Immunological Methods 193 (1): 29–40.). Multicistronic vectors are sometimes constructed to express more than one immunogen, or to express an immunogen and an immunostimulatory protein (Lewis et al., (1999). Advances in Virus Research (Academic Press) 54: 129–88).

[00143] Because the plasmid is the "vehicle" from which the immunogen is expressed, optimising vector design for maximal protein expression is essential (Lewis et al., (1999). Advances in Virus Research (Academic Press) 54: 129–88). One way of enhancing protein expression is by optimising the codon usage of pathogenic mRNAs for eukaryotic cells. Another consideration is the choice of promoter. Such promoters may be the SV40 promoter or Rous Sarcoma Virus (RSV).

[00144] Plasmids may be introduced into animal tissues by a number of different methods. The two most popular approaches are injection of DNA in saline, using a standard hypodermic needle, and gene gun delivery. A schematic outline of the construction of a DNA vaccine plasmid and its subsequent delivery by these two methods into a host is illustrated at Scientific American (Weiner et al., (1999) Scientific American 281 (1): 34–41). Injection in saline is normally conducted intramuscularly (IM) in skeletal muscle, or intradermally (ID), with DNA being delivered to the extracellular spaces. This can be assisted by electroporation by temporarily damaging muscle fibres with myotoxins such as bupivacaine; or by using hypertonic solutions of saline or sucrose (Alarcon et al., (1999). Adv. Parasitol. Advances in Parasitology 42: 343–410). Immune responses to this method of delivery can be affected by many factors, including needle type, needle alignment, speed of injection, volume of injection, muscle type, and age, sex and physiological condition of the animal being injected(Alarcon et al., (1999). Adv. Parasitol. Advances in Parasitology 42: 343–410).

[00145] Gene gun delivery, the other commonly used method of delivery, ballistically accelerates plasmid DNA (pDNA) that has been adsorbed onto gold or tungsten microparticles into the target cells, using compressed helium as an accelerant (Alarcon et al., (1999). Adv.

Parasitol. Advances in Parasitology 42: 343–410; Lewis et al., (1999). Advances in Virus Research (Academic Press) 54: 129–88).

[00146] Alternative delivery methods may include aerosol instillation of naked DNA on mucosal surfaces, such as the nasal and lung mucosa, (Lewis et al., (1999). Advances in Virus Research (Academic Press) 54: 129–88) and topical administration of pDNA to the eye and vaginal mucosa (Lewis et al., (1999) Advances in Virus Research (Academic Press) 54: 129–88). Mucosal surface delivery has also been achieved using cationic liposome-DNA preparations, biodegradable microspheres, attenuated Shigella or Listeria vectors for oral administration to the intestinal mucosa, and recombinant adenovirus vectors. DNA or RNA may also be delivered to cells following mild mechanical disruption of the cell membrane, temporarily permeabilizing the cells. Such a mild mechanical disruption of the membrane can be accomplished by gently forcing cells through a small aperture (Ex Vivo Cytosolic Delivery of Functional Macromolecules to Immune Cells, Sharei et al, PLOS ONE | DOI:10.1371/journal.pone.0118803 April 13, 2015).

[00147] The method of delivery determines the dose of DNA required to raise an effective immune response. Saline injections require variable amounts of DNA, from 10 µg-1 mg, whereas gene gun deliveries require 100 to 1000 times less DNA than intramuscular saline injection to raise an effective immune response. Generally, 0.2 µg – 20 µg are required, although quantities as low as 16 ng have been reported. These quantities vary from species to species, with mice, for example, requiring approximately 10 times less DNA than primates. Saline injections require more DNA because the DNA is delivered to the extracellular spaces of the target tissue (normally muscle), where it has to overcome physical barriers (such as the basal lamina and large amounts of connective tissue, to mention a few) before it is taken up by the cells, while gene gun deliveries bombard DNA directly into the cells, resulting in less "wastage" (See e.g., Sedegah et al., (1994). Proceedings of the National Academy of Sciences of the United States of America 91 (21): 9866–9870; Daheshiaet al., (1997). The Journal of Immunology 159 (4): 1945–1952; Chen et al., (1998). The Journal of Immunology 160 (5): 2425–2432; Sizemore (1995) Science 270 (5234): 299–302; Fynan et al., (1993) Proc. Natl. Acad. Sci. U.S.A. 90 (24): 11478–82).

[00148] In one embodiment, a neoplasia vaccine or immunogenic composition may include separate DNA plasmids encoding, for example, one or more neoantigenic peptides/polypeptides as identified in according to the invention. As discussed herein, the exact choice of expression

vectors can depend upon the peptide/polypeptides to be expressed, and is well within the skill of the ordinary artisan. The expected persistence of the DNA constructs (e.g., in an episomal, non-replicating, non-integrated form in the muscle cells) is expected to provide an increased duration of protection.

[00149] One or more neoantigenic peptides of the invention may be encoded and expressed in vivo using a viral based system (e.g., an adenovirus system, an adeno associated virus (AAV) vector, a poxvirus, or a lentivirus). In one embodiment, the neoplasia vaccine or immunogenic composition may include a viral based vector for use in a human patient in need thereof, such as, for example, an adenovirus (see, e.g., Baden et al. First-in-human evaluation of the safety and immunogenicity of a recombinant adenovirus serotype 26 HIV-1 Env vaccine (IPCAVD 001). J Infect Dis. 2013 Jan 15;207(2):240-7, hereby incorporated by reference in its entirety). Plasmids that can be used for adeno associated virus, adenovirus, and lentivirus delivery have been described previously (see e.g., U.S. Patent Nos. 6,955,808 and 6,943,019, and U.S. Patent application No. 20080254008, hereby incorporated by reference).

[00150] The peptides and polypeptides of the invention can also be expressed by a vector, e.g., a nucleic acid molecule as herein-discussed, e.g., RNA or a DNA plasmid, a viral vector such as a poxvirus, e.g., orthopox virus, avipox virus, or adenovirus, AAV or lentivirus. This approach involves the use of a vector to express nucleotide sequences that encode the peptide of the invention. Upon introduction into an acutely or chronically infected host or into a noninfected host, the vector expresses the immunogenic peptide, and thereby elicits a host CTL response.

[00151] Among vectors that may be used in the practice of the invention, integration in the host genome of a cell is possible with retrovirus gene transfer methods, often resulting in long term expression of the inserted transgene. In a preferred embodiment the retrovirus is a lentivirus. Additionally, high transduction efficiencies have been observed in many different cell types and target tissues. The tropism of a retrovirus can be altered by incorporating foreign envelope proteins, expanding the potential target population of target cells. A retrovirus can also be engineered to allow for conditional expression of the inserted transgene, such that only certain cell types are infected by the lentivirus. Cell type specific promoters can be used to target expression in specific cell types. Lentiviral vectors are retroviral vectors (and hence both lentiviral and retroviral vectors may be used in the practice of the invention). Moreover,

lentiviral vectors are preferred as they are able to transduce or infect non-dividing cells and typically produce high viral titers. Selection of a retroviral gene transfer system may therefore depend on the target tissue. Retroviral vectors are comprised of cis-acting long terminal repeats with packaging capacity for up to 6-10 kb of foreign sequence. The minimum cis-acting LTRs are sufficient for replication and packaging of the vectors, which are then used to integrate the desired nucleic acid into the target cell to provide permanent expression. Widely used retroviral vectors that may be used in the practice of the invention include those based upon murine leukemia virus (MuLV), gibbon ape leukemia virus (GaLV), Simian Immuno deficiency virus (SIV), human immuno deficiency virus (HIV), and combinations thereof (see, e.g., Buchscher et al., (1992) J. Virol. 66:2731-2739; Johann et al., (1992) J. Virol. 66:1635-1640; Sommnerfelt et al., (1990) Virol. 176:58-59; Wilson et al., (1998) J. Virol. 63:2374-2378; Miller et al., (1991) J. Virol. 65:2220-2224; PCT/US94/05700).

[00152] Also useful in the practice of the invention is a minimal non-primate lentiviral vector, such as a lentiviral vector based on the equine infectious anemia virus (EIAV) (see, e.g., Balagaan, (2006) J Gene Med; 8: 275 – 285, Published online 21 November 2005 in Wiley InterScience (www.interscience.wiley.com). DOI: 10.1002/jgm.845). The vectors may have cytomegalovirus (CMV) promoter driving expression of the target gene. Accordingly, the invention contemplates amongst vector(s) useful in the practice of the invention: viral vectors, including retroviral vectors and lentiviral vectors.

[00153] Lentiviral vectors have been disclosed as in the treatment for Parkinson's Disease, see, e.g., US Patent Publication No. 20120295960 and US Patent Nos. 7303910 and 7351585. Lentiviral vectors have also been disclosed for delivery to the Brain, see, e.g., US Patent Publication Nos. US20110293571; US20040013648, US20070025970, US20090111106 and US Patent No. US7259015. In another embodiment lentiviral vectors are used to deliver vectors to the brain of those being treated for a disease.

[00154] As to lentivirus vector systems useful in the practice of the invention, mention is made of US Patents Nos. 6428953, 6165782, 6013516, 5994136, 6312682, and 7,198,784, and documents cited therein.

[00155] In an embodiment herein the delivery is via an lentivirus. Zou et al. administered about 10 µl of a recombinant lentivirus having a titer of 1 x 10^9 transducing units (TU)/ml by an intrathecal catheter. These sort of dosages can be adapted or extrapolated to use of a retroviral or

lentiviral vector in the present invention. For transduction in tissues such as the brain, it is necessary to use very small volumes, so the viral preparation is concentrated by ultracentrifugation. The resulting preparation should have at least 10^8 TU/ml, preferably from 10^8 to 10^9 TU/ml, more preferably at least 10^9 TU/ml. Other methods of concentration such as ultrafiltration or binding to and elution from a matrix may be used.

[00156] In other embodiments the amount of lentivirus administered may be $1.x.10^5$ or about $1.x.10^5$ plaque forming units (PFU), $5.x.10^5$ or about $5.x.10^5$ PFU, $1.x.10^6$ or about $1.x10^6$ PFU, $5.x.10^6$ or about $5.x.10^6$ PFU, $1.x.10^7$ or about $1.x.10^7$ PFU, $5.x.10^7$ or about $5.x.10^7$ PFU, $1.x.10^8$ or about $1.x.10^8$ PFU, $5.x.10^8$ or about $5.x.10^8$ PFU, $1.x.10^9$ or about $1.x.10^9$ PFU, $5.x.10^9$ or about $5.x.10^9$ PFU, $1.x.10^{10}$ or about $1.x.10^{10}$ PFU or $5.x.10^{10}$ or about $5.x.10^{10}$ PFU as total single dosage for an average human of 75 kg or adjusted for the weight and size and species of the subject. One of skill in the art can determine suitable dosage. Suitable dosages for a virus can be determined empirically.

[00157] Also useful in the practice of the invention is an adenovirus vector. One advantage is the ability of recombinant adenoviruses to efficiently transfer and express recombinant genes in a variety of mammalian cells and tissues in vitro and in vivo, resulting in the high expression of the transferred nucleic acids. Further, the ability to productively infect quiescent cells, expands the utility of recombinant adenoviral vectors. In addition, high expression levels ensure that the products of the nucleic acids will be expressed to sufficient levels to generate an immune response (see e.g., U.S. Patent No. 7,029,848, hereby incorporated by reference).

[00158] As to adenovirus vectors useful in the practice of the invention, mention is made of US Patent No. 6,955,808. The adenovirus vector used can be selected from the group consisting of the Ad5, Ad35, Ad11, C6, and C7 vectors. The sequence of the Adenovirus 5 ("Ad5") genome has been published. (Chroboczek, J., Bieber, F., and Jacrot, B. (1992) The Sequence of the Genome of Adenovirus Type 5 and Its Comparison with the Genome of Adenovirus Type 2, Virology 186, 280-285; the contents if which is hereby incorporated by reference). Ad35 vectors are described in U.S. Pat. Nos. 6,974,695, 6,913,922, and 6,869,794. Ad11 vectors are described in U.S. Pat. No. 6,913,922. C6 adenovirus vectors are described in U.S. Pat. Nos. 6,780,407; 6,537,594; 6,309,647; 6,265,189; 6,156,567; 6,090,393; 5,942,235 and 5,833,975. C7 vectors are described in U.S. Pat. No. 6,277,558. Adenovirus vectors that are E1-defective or deleted, E3-defective or deleted, and/or E4-defective or deleted may also be used. Certain adenoviruses

having mutations in the E1 region have improved safety margin because E1-defective adenovirus mutants are replication-defective in non-permissive cells, or, at the very least, are highly attenuated. Adenoviruses having mutations in the E3 region may have enhanced the immunogenicity by disrupting the mechanism whereby adenovirus down-regulates MHC class I molecules. Adenoviruses having E4 mutations may have reduced immunogenicity of the adenovirus vector because of suppression of late gene expression. Such vectors may be particularly useful when repeated re-vaccination utilizing the same vector is desired. Adenovirus vectors that are deleted or mutated in E1, E3, E4, E1 and E3, and E1 and E4 can be used in accordance with the present invention. Furthermore, "gutless" adenovirus vectors, in which all viral genes are deleted, can also be used in accordance with the present invention. Such vectors require a helper virus for their replication and require a special human 293 cell line expressing both E1a and Cre, a condition that does not exist in natural environment. Such "gutless" vectors are non-immunogenic and thus the vectors may be inoculated multiple times for re-vaccination. The "gutless" adenovirus vectors can be used for insertion of heterologous inserts/genes such as the transgenes of the present invention, and can even be used for co-delivery of a large number of heterologous inserts/genes.

[00159] In an embodiment herein the delivery is via an adenovirus, which may be at a single booster dose containing at least 1 x 10^5 particles (also referred to as particle units, pu) of adenoviral vector. In an embodiment herein, the dose preferably is at least about 1 x 10^6 particles (for example, about 1 x 10^6-1 x 10^{12} particles), more preferably at least about 1 x 10^7 particles, more preferably at least about 1 x 10^8 particles (e.g., about 1 x 10^8-1 x 10^{11} particles or about 1 x 10^8-1 x 10^{12} particles), and most preferably at least about 1 x 10^9 particles (e.g., about 1 x 10^9-1 x 10^{10} particles or about 1 x 10^9-1 x 10^{12} particles), or even at least about 1 x 10^{10} particles (e.g., about 1 x 10^{10}-1 x 10^{12} particles) of the adenoviral vector. Alternatively, the dose comprises no more than about 1 x 10^{14} particles, preferably no more than about 1 x 10^{13} particles, even more preferably no more than about 1 x 10^{12} particles, even more preferably no more than about 1 x 10^{11} particles, and most preferably no more than about 1 x 10^{10} particles (e.g., no more than about 1 x 10^9 articles). Thus, the dose may contain a single dose of adenoviral vector with, for example, about 1 x 10^6 particle units (pu), about 2 x 10^6 pu, about 4 x 10^6 pu, about 1 x 10^7 pu, about 2 x 10^7 pu, about 4 x 10^7 pu, about 1 x 10^8 pu, about 2 x 10^8 pu, about 4 x 10^8 pu, about 1 x 10^9 pu, about 2 x 10^9 pu, about 4 x 10^9 pu, about 1 x 10^{10} pu, about 2 x 10^{10} pu, about 4 x 10^{10}

pu, about 1 x 10^{11} pu, about 2 x 10^{11} pu, about 4 x 10^{11} pu, about 1 x 10^{12} pu, about 2 x 10^{12} pu, or about 4 x 10^{12} pu of adenoviral vector. See, for example, the adenoviral vectors in U.S. Patent No. 8,454,972 B2 to Nabel, et. al., granted on June 4, 2013; incorporated by reference herein, and the dosages at col 29, lines 36-58 thereof. In an embodiment herein, the adenovirus is delivered via multiple doses.

[00160] In terms of in vivo delivery, AAV is advantageous over other viral vectors due to low toxicity and low probability of causing insertional mutagenesis because it doesn't integrate into the host genome. AAV has a packaging limit of 4.5 or 4.75 Kb. Constructs larger than 4.5 or 4.75 Kb result in significantly reduced virus production. There are many promoters that can be used to drive nucleic acid molecule expression. AAV ITR can serve as a promoter and is advantageous for eliminating the need for an additional promoter element. For ubiquitous expression, the following promoters can be used: CMV, CAG, CBh, PGK, SV40, Ferritin heavy or light chains, etc. For brain expression, the following promoters can be used: SynapsinI for all neurons, CaMKIIalpha for excitatory neurons, GAD67 or GAD65 or VGAT for GABAergic neurons, etc. Promoters used to drive RNA synthesis can include: Pol III promoters such as U6 or H1. The use of a Pol II promoter and intronic cassettes can be used to express guide RNA (gRNA).

[00161] With regard to AAV vectors useful in the practice of the invention, mention is made of US Patent Nos. 5658785, 7115391, 7172893, 6953690, 6936466, 6924128, 6893865, 6793926, 6537540, 6475769 and 6258595, and documents cited therein.

[00162] As to AAV, the AAV can be AAV1, AAV2, AAV5 or any combination thereof. One can select the AAV with regard to the cells to be targeted; e.g., one can select AAV serotypes 1, 2, 5 or a hybrid capsid AAV1, AAV2, AAV5 or any combination thereof for targeting brain or neuronal cells; and one can select AAV4 for targeting cardiac tissue. AAV8 is useful for delivery to the liver. The above promoters and vectors are preferred individually.

[00163] In an embodiment herein, the delivery is via an AAV. A therapeutically effective dosage for in vivo delivery of the AAV to a human is believed to be in the range of from about 20 to about 50 ml of saline solution containing from about 1 x 10^{10} to about 1 x 10^{50} functional AAV/ml solution. The dosage may be adjusted to balance the therapeutic benefit against any side effects. In an embodiment herein, the AAV dose is generally in the range of concentrations of from about 1 x 10^{5} to 1 x 10^{50} genomes AAV, from about 1 x 10^{8} to 1 x 10^{20} genomes AAV,

from about 1 x 10^{10} to about 1 x 10^{16} genomes, or about 1 x 10^{11} to about 1 x 10^{16} genomes AAV. A human dosage may be about 1 x 10^{13} genomes AAV. Such concentrations may be delivered in from about 0.001 ml to about 100 ml, about 0.05 to about 50 ml, or about 10 to about 25 ml of a carrier solution. In a preferred embodiment, AAV is used with a titer of about 2 x 10^{13} viral genomes/milliliter, and each of the striatal hemispheres of a mouse receives one 500 nanoliter injection. Other effective dosages can be readily established by one of ordinary skill in the art through routine trials establishing dose response curves. See, for example, U.S. Patent No. 8,404,658 B2 to Hajjar, et al., granted on March 26, 2013, at col. 27, lines 45-60.

[00164] In another embodiment effectively activating a cellular immune response for a neoplasia vaccine or immunogenic composition can be achieved by expressing the relevant neoantigens in a vaccine or immunogenic composition in a non-pathogenic microorganism. Well-known examples of such microorganisms are Mycobacterium bovis BCG, Salmonella and Pseudomona (See, U.S. Patent No. 6,991,797, hereby incorporated by reference in its entirety).

[00165] In another embodiment a Poxvirus is used in the neoplasia vaccine or immunogenic composition. These include orthopoxvirus, avipox, vaccinia, MVA, NYVAC, canarypox, ALVAC, fowlpox, TROVAC, etc. (see e.g., Verardiet al., Hum Vaccin Immunother. 2012 Jul;8(7):961-70; and Moss, Vaccine. 2013; 31(39): 4220–4222). Poxvirus expression vectors were described in 1982 and quickly became widely used for vaccine development as well as research in numerous fields. Advantages of the vectors include simple construction, ability to accommodate large amounts of foreign DNA and high expression levels.

[00166] Information concerning poxviruses that may be used in the practice of the invention, such as *Chordopoxvirinae* subfamily poxviruses (poxviruses of vertebrates), for instance, orthopoxviruses and avipoxviruses, e.g., vaccinia virus (e.g., Wyeth Strain, WR Strain (e.g., ATCC® VR-1354), Copenhagen Strain, NYVAC, NYVAC.1, NYVAC.2, MVA, MVA-BN), canarypox virus (e.g., Wheatley C93 Strain, ALVAC), fowlpox virus (e.g., FP9 Strain, Webster Strain, TROVAC), dovepox, pigeonpox, quailpox, and raccoon pox, *inter alia*, synthetic or non-naturally occurring recombinants thereof, uses thereof, and methods for making and using such recombinants may be found in scientific and patent literature, such as:

- US Patents Nos. 4,603,112, 4,769,330, 5,110,587, 5,174,993, 5,364,773, 5,762,938, 5,494,807, 5,766,597, 7,767,449, 6,780,407, 6,537,594, 6,265,189, 6,214,353, 6,130,066, 6,004,777, 5,990,091, 5,942,235, 5,833,975, 5,766,597, 5,756,101, 7,045,313, 6,780,417,

8,470,598, 8,372,622, 8,268,329, 8,268,325, 8,236,560, 8,163,293, 7,964,398, 7,964,396, 7,964,395, 7,939,086, 7,923,017, 7,897,156, 7,892,533, 7,628,980, 7,459,270, 7,445,924, 7,384,644, 7,335,364, 7,189,536, 7,097,842, 6,913,752, 6,761,893, 6,682,743, 5,770,212, 5,766,882, and 5,989,562, and

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each of which is incorporated herein by reference.

[00167] In another embodiment the vaccinia virus is used in the neoplasia vaccine or immunogenic composition to express a neoantigen. (Rolph et al., Recombinant viruses as vaccines and immunological tools. Curr Opin Immunol 9:517-524, 1997). The recombinant vaccinia virus is able to replicate within the cytoplasm of the infected host cell and the polypeptide of interest can therefore induce an immune response. Moreover, Poxviruses have been widely used as vaccine or immunogenic composition vectors because of their ability to target encoded antigens for processing by the major histocompatibility complex class I pathway by directly infecting immune cells, in particular antigen-presenting cells, but also due to their ability to self-adjuvant.

[00168] In another embodiment ALVAC is used as a vector in a neoplasia vaccine or immunogenic composition. ALVAC is a canarypox virus that can be modified to express foreign transgenes and has been used as a method for vaccination against both prokaryotic and eukaryotic antigens (Horig H, Lee DS, Conkright W, et al. Phase I clinical trial of a recombinant canarypoxvirus (ALVAC) vaccine expressing human carcinoembryonic antigen and the B7.1 co-stimulatory molecule. Cancer Immunol Immunother 2000;49:504–14; von Mehren M, Arlen P, Tsang KY, et al. Pilot study of a dual gene recombinant avipox vaccine containing both carcinoembryonic antigen (CEA) and B7.1 transgenes in patients with recurrent CEA-expressing adenocarcinomas. Clin Cancer Res 2000;6:2219–28; Musey L, Ding Y, Elizaga M, et al. HIV-1 vaccination administered intramuscularly can induce both systemic and mucosal T cell immunity

in HIV-1-uninfected individuals. J Immunol 2003;171:1094–101; Paoletti E. Applications of pox virus vectors to vaccination: an update. Proc Natl Acad Sci U S A 1996;93:11349–53; U.S. Patent No. 7,255,862). In a phase I clinical trial, an ALVAC virus expressing the tumor antigen CEA showed an excellent safety profile and resulted in increased CEA-specific T-cell responses in selected patients; objective clinical responses, however, were not observed (Marshall JL, Hawkins MJ, Tsang KY, et al. Phase I study in cancer patients of a replication-defective avipox recombinant vaccine that expresses human carcinoembryonic antigen. J Clin Oncol 1999;17:332–7).

[00169] In another embodiment a Modified Vaccinia Ankara (MVA) virus may be used as a viral vector for a neoantigen vaccine or immunogenic composition. MVA is a member of the Orthopoxvirus family and has been generated by about 570 serial passages on chicken embryo fibroblasts of the Ankara strain of Vaccinia virus (CVA) (for review see Mayr, A., et al., Infection 3, 6-14, 1975). As a consequence of these passages, the resulting MVA virus contains 31 kilobases less genomic information compared to CVA, and is highly host-cell restricted (Meyer, H. et al., J. Gen. Virol. 72, 1031-1038, 1991). MVA is characterized by its extreme attenuation, namely, by a diminished virulence or infectious ability, but still holds an excellent immunogenicity. When tested in a variety of animal models, MVA was proven to be avirulent, even in immuno-suppressed individuals. Moreover, MVA-BN®-HER2 is a candidate immunotherapy designed for the treatment of HER-2-positive breast cancer and is currently in clinical trials. (Mandl et al., Cancer Immunol Immunother. Jan 2012; 61(1): 19–29). Methods to make and use recombinant MVA has been described (e.g., see U.S. Patent Nos. 8,309,098 and 5,185,146 hereby incorporated in its entirety).

[00170] In another embodiment the modified Copenhagen strain of vaccinia virus, NYVAC and NYVAC variations are used as a vector (see U.S. Patent No. 7,255,862; PCT WO 95/30018; U.S. Pat. Nos. 5,364,773 and 5,494,807, hereby incorporated by reference in its entirety).

[00171] In one embodiment recombinant viral particles of the vaccine or immunogenic composition are administered to patients in need thereof. Dosages of expressed neoantigen can range from a few to a few hundred micrograms, e.g., 5 to 500 .mu.g. The vaccine or immunogenic composition can be administered in any suitable amount to achieve expression at these dosage levels. The viral particles can be administered to a patient in need thereof or transfected into cells in an amount of about at least $10^{3.5}$ pfu; thus, the viral particles are

preferably administered to a patient in need thereof or infected or transfected into cells in at least about 10^4 pfu to about 10^6 pfu; however, a patient in need thereof can be administered at least about 10^8 pfu such that a more preferred amount for administration can be at least about 10^7 pfu to about 10^9 pfu. Doses as to NYVAC are applicable as to ALVAC, MVA, MVA-BN, and avipoxes, such as canarypox and fowlpox.

Vaccine or Immunogenic Composition Adjuvant

[00172] Effective vaccine or immunogenic compositions advantageously include a strong adjuvant to initiate an immune response. As described herein, poly-ICLC, an agonist of TLR3 and the RNA helicase –domains of MDA5 and RIG3, has shown several desirable properties for a vaccine or immunogenic composition adjuvant. These properties include the induction of local and systemic activation of immune cells in vivo, production of stimulatory chemokines and cytokines, and stimulation of antigen-presentation by DCs. Furthermore, poly-ICLC can induce durable CD4+ and CD8+ responses in humans. Importantly, striking similarities in the upregulation of transcriptional and signal transduction pathways were seen in subjects vaccinated with poly-ICLC and in volunteers who had received the highly effective, replication-competent yellow fever vaccine. Furthermore, >90% of ovarian carcinoma patients immunized with poly-ICLC in combination with a NY-ESO-1 peptide vaccine (in addition to Montanide) showed induction of CD4+ and CD8+ T cell, as well as antibody responses to the peptide in a recent phase 1 study. At the same time, poly-ICLC has been extensively tested in more than 25 clinical trials to date and exhibited a relatively benign toxicity profile. In addition to a powerful and specific immunogen the neoantigen peptides may be combined with an adjuvant (e.g., poly-ICLC) or another anti-neoplastic agent. Without being bound by theory, these neoantigens are expected to bypass central thymic tolerance (thus allowing stronger anti-tumor T cell response), while reducing the potential for autoimmunity (e.g., by avoiding targeting of normal self-antigens). An effective immune response advantageously includes a strong adjuvant to activate the immune system (Speiser and Romero, Molecularly defined vaccines for cancer immunotherapy, and protective T cell immunity Seminars in Immunol 22:144 (2010)). For example, Toll-like receptors (TLRs) have emerged as powerful sensors of microbial and viral pathogen "danger signals", effectively inducing the innate immune system, and in turn, the adaptive immune system (Bhardwaj and Gnjatic, TLR AGONISTS: Are They Good Adjuvants?

Cancer J. 16:382-391 (2010)). Among the TLR agonists, poly-ICLC (a synthetic double-stranded RNA mimic) is one of the most potent activators of myeloid-derived dendritic cells. In a human volunteer study, poly-ICLC has been shown to be safe and to induce a gene expression profile in peripheral blood cells comparable to that induced by one of the most potent live attenuated viral vaccines, the yellow fever vaccine YF-17D (Caskey et al, Synthetic double-stranded RNA induces innate immune responses similar to a live viral vaccine in humans J Exp Med 208:2357 (2011)). In a preferred embodiment Hiltonol®, a GMP preparation of poly-ICLC prepared by Oncovir, Inc, is utilized as the adjuvant. In other embodiments, other adjuvants described herein are envisioned. For instance oil-in-water, water-in-oil or multiphasic W/O/W; see, e.g., US 7,608,279 and Aucouturier et al, Vaccine 19 (2001), 2666-2672, and documents cited therein.

Indications

[00173] Examples of cancers and cancer conditions that can be treated with the therapy of this document include, but are not limited to a patient in need thereof that has been diagnosed as having cancer, or at risk of developing cancer. The subject may have a solid tumor such as breast, ovarian, prostate, lung, kidney, gastric, colon, testicular, head and neck, pancreas, brain, melanoma, and other tumors of tissue organs and hematological tumors, such as lymphomas and leukemias, including acute myelogenous leukemia, chronic myelogenous leukemia, chronic lymphocytic leukemia, T cell lymphocytic leukemia, and B cell lymphomas, tumors of the brain and central nervous system (e.g., tumors of the meninges, brain, spinal cord, cranial nerves and other parts of the CNS, such as glioblastomas or medulla blastomas); head and/or neck cancer, breast tumors, tumors of the circulatory system (e.g., heart, mediastinum and pleura, and other intrathoracic organs, vascular tumors, and tumor-associated vascular tissue); tumors of the blood and lymphatic system (e.g., Hodgkin's disease, Non-Hodgkin's disease lymphoma, Burkitt's lymphoma, AIDS-related lymphomas, malignant immunoproliferative diseases, multiple myeloma, and malignant plasma cell neoplasms, lymphoid leukemia, myeloid leukemia, acute or chronic lymphocytic leukemia, monocytic leukemia, other leukemias of specific cell type, leukemia of unspecified cell type, unspecified malignant neoplasms of lymphoid, hematopoietic and related tissues, such as diffuse large cell lymphoma, T-cell lymphoma or cutaneous T-cell lymphoma); tumors of the excretory system (e.g., kidney, renal pelvis, ureter, bladder, and other

urinary organs); tumors of the gastrointestinal tract (e.g., esophagus, stomach, small intestine, colon, colorectal, rectosigmoid junction, rectum, anus, and anal canal); tumors involving the liver and intrahepatic bile ducts, gall bladder, and other parts of the biliary tract, pancreas, and other digestive organs; tumors of the oral cavity (e.g., lip, tongue, gum, floor of mouth, palate, parotid gland, salivary glands, tonsil, oropharynx, nasopharynx, puriform sinus, hypopharynx, and other sites of the oral cavity); tumors of the reproductive system (e.g., vulva, vagina, Cervix uteri, uterus, ovary, and other sites associated with female genital organs, placenta, penis, prostate, testis, and other sites associated with male genital organs); tumors of the respiratory tract (e.g., nasal cavity, middle ear, accessory sinuses, larynx, trachea, bronchus and lung, such as small cell lung cancer and non-small cell lung cancer); tumors of the skeletal system (e.g., bone and articular cartilage of limbs, bone articular cartilage and other sites); tumors of the skin (e.g., malignant melanoma of the skin, non-melanoma skin cancer, basal cell carcinoma of skin, squamous cell carcinoma of skin, mesothelioma, Kaposi's sarcoma); and tumors involving other tissues including peripheral nerves and autonomic nervous system, connective and soft tissue, retroperitoneoum and peritoneum, eye, thyroid, adrenal gland, and other endocrine glands and related structures, secondary and unspecified malignant neoplasms of lymph nodes, secondary malignant neoplasm of respiratory and digestive systems and secondary malignant neoplasm of other sites. Thus the population of subjects described herein may be suffering from one of the above cancer types. In other embodiments, the population of subjects may be all subjects suffering from solid tumors, or all subjects suffering from liquid tumors.

[00174] Of special interest is the treatment of Non-Hodgkin's Lymphoma (NHL), clear cell Renal Cell Carcinoma (ccRCC), metastatic melanoma, sarcoma, leukemia or a cancer of the bladder, colon, brain, breast, head and neck, endometrium, lung, ovary, pancreas or prostate. In certain embodiments, the melanoma is high risk melanoma.

[00175] Cancers that can be treated using the therapy described herein may include among others cases which are refractory to treatment with other chemotherapeutics. The term "refractory, as used herein refers to a cancer (and/or metastases thereof), which shows no or only weak antiproliferative response (e.g., no or only weak inhibition of tumor growth) after treatment with another chemotherapeutic agent. These are cancers that cannot be treated satisfactorily with other chemotherapeutics. Refractory cancers encompass not only (i) cancers where one or more chemotherapeutics have already failed during treatment of a patient, but also (ii) cancers that can

be shown to be refractory by other means, e.g., biopsy and culture in the presence of chemotherapeutics.

[00176] The therapy described herein is also applicable to the treatment of patients in need thereof who have not been previously treated.

[00177] The therapy described herein is also applicable where the subject has no detectable neoplasia but is at high risk for disease recurrence.

[00178] Also of special interest is the treatment of patients in need thereof who have undergone Autologous Hematopoietic Stem Cell Transplant (AHSCT), and in particular patients who demonstrate residual disease after undergoing AHSCT. The post-AHSCT setting is characterized by a low volume of residual disease, the infusion of immune cells to a situation of homeostatic expansion, and the absence of any standard relapse-delaying therapy. These features provide a unique opportunity to use the claimed neoplastic vaccine or immunogenic composition compositions to delay disease relapse.

Pharmaceutical Compositions/Methods of Delivery

[00179] The present invention is also directed to pharmaceutical compositions comprising an effective amount of one or more neoantigenic peptides as described herein (including a pharmaceutically acceptable salt, thereof), optionally in combination with a pharmaceutically acceptable carrier, excipient or additive.

[00180] When administered as a combination, the therapeutic agents (i.e. the neoantigenic peptides) can be formulated as separate compositions that are given at the same time or different times, or the therapeutic agents can be given as a single composition.

[00181] The compositions may be administered once daily, twice daily, once every two days, once every three days, once every four days, once every five days, once every six days, once every seven days, once every two weeks, once every three weeks, once every four weeks, once every two months, once every six months, or once per year. The dosing interval can be adjusted according to the needs of individual patients. For longer intervals of administration, extended release or depot formulations can be used.

[00182] The compositions of the invention can be used to treat diseases and disease conditions that are acute, and may also be used for treatment of chronic conditions. In particular, the compositions of the invention are used in methods to treat or prevent a neoplasia. In certain

embodiments, the compounds of the invention are administered for time periods exceeding two weeks, three weeks, one month, two months, three months, four months, five months, six months, one year, two years, three years, four years, or five years, ten years, or fifteen years; or for example, any time period range in days, months or years in which the low end of the range is any time period between 14 days and 15 years and the upper end of the range is between 15 days and 20 years (e.g., 4 weeks and 15 years, 6 months and 20 years). In some cases, it may be advantageous for the compounds of the invention to be administered for the remainder of the patient's life. In preferred embodiments, the patient is monitored to check the progression of the disease or disorder, and the dose is adjusted accordingly. In preferred embodiments, treatment according to the invention is effective for at least two weeks, three weeks, one month, two months, three months, four months, five months, six months, one year, two years, three years, four years, or five years, ten years, fifteen years, twenty years, or for the remainder of the subject's life.

[00183] Surgical resection uses surgery to remove abnormal tissue in cancer, such as mediastinal, neurogenic, or germ cell tumors, or thymoma. In certain embodiments, administration of the composition is initiated following tumor resection. In other embodiments, administration of the neoplasia vaccine or immunogenic composition is initiated 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15 or more weeks after tumor resection. Preferably, administration of the neoplasia vaccine or immunogenic composition is initiated 4, 5, 6, 7, 8, 9, 10, 11 or 12 weeks after tumor resection.

[00184] Prime/ boost regimens refer to the successive administrations of a vaccine or immunogenic or immunological compositions. In certain embodiments, administration of the neoplasia vaccine or immunogenic composition is in a prime/ boost dosing regimen, for example administration of the neoplasia vaccine or immunogenic composition at weeks 1, 2, 3 or 4 as a prime and administration of the neoplasia vaccine or immunogenic composition is at months 2, 3 or 4 as a boost. In another embodiment heterologous prime-boost strategies are used to ellicit a greater cytotoxic T-cell response (see Schneider et al., Induction of CD8+ T cells using heterologous prime-boost immunisation strategies, Immunological Reviews Volume 170, Issue 1, pages 29–38, August 1999). In another embodiment DNA encoding neoantigens is used to prime followed by a protein boost. In another embodiment protein is used to prime followed by boosting with a virus encoding the neoantigen. In another embodiment a virus encoding the

neoantigen is used to prime and another virus is used to boost. In another embodiment protein is used to prime and DNA is used to boost. In a preferred embodiment a DNA vaccine or immunogenic composition is used to prime a T-cell response and a recombinant viral vaccine or immunogenic composition is used to boost the response. In another preferred embodiment a viral vaccine or immunogenic composition is coadministered with a protein or DNA vaccine or immunogenic composition to act as an adjuvant for the protein or DNA vaccine or immunogenic composition. The patient can then be boosted with either the viral vaccine or immunogenic composition, protein, or DNA vaccine or immunogenic composition (see Hutchings et al., Combination of protein and viral vaccines induces potent cellular and humoral immune responses and enhanced protection from murine malaria challenge. Infect Immun. 2007 Dec;75(12):5819-26. Epub 2007 Oct 1).

[00185] The pharmaceutical compositions can be processed in accordance with conventional methods of pharmacy to produce medicinal agents for administration to patients in need thereof, including humans and other mammals.

[00186] Modifications of the neoantigenic peptides can affect the solubility, bioavailability and rate of metabolism of the peptides, thus providing control over the delivery of the active species. Solubility can be assessed by preparing the neoantigenic peptide and testing according to known methods well within the routine practitioner's skill in the art.

[00187] In certain embodiments of the pharmaceutical composition the pharmaceutically acceptable carrier comprises water. In certain embodiments, the pharmaceutically acceptable carrier further comprises dextrose. In certain embodiments, the pharmaceutically acceptable carrier further comprises dimethylsulfoxide. In certain embodiments, the pharmaceutical composition further comprises an immunomodulator or adjuvant. In certain embodiments, the immunodulator or adjuvant is selected from the group consisting of poly-ICLC, STING agonist, 1018 ISS, aluminum salts, Amplivax, AS15, BCG, CP-870,893, CpG7909, CyaA, dSLIM, GM-CSF, IC30, IC31, Imiquimod, ImuFact IMP321, IS Patch, ISS, ISCOMATRIX, JuvImmune, LipoVac, MF59, monophosphoryl lipid A, Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, OK-432, OM-174, OM-197-MP-EC, ONTAK, PEPTEL, vector system, PLGA microparticles, resiquimod, SRL172, Virosomes and other Virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, and Aquila's QS21 stimulon. In certain embodiments, the immunomodulator or adjuvant comprises poly-ICLC.

[00188] Xanthenone derivatives such as, for example, Vadimezan or AsA404 (also known as 5,6-dimethylaxanthenone-4-acetic acid (DMXAA)), may also be used as adjuvants according to embodiments of the invention. Alternatively, such derivatives may also be administered in parallel to the vaccine or immunogenic composition of the invention, for example via systemic or intratumoral delivery, to stimulate immunity at the tumor site. Without being bound by theory, it is believed that such xanthenone derivatives act by stimulating interferon (IFN) production via the stimulator of IFN gene ISTING) receptor (see e.g., Conlon et al. (2013) Mouse, but not Human STING, Binds and Signals in Response to the Vascular Disrupting Agent 5,6-Dimethylxanthenone-4-Acetic Acid, Journal of Immunology, 190:5216-25 and Kim et al. (2013) Anticancer Flavonoids are Mouse-Selective STING Agonists, 8:1396-1401).

[00189] The vaccine or immunological composition may also include an adjuvant compound chosen from the acrylic or methacrylic polymers and the copolymers of maleic anhydride and an alkenyl derivative. It is in particular a polymer of acrylic or methacrylic acid cross-linked with a polyalkenyl ether of a sugar or polyalcohol (carbomer), in particular cross-linked with an allyl sucrose or with allylpentaerythritol. It may also be a copolymer of maleic anhydride and ethylene cross-linked, for example, with divinyl ether (see U.S. Patent No. 6,713,068 hereby incorporated by reference in its entirety)..

[00190] In certain embodiments, the pH modifier can stabilize the adjuvant or immunomodulator as described herein.

[00191] In certain embodiments, a pharmaceutical composition comprises: one to five peptides, dimethylsulfoxide (DMSO), dextrose, water, succinate, poly I: poly C, poly-L-lysine, carboxymethylcellulose, and chloride. In certain embodiments, each of the one to five peptides is present at a concentration of 300 μg/ml. In certain embodiments, the pharmaceutical composition comprises ≤ 3% DMSO by volume. In certain embodiments, the pharmaceutical composition comprises 3.6 – 3.7 % dextrose in water. In certain embodiments, the pharmaceutical composition comprises 3.6 – 3.7 mM succinate (e.g., as sodium succinate) or a salt thereof. In certain embodiments, the pharmaceutical composition comprises 0.5 mg/ml poly I: poly C. In certain embodiments, the pharmaceutical composition comprises 0.375 mg/ml poly-L-Lysine. In certain embodiments, the pharmaceutical composition comprises 1.25 mg/ml sodium carboxymethylcellulose. In certain embodiments, the pharmaceutical composition comprises 0.225% sodium chloride.

[00192] Pharmaceutical compositions comprise the herein-described tumor specific neoantigenic peptides in a therapeutically effective amount for treating diseases and conditions (e.g., a neoplasia/tumor), which have been described herein, optionally in combination with a pharmaceutically acceptable additive, carrier and/or excipient. One of ordinary skill in the art from this disclosure and the knowledge in the art will recognize that a therapeutically effective amount of one of more compounds according to the present invention may vary with the condition to be treated, its severity, the treatment regimen to be employed, the pharmacokinetics of the agent used, as well as the patient (animal or human) treated.

[00193] To prepare the pharmaceutical compositions according to the present invention, a therapeutically effective amount of one or more of the compounds according to the present invention is preferably intimately admixed with a pharmaceutically acceptable carrier according to conventional pharmaceutical compounding techniques to produce a dose. A carrier may take a wide variety of forms depending on the form of preparation desired for administration, e.g., ocular, oral, topical or parenteral, including gels, creams ointments, lotions and time released implantable preparations, among numerous others. In preparing pharmaceutical compositions in oral dosage form, any of the usual pharmaceutical media may be used. Thus, for liquid oral preparations such as suspensions, elixirs and solutions, suitable carriers and additives including water, glycols, oils, alcohols, flavoring agents, preservatives, coloring agents and the like may be used. For solid oral preparations such as powders, tablets, capsules, and for solid preparations such as suppositories, suitable carriers and additives including starches, sugar carriers, such as dextrose, mannitol, lactose and related carriers, diluents, granulating agents, lubricants, binders, disintegrating agents and the like may be used. If desired, the tablets or capsules may be enteric-coated or sustained release by standard techniques.

[00194] The active compound is included in the pharmaceutically acceptable carrier or diluent in an amount sufficient to deliver to a patient a therapeutically effective amount for the desired indication, without causing serious toxic effects in the patient treated.

[00195] Oral compositions generally include an inert diluent or an edible carrier. They may be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound or its prodrug derivative can be incorporated with excipients and used in the form of tablets, troches, or capsules. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition.

[00196] The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a dispersing agent such as alginic acid or corn starch; a lubricant such as magnesium stearate; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring. When the dosage unit form is a capsule, it can contain, in addition to material herein discussed, a liquid carrier such as a fatty oil. In addition, dosage unit forms can contain various other materials which modify the physical form of the dosage unit, for example, coatings of sugar, shellac, or enteric agents.

[00197] Formulations of the present invention suitable for oral administration may be presented as discrete units such as capsules, cachets or tablets each containing a predetermined amount of the active ingredient; as a powder or granules; as a solution or a suspension in an aqueous liquid or a non-aqueous liquid; or as an oil-in-water liquid emulsion or a water-in-oil emulsion and as a bolus, etc.

[00198] A tablet may be made by compression or molding, optionally with one or more accessory ingredients. Compressed tablets may be prepared by compressing in a suitable machine the active ingredient in a free-flowing form such as a powder or granules, optionally mixed with a binder, lubricant, inert diluent, preservative, surface-active or dispersing agent. Molded tablets may be made by molding in a suitable machine a mixture of the powdered compound moistened with an inert liquid diluent. The tablets optionally may be coated or scored and may be formulated so as to provide slow or controlled release of the active ingredient therein.

[00199] Methods of formulating such slow or controlled release compositions of pharmaceutically active ingredients, are known in the art and described in several issued US Patents, some of which include, but are not limited to, US Patent Nos. 3,870,790; 4,226,859; 4,369,172; 4,842,866 and 5,705,190, the disclosures of which are incorporated herein by reference in their entireties. Coatings can be used for delivery of compounds to the intestine (see, e.g., U.S. Patent Nos. 6,638,534, 5,541,171, 5,217,720, and 6,569,457, and references cited therein).

[00200] The active compound or pharmaceutically acceptable salt thereof may also be administered as a component of an elixir, suspension, syrup, wafer, chewing gum or the like. A

syrup may contain, in addition to the active compounds, sucrose or fructose as a sweetening agent and certain preservatives, dyes and colorings and flavors.

[00201] Solutions or suspensions used for ocular, parenteral, intradermal, subcutaneous, or topical application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates; and agents for the adjustment of tonicity such as sodium chloride or dextrose.

[00202] In certain embodiments, the pharmaceutically acceptable carrier is an aqueous solvent, i.e., a solvent comprising water, optionally with additional co-solvents. Exemplary pharmaceutically acceptable carriers include water, buffer solutions in water (such as phosphate-buffered saline (PBS), and 5% dextrose in water (D5W). In certain embodiments, the aqueous solvent further comprises dimethyl sulfoxide (DMSO), e.g., in an amount of about 1-4%, or 1-3%. In certain embodiments, the pharmaceutically acceptable carrier is isotonic (i.e., has substantially the same osmotic pressure as a body fluid such as plasma).

[00203] In one embodiment, the active compounds are prepared with carriers that protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, polylactic acid, and polylactic-co-glycolic acid (PLGA). Methods for preparation of such formulations are within the ambit of the skilled artisan in view of this disclosure and the knowledge in the art.

[00204] A skilled artisan from this disclosure and the knowledge in the art recognizes that in addition to tablets, other dosage forms can be formulated to provide slow or controlled release of the active ingredient. Such dosage forms include, but are not limited to, capsules, granulations and gel-caps.

[00205] Liposomal suspensions may also be pharmaceutically acceptable carriers. These may be prepared according to methods known to those skilled in the art. For example, liposomal formulations may be prepared by dissolving appropriate lipid(s) in an inorganic solvent that is then evaporated, leaving behind a thin film of dried lipid on the surface of the container. An

aqueous solution of the active compound are then introduced into the container. The container is then swirled by hand to free lipid material from the sides of the container and to disperse lipid aggregates, thereby forming the liposomal suspension. Other methods of preparation well known by those of ordinary skill may also be used in this aspect of the present invention.

[00206] The formulations may conveniently be presented in unit dosage form and may be prepared by conventional pharmaceutical techniques. Such techniques include the step of bringing into association the active ingredient and the pharmaceutical carrier(s) or excipient(s). In general, the formulations are prepared by uniformly and intimately bringing into association the active ingredient with liquid carriers or finely divided solid carriers or both, and then, if necessary, shaping the product.

[00207] Formulations and compositions suitable for topical administration in the mouth include lozenges comprising the ingredients in a flavored basis, usually sucrose and acacia or tragacanth; pastilles comprising the active ingredient in an inert basis such as gelatin and glycerin, or sucrose and acacia; and mouthwashes comprising the ingredient to be administered in a suitable liquid carrier.

[00208] Formulations suitable for topical administration to the skin may be presented as ointments, creams, gels and pastes comprising the ingredient to be administered in a pharmaceutical acceptable carrier. A preferred topical delivery system is a transdermal patch containing the ingredient to be administered.

[00209] Formulations for rectal administration may be presented as a suppository with a suitable base comprising, for example, cocoa butter or a salicylate.

[00210] Formulations suitable for nasal administration, wherein the carrier is a solid, include a coarse powder having a particle size, for example, in the range of 20 to 500 microns which is administered in the manner in which snuff is administered, i.e., by rapid inhalation through the nasal passage from a container of the powder held close up to the nose. Suitable formulations, wherein the carrier is a liquid, for administration, as for example, a nasal spray or as nasal drops, include aqueous or oily solutions of the active ingredient.

[00211] Formulations suitable for vaginal administration may be presented as pessaries, tampons, creams, gels, pastes, foams or spray formulations containing in addition to the active ingredient such carriers as are known in the art to be appropriate.

[00212] The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic. If administered intravenously, preferred carriers include, for example, physiological saline or phosphate buffered saline (PBS).

[00213] For parenteral formulations, the carrier usually comprises sterile water or aqueous sodium chloride solution, though other ingredients including those which aid dispersion may be included. Of course, where sterile water is to be used and maintained as sterile, the compositions and carriers are also sterilized. Injectable suspensions may also be prepared, in which case appropriate liquid carriers, suspending agents and the like may be employed.

[00214] Formulations suitable for parenteral administration include aqueous and non-aqueous sterile injection solutions which may contain antioxidants, buffers, bacteriostats and solutes which render the formulation isotonic with the blood of the intended recipient; and aqueous and non-aqueous sterile suspensions which may include suspending agents and thickening agents. The formulations may be presented in unit-dose or multi-dose containers, for example, sealed ampules and vials, and may be stored in a freeze-dried (lyophilized) condition requiring only the addition of the sterile liquid carrier, for example, water for injections, immediately prior to use. Extemporaneous injection solutions and suspensions may be prepared from sterile powders, granules and tablets of the kind previously described.

[00215] Administration of the active compound may range from continuous (intravenous drip) to several oral administrations per day (for example, Q.I.D.) and may include oral, topical, eye or ocular, parenteral, intramuscular, intravenous, sub-cutaneous, transdermal (which may include a penetration enhancement agent), buccal and suppository administration, among other routes of administration, including through an eye or ocular route.

[00216] The neoplasia vaccine or immunogenic composition, and any additional agents, may be administered by injection, orally, parenterally, by inhalation spray, rectally, vaginally, or topically in dosage unit formulations containing conventional pharmaceutically acceptable carriers, adjuvants, and vehicles. The term parenteral as used herein includes, into a lymph node or nodes, subcutaneous, intravenous, intramuscular, intrasternal, infusion techniques, intraperitoneally, eye or ocular, intravitreal, intrabuccal, transdermal, intranasal, into the brain, including intracranial and intradural, into the joints, including ankles, knees, hips, shoulders, elbows, wrists, directly into tumors, and the like, and in suppository form.

[00217] In certain embodiments, the vaccine or immunogenic composition is administered intravenously or subcutaneously. Various techniques can be used for providing the subject compositions at the site of interest, such as injection, use of catheters, trocars, projectiles, pluronic gel, stents, sustained drug release polymers or other device which provides for internal access. Where an organ or tissue is accessible because of removal from the patient, such organ or tissue may be bathed in a medium containing the subject compositions, the subject compositions may be painted onto the organ, or may be applied in any convenient way.

[00218] The tumor specific neoantigenic peptides may be administered through a device suitable for the controlled and sustained release of a composition effective in obtaining a desired local or systemic physiological or pharmacological effect. The method includes positioning the sustained released drug delivery system at an area wherein release of the agent is desired and allowing the agent to pass through the device to the desired area of treatment.

[00219] The tumor specific neoantigenic peptides may be utilized in combination with at least one known other therapeutic agent, or a pharmaceutically acceptable salt of said agent. Examples of known therapeutic agents which can be used for combination therapy include, but are not limited to, corticosteroids (e.g., cortisone, prednisone, dexamethasone), non-steroidal anti-inflammatory drugs (NSAIDS) (e.g., ibuprofen, celecoxib, aspirin, indomethicin, naproxen), alkylating agents such as busulfan, cis-platin, mitomycin C, and carboplatin; antimitotic agents such as colchicine, vinblastine, paclitaxel, and docetaxel; topo I inhibitors such as camptothecin and topotecan; topo II inhibitors such as doxorubicin and etoposide; and/or RNA/DNA antimetabolites such as 5-azacytidine, 5-fluorouracil and methotrexate; DNA antimetabolites such as 5-fluoro-2'-deoxy-uridine, ara-C, hydroxyurea and thioguanine; antibodies such as HERCEPTIN and RITUXAN.

[00220] It should be understood that in addition to the ingredients particularly mentioned herein, the formulations of the present invention may include other agents conventional in the art having regard to the type of formulation in question, for example, those suitable for oral administration may include flavoring agents.

[00221] Pharmaceutically acceptable salt forms may be the preferred chemical form of compounds according to the present invention for inclusion in pharmaceutical compositions according to the present invention.

[00222] The present compounds or their derivatives, including prodrug forms of these agents, can be provided in the form of pharmaceutically acceptable salts. As used herein, the term pharmaceutically acceptable salts or complexes refers to appropriate salts or complexes of the active compounds according to the present invention which retain the desired biological activity of the parent compound and exhibit limited toxicological effects to normal cells. Nonlimiting examples of such salts are (a) acid addition salts formed with inorganic acids (for example, hydrochloric acid, hydrobromic acid, sulfuric acid, phosphoric acid, nitric acid, and the like), and salts formed with organic acids such as acetic acid, oxalic acid, tartaric acid, succinic acid, malic acid, ascorbic acid, benzoic acid, tannic acid, pamoic acid, alginic acid, and polyglutamic acid, among others; (b) base addition salts formed with metal cations such as zinc, calcium, sodium, potassium, and the like, among numerous others.

[00223] The compounds herein are commercially available or can be synthesized. As can be appreciated by the skilled artisan, further methods of synthesizing the compounds of the formulae herein is evident to those of ordinary skill in the art. Additionally, the various synthetic steps may be performed in an alternate sequence or order to give the desired compounds. Synthetic chemistry transformations and protecting group methodologies (protection and deprotection) useful in synthesizing the compounds described herein are known in the art and include, for example, those such as described in R. Larock, Comprehensive Organic Transformations, 2nd. Ed., Wiley-VCH Publishers (1999); T.W. Greene and P.G.M. Wuts, Protective Groups in Organic Synthesis, 3rd. Ed., John Wiley and Sons (1999); L. Fieser and M. Fieser, Fieser and Fieser's Reagents for Organic Synthesis, John Wiley and Sons (1999); and L. Paquette, ed., Encyclopedia of Reagents for Organic Synthesis, John Wiley and Sons (1995), and subsequent editions thereof.

[00224] The additional agents that may be included with the tumor specific neo-antigenic peptides of this invention may contain one or more asymmetric centers and thus occur as racemates and racemic mixtures, single enantiomers, individual diastereomers and diastereomeric mixtures. All such isomeric forms of these compounds are expressly included in the present invention. The compounds of this invention may also be represented in multiple tautomeric forms, in such instances, the invention expressly includes all tautomeric forms of the compounds described herein (e.g., alkylation of a ring system may result in alkylation at multiple sites, the invention expressly includes all such reaction products). All such isomeric forms of

such compounds are expressly included in the present invention. All crystal forms of the compounds described herein are expressly included in the present invention.

Dosage

[00225] When the agents described herein are administered as pharmaceuticals to humans or animals, they can be given per se or as a pharmaceutical composition containing active ingredient in combination with a pharmaceutically acceptable carrier, excipient, or diluent.

[00226] Actual dosage levels and time course of administration of the active ingredients in the pharmaceutical compositions of the invention can be varied so as to obtain an amount of the active ingredient which is effective to achieve the desired therapeutic response for a particular patient, composition, and mode of administration, without being toxic to the patient. Generally, agents or pharmaceutical compositions of the invention are administered in an amount sufficient to reduce or eliminate symptoms associated with neoplasia, e.g. cancer or tumors.

[00227] A preferred dose of an agent is the maximum that a patient can tolerate and not develop serious or unacceptable side effects. Exemplary dose ranges include 0.01 mg to 250 mg per day, 0.01 mg to 100 mg per day, 1 mg to 100 mg per day, 10 mg to 100 mg per day, 1 mg to 10 mg per day, and 0.01 mg to 10 mg per day. A preferred dose of an agent is the maximum that a patient can tolerate and not develop serious or unacceptable side effects. In embodiments, the agent is administered at a concentration of about 10 micrograms to about 100 mg per kilogram of body weight per day, about 0.1 to about 10 mg/kg per day, or about 1.0 mg to about 10 mg/kg of body weight per day.

[00228] In embodiments, the pharmaceutical composition comprises an agent in an amount ranging between 1 and 10 mg, such as 1, 2, 3, 4, 5, 6, 7, 8, 9, or 10 mg.

[00229] In embodiments, the therapeutically effective dosage produces a serum concentration of an agent of from about 0.1 ng/ml to about 50-100 mg/ml. The pharmaceutical compositions 5 typically should provide a dosage of from about 0.001 mg to about 2000 mg of compound per kilogram of body weight per day. For example, dosages for systemic administration to a human patient can range from 1-10 mglkg, 20-80 mglkg, 5-50 mg/kg, 75-150 mg/kg, 100-500 mg/kg, 250-750 mg/kg, 500-1000 mg/kg, 1-10 mg/kg, 5-50 mg/kg, 25-75 mg/kg, 50-100 mg/kg, 100-250 mg/kg, 50-100 mg/kg, 250-500 mg/kg, 500-750 mg/kg, 750-1000 mg/kg, 1000-1500 mg/kg, 10 1500-2000 mg/kg, 5 mg/kg, 20 mg/kg, 50 mg/kg, 100 mg/kg, 500 mg/kg, 1000 mg/kg, 1500

mg/kg, or 2000 mg/kg. Pharmaceutical dosage unit forms are prepared to provide from about 1 mg to about 5000 mg, for example from about 100 to about 2500 mg of the compound or a combination of essential ingredients per dosage unit form.

[00230] In embodiments, about 50 nM to about 1μM of an agent is administered to a subject. In related embodiments, about 50-100 nM, 50-250 nM, 100-500 nM, 250-500 nM, 250-750 nM, 500-750 nM, 500 nM to 1μM, or 750 nM to 1μM of an agent is administered to a subject.

[00231] Determination of an effective amount is well within the capability of those skilled in the art, especially in light of the detailed disclosure provided herein. Generally, an efficacious or effective amount of an agent is determined by first administering a low dose of the agent(s) and then incrementally increasing the administered dose or dosages until a desired effect (e.g., reduce or eliminate symptoms associated with viral infection or autoimmune disease) is observed in the treated subject, with minimal or acceptable toxic side effects. Applicable methods for determining an appropriate dose and dosing schedule for administration of a pharmaceutical composition of the present invention are described, for example, in Goodman and Gilman's The Pharmacological Basis of Therapeutics, Goodman et al., eds., 11th Edition, McGraw-Hill 2005, and Remington: The Science and Practice of Pharmacy, 20th and 21st Editions, Gennaro and University of the Sciences in Philadelphia, Eds., Lippencott Williams & Wilkins (2003 and 2005), each of which is hereby incorporated by reference.

[00232] Preferred unit dosage formulations are those containing a daily dose or unit, daily sub-dose, as herein discussed, or an appropriate fraction thereof, of the administered ingredient.

[00233] The dosage regimen for treating a disorder or a disease with the tumor specific neoantigenic peptides of this invention and/or compositions of this invention is based on a variety of factors, including the type of disease, the age, weight, sex, medical condition of the patient, the severity of the condition, the route of administration, and the particular compound employed. Thus, the dosage regimen may vary widely, but can be determined routinely using standard methods.

[00234] The amounts and dosage regimens administered to a subject can depend on a number of factors, such as the mode of administration, the nature of the condition being treated, the body weight of the subject being treated and the judgment of the prescribing physician; all such factors being within the ambit of the skilled artisan from this disclosure and the knowledge in the art.

[00235] The amount of compound included within therapeutically active formulations according to the present invention is an effective amount for treating the disease or condition. In general, a therapeutically effective amount of the present preferred compound in dosage form usually ranges from slightly less than about 0.025 mg/kg/day to about 2.5 g/kg/day, preferably about 0.1 mg/kg/day to about 100 mg/kg/day of the patient or considerably more, depending upon the compound used, the condition or infection treated and the route of administration, although exceptions to this dosage range may be contemplated by the present invention. In its most preferred form, compounds according to the present invention are administered in amounts ranging from about 1 mg/kg/day to about 100 mg/kg/day. The dosage of the compound can depend on the condition being treated, the particular compound, and other clinical factors such as weight and condition of the patient and the route of administration of the compound. It is to be understood that the present invention has application for both human and veterinary use.

[00236] For oral administration to humans, a dosage of between approximately 0.1 to 100 mg/kg/day, preferably between approximately 1 and 100 mg/kg/day, is generally sufficient.

[00237] Where drug delivery is systemic rather than topical, this dosage range generally produces effective blood level concentrations of active compound ranging from less than about 0.04 to about 400 micrograms/cc or more of blood in the patient. The compound is conveniently administered in any suitable unit dosage form, including but not limited to one containing 0.001 to 3000 mg, preferably 0.05 to 500 mg of active ingredient per unit dosage form. An oral dosage of 10-250 mg is usually convenient.

[00238] According to certain exemplary embodiments, the vaccine or immunogenic composition is administered at a dose of about 10 μg to 1 mg per neoantigenic peptide. According to certain exemplary embodiments, the vaccine or immunogenic composition is administered at an average weekly dose level of about 10 μg to 2000 μg per neoantigenic peptide.

[00239] The concentration of active compound in the drug composition will depend on absorption, distribution, inactivation, and excretion rates of the drug as well as other factors known to those of skill in the art. It is to be noted that dosage values will also vary with the severity of the condition to be alleviated. It is to be further understood that for any particular subject, specific dosage regimens should be adjusted over time according to the individual need and the professional judgment of the person administering or supervising the administration of

the compositions, and that the concentration ranges set forth herein are exemplary only and are not intended to limit the scope or practice of the claimed composition. The active ingredient may be administered at once, or may be divided into a number of smaller doses to be administered at varying intervals of time.

[00240] The invention provides for pharmaceutical compositions containing at least one tumor specific neoantigen described herein. In embodiments, the pharmaceutical compositions contain a pharmaceutically acceptable carrier, excipient, or diluent, which includes any pharmaceutical agent that does not itself induce the production of an immune response harmful to a subject receiving the composition, and which may be administered without undue toxicity. As used herein, the term "pharmaceutically acceptable" means being approved by a regulatory agency of the Federal or a state government or listed in the U.S. Pharmacopia, European Pharmacopia or other generally recognized pharmacopia for use in mammals, and more particularly in humans. These compositions can be useful for treating and/or preventing viral infection and/or autoimmune disease.

[00241] A thorough discussion of pharmaceutically acceptable carriers, diluents, and other excipients is presented in Remington's Pharmaceutical Sciences (17th ed., Mack Publishing Company) and Remington: The Science and Practice of Pharmacy (21st ed., Lippincott Williams & Wilkins), which are hereby incorporated by reference. The formulation of the pharmaceutical composition should suit the mode of administration. In embodiments, the pharmaceutical composition is suitable for administration to humans, and can be sterile, non-particulate and/or non-pyrogenic.

[00242] Pharmaceutically acceptable carriers, excipients, or diluents include, but are not limited, to saline, buffered saline, dextrose, water, glycerol, ethanol, sterile isotonic aqueous buffer, and combinations thereof.

[00243] Wetting agents, emulsifiers and lubricants, such as sodium lauryl sulfate and magnesium stearate, as well as coloring agents, release agents, coating agents, sweetening, flavoring and perfuming agents, preservatives, and antioxidants can also be present in the compositions.

[00244] Examples of pharmaceutically-acceptable antioxidants include, but are not limited to: (1) water soluble antioxidants, such as ascorbic acid, cysteine hydrochloride, sodium bisulfate, sodium metabisulfite, sodium sulfite and the like; (2) oil-soluble antioxidants, such as ascorbyl

palmitate, butylated hydroxyanisole (BHA), butylated hydroxytoluene (BHT), lecithin, propyl gallate, alpha-tocopherol, and the like; and (3) metal chelating agents, such as citric acid, ethylenediamine tetraacetic acid (EDTA), sorbitol, tartaric acid, phosphoric acid, and the like.

[00245] In embodiments, the pharmaceutical composition is provided in a solid form, such as a lyophilized powder suitable for reconstitution, a liquid solution, suspension, emulsion, tablet, pill, capsule, sustained release formulation, or powder.

[00246] In embodiments, the pharmaceutical composition is supplied in liquid form, for example, in a sealed container indicating the quantity and concentration of the active ingredient in the pharmaceutical composition. In related embodiments, the liquid form of the pharmaceutical composition is supplied in a hermetically sealed container.

[00247] Methods for formulating the pharmaceutical compositions of the present invention are conventional and well known in the art (see Remington and Remington's). One of skill in the art can readily formulate a pharmaceutical composition having the desired characteristics (e.g., route of administration, biosafety, and release profile).

[00248] Methods for preparing the pharmaceutical compositions include the step of bringing into association the active ingredient with a pharmaceutically acceptable carrier and, optionally, one or more accessory ingredients. The pharmaceutical compositions can be prepared by uniformly and intimately bringing into association the active ingredient with liquid carriers, or finely divided solid carriers, or both, and then, if necessary, shaping the product. Additional methodology for preparing the pharmaceutical compositions, including the preparation of multilayer dosage forms, are described in Ansel's Pharmaceutical Dosage Forms and Drug Delivery Systems (9th ed., Lippincott Williams & Wilkins), which is hereby incorporated by reference.

[00249] Pharmaceutical compositions suitable for oral administration can be in the form of capsules, cachets, pills, tablets, lozenges (using a flavored basis, usually sucrose and acacia or tragacanth), powders, granules, or as a solution or a suspension in an aqueous or non-aqueous liquid, or as an oil-in-water or water-in-oil liquid emulsion, or as an elixir or syrup, or as pastilles (using an inert base, such as gelatin and glycerin, or sucrose and acacia) and/or as mouth washes and the like, each containing a predetermined amount of a compound(s) described herein, a derivative thereof, or a pharmaceutically acceptable salt or prodrug thereof as the active ingredient(s). The active ingredient can also be administered as a bolus, electuary, or paste.

[00250] In solid dosage forms for oral administration (e.g., capsules, tablets, pills, dragees, powders, granules and the like), the active ingredient is mixed with one or more pharmaceutically acceptable carriers, excipients, or diluents, such as sodium citrate or dicalcium phosphate, and/or any of the following: (1) fillers or extenders, such as starches, lactose, sucrose, glucose, mannitol, and/or silicic acid; (2) binders, such as, for example, carboxymethylcellulose, alginates, gelatin, polyvinyl pyrrolidone, sucrose and/or acacia; (3) humectants, such as glycerol; (4) disintegrating agents, such as agar-agar, calcium carbonate, potato or tapioca starch, alginic acid, certain silicates, and sodium carbonate; (5) solution retarding agents, such as paraffin; (6) absorption accelerators, such as quaternary ammonium compounds; (7) wetting agents, such as, for example, acetyl alcohol and glycerol monostearate; (8) absorbents, such as kaolin and bentonite clay; (9) lubricants, such a talc, calcium stearate, magnesium stearate, solid polyethylene glycols, sodium lauryl sulfate, and mixtures thereof; and (10) coloring agents. In the case of capsules, tablets, and pills, the pharmaceutical compositions can also comprise buffering agents. Solid compositions of a similar type can also be prepared using fillers in soft and hard-filled gelatin capsules, and excipients such as lactose or milk sugars, as well as high molecular weight polyethylene glycols and the like.

[00251] A tablet can be made by compression or molding, optionally with one or more accessory ingredients. Compressed tablets can be prepared using binders (for example, gelatin or hydroxypropylmethyl cellulose), lubricants, inert diluents, preservatives, disintegrants (for example, sodium starch glycolate or cross-linked sodium carboxymethyl cellulose), surface-actives, and/ or dispersing agents. Molded tablets can be made by molding in a suitable machine a mixture of the powdered active ingredient moistened with an inert liquid diluent.

[00252] The tablets and other solid dosage forms, such as dragees, capsules, pills, and granules, can optionally be scored or prepared with coatings and shells, such as enteric coatings and other coatings well known in the art.

[00253] In some embodiments, in order to prolong the effect of an active ingredient, it is desirable to slow the absorption of the compound from subcutaneous or intramuscular injection. This can be accomplished by the use of a liquid suspension of crystalline or amorphous material having poor water solubility. The rate of absorption of the active ingredient then depends upon its rate of dissolution which, in turn, can depend upon crystal size and crystalline form. Alternatively, delayed absorption of a parenterally-administered active ingredient is

accomplished by dissolving or suspending the compound in an oil vehicle. In addition, prolonged absorption of the injectable pharmaceutical form can be brought about by the inclusion of agents that delay absorption such as aluminum monostearate and gelatin.

[00254] Controlled release parenteral compositions can be in form of aqueous suspensions, microspheres, microcapsules, magnetic microspheres, oil solutions, oil suspensions, emulsions, or the active ingredient can be incorporated in biocompatible carrier(s), liposomes, nanoparticles, implants or infusion devices.

[00255] Materials for use in the preparation of microspheres and/or microcapsules include biodegradable/bioerodible polymers such as polyglactin, poly-(isobutyl cyanoacrylate), poly(2-hydroxyethyl-L-glutamine) and poly(lactic acid).

[00256] Biocompatible carriers which can be used when formulating a controlled release parenteral formulation include carbohydrates such as dextrans, proteins such as albumin, lipoproteins or antibodies.

[00257] Materials for use in implants can be non-biodegradable, e.g., polydimethylsiloxane, or biodegradable such as, e.g., poly(caprolactone), poly(lactic acid), poly(glycolic acid) or poly(ortho esters).

[00258] In embodiments, the active ingredient(s) are administered by aerosol. This is accomplished by preparing an aqueous aerosol, liposomal preparation, or solid particles containing the compound. A nonaqueous (e.g., fluorocarbon propellant) suspension can be used. The pharmaceutical composition can also be administered using a sonic nebulizer, which would minimize exposing the agent to shear, which can result in degradation of the compound.

[00259] Ordinarily, an aqueous aerosol is made by formulating an aqueous solution or suspension of the active ingredient(s) together with conventional pharmaceutically-acceptable carriers and stabilizers. The carriers and stabilizers vary with the requirements of the particular compound, but typically include nonionic surfactants (Tweens, Pluronics, or polyethylene glycol), innocuous proteins like serum albumin, sorbitan esters, oleic acid, lecithin, amino acids such as glycine, buffers, salts, sugars or sugar alcohols. Aerosols generally are prepared from isotonic solutions.

[00260] Dosage forms for topical or transdermal administration of an active ingredient(s) includes powders, sprays, ointments, pastes, creams, lotions, gels, solutions, patches and

inhalants. The active ingredient(s) can be mixed under sterile conditions with a pharmaceutically acceptable carrier, and with any preservatives, buffers, or propellants as appropriate.

[00261] Transdermal patches suitable for use in the present invention are disclosed in Transdermal Drug Delivery: Developmental Issues and Research Initiatives (Marcel Dekker Inc., 1989) and U.S. Pat. Nos. 4,743,249, 4,906,169, 5,198,223, 4,816,540, 5,422,119, 5,023,084, which are hereby incorporated by reference. The transdermal patch can also be any transdermal patch well known in the art, including transscrotal patches. Pharmaceutical compositions in such transdermal patches can contain one or more absorption enhancers or skin permeation enhancers well known in the art (see, e.g., U.S. Pat. Nos. 4,379,454 and 4,973,468, which are hereby incorporated by reference). Transdermal therapeutic systems for use in the present invention can be based on iontophoresis, diffusion, or a combination of these two effects.

[00262] Transdermal patches have the added advantage of providing controlled delivery of active ingredient(s) to the body. Such dosage forms can be made by dissolving or dispersing the active ingredient(s) in a proper medium. Absorption enhancers can also be used to increase the flux of the active ingredient across the skin. The rate of such flux can be controlled by either providing a rate controlling membrane or dispersing the active ingredient(s) in a polymer matrix or gel.

[00263] Such pharmaceutical compositions can be in the form of creams, ointments, lotions, liniments, gels, hydrogels, solutions, suspensions, sticks, sprays, pastes, plasters and other kinds of transdermal drug delivery systems. The compositions can also include pharmaceutically acceptable carriers or excipients such as emulsifying agents, antioxidants, buffering agents, preservatives, humectants, penetration enhancers, chelating agents, gel-forming agents, ointment bases, perfumes, and skin protective agents.

[00264] Examples of emulsifying agents include, but are not limited to, naturally occurring gums, e.g. gum acacia or gum tragacanth, naturally occurring phosphatides, e.g. soybean lecithin and sorbitan monooleate derivatives.

[00265] Examples of antioxidants include, but are not limited to, butylated hydroxy anisole (BHA), ascorbic acid and derivatives thereof, tocopherol and derivatives thereof, and cysteine.

[00266] Examples of preservatives include, but are not limited to, parabens, such as methyl or propyl p-hydroxybenzoate and benzalkonium chloride.

[00267] Examples of humectants include, but are not limited to, glycerin, propylene glycol, sorbitol and urea.

[00268] Examples of penetration enhancers include, but are not limited to, propylene glycol, DMSO, triethanolamine, N,N-dimethylacetamide, N,N-dimethylformamide, 2-pyrrolidone and derivatives thereof, tetrahydrofurfuryl alcohol, propylene glycol, diethylene glycol monoethyl or monomethyl ether with propylene glycol monolaurate or methyl laurate, eucalyptol, lecithin, TRANSCUTOL, and AZONE.

[00269] Examples of chelating agents include, but are not limited to, sodium EDTA, citric acid and phosphoric acid.

[00270] Examples of gel forming agents include, but are not limited to, Carbopol, cellulose derivatives, bentonite, alginates, gelatin and polyvinylpyrrolidone.

[00271] In addition to the active ingredient(s), the ointments, pastes, creams, and gels of the present invention can contain excipients, such as animal and vegetable fats, oils, waxes, paraffins, starch, tragacanth, cellulose derivatives, polyethylene glycols, silicones, bentonites, silicic acid, talc and zinc oxide, or mixtures thereof.

[00272] Powders and sprays can contain excipients such as lactose, talc, silicic acid, aluminum hydroxide, calcium silicates and polyamide powder, or mixtures of these substances. Sprays can additionally contain customary propellants, such as chlorofluorohydrocarbons, and volatile unsubstituted hydrocarbons, such as butane and propane.

[00273] Injectable depot forms are made by forming microencapsule matrices of compound(s) of the invention in biodegradable polymers such as polylactide-polyglycolide. Depending on the ratio of compound to polymer, and the nature of the particular polymer employed, the rate of compound release can be controlled. Examples of other biodegradable polymers include poly(orthoesters) and poly(anhydrides). Depot injectable formulations are also prepared by entrapping the drug in liposomes or microemulsions which are compatible with body tissue.

[00274] Subcutaneous implants are well known in the art and are suitable for use in the present invention. Subcutaneous implantation methods are preferably non-irritating and mechanically resilient. The implants can be of matrix type, of reservoir type, or hybrids thereof. In matrix type devices, the carrier material can be porous or non-porous, solid or semi-solid, and permeable or impermeable to the active compound or compounds. The carrier material can be biodegradable or may slowly erode after administration. In some instances, the matrix is non-

degradable but instead relies on the diffusion of the active compound through the matrix for the carrier material to degrade. Alternative subcutaneous implant methods utilize reservoir devices where the active compound or compounds are surrounded by a rate controlling membrane, e.g., a membrane independent of component concentration (possessing zero-order kinetics). Devices consisting of a matrix surrounded by a rate controlling membrane also suitable for use.

[00275] Both reservoir and matrix type devices can contain materials such as polydimethylsiloxane, such as SILASTIC, or other silicone rubbers. Matrix materials can be insoluble polypropylene, polyethylene, polyvinyl chloride, ethylvinyl acetate, polystyrene and polymethacrylate, as well as glycerol esters of the glycerol palmitostearate, glycerol stearate, and glycerol behenate type. Materials can be hydrophobic or hydrophilic polymers and optionally contain solubilizing agents.

[00276] Subcutaneous implant devices can be slow-release capsules made with any suitable polymer, e.g., as described in U.S. Pat. Nos. 5,035,891 and 4,210,644, which are hereby incorporated by reference.

[00277] In general, at least four different approaches are applicable in order to provide rate control over the release and transdermal permeation of a drug compound. These approaches are: membrane-moderated systems, adhesive diffusion-controlled systems, matrix dispersion-type systems and microreservoir systems. It is appreciated that a controlled release percutaneous and/or topical composition can be obtained by using a suitable mixture of these approaches.

[00278] In a membrane-moderated system, the active ingredient is present in a reservoir which is totally encapsulated in a shallow compartment molded from a drug-impermeable laminate, such as a metallic plastic laminate, and a rate-controlling polymeric membrane such as a microporous or a non-porous polymeric membrane, e.g., ethylene-vinyl acetate copolymer. The active ingredient is released through the rate controlling polymeric membrane. In the drug reservoir, the active ingredient can either be dispersed in a solid polymer matrix or suspended in an unleachable, viscous liquid medium such as silicone fluid. On the external surface of the polymeric membrane, a thin layer of an adhesive polymer is applied to achieve an intimate contact of the transdermal system with the skin surface. The adhesive polymer is preferably a polymer which is hypoallergenic and compatible with the active drug substance.

[00279] In an adhesive diffusion-controlled system, a reservoir of the active ingredient is formed by directly dispersing the active ingredient in an adhesive polymer and then by, e.g.,

solvent casting, spreading the adhesive containing the active ingredient onto a flat sheet of substantially drug-impermeable metallic plastic backing to form a thin drug reservoir layer.

[00280] A matrix dispersion-type system is characterized in that a reservoir of the active ingredient is formed by substantially homogeneously dispersing the active ingredient in a hydrophilic or lipophilic polymer matrix. The drug-containing polymer is then molded into disc with a substantially well-defined surface area and controlled thickness. The adhesive polymer is spread along the circumference to form a strip of adhesive around the disc.

[00281] A microreservoir system can be considered as a combination of the reservoir and matrix dispersion type systems. In this case, the reservoir of the active substance is formed by first suspending the drug solids in an aqueous solution of water-soluble polymer and then dispersing the drug suspension in a lipophilic polymer to form a multiplicity of unleachable, microscopic spheres of drug reservoirs.

[00282] Any of the herein-described controlled release, extended release, and sustained release compositions can be formulated to release the active ingredient in about 30 minutes to about 1 week, in about 30 minutes to about 72 hours, in about 30 minutes to 24 hours, in about 30 minutes to 12 hours, in about 30 minutes to 6 hours, in about 30 minutes to 4 hours, and in about 3 hours to 10 hours. In embodiments, an effective concentration of the active ingredient(s) is sustained in a subject for 4 hours, 6 hours, 8 hours, 10 hours, 12 hours, 16 hours, 24 hours, 48 hours, 72 hours, or more after administration of the pharmaceutical compositions to the subject.

Vaccine or immunogenic compositions

[00283] The present invention is directed in some aspects to pharmaceutical compositions suitable for the prevention or treatment of cancer. In one embodiment, the composition comprises at least an immunogenic composition, e.g., a neoplasia vaccine or immunogenic composition capable of raising a specific T-cell response. The neoplasia vaccine or immunogenic composition comprises neoantigenic peptides and/or neoantigenic polypeptides corresponding to tumor specific neoantigens as described herein.

[00284] A suitable neoplasia vaccine or immunogenic composition can preferably contain a plurality of tumor specific neoantigenic peptides. In an embodiment, the vaccine or immunogenic composition can include between 1 and 100 sets of peptides, more preferably between 1 and 50 such peptides, even more preferably between 10 and 30 sets peptides, even

more preferably between 15 and 25 peptides. According to another preferred embodiment, the vaccine or immunogenic composition can include at least one peptides, more preferably 2, 3, 4, or 5 peptides, In certain embodiments, the vaccine or immunogenic composition can comprise 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, or 30 different peptides.

[00285] The optimum amount of each peptide to be included in the vaccine or immunogenic composition and the optimum dosing regimen can be determined by one skilled in the art without undue experimentation. For example, the peptide or its variant may be prepared for intravenous (i.v.) injection, sub-cutaneous (s.c.) injection, intradermal (i.d.) injection, intraperitoneal (i.p.) injection, intramuscular (i.m.) injection. Preferred methods of peptide injection include s.c, i.d., i.p., i.m., and i.v. Preferred methods of DNA injection include i.d., i.m., s.c, i.p. and i.v. For example, doses of between 1 and 500 mg 50 μg and 1.5 mg, preferably 10 μg to 500 μg, of peptide or DNA may be given and can depend from the respective peptide or DNA. Doses of this range were successfully used in previous trials (Brunsvig P F, et al., Cancer Immunol Immunother. 2006; 55(12): 1553- 1564; M. Staehler, et al., ASCO meeting 2007; Abstract No 3017). Other methods of administration of the vaccine or immunogenic composition are known to those skilled in the art.

[00286] In one embodiment of the present invention the different tumor specific neoantigenic peptides and/or polypeptides are selected for use in the neoplasia vaccine or immunogenic composition so as to maximize the likelihood of generating an immune attack against the neoplasias/tumors in a high proportion of subjects in the population. Without being bound by theory, it is believed that the inclusion of a diversity of tumor specific neoantigenic peptides can generate a broad scale immune attack against a neoplasia/tumor. In one embodiment, the selected tumor specific neoantigenic peptides/polypeptides are encoded by missense mutations. In a second embodiment, the selected tumor specific neoantigenic peptides/polypeptides are encoded by a combination of missense mutations and neoORF mutations. In a third embodiment, the selected tumor specific neoantigenic peptides/polypeptides are encoded by neoORF mutations.

[00287] In one embodiment in which the selected tumor specific neoantigenic peptides/polypeptides are encoded by missense mutations, the peptides and/or polypeptides are chosen based on their capability to associate with the MHC molecules of a high proportion of

subjects in the population. Peptides/polypeptides derived from neoORF mutations can also be selected on the basis of their capability to associate with the MHC molecules of the patient population.

[00288] The vaccine or immunogenic composition is capable of raising a specific cytotoxic T-cells response and/or a specific helper T-cell response.

[00289] The vaccine or immunogenic composition can further comprise an adjuvant and/or a carrier. Examples of useful adjuvants and carriers are given herein herein. The peptides and/or polypeptides in the composition can be associated with a carrier such as, e.g., a protein or an antigen-presenting cell such as e.g. a dendritic cell (DC) capable of presenting the peptide to a T-cell.

[00290] Adjuvants are any substance whose admixture into the vaccine or immunogenic composition increases or otherwise modifies the immune response to the mutant peptide. Carriers are scaffold structures, for example a polypeptide or a polysaccharide, to which the neoantigenic peptides, is capable of being associated. Optionally, adjuvants are conjugated covalently or non-covalently to the peptides or polypeptides of the invention.

[00291] The ability of an adjuvant to increase the immune response to an antigen is typically manifested by a significant increase in immune-mediated reaction, or reduction in disease symptoms. For example, an increase in humoral immunity is typically manifested by a significant increase in the titer of antibodies raised to the antigen, and an increase in T-cell activity is typically manifested in increased cell proliferation, or cellular cytotoxicity, or cytokine secretion. An adjuvant may also alter an immune response, for example, by changing a primarily humoral or Th2 response into a primarily cellular, or Th1 response.

[00292] Suitable adjuvants include, but are not limited to 1018 ISS, aluminum salts, Amplivax, AS15, BCG, CP-870,893, CpG7909, CyaA, dSLIM, GM-CSF, IC30, IC31, Imiquimod, ImuFact IMP321, IS Patch, ISS, ISCOMATRIX, Juvlmmune, LipoVac, MF59, monophosphoryl lipid A, Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, OK-432, OM-174, OM-197-MP-EC, ONTAK, PEPTEL. vector system, PLG microparticles, resiquimod, SRL172, Virosomes and other Virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, Aquila's QS21 stimulon (Aquila Biotech, Worcester, Mass., USA) which is derived from saponin, mycobacterial extracts and synthetic bacterial cell wall mimics, and other proprietary adjuvants such as Ribi's Detox. Quil or Superfos. Several

immunological adjuvants (e.g., MF59) specific for dendritic cells and their preparation have been described previously (Dupuis M, et al., Cell Immunol. 1998; 186(1): 18-27; Allison A C; Dev Biol Stand. 1998; 92:3-11). Also cytokines may be used. Several cytokines have been directly linked to influencing dendritic cell migration to lymphoid tissues (e.g., TNF-alpha), accelerating the maturation of dendritic cells into efficient antigen-presenting cells for T-lymphocytes (e.g., GM-CSF, IL-1 and IL-4) (U.S. Pat. No. 5,849,589, specifically incorporated herein by reference in its entirety) and acting as immunoadjuvants (e.g., IL-12) (Gabrilovich D I, et al., J Immunother Emphasis Tumor Immunol. 1996 (6):414-418).

[00293] Toll like receptors (TLRs) may also be used as adjuvants, and are important members of the family of pattern recognition receptors (PRRs) which recognize conserved motifs shared by many micro-organisms, termed "pathogen-associated molecular patterns" (PAMPS). Recognition of these "danger signals" activates multiple elements of the innate and adaptive immune system. TLRs are expressed by cells of the innate and adaptive immune systems such as dendritic cells (DCs), macrophages, T and B cells, mast cells, and granulocytes and are localized in different cellular compartments, such as the plasma membrane, lysosomes, endosomes, and endolysosomes. Different TLRs recognize distinct PAMPS. For example, TLR4 is activated by LPS contained in bacterial cell walls, TLR9 is activated by unmethylated bacterial or viral CpG DNA, and TLR3 is activated by double stranded RNA. TLR ligand binding leads to the activation of one or more intracellular signaling pathways, ultimately resulting in the production of many key molecules associated with inflammation and immunity (particularly the transcription factor NF-κB and the Type-I interferons). TLR mediated DC activation leads to enhanced DC activation, phagocytosis, upregulation of activation and co-stimulation markers such as CD80, CD83, and CD86, expression of CCR7 allowing migration of DC to draining lymph nodes and facilitating antigen presentation to T cells, as well as increased secretion of cytokines such as type I interferons, IL-12, and IL-6. All of these downstream events are critical for the induction of an adaptive immune response.

[00294] Among the most promising cancer vaccine or immunogenic composition adjuvants currently in clinical development are the TLR9 agonist CpG and the synthetic double-stranded RNA (dsRNA) TLR3 ligand poly-ICLC. In preclinical studies poly-ICLC appears to be the most potent TLR adjuvant when compared to LPS and CpG due to its induction of pro-inflammatory cytokines and lack of stimulation of IL-10, as well as maintenance of high levels of co-

stimulatory molecules in DCs1. Furthermore, poly-ICLC was recently directly compared to CpG in non-human primates (rhesus macaques) as adjuvant for a protein vaccine or immunogenic composition consisting of human papillomavirus (HPV)16 capsomers (Stahl-Hennig C, Eisenblatter M, Jasny E, et al. Synthetic double-stranded RNAs are adjuvants for the induction of T helper 1 and humoral immune responses to human papillomavirus in rhesus macaques. PLoS pathogens. Apr 2009;5(4)).

[00295] CpG immuno stimulatory oligonucleotides have also been reported to enhance the effects of adjuvants in a vaccine or immunogenic composition setting. Without being bound by theory, CpG oligonucleotides act by activating the innate (non- adaptive) immune system via Toll-like receptors (TLR), mainly TLR9. CpG triggered TLR9 activation enhances antigen-specific humoral and cellular responses to a wide variety of antigens, including peptide or protein antigens, live or killed viruses, dendritic cell vaccines, autologous cellular vaccines and polysaccharide conjugates in both prophylactic and therapeutic vaccines. More importantly, it enhances dendritic cell maturation and differentiation, resulting in enhanced activation of Thl cells and strong cytotoxic T- lymphocyte (CTL) generation, even in the absence of CD4 T-cell help. The Thl bias induced by TLR9 stimulation is maintained even in the presence of vaccine adjuvants such as alum or incomplete Freund's adjuvant (IFA) that normally promote a Th2 bias. CpG oligonucleotides show even greater adjuvant activity when formulated or co-administered with other adjuvants or in formulations such as microparticles, nano particles, lipid emulsions or similar formulations, which are especially necessary for inducing a strong response when the antigen is relatively weak. They also accelerate the immune response and enabled the antigen doses to be reduced by approximately two orders of magnitude, with comparable antibody responses to the full-dose vaccine without CpG in some experiments (Arthur M. Krieg, Nature Reviews, Drug Discovery, 5, Jun. 2006, 471-484). U.S. Pat. No. 6,406,705 Bl describes the combined use of CpG oligonucleotides, non-nucleic acid adjuvants and an antigen to induce an antigen- specific immune response. A commercially available CpG TLR9 antagonist is dSLIM (double Stem Loop Immunomodulator) by Mologen (Berlin, GERMANY), which is a preferred component of the pharmaceutical composition of the present invention. Other TLR binding molecules such as RNA binding TLR 7, TLR 8 and/or TLR 9 may also be used.

[00296] Other examples of useful adjuvants include, but are not limited to, chemically modified CpGs (e.g. CpR, Idera), Poly(I:C)(e.g. polyi:CI2U), non-CpG bacterial DNA or RNA

as well as immunoactive small molecules and antibodies such as cyclophosphamide, sunitinib, bevacizumab, celebrex, NCX-4016, sildenafil, tadalafil, vardenafil, sorafinib, XL-999, CP-547632, pazopanib, ZD2171, AZD2171, ipilimumab, tremelimumab, and SC58175, which may act therapeutically and/or as an adjuvant. The amounts and concentrations of adjuvants and additives useful in the context of the present invention can readily be determined by the skilled artisan without undue experimentation. Additional adjuvants include colony- stimulating factors, such as Granulocyte Macrophage Colony Stimulating Factor (GM-CSF, sargramostim).

[00297] Poly-ICLC is a synthetically prepared double-stranded RNA consisting of polyI and polyC strands of average length of about 5000 nucleotides, which has been stabilized to thermal denaturation and hydrolysis by serum nucleases by the addition of polylysine and carboxymethylcellulose. The compound activates TLR3 and the RNA helicase-domain of MDA5, both members of the PAMP family, leading to DC and natural killer (NK) cell activation and production of a "natural mix" of type I interferons, cytokines, and chemokines. Furthermore, poly-ICLC exerts a more direct, broad host-targeted anti-infectious and possibly antitumor effect mediated by the two IFN-inducible nuclear enzyme systems, the 2'5'-OAS and the P1/eIF2a kinase, also known as the PKR (4-6), as well as RIG-I helicase and MDA5.

[00298] In rodents and non-human primates, poly-ICLC was shown to enhance T cell responses to viral antigens, cross-priming, and the induction of tumor-, virus-, and autoantigen-specific CD8+ T-cells. In a recent study in non-human primates, poly-ICLC was found to be essential for the generation of antibody responses and T-cell immunity to DC targeted or non-targeted HIV Gag p24 protein, emphasizing its effectiveness as a vaccine adjuvant.

[00299] In human subjects, transcriptional analysis of serial whole blood samples revealed similar gene expression profiles among the 8 healthy human volunteers receiving one single s.c. administration of poly-ICLC and differential expression of up to 212 genes between these 8 subjects versus 4 subjects receiving placebo. Remarkably, comparison of the poly-ICLC gene expression data to previous data from volunteers immunized with the highly effective yellow fever vaccine YF17D showed that a large number of transcriptional and signal transduction canonical pathways, including those of the innate immune system, were similarly upregulated at peak time points.

[00300] More recently, an immunologic analysis was reported on patients with ovarian, fallopian tube, and primary peritoneal cancer in second or third complete clinical remission who

were treated on a phase 1 study of subcutaneous vaccination with synthetic overlapping long peptides (OLP) from the cancer testis antigen NY-ESO-1 alone or with Montanide-ISA-51, or with 1.4 mg poly-ICLC and Montanide. The generation of NY-ESO-1-specific CD4+ and CD8+ T-cell and antibody responses were markedly enhanced with the addition of poly-ICLC and Montanide compared to OLP alone or OLP and Montanide.

[00301] A vaccine or immunogenic composition according to the present invention may comprise more than one different adjuvant. Furthermore, the invention encompasses a therapeutic composition comprising any adjuvant substance including any of those herein discussed. It is also contemplated that the peptide or polypeptide, and the adjuvant can be administered separately in any appropriate sequence.

[00302] A carrier may be present independently of an adjuvant. The carrier may be covalently linked to the antigen. A carrier can also be added to the antigen by inserting DNA encoding the carrier in frame with DNA encoding the antigen. The function of a carrier can for example be to confer stability, to increase the biological activity, or to increase serum half-life. Extension of the half-life can help to reduce the number of applications and to lower doses, thus are beneficial for therapeutic but also economic reasons. Furthermore, a carrier may aid presenting peptides to T-cells. The carrier may be any suitable carrier known to the person skilled in the art, for example a protein or an antigen presenting cell. A carrier protein could be but is not limited to keyhole limpet hemocyanin, serum proteins such as transferrin, bovine serum albumin, human serum albumin, thyroglobulin or ovalbumin, immunoglobulins, or hormones, such as insulin or palmitic acid. For immunization of humans, the carrier may be a physiologically acceptable carrier acceptable to humans and safe. However, tetanus toxoid and/or diptheria toxoid are suitable carriers in one embodiment of the invention. Alternatively, the carrier may be dextrans for example sepharose.

[00303] Cytotoxic T-cells (CTLs) recognize an antigen in the form of a peptide bound to an MHC molecule rather than the intact foreign antigen itself. The MHC molecule itself is located at the cell surface of an antigen presenting cell. Thus, an activation of CTLs is only possible if a trimeric complex of peptide antigen, MHC molecule, and APC is present. Correspondingly, it may enhance the immune response if not only the peptide is used for activation of CTLs, but if additionally APCs with the respective MHC molecule are added. Therefore, in some

embodiments the vaccine or immunogenic composition according to the present invention additionally contains at least one antigen presenting cell.

[00304] The antigen-presenting cell (or stimulator cell) typically has an MHC class I or II molecule on its surface, and in one embodiment is substantially incapable of itself loading the MHC class I or II molecule with the selected antigen. As is described in more detail herein, the MHC class I or II molecule may readily be loaded with the selected antigen in vitro.

[00305] CD8+ cell activity may be augmented through the use of CD4+ cells. The identification of CD4 T+ cell epitopes for tumor antigens has attracted interest because many immune based therapies against cancer may be more effective if both CD8+ and CD4+ T lymphocytes are used to target a patient's tumor. CD4+ cells are capable of enhancing CD8 T cell responses. Many studies in animal models have clearly demonstrated better results when both CD4+ and CD8+ T cells participate in anti-tumor responses (see e.g., Nishimura et al. (1999) Distinct role of antigen-specific T helper type 1 (TH1) and Th2 cells in tumor eradication in vivo. J Ex Med 190:617-27). Universal CD4+ T cell epitopes have been identified that are applicable to developing therapies against different types of cancer (see e.g., Kobayashi et al. (2008) Current Opinion in Immunology 20:221-27). For example, an HLA-DR restricted helper peptide from tetanus toxoid was used in melanoma vaccines to activate CD4+ T cells non-specifically (see e.g., Slingluff et al. (2007) Immunologic and Clinical Outcomes of a Randomized Phase II Trial of Two Multipeptide Vaccines for Melanoma in the Adjuvant Setting, Clinical Cancer Research 13(21):6386-95). It is contemplated within the scope of the invention that such CD4+ cells may be applicable at three levels that vary in their tumor specificity: 1) a broad level in which universal CD4+ epitopes (e.g., tetanus toxoid) may be used to augment CD8+ cells; 2) an intermediate level in which native, tumor-associated CD4+ epitopes may be used to augment CD8+ cells; and 3) a patient specific level in which neoantigen CD4+ epitopes may be used to augment CD8+ cells in a patient specific manner. Although current algorithms for predicting CD4 epitopes are limited in accuracy, it is a reasonable expectation that many long peptides containing predicted CD8 neoepitopes will also include CD4 epitopes. CD4 epitopes are longer than CD8 epitopes and typically are 10 -12 amino acids in length although some can be longer (Kreiter et al, Mutant MHC Class II epitopes drive therapeutic immune responses to cancer, Nature (2015). Thus the neoantigenic epitopes described herein, either in the form of

long peptides (>25 amino acids) or nucleic acids encoding such long peptides, may also boost CD4 responses in a tumor and patient-specific manner (level (3) above).

[00306] CD8+ cell immunity may also be generated with neoantigen loaded dendritic cell (DC) vaccine. DCs are potent antigen-presenting cells that initiate T cell immunity and can be used as cancer vaccines when loaded with one or more peptides of interest, for example, by direct peptide injection. For example, patients that were newly diagnosed with metastatic melanoma were shown to be immunized against 3 HLA-A*0201-restricted gp100 melanoma antigen-derived peptides with autologous peptide pulsed CD40L/IFN-g-activated mature DCs via an IL-12p70-producing patient DC vaccine (see e.g., Carreno et al (2013) L-12p70-producing patient DC vaccine elicits Tc1-polarized immunity, Journal of Clinical Investigation, 123(8):3383-94 and Ali et al. (2009) In situ regulation of DC subsets and T cells mediates tumor regression in mice, Cancer Immunotherapy, 1(8):1-10). It is contemplated within the scope of the invention that neoantigen loaded DCs may be prepared using the synthetic TLR 3 agonist Polyinosinic-Polycytidylic Acid-poly-L-lysine Carboxymethylcellulose (Poly-ICLC) to stimulate the DCs. Poly-ICLC is a potent individual maturation stimulus for human DCs as assessed by an upregulation of CD83 and CD86, induction of interleukin-12 (IL-12), tumor necrosis factor (TNF), interferon gamma-induced protein 10 (IP-10), interleukin 1 (IL-1), and type I interferons (IFN), and minimal interleukin 10 (IL-10) production. DCs may be differentiated from frozen peripheral blood mononuclear cells (PBMCs) obtained by leukapheresis, while PBMCs may be isolated by Ficoll gradient centrifugation and frozen in aliquots.

[00307] Illustratively, the following 7 day activation protocol may be used. Day 1—PBMCs are thawed and plated onto tissue culture flasks to select for monocytes which adhere to the plastic surface after 1-2 hr incubation at 37°C in the tissue culture incubator. After incubation, the lymphocytes are washed off and the adherent monocytes are cultured for 5 days in the presence of interleukin-4 (IL-4) and granulocyte macrophage-colony stimulating factor (GM-CSF) to differentiate to immature DCs. On Day 6, immature DCs are pulsed with the keyhole limpet hemocyanin (KLH) protein which serves as a control for the quality of the vaccine and may boost the immunogenicity of the vaccine. The DCs are stimulated to mature, loaded with peptide antigens, and incubated overnight. On Day 7, the cells are washed, and frozen in 1 ml aliquots containing 4-20 x 10(6) cells using a controlled-rate freezer. Lot release testing for the batches of DCs may be performed to meet minimum specifications before the DCs are injected

into patients (see e.g., Sabado et al. (2013) Preparation of tumor antigen-loaded mature dendritic cells for immunotherapy, J. Vis Exp. Aug 1;(78). doi: 10.3791/50085).

[00308] A DC vaccine may be incorporated into a scaffold system to facilitate delivery to a patient. Therapeutic treatment of a patients neoplasia with a DC vaccine may utilize a biomaterial system that releases factors that recruit host dendritic cells into the device, differentiates the resident, immature DCs by locally presenting adjuvants (e.g., danger signals) while releasing antigen, and promotes the release of activated, antigen loaded DCs to the lymph nodes (or desired site of action) where the DCs may interact with T cells to generate a potent cytotoxic T lymphocyte response to the cancer neoantigens. Implantable biomaterials may be used to generate a potent cytotoxic T lymphocyte response against a neoplasia in a patient specific manner. The biomaterial-resident dendritic cells may then be activated by exposing them to danger signals mimicking infection, in concert with release of antigen from the biomaterial. The activated dendritic cells then migrate from the biomaterials to lymph nodes to induce a cytotoxic T effector response. This approach has previously been demonstrated to lead to regression of established melanoma in preclinical studies using a lysate prepared from tumor biopsies (see e.g., Ali et al. (2209) In situ regulation of DC subsets and T cells mediates tumor regression in mice, Cancer Immunotherapy 1(8):1-10; Ali et al. (2009) Infection-mimicking materials to program dendritic cells in situ. Nat Mater 8:151-8), and such a vaccine is currently being tested in a Phase I clinical trial recently initiated at the Dana-Farber Cancer Institute. This approach has also been shown to lead to regression of glioblastoma, as well as the induction of a potent memory response to prevent relapse, using the C6 rat glioma model.24 in the current proposal. The ability of such an implantable, biomatrix vaccine delivery scaffold to amplify and sustain tumor specific dendritic cell activation may lead to more robust anti-tumor immunosensitization than can be achieved by traditional subcutaneous or intra-nodal vaccine administrations.

[00309] The present invention may include any method for loading a neoantigenic peptide onto a dendritic cell. One such method applicable to the present invention is a microfluidic intracellular delivery system. Such systems cause temporary membrane disruption by rapid mechanical deformation of human and mouse immune cells, thus allowing the intracellular delivery of biomolecules (Sharei et al., 2015, PLOS ONE).

[00310] Preferably, the antigen presenting cells are dendritic cells. Suitably, the dendritic cells are autologous dendritic cells that are pulsed with the neoantigenic peptide. The peptide may be any suitable peptide that gives rise to an appropriate T-cell response. T-cell therapy using autologous dendritic cells pulsed with peptides from a tumor associated antigen is disclosed in Murphy et al. (1996) The Prostate 29, 371-380 and Tjua et al. (1997) The Prostate 32, 272-278. In certain embodiments the dendritic cells are targeted using CD141, DEC205, or XCR1 markers. CD141+XCR1+ DC's were identified as a subset that may be better suited to the induction of anti-tumor responses (Bachem et al., J. Exp. Med. 207, 1273-1281 (2010); Crozat et al., J. Exp. Med. 207, 1283-1292 (2010); and Gallois & Bhardwaj, Nature Med. 16, 854-856 (2010)).

[00311] Thus, in one embodiment of the present invention the vaccine or immunogenic composition containing at least one antigen presenting cell is pulsed or loaded with one or more peptides of the present invention. Alternatively, peripheral blood mononuclear cells (PBMCs) isolated from a patient may be loaded with peptides ex vivo and injected back into the patient. As an alternative the antigen presenting cell comprises an expression construct encoding a peptide of the present invention. The polynucleotide may be any suitable polynucleotide and it is preferred that it is capable of transducing the dendritic cell, thus resulting in the presentation of a peptide and induction of immunity.

[00312] The inventive pharmaceutical composition may be compiled so that the selection, number and/or amount of peptides present in the composition covers a high proportion of subjects in the population. The selection may be dependent on the specific type of cancer, the status of the disease, earlier treatment regimens, and, of course, the HLA-haplotypes present in the patient population.

[00313] Pharmaceutical compositions comprising the peptide of the invention may be administered to an individual already suffering from cancer. In therapeutic applications, compositions are administered to a patient in an amount sufficient to elicit an effective CTL response to the tumor antigen and to cure or at least partially arrest symptoms and/or complications. An amount adequate to accomplish this is defined as "therapeutically effective dose." Amounts effective for this use can depend on, e.g., the peptide composition, the manner of administration, the stage and severity of the disease being treated, the weight and general state of health of the patient, and the judgment of the prescribing physician, but generally range for the

initial immunization (that is for therapeutic or prophylactic administration) from about 1.0 μg to about 50,000 μg of peptide for a 70 kg patient, followed by boosting dosages or from about 1.0 μg to about 10,000 μg of peptide pursuant to a boosting regimen over weeks to months depending upon the patient's response and condition and possibly by measuring specific CTL activity in the patient's blood. It should be kept in mind that the peptide and compositions of the present invention may generally be employed in serious disease states, that is, life-threatening or potentially life threatening situations, especially when the cancer has metastasized. For therapeutic use, administration should begin as soon as possible after the detection or surgical removal of tumors. This is followed by boosting doses until at least symptoms are substantially abated and for a period thereafter.

[00314] The pharmaceutical compositions (e.g., vaccine compositions) for therapeutic treatment are intended for parenteral, topical, nasal, oral or local administration. Preferably, the pharmaceutical compositions are administered parenterally, e.g., intravenously, subcutaneously, intradermally, or intramuscularly. The compositions may be administered at the site of surgical excision to induce a local immune response to the tumor. The invention provides compositions for parenteral administration which comprise a solution of the peptides and vaccine or immunogenic compositions are dissolved or suspended in an acceptable carrier, preferably an aqueous carrier. A variety of aqueous carriers may be used, e.g., water, buffered water, 0.9% saline, 0.3% glycine, hyaluronic acid and the like. These compositions may be sterilized by conventional, well known sterilization techniques, or may be sterile filtered. The resulting aqueous solutions may be packaged for use as is, or lyophilized, the lyophilized preparation being combined with a sterile solution prior to administration. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH adjusting and buffering agents, tonicity adjusting agents, wetting agents and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, etc.

[00315] A liposome suspension containing a peptide may be administered intravenously, locally, topically, etc. in a dose which varies according to, inter alia, the manner of administration, the peptide being delivered, and the stage of the disease being treated. For targeting to the immune cells, a ligand, such as, e.g., antibodies or fragments thereof specific for

cell surface determinants of the desired immune system cells, can be incorporated into the liposome.

[00316] For solid compositions, conventional or nanoparticle nontoxic solid carriers may be used which include, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharin, talcum, cellulose, glucose, sucrose, magnesium carbonate, and the like. For oral administration, a pharmaceutically acceptable nontoxic composition is formed by incorporating any of the normally employed excipients, such as those carriers previously listed, and generally 10-95% of active ingredient, that is, one or more peptides of the invention, and more preferably at a concentration of 25%-75%.

[00317] For aerosol administration, the immunogenic peptides are preferably supplied in finely divided form along with a surfactant and propellant. Typical percentages of peptides are 0.01 %-20% by weight, preferably 1%-10%. The surfactant can, of course, be nontoxic, and preferably soluble in the propellant. Representative of such agents are the esters or partial esters of fatty acids containing from 6 to 22 carbon atoms, such as caproic, octanoic, lauric, palmitic, stearic, linoleic, linolenic, olesteric and oleic acids with an aliphatic polyhydric alcohol or its cyclic anhydride. Mixed esters, such as mixed or natural glycerides may be employed. The surfactant may constitute 0.1%-20% by weight of the composition, preferably 0.25-5%. The balance of the composition is ordinarily propellant. A carrier can also be included as desired, as with, e.g., lecithin for intranasal delivery.

[00318] The peptides and polypeptides of the invention can be readily synthesized chemically utilizing reagents that are free of contaminating bacterial or animal substances (Merrifield RB: Solid phase peptide synthesis. I. The synthesis of a tetrapeptide. J. Am. Chem. Soc. 85:2149-54, 1963).

[00319] The peptides and polypeptides of the invention can also be expressed by a vector, e.g., a nucleic acid molecule as herein-discussed, e.g., RNA or a DNA plasmid, a viral vector such as a poxvirus, e.g., orthopox virus, avipox virus, or adenovirus, AAV or lentivirus. This approach involves the use of a vector to express nucleotide sequences that encode the peptide of the invention. Upon introduction into an acutely or chronically infected host or into a noninfected host, the vector expresses the immunogenic peptide, and thereby elicits a host CTL response.

[00320] For therapeutic or immunization purposes, nucleic acids encoding the peptide of the invention and optionally one or more of the peptides described herein can also be administered to the patient. A number of methods are conveniently used to deliver the nucleic acids to the patient. For instance, the nucleic acid can be delivered directly, as "naked DNA". This approach is described, for instance, in Wolff et al., Science 247: 1465-1468 (1990) as well as U.S. Patent Nos. 5,580,859 and 5,589,466. The nucleic acids can also be administered using ballistic delivery as described, for instance, in U.S. Patent No. 5,204,253. Particles comprised solely of DNA can be administered. Alternatively, DNA can be adhered to particles, such as gold particles. Generally, a plasmid for a vaccine or immunological composition can comprise DNA encoding an antigen (e.g., one or more neoantigens) operatively linked to regulatory sequences which control expression or expression and secretion of the antigen from a host cell, e.g., a mammalian cell; for instance, from upstream to downstream, DNA for a promoter, such as a mammalian virus promoter (e.g., a CMV promoter such as an hCMV or mCMV promoter, e.g., an early-intermediate promoter, or an SV40 promoter--see documents cited or incorporated herein for useful promoters), DNA for a eukaryotic leader peptide for secretion (e.g., tissue plasminogen activator), DNA for the neoantigen(s), and DNA encoding a terminator (e.g., the 3' UTR transcriptional terminator from the gene encoding Bovine Growth Hormone or bGH polyA). A composition can contain more than one plasmid or vector, whereby each vector contains and expresses a different neoantigen. Mention is also made of Wasmoen U.S. Pat. No. 5,849,303, and Dale U.S. Pat. No. 5,811,104, whose text may be useful. DNA or DNA plasmid formulations can be formulated with or inside cationic lipids; and, as to cationic lipids, as well as adjuvants, mention is also made of Loosmore U.S. Patent Application 2003/0104008. Also, teachings in Audonnet U.S. Pat. Nos. 6,228,846 and 6,159,477 may be relied upon for DNA plasmid teachings that can be employed in constructing and using DNA plasmids that contain and express in vivo.

[00321] The nucleic acids can also be delivered complexed to cationic compounds, such as cationic lipids. Lipid-mediated gene delivery methods are described, for instance, in WO1996/18372; WO 1993/24640; Mannino & Gould-Fogerite , BioTechniques 6(7): 682-691 (1988); U.S. Patent No. 5,279,833; WO 1991/06309; and Feigner et al., Proc. Natl. Acad. Sci. USA 84: 7413-7414 (1987).

[00322] RNA encoding the peptide of interest (e.g., mRNA) can also be used for delivery (see, e.g., Kiken et al, 2011; Su et al , 2011; see also US 8278036; Halabi et al. J Clin Oncol (2003) 21:1232-1237; Petsch et al, Nature Biotechnology 2012 Dec 7;30(12):1210-6).

[00323] Viral vectors as described herein can also be used to deliver the neoantigenic peptides of the invention. Vectors can be administered so as to have in vivo expression and response akin to doses and/or responses elicited by antigen administration.

[00324] A preferred means of administering nucleic acids encoding the peptide of the invention uses minigene constructs encoding multiple epitopes. To create a DNA sequence encoding the selected CTL epitopes (minigene) for expression in human cells, the amino acid sequences of the epitopes are reverse translated. A human codon usage table is used to guide the codon choice for each amino acid. These epitope-encoding DNA sequences are directly adjoined, creating a continuous polypeptide sequence. To optimize expression and/or immunogenicity, additional elements can be incorporated into the minigene design. Examples of amino acid sequence that could be reverse translated and included in the minigene sequence include: helper T lymphocyte, epitopes, a leader (signal) sequence, and an endoplasmic reticulum retention signal. In addition, MHC presentation of CTL epitopes may be improved by including synthetic (e.g. poly-alanine) or naturally- occurring flanking sequences adjacent to the CTL epitopes.

[00325] The minigene sequence is converted to DNA by assembling oligonucleotides that encode the plus and minus strands of the minigene. Overlapping oligonucleotides (30-100 bases long) are synthesized, phosphorylated, purified and annealed under appropriate conditions using well known techniques. The ends of the oligonucleotides are joined using T4 DNA ligase. This synthetic minigene, encoding the CTL epitope polypeptide, can then cloned into a desired expression vector.

[00326] Standard regulatory sequences well known to those of skill in the art are included in the vector to ensure expression in the target cells. Several vector elements are required: a promoter with a down-stream cloning site for minigene insertion; a polyadenylation signal for efficient transcription termination; an E. coli origin of replication; and an E. coli selectable marker (e.g. ampicillin or kanamycin resistance). Numerous promoters can be used for this purpose, e.g., the human cytomegalovirus (hCMV) promoter. See, U.S. Patent Nos. 5,580,859 and 5,589,466 for other suitable promoter sequences.

[00327] Additional vector modifications may be desired to optimize minigene expression and immunogenicity. In some cases, introns are required for efficient gene expression, and one or more synthetic or naturally-occurring introns could be incorporated into the transcribed region of the minigene. The inclusion of mRNA stabilization sequences can also be considered for increasing minigene expression. It has recently been proposed that immuno stimulatory sequences (ISSs or CpGs) play a role in the immunogenicity of DNA' vaccines. These sequences could be included in the vector, outside the minigene coding sequence, if found to enhance immunogenicity.

[00328] In some embodiments, a bicistronic expression vector, to allow production of the minigene-encoded epitopes and a second protein included to enhance or decrease immunogenicity can be used. Examples of proteins or polypeptides that could beneficially enhance the immune response if co-expressed include cytokines (e.g., IL2, IL12, GM-CSF), cytokine-inducing molecules (e.g. LeIF) or costimulatory molecules. Helper (HTL) epitopes could be joined to intracellular targeting signals and expressed separately from the CTL epitopes. This would allow direction of the HTL epitopes to a cell compartment different than the CTL epitopes. If required, this could facilitate more efficient entry of HTL epitopes into the MHC class II pathway, thereby improving CTL induction. In contrast to CTL induction, specifically decreasing the immune response by co-expression of immunosuppressive molecules (e.g. TGF-β) may be beneficial in certain diseases.

[00329] Once an expression vector is selected, the minigene is cloned into the polylinker region downstream of the promoter. This plasmid is transformed into an appropriate E. coli strain, and DNA is prepared using standard techniques. The orientation and DNA sequence of the minigene, as well as all other elements included in the vector, are confirmed using restriction mapping and DNA sequence analysis. Bacterial cells harboring the correct plasmid can be stored as a master cell bank and a working cell bank.

[00330] Purified plasmid DNA can be prepared for injection using a variety of formulations. The simplest of these is reconstitution of lyophilized DNA in sterile phosphate-buffer saline (PBS). A variety of methods have been described, and new techniques may become available. As noted herein, nucleic acids are conveniently formulated with cationic lipids. In addition, glycolipids, fusogenic liposomes, peptides and compounds referred to collectively as protective, interactive, non-condensing (PINC) could also be complexed to purified plasmid DNA to

influence variables such as stability, intramuscular dispersion, or trafficking to specific organs or cell types.

[00331] Target cell sensitization can be used as a functional assay for expression and MHC class I presentation of minigene-encoded CTL epitopes. The plasmid DNA is introduced into a mammalian cell line that is suitable as a target for standard CTL chromium release assays. The transfection method used is dependent on the final formulation. Electroporation can be used for "naked" DNA, whereas cationic lipids allow direct in vitro transfection. A plasmid expressing green fluorescent protein (GFP) can be co-transfected to allow enrichment of transfected cells using fluorescence activated cell sorting (FACS). These cells are then chromium-51 labeled and used as target cells for epitope- specific CTL lines. Cytolysis, detected by 51 Cr release, indicates production of MHC presentation of mini gene-encoded CTL epitopes.

[00332] In vivo immunogenicity is a second approach for functional testing of minigene DNA formulations. Transgenic mice expressing appropriate human MHC molecules are immunized with the DNA product. The dose and route of administration are formulation dependent (e.g. IM for DNA in PBS, IP for lipid-complexed DNA). Twenty-one days after immunization, splenocytes are harvested and restimulated for 1 week in the presence of peptides encoding each epitope being tested. These effector cells (CTLs) are assayed for cytolysis of peptide-loaded, chromium-51 labeled target cells using standard techniques. Lysis of target cells sensitized by MHC loading of peptides corresponding to minigene-encoded epitopes demonstrates DNA vaccine function for in vivo induction of CTLs.

[00333] Peptides may be used to elicit CTL ex vivo, as well. The resulting CTL, can be used to treat chronic tumors in patients in need thereof that do not respond to other conventional forms of therapy, or does not respond to a peptide vaccine approach of therapy. Ex vivo CTL responses to a particular tumor antigen are induced by incubating in tissue culture the patient's CTL precursor cells (CTLp) together with a source of antigen-presenting cells (APC) and the appropriate peptide. After an appropriate incubation time (typically 1-4 weeks), in which the CTLp are activated and mature and expand into effector CTL, the cells are infused back into the patient, where they destroy their specific target cell (i.e., a tumor cell). In order to optimize the in vitro conditions for the generation of specific cytotoxic T cells, the culture of stimulator cells are maintained in an appropriate serum-free medium.

[00334] Prior to incubation of the stimulator cells with the cells to be activated, e.g., precursor CD8+ cells, an amount of antigenic peptide is added to the stimulator cell culture, of sufficient quantity to become loaded onto the human Class I molecules to be expressed on the surface of the stimulator cells. In the present invention, a sufficient amount of peptide is an amount that allows about 200, and preferably 200 or more, human Class I MHC molecules loaded with peptide to be expressed on the surface of each stimulator cell. Preferably, the stimulator cells are incubated with >2μg/ml peptide. For example, the stimulator cells are incubates with > 3, 4, 5, 10, 15, or more μg/ml peptide.

[00335] Resting or precursor CD8+ cells are then incubated in culture with the appropriate stimulator cells for a time period sufficient to activate the CD8+ cells. Preferably, the CD8+ cells are activated in an antigen- specific manner. The ratio of resting or precursor CD8+ (effector) cells to stimulator cells may vary from individual to individual and may further depend upon variables such as the amenability of an individual's lymphocytes to culturing conditions and the nature and severity of the disease condition or other condition for which the within-described treatment modality is used. Preferably, however, the lymphocyte: stimulator cell ratio is in the range of about 30: 1 to 300: 1. The effector/stimulator culture may be maintained for as long a time as is necessary to stimulate a therapeutically useable or effective number of CD8+ cells.

[00336] The induction of CTL in vitro requires the specific recognition of peptides that are bound to allele specific MHC class I molecules on APC. The number of specific MHC/peptide complexes per APC is crucial for the stimulation of CTL, particularly in primary immune responses. While small amounts of peptide/MHC complexes per cell are sufficient to render a cell susceptible to lysis by CTL, or to stimulate a secondary CTL response, the successful activation of a CTL precursor (pCTL) during primary response requires a significantly higher number of MHC/peptide complexes. Peptide loading of empty major histocompatability complex molecules on cells allows the induction of primary cytotoxic T lymphocyte responses.

[00337] Since mutant cell lines do not exist for every human MHC allele, it is advantageous to use a technique to remove endogenous MHC- associated peptides from the surface of APC, followed by loading the resulting empty MHC molecules with the immunogenic peptides of interest. The use of non-transformed (non-tumorigenic), noninfected cells, and preferably, autologous cells of patients as APC is desirable for the design of CTL induction protocols

directed towards development of ex vivo CTL therapies. This application discloses methods for stripping the endogenous MHC-associated peptides from the surface of APC followed by the loading of desired peptides.

[00338] A stable MHC class I molecule is a trimeric complex formed of the following elements: 1) a peptide usually of 8 - 10 residues, 2) a transmembrane heavy polymorphic protein chain which bears the peptide-binding site in its al and a2 domains, and 3) a non-covalently associated non-polymorphic light chain, p2microglobuiin. Removing the bound peptides and/or dissociating the p2microglobulin from the complex renders the MHC class I molecules nonfunctional and unstable, resulting in rapid degradation. All MHC class I molecules isolated from PBMCs have endogenous peptides bound to them. Therefore, the first step is to remove all endogenous peptides bound to MHC class I molecules on the APC without causing their degradation before exogenous peptides can be added to them.

[00339] Two possible ways to free up MHC class I molecules of bound peptides include lowering the culture temperature from 37°C to 26°C overnight to destablize p2microglobulin and stripping the endogenous peptides from the cell using a mild acid treatment. The methods release previously bound peptides into the extracellular environment allowing new exogenous peptides to bind to the empty class I molecules. The cold-temperature incubation method enables exogenous peptides to bind efficiently to the MHC complex, but requires an overnight incubation at 26°C which may slow the cell's metabolic rate. It is also likely that cells not actively synthesizing MHC molecules (e.g., resting PBMC) would not produce high amounts of empty surface MHC molecules by the cold temperature procedure.

[00340] Harsh acid stripping involves extraction of the peptides with trifluoroacetic acid, pH 2, or acid denaturation of the immunoaffinity purified class I-peptide complexes. These methods are not feasible for CTL induction, since it is important to remove the endogenous peptides while preserving APC viability and an optimal metabolic state which is critical for antigen presentation. Mild acid solutions of pH 3 such as glycine or citrate -phosphate buffers have been used to identify endogenous peptides and to identify tumor associated T cell epitopes. The treatment is especially effective, in that only the MHC class I molecules are destabilized (and associated peptides released), while other surface antigens remain intact, including MHC class II molecules. Most importantly, treatment of cells with the mild acid solutions do not affect the cell's viability or metabolic state. The mild acid treatment is rapid since the stripping of the

endogenous peptides occurs in two minutes at 4°C and the APC is ready to perform its function after the appropriate peptides are loaded. The technique is utilized herein to make peptide-specific APCs for the generation of primary antigen- specific CTL. The resulting APC are efficient in inducing peptide- specific CD8+ CTL.

[00341] Activated CD8+ cells may be effectively separated from the stimulator cells using one of a variety of known methods. For example, monoclonal antibodies specific for the stimulator cells, for the peptides loaded onto the stimulator cells, or for the CD8+ cells (or a segment thereof) may be utilized to bind their appropriate complementary ligand. Antibody-tagged molecules may then be extracted from the stimulator-effector cell admixture via appropriate means, e.g., via well-known immunoprecipitation or immunoassay methods.

[00342] Effective, cytotoxic amounts of the activated CD8+ cells can vary between in vitro and in vivo uses, as well as with the amount and type of cells that are the ultimate target of these killer cells. The amount can also vary depending on the condition of the patient and should be determined via consideration of all appropriate factors by the practitioner. Preferably, however, about 1 X 10^6 to about 1 X 10^{12}, more preferably about 1 X 10^8 to about 1 X 10^{11}, and even more preferably, about 1 X 10^9 to about 1 X 10^{10} activated CD8+ cells are utilized for adult humans, compared to about 5 X 10^6 - 5 X 10^7 cells used in mice.

[00343] Preferably, as discussed herein, the activated CD8+ cells are harvested from the cell culture prior to administration of the CD8+ cells to the individual being treated. It is important to note, however, that unlike other present and proposed treatment modalities, the present method uses a cell culture system that is not tumorigenic. Therefore, if complete separation of stimulator cells and activated CD8+ cells are not achieved, there is no inherent danger known to be associated with the administration of a small number of stimulator cells, whereas administration of mammalian tumor-promoting cells may be extremely hazardous.

[00344] Methods of re-introducing cellular components are known in the art and include procedures such as those exemplified in U.S. Patent No. 4,844,893 to Honsik, et al. and U.S. Patent No. 4,690,915 to Rosenberg. For example, administration of activated CD8+ cells via intravenous infusion is appropriate.

[00345] The practice of the present invention employs, unless otherwise indicated, conventional techniques of molecular biology (including recombinant techniques), microbiology, cell biology, biochemistry and immunology, which are well within the purview of the skilled

artisan. Such techniques are explained fully in the literature, such as, "Molecular Cloning: A Laboratory Manual", second edition (Sambrook, 1989); "Oligonucleotide Synthesis" (Gait, 1984); "Animal Cell Culture" (Freshney, 1987); "Methods in Enzymology" "Handbook of Experimental Immunology" (Wei, 1996); "Gene Transfer Vectors for Mammalian Cells" (Miller and Calos, 1987); "Current Protocols in Molecular Biology" (Ausubel, 1987); "PCR: The Polymerase Chain Reaction", (Mullis, 1994); "Current Protocols in Immunology" (Coligan, 1991). These techniques are applicable to the production of the polynucleotides and polypeptides of the invention, and, as such, may be considered in making and practicing the invention. Particularly useful techniques for particular embodiments are discussed in the sections that follow.

Therapeutic Methods

[00346] The present invention provides methods of inducing a neoplasia/tumor specific immune response in a subject, vaccinating against a neoplasia/tumor, treating and or alleviating a symptom of cancer in a subject by administering the subject a plurality of neoantigenic peptides or composition of the invention.

[00347] According to the invention, the herein-described neoplasia vaccine or immunogenic composition may be used for a patient that has been diagnosed as having cancer, or at risk of developing cancer.

[00348] The claimed combination of the invention is administered in an amount sufficient to induce a CTL response.

Additional Therapies

[00349] The tumor specific neoantigen peptides and pharmaceutical compositions described herein can also be administered in a combination therapy with another agent, for example a therapeutic agent. In certain embodiments, the additional agents can be, but are not limited to, chemotherapeutic agents, anti-angiogenesis agents and agents that reduce immune-suppression.

[00350] The neoplasia vaccine or immunogenic composition can be administered before, during, or after administration of the additional agent. In embodiments, the neoplasia vaccine or immunogenic composition is administered before the first administration of the additional agent. In other embodiments, the neoplasia vaccine or immunogenic composition is administered after the first administration of the additional therapeutic agent (e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12,

13, 14 days or more). In embodiments, the neoplasia vaccine or immunogenic composition is administered simultaneously with the first administration of the additional therapeutic agent.

[00351] The therapeutic agent is for example, a chemotherapeutic or biotherapeutic agent, radiation, or immunotherapy. Any suitable therapeutic treatment for a particular cancer may be administered. Examples of chemotherapeutic and biotherapeutic agents include, but are not limited to, an angiogenesis inhibitor, such ashydroxy angiostatin K1-3, DL-α-Difluoromethyl-ornithine, endostatin, fumagillin, genistein, minocycline, staurosporine, and thalidomide; a DNA intercaltor/cross-linker, such as Bleomycin, Carboplatin, Carmustine, Chlorambucil, Cyclophosphamide, cis-Diammineplatinum(II) dichloride (Cisplatin), Melphalan, Mitoxantrone, and Oxaliplatin; a DNA synthesis inhibitor, such as (±)-Amethopterin (Methotrexate), 3-Amino-1,2,4-benzotriazine 1,4-dioxide, Aminopterin, Cytosine β-D-arabinofuranoside, 5-Fluoro-5'-deoxyuridine, 5-Fluorouracil, Ganciclovir, Hydroxyurea, and Mitomycin C; a DNA-RNA transcription regulator, such as Actinomycin D, Daunorubicin, Doxorubicin, Homoharringtonine, and Idarubicin; an enzyme inhibitor, such as S(+)-Camptothecin, Curcumin, (-)-Deguelin, 5,6-Dichlorobenzimidazole 1-β-D-ribofuranoside, Etoposide, Formestane, Fostriecin, Hispidin, 2-Imino-1-imidazoli-dineacetic acid (Cyclocreatine), Mevinolin, Trichostatin A, Tyrphostin AG 34, and Tyrphostin AG 879; a gene regulator, such as 5-Aza-2'-deoxycytidine, 5-Azacytidine, Cholecalciferol (Vitamin D3), 4-Hydroxytamoxifen, Melatonin, Mifepristone, Raloxifene, all trans-Retinal (Vitamin A aldehyde), Retinoic acid all trans (Vitamin A acid), 9-cis-Retinoic Acid, 13-cis-Retinoic acid, Retinol (Vitamin A), Tamoxifen, and Troglitazone; a microtubule inhibitor, such as Colchicine, docetaxel, Dolastatin 15, Nocodazole, Paclitaxel, Podophyllotoxin, Rhizoxin, Vinblastine, Vincristine, Vindesine, and Vinorelbine (Navelbine); and an unclassified therapeutic agent, such as 17-(Allylamino)-17-demethoxygeldanamycin, 4-Amino-1,8-naphthalimide, Apigenin, Brefeldin A, Cimetidine, Dichloromethylene-diphosphonic acid, Leuprolide (Leuprorelin), Luteinizing Hormone-Releasing Hormone, Pifithrin-α, Rapamycin, Sex hormone-binding globulin, Thapsigargin, and Urinary trypsin inhibitor fragment (Bikunin). The therapeutic agent may be altretamine, amifostine, asparaginase, capecitabine, cladribine, cisapride, cytarabine, dacarbazine (DTIC), dactinomycin, dronabinol, epoetin alpha, filgrastim, fludarabine, gemcitabine, granisetron, ifosfamide, irinotecan, lansoprazole, levamisole, leucovorin, megestrol, mesna, metoclopramide, mitotane, omeprazole, ondansetron, pilocarpine, prochloroperazine, or topotecan hydrochloride. The therapeutic agent may be a monoclonal

antibody or small molecule such as rituximab (Rituxan®), alemtuzumab (Campath®), Bevacizumab (Avastin®), Cetuximab (Erbitux®), panitumumab (Vectibix®), and trastuzumab (Herceptin®), Vemurafenib (Zelboraf®) imatinib mesylate (Gleevec®), erlotinib (Tarceva®), gefitinib (Iressa®), Vismodegib (Erivedge™), 90Y-ibritumomab tiuxetan, 131I-tositumomab, ado-trastuzumab emtansine, lapatinib (Tykerb®), pertuzumab (Perjeta™), ado-trastuzumab emtansine (Kadcyla™), regorafenib (Stivarga®), sunitinib (Sutent®), Denosumab (Xgeva®), sorafenib (Nexavar®), pazopanib (Votrient®), axitinib (Inlyta®), dasatinib (Sprycel®), nilotinib (Tasigna®), bosutinib (Bosulif®), ofatumumab (Arzerra®), obinutuzumab (Gazyva™), ibrutinib (Imbruvica™), idelalisib (Zydelig®), crizotinib (Xalkori®), erlotinib (Tarceva®), afatinib dimaleate (Gilotrif®), ceritinib (LDK378/Zykadia), Tositumomab and 131I-tositumomab (Bexxar®), ibritumomab tiuxetan (Zevalin®), brentuximab vedotin (Adcetris®), bortezomib (Velcade®), siltuximab (Sylvant™), trametinib (Mekinist®), dabrafenib (Tafinlar®), pembrolizumab (Keytruda®), carfilzomib (Kyprolis®), Ramucirumab (Cyramza™), Cabozantinib (Cometriq™), vandetanib (Caprelsa®), Optionally, the therapeutic agent is a neoantigen. The therapeutic agent may be a cytokine such as interferons (INFs), interleukins (ILs), or hematopoietic growth factors. The therapeutic agent may be INF-α, IL-2, Aldesleukin, IL-2, Erythropoietin, Granulocyte-macrophage colony-stimulating factor (GM-CSF) or granulocyte colony-stimulating factor. The therapeutic agent may be a targeted therapy such as toremifene (Fareston®), fulvestrant (Faslodex®), anastrozole (Arimidex®), exemestane (Aromasin®), letrozole (Femara®), ziv-aflibercept (Zaltrap®), Alitretinoin (Panretin®), temsirolimus (Torisel®), Tretinoin (Vesanoid®), denileukin diftitox (Ontak®), vorinostat (Zolinza®), romidepsin (Istodax®), bexarotene (Targretin®), pralatrexate (Folotyn®), lenaliomide (Revlimid®), belinostat (Beleodaq™), lenaliomide (Revlimid®), pomalidomide (Pomalyst®), Cabazitaxel (Jevtana®), enzalutamide (Xtandi®), abiraterone acetate (Zytiga®), radium 223 chloride (Xofigo®), or everolimus (Afinitor®). Aditionally, the therapeutic agent may be an epigenetic targeted drug such as HDAC inhibitors, kinase inhibitors, DNA methyltransferase inhibitors, histone demethylase inhibitors, or histone methylation inhibitors. The epigenetic drugs may be Azacitidine (Vidaza), Decitabine (Dacogen), Vorinostat (Zolinza), Romidepsin (Istodax), or Ruxolitinib (Jakafi). For prostate cancer treatment, a preferred chemotherapeutic agent with which anti- CTLA-4 can be combined is paclitaxel (TAXOL).

[00352] In certain embodiments, the one or more additional agents are one or more anti-glucocorticoid-induced tumor necrosis factor family receptor (GITR) agonistic antibodies. GITR is a costimulatory molecule for T lymphocytes, modulates innate and adaptive immune system and has been found to participate in a variety of immune responses and inflammatory processes. GITR was originally described by Nocentini et al. after being cloned from dexamethasone-treated murine T cell hybridomas (Nocentini et al. Proc Natl Acad Sci USA 94:6216–6221.1997). Unlike CD28 and CTLA-4, GITR has a very low basal expression on naive CD4+ and CD8+ T cells (Ronchetti et al. Eur J Immunol 34:613–622. 2004). The observation that GITR stimulation has immunostimulatory effects in vitro and induced autoimmunity in vivo prompted the investigation of the antitumor potency of triggering this pathway. A review of Modulation Of Ctla 4 And Gitr For Cancer Immunotherapy can be found in Cancer Immunology and Immunotherapy (Avogadri et al. Current Topics in Microbiology and Immunology 344. 2011). Other agents that can contribute to relief of immune suppression include checkpoint inhibitors targeted at another member of the CD28/CTLA4 Ig superfamily such as BTLA, LAG3, ICOS, PDL1 or KIR (Page et a, Annual Review of Medicine 65:27 (2014)). In further additional embodiments, the checkpoint inhibitor is targeted at a member of the TNFR superfamily such as CD40, OX40, CD137, GITR, CD27 or TIM-3. In some cases targeting a checkpoint inhibitor is accomplished with an inhibitory antibody or similar molecule. In other cases, it is accomplished with an agonist for the target; examples of this class include the stimulatory targets OX40 and GITR.

[00353] In certain embodiments, the one or more additional agents are synergistic in that they increase immunogenicity after treatment. In one embodiment the additional agent allows for lower toxicity and/or lower discomfort due to lower doses of the additional therapeutic agents or any components of the combination therapy described herein. In another embodiment the additional agent results in longer lifespan due to increased effectiveness of the combination therapy described herein. Chemotherapeutic treatments that enhance the immunological response in a patient have been reviewed (Zitvogel et al., Immunological aspects of cancer chemotherapy. Nat Rev Immunol. 2008 Jan;8(1):59-73). Aditionally, chemotherapeutic agents can be administered safely with immunotherapy without inhibiting vaccine specific T-cell responses (Perez et al., A new era in anticancer peptide vaccines. Cancer May 2010). In one embodiment the additional agent is administered to increase the efficacy of the therapy described herein. In

one embodiment the additional agent is a chemotherapy treatment. In one embodiment low doses of chemotherapy potentiate delayed-type hypersensitivity (DTH) responses. In one embodiment the chemotheray agent targets regulatory T-cells. In one embodiment cyclophosphamide is the therapeutic agent. In one embodiment cyclophosphamide is administered prior to vaccination. In one embodiment cyclophosphamide is administered as a single dose before vaccination (Walter et al., Multipeptide immune response to cancer vaccine IMA901 after single-dose cyclophosphamide associates with longer patient survival. Nature Medicine; 18:8 2012). In another embodiment, cyclophosphamide is administered according to a metronomic program, where a daily dose is administered for one month (Ghiringhelli et al., Metronomic cyclophosphamide regimen selectively depletes CD4+CD25+ regulatory T cells and restores T and NK effector functions in end stage cancer patients. Cancer Immunol Immunother 2007 56:641–648). In another embodiment taxanes are administered before vaccination to enhance T-cell and NK-cell functions (Zitvogel et al., 2008). In another embodiment a low dose of a chemotherapeutic agent is administered with the therapy described herein. In one embodiment the chemotherapeutic agent is estramustine. In one embodiment the cancer is hormone resistant prostate cancer. A ≥50% decrease in serum prostate specific antigen (PSA) was seen in 8.7% of advanced hormone refractory prostate cancer patients by personalized vaccination alone, whereas such a decrease was seen in 54% of patients when the personalized vaccination was combined with a low dose of estramustine (Itoh et al., Personalized peptide vaccines: A new therapeutic modality for cancer. Cancer Sci 2006; 97: 970–976). In another embodiment glucocorticoids are administered with or before the therapy described herein (Zitvogel et al., 2008). In another embodiment glucocorticoids are administered after the therapy described herein. In another embodiment Gemcitabine is administered before, simultaneously, or after the therapy described herein to enhance the frequency of tumor specific CTL precursors (Zitvogel et al., 2008). In another embodiment 5-fluorouracil is administered with the therapy described herein as synergistic effects were seen with a peptide based vaccine (Zitvogel et al., 2008). In another embodiment an inhibitor of Braf, such as Vemurafenib, is used as an additional agent. Braf inhibition has been shown to be associated with an increase in melanoma antigen expression and T-cell infiltrate and a decrease in immunosuppressive cytokines in tumors of treated patients (Frederick et al., BRAF inhibition is associated with enhanced melanoma antigen expression and a more favorable tumor microenvironment in patients with metastatic melanoma. Clin Cancer

Res. 2013; 19:1225-1231). In another embodiment an inhibitor of tyrosine kinases is used as an additional agent. In one embodiment the tyrosine kinase inhibitor is used before vaccination with the therapy described herein. In one embodiment the tyrosine kinase inhibitor is used simultaneously with the therapy described herein. In another embodiment the tyrosine kinase inhibitor is used to create a more immune permissive environment. In another embodiment the tyrosine kinase inhibitor is sunitinib or imatinib mesylate. It has previously been shown that favorable outcomes could be achieved with sequential administration of continuous daily dosing of sunitinib and recombinant vaccine (Farsaci et al., Consequence of dose scheduling of sunitinib on host immune response elements and vaccine combination therapy. Int J Cancer; 130: 1948-1959). Sunitinib has also been shown to reverse type-1 immune suppression using a daily dose of 50 mg/day (Finke et al., Sunitinib Reverses Type-1 Immune Suppression and Decreases T-Regulatory Cells in Renal Cell Carcinoma Patients. Clin Cancer Res 2008;14(20)). In another embodiment targeted therapies are administered in combination with the therapy described herein. Doses of targeted therapies has been described previously (Alvarez, Present and future evolution of advanced breast cancer therapy. Breast Cancer Research 2010, 12(Suppl 2):S1). In another embodiment temozolomide is administered with the therapy described herein. In one embodiment temozolomide is administered at 200 mg/day for 5 days every fourth week of a combination therapy with the therapy described herein. Results of a similar strategy have been shown to have low toxicity (Kyte et al., Telomerase Peptide Vaccination Combined with Temozolomide: A Clinical Trial in Stage IV Melanoma Patients. Clin Cancer Res; 17(13) 2011). In another embodiment the therapy is administered with an additional therapeutic agent that results in lymphopenia. In one embodiment the additional agent is temozolomide. An immune response can still be induced under these conditions (Sampson et al., Greater chemotherapy-induced lymphopenia enhances tumor-specific immune responses that eliminate EGFRvIII-expressing tumor cells in patients with glioblastoma. Neuro-Oncology 13(3):324–333, 2011).

[00354] Patients in need thereof may receive a series of priming vaccinations with a mixture of tumor-specific peptides. Additionally, over a 4 week period the priming may be followed by two boosts during a maintenance phase. All vaccinations are subcutaneously delivered. The vaccine or immunogenic composition is evaluated for safety, tolerability, immune response and clinical effect in patients and for feasibility of producing vaccine or immunogenic composition and successfully initiating vaccination within an appropriate time frame. The first cohort can

consist of 5 patients, and after safety is adequately demonstrated, an additional cohort of 10 patients may be enrolled. Peripheral blood is extensively monitored for peptide-specific T-cell responses and patients are followed for up to two years to assess disease recurrence.

Administering a combination therapy consistent with standard of care

[00355] In another aspect, the therapy described herein provides selecting the appropriate point to administer a combination therapy in relation to and within the standard of care for the cancer being treated for a patient in need thereof. The studies described herein show that the combination therapy can be effectively administered even within the standard of care that includes surgery, radiation, or chemotherapy. The standards of care for the most common cancers can be found on the website of National Cancer Institute (www.cancer.gov/cancertopics). The standard of care is the current treatment that is accepted by medical experts as a proper treatment for a certain type of disease and that is widely used by healthcare professionals. Standard or care is also called best practice, standard medical care, and standard therapy. Standards of Care for cancer generally include surgery, lymph node removal, radiation, chemotherapy, targeted therapies, antibodies targeting the tumor, and immunotherapy. Immunotherapy can include checkpoint blockers (CBP), chimeric antigen receptors (CARs), and adoptive T-cell therapy. The combination therapy described herein can be incorporated within the standard of care. The combination therapy described herein may also be administered where the standard of care has changed due to advances in medicine.

[00356] Incorporation of the combination therapy described herein may depend on a treatment step in the standard of care that can lead to activation of the immune system. Treatment steps that can activate and function synergistically with the combination therapy have been described herein. The therapy can be advantageously administered simultaneously or after a treatment that activates the immune system.

[00357] Incorporation of the combination therapy described herein may depend on a treatment step in the standard of care that causes the immune system to be suppressed. Such treatment steps may include irradiation, high doses of alkylating agents and/or methotrexate, steroids such as glucosteroids, surgery, such as to remove the lymph nodes, imatinib mesylate, high doses of TNF, and taxanes (Zitvogel et al., 2008). The combination therapy may be administered before such steps or may be administered after.

[00358] In one embodiment the combination therapy may be administered after bone marrow transplants and peripheral blood stem cell transplantation. Bone marrow transplantation and peripheral blood stem cell transplantation are procedures that restore stem cells that were destroyed by high doses of chemotherapy and/or radiation therapy. After being treated with high-dose anticancer drugs and/or radiation, the patient receives harvested stem cells, which travel to the bone marrow and begin to produce new blood cells. A "mini-transplant" uses lower, less toxic doses of chemotherapy and/or radiation to prepare the patient for transplant. A "tandem transplant" involves two sequential courses of high-dose chemotherapy and stem cell transplant. In autologous transplants, patients receive their own stem cells. In syngeneic transplants, patients receive stem cells from their identical twin. In allogeneic transplants, patients receive stem cells from their brother, sister, or parent. A person who is not related to the patient (an unrelated donor) also may be used. In some types of leukemia, the graft-versus-tumor (GVT) effect that occurs after allogeneic BMT and PBSCT is crucial to the effectiveness of the treatment. GVT occurs when white blood cells from the donor (the graft) identify the cancer cells that remain in the patient's body after the chemotherapy and/or radiation therapy (the tumor) as foreign and attack them. Immunotherapy with the combination therapy described herein can take advantage of this by vaccinating after a transplant. Additionally, the transferred cells may be presented with neoantigens of the combination therapy described herein before transplantation.

[00359] In one embodiment the combination therapy is administered to a patient in need thereof with a cancer that requires surgery. In one embodiment the combination therapy described herein is administered to a patient in need thereof in a cancer where the standard of care is primarily surgery followed by treatment to remove possible micro-metastases, such as breast cancer. Breast cancer is commonly treated by various combinations of surgery, radiation therapy, chemotherapy, and hormone therapy based on the stage and grade of the cancer. Adjuvant therapy for breast cancer is any treatment given after primary therapy to increase the chance of long-term survival. Neoadjuvant therapy is treatment given before primary therapy. Adjuvant therapy for breast cancer is any treatment given after primary therapy to increase the chance of long-term disease-free survival. Primary therapy is the main treatment used to reduce or eliminate the cancer. Primary therapy for breast cancer usually includes surgery, a mastectomy (removal of the breast) or a lumpectomy (surgery to remove the tumor and a small amount of normal tissue around it; a type of breast-conserving surgery). During either type of

surgery, one or more nearby lymph nodes are also removed to see if cancer cells have spread to the lymphatic system. When a woman has breast-conserving surgery, primary therapy almost always includes radiation therapy. Even in early-stage breast cancer, cells may break away from the primary tumor and spread to other parts of the body (metastasize). Therefore, doctors give adjuvant therapy to kill any cancer cells that may have spread, even if they cannot be detected by imaging or laboratory tests.

[00360] In one embodiment the combination therapy is administered consistent with the standard of care for Ductal carcinoma *in situ* (DCIS). The standard of care for this breast cancer type is:

1. Breast-conserving surgery and radiation therapy with or without tamoxifen.
2. Total mastectomy with or without tamoxifen.
3. Breast-conserving surgery without radiation therapy.

[00361] The combination therapy may be administered before breast conserving surgery or total mastectomy to shrink the tumor before surgery. In another embodiment the combination therapy can be administered as an adjuvant therapy to remove any remaining cancer cells.

In another embodiment patients diagnosed with stage I, II, IIIA, and Operable IIIC breast cancer are treated with the combination therapy as described herein. The standard of care for this breast cancer type is:

1. Local-regional treatment:

- Breast-conserving therapy (lumpectomy, breast radiation, and surgical staging of the axilla).
- Modified radical mastectomy (removal of the entire breast with level I–II axillary dissection) with or without breast reconstruction.
- Sentinel node biopsy.

2. Adjuvant radiation therapy postmastectomy in axillary node-positive tumors:

- For one to three nodes: unclear role for regional radiation (infra/supraclavicular nodes, internal mammary nodes, axillary nodes, and chest wall).
- For more than four nodes or extranodal involvement: regional radiation is advised.

3. Adjuvant systemic therapy

[00362] In one embodiment the combination therapy is administered as a neoadjuvant therapy to shrink the tumor. In another embodiment the combination is administered as an adjuvant systemic therapy.

[00363] In another embodiment patients diagnosed with inoperable stage IIIB or IIIC or inflammatory breast cancer are treated with the combination therapy as described herein. The standard of care for this breast cancer type is:

1. Multimodality therapy delivered with curative intent is the standard of care for patients with clinical stage IIIB disease.

2. Initial surgery is generally limited to biopsy to permit the determination of histology, estrogen-receptor (ER) and progesterone-receptor (PR) levels, and human epidermal growth factor receptor 2 (HER2/neu) overexpression. Initial treatment with anthracycline-based chemotherapy and/or taxane-based therapy is standard. For patients who respond to neoadjuvant chemotherapy, local therapy may consist of total mastectomy with axillary lymph node dissection followed by postoperative radiation therapy to the chest wall and regional lymphatics. Breast-conserving therapy can be considered in patients with a good partial or complete response to neoadjuvant chemotherapy. Subsequent systemic therapy may consist of further chemotherapy. Hormone therapy should be administered to patients whose tumors are ER-positive or unknown. All patients should be considered candidates for clinical trials to evaluate the most appropriate fashion in which to administer the various components of multimodality regimens.

[00364] In one embodiment the combination therapy is administered as part of the various components of multimodality regimens. In another embodiment the combination therapy is administered before, simultaneously with, or after the multimodality regimens. In another embodiment the combination therapy is administered based on synergism between the modalities. In another embodiment the combination therapy is administered after treatment with anthracycline-based chemotherapy and/or taxane-based therapy (Zitvogel et al., 2008). Treatment after administering the combination therapy may negatively affect dividing effector T-cells. The combination therapy may also be administered after radiation.

[00365] In another embodiment the combination therapy described herein is used in the treatment in a cancer where the standard of care is primarily not surgery and is primarily based on systemic treatments, such as Chronic Lymphocytic Leukemia (CLL).

[00366] In another embodiment patients diagnosed with stage I, II, III, and IV Chronic Lymphocytic Leukemia are treated with the combination therapy as described herein. The standard of care for this cancer type is:

1. Observation in asymptomatic or minimally affected patients
2. Rituximab
3. Ofatumomab
4. Oral alkylating agents with or without corticosteroids
5. Fludarabine, 2-chlorodeoxyadenosine, or pentostatin
6. Bendamustine
7. Lenalidomide
8. Combination chemotherapy.

   combination chemotherapy regimens include the following:

   - Fludarabine plus cyclophosphamide plus rituximab.
   - Fludarabine plus rituximab as seen in the CLB-9712 and CLB-9011 trials.
   - Fludarabine plus cyclophosphamide versus fludarabine plus cyclophosphamide plus rituximab.
   - Pentostatin plus cyclophosphamide plus rituximab as seen in the MAYO-MC0183 trial, for example.
   - Ofatumumab plus fludarabine plus cyclophosphamide.
   - CVP: cyclophosphamide plus vincristine plus prednisone.
   - CHOP: cyclophosphamide plus doxorubicin plus vincristine plus prednisone.
   - Fludarabine plus cyclophosphamide versus fludarabine as seen in the E2997 trial [NCT00003764] and the LRF-CLL4 trial, for example.
   - Fludarabine plus chlorambucil as seen in the CLB-9011 trial, for example.
9. Involved-field radiation therapy.
10. Alemtuzumab
11. Bone marrow and peripheral stem cell transplantations are under clinical evaluation.
12. Ibrutinib

[00367] In one embodiment the combination therapy is administered before, simultaneously with or after treatment with Rituximab or Ofatumomab. As these are monoclonal antibodies that target B-cells, treatment with the combination therapy may be synergistic. In another

embodiment the combination therapy is administered after treatment with oral alkylating agents with or without corticosteroids, and Fludarabine, 2-chlorodeoxyadenosine, or pentostatin, as these treatments may negatively affect the immune system if administered before. In one embodiment bendamustine is administered with the combination therapy in low doses based on the results for prostate cancer described herein. In one embodiment the combination therapy is administered after treatment with bendamustine.

[00368] In another embodiment, therapies targeted to specific recurrent mutations in genes that include extracellular domains are used in the treatment of a patient in need thereof suffering from cancer. The genes may advantageously be well-expressed genes. Well expressed may be expressed in "transcripts per million" (TPM). A TPM greater than 100 is considered well expressed. Well expressed genes may be FGFR3, ERBB3, EGFR, MUC4, PDGFRA, MMP12, TMEM52, and PODXL. The therapies may be a ligand capable of binding to an extracellular neoantigen epitope. Such ligands are well known in the art and may include therapeutic antibodies or fragments thereof, antibody-drug conjugates, engineered T cells, or aptamers. Engineered T cells may be chimeric antigen receptors (CARs). Antibodies may be fully humanized, humanized, or chimeric. The antibody fragments may be a nanobody, Fab, Fab', (Fab')2, Fv, ScFv, diabody, triabody, tetrabody, Bis-scFv, minibody, Fab2, or Fab3 fragment. Antibodies may be developed against tumor-specific neoepitopes using known methods in the art.

Adoptive cell transfer (ACT)

[00369] Aspects of the invention involve the adoptive transfer of immune system cells, such as T cells, specific for selected antigens, such as tumor associated antigens (see Maus et al., 2014, Adoptive Immunotherapy for Cancer or Viruses, Annual Review of Immunology, Vol. 32: 189-225; Rosenberg and Restifo, 2015, Adoptive cell transfer as personalized immunotherapy for human cancer, Science Vol. 348 no. 6230 pp. 62-68; Restifo et al., 2015, Adoptive immunotherapy for cancer: harnessing the T cell response. Nat. Rev. Immunol. 12(4): 269-281; and Jenson and Riddell, 2014, Design and implementation of adoptive therapy with chimeric antigen receptor-modified T cells. Immunol Rev. 257(1): 127–144). Various strategies may for example be employed to genetically modify T cells by altering the specificity of the T cell receptor (TCR) for example by introducing new TCR α and β chains with selected peptide

specificity (see U.S. Patent No. 8,697,854; PCT Patent Publications: WO2003020763, WO2004033685, WO2004044004, WO2005114215, WO2006000830, WO2008038002, WO2008039818, WO2004074322, WO2005113595, WO2006125962, WO2013166321, WO2013039889, WO2014018863, WO2014083173; U.S. Patent No. 8,088,379).

[00370] As an alternative to, or addition to, TCR modifications, chimeric antigen receptors (CARs) may be used in order to generate immunoresponsive cells, such as T cells, specific for selected targets, such as malignant cells, with a wide variety of receptor chimera constructs having been described (see U.S. Patent Nos. 5,843,728; 5,851,828; 5,912,170; 6,004,811; 6,284,240; 6,392,013; 6,410,014; 6,753,162; 8,211,422; and, PCT Publication WO9215322). Alternative CAR constructs may be characterized as belonging to successive generations. First-generation CARs typically consist of a single-chain variable fragment of an antibody specific for an antigen, for example comprising a V_L linked to a V_H of a specific antibody, linked by a flexible linker, for example by a CD8α hinge domain and a CD8α transmembrane domain, to the transmembrane and intracellular signaling domains of either CD3ζ or FcRγ (scFv-CD3ζ or scFv-FcRγ; see U.S. Patent No. 7,741,465; U.S. Patent No. 5,912,172; U.S. Patent No. 5,906,936). Second-generation CARs incorporate the intracellular domains of one or more costimulatory molecules, such as CD28, OX40 (CD134), or 4-1BB (CD137) within the endodomain (for example scFv-CD28/OX40/4-1BB-CD3ζ; see U.S. Patent Nos. 8,911,993; 8,916,381; 8,975,071; 9,101,584; 9,102,760; 9,102,761). Third-generation CARs include a combination of costimulatory endodomains, such a CD3ζ-chain, CD97, GDI la-CD18, CD2, ICOS, CD27, CD154, CDS, OX40, 4-1BB, or CD28 signaling domains (for example scFv-CD28-4-1BB-CD3ζ or scFv-CD28-OX40-CD3ζ; see U.S. Patent No. 8,906,682; U.S. Patent No. 8,399,645; U.S. Pat. No. 5,686,281; PCT Publication No. WO2014134165; PCT Publication No. WO2012079000). Alternatively, costimulation may be orchestrated by expressing CARs in antigen-specific T cells, chosen so as to be activated and expanded following engagement of their native αβTCR, for example by antigen on professional antigen-presenting cells, with attendant costimulation. In addition, additional engineered receptors may be provided on the immunoresponsive cells, for example to improve targeting of a T-cell attack and/or minimize side effects.

[00371] Alternative techniques may be used to transform target immunoresponsive cells, such as protoplast fusion, lipofection, transfection or electroporation. A wide variety of vectors may be used, such as retroviral vectors, lentiviral vectors, adenoviral vectors, adeno-associated viral

vectors, plasmids or transposons, such as a Sleeping Beauty transposon (see U.S. Patent Nos. 6,489,458; 7,148,203; 7,160,682; 7,985,739; 8,227,432), may be used to introduce CARs, for example using 2nd generation antigen-specific CARs signaling through CD3ζ and either CD28 or CD137. Viral vectors may for example include vectors based on HIV, SV40, EBV, HSV or BPV.

[00372] Cells that are targeted for transformation may for example include T cells, Natural Killer (NK) cells, cytotoxic T lymphocytes (CTL), regulatory T cells, human embryonic stem cells, tumor-infiltrating lymphocytes (TIL) or a pluripotent stem cell from which lymphoid cells may be differentiated. T cells expressing a desired CAR may for example be selected through co-culture with γ-irradiated activating and propagating cells (AaPC), which co-express the cancer antigen and co-stimulatory molecules. The engineered CAR T-cells may be expanded, for example by co-culture on AaPC in presence of soluble factors, such as IL-2 and IL-21. This expansion may for example be carried out so as to provide memory CAR+ T cells (which may for example be assayed by non-enzymatic digital array and/or multi-panel flow cytometry). In this way, CAR T cells may be provided that have specific cytotoxic activity against antigen-bearing tumors (optionally in conjunction with production of desired chemokines such as interferon-γ). CAR T cells of this kind may for example be used in animal models, for example to treat tumor xenografts.

[00373] Approaches such as the foregoing may be adapted to provide methods of treating and/or increasing survival of a subject having a disease, such as a neoplasia, for example by administering an effective amount of an immunoresponsive cell comprising an antigen recognizing receptor that binds a selected antigen, wherein the binding activates the immunoreponsive cell, thereby treating or preventing the disease (such as a neoplasia, a pathogen infection, an autoimmune disorder, or an allogeneic transplant reaction).

[00374] In one embodiment, the treatment can be administrated into patients undergoing an immunosuppressive treatment. The cells or population of cells, may be made resistant to at least one immunosuppressive agent due to the inactivation of a gene encoding a receptor for such immunosuppressive agent. Not being bound by a theory, the immunosuppressive treatment should help the selection and expansion of the immunoresponsive or T cells according to the invention within the patient.

[00375] The administration of the cells or population of cells according to the present invention may be carried out in any convenient manner, including by aerosol inhalation, injection, ingestion, transfusion, implantation or transplantation. The cells or population of cells may be administered to a patient subcutaneously, intradermally, intratumorally, intranodally, intramedullary, intramuscularly, by intravenous or intralymphatic injection, or intraperitoneally. In one embodiment, the cell compositions of the present invention are preferably administered by intravenous injection.

[00376] The administration of the cells or population of cells can consist of the administration of 10^4- 10^9 cells per kg body weight, preferably 10^5 to 10^6 cells/kg body weight including all integer values of cell numbers within those ranges. Dosing in CAR T cell therapies may for example involve administration of from 10^6 to 10^9 cells/kg, with or without a course of lymphodepletion, for example with cyclophosphamide. The cells or population of cells can be administrated in one or more doses. In another embodiment, the effective amount of cells are administrated as a single dose. In another embodiment, the effective amount of cells are administrated as more than one dose over a period time. Timing of administration is within the judgment of managing physician and depends on the clinical condition of the patient. The cells or population of cells may be obtained from any source, such as a blood bank or a donor. While individual needs vary, determination of optimal ranges of effective amounts of a given cell type for a particular disease or conditions are within the skill of one in the art. An effective amount means an amount which provides a therapeutic or prophylactic benefit. The dosage administrated will be dependent upon the age, health and weight of the recipient, kind of concurrent treatment, if any, frequency of treatment and the nature of the effect desired.

[00377] In another embodiment, the effective amount of cells or composition comprising those cells are administrated parenterally. The administration can be an intravenous administration. The administration can be directly done by injection within a tumor.

[00378] To guard against possible adverse reactions, engineered immunoresponsive cells may be equipped with a transgenic safety switch, in the form of a transgene that renders the cells vulnerable to exposure to a specific signal. For example, the herpes simplex viral thymidine kinase (TK) gene may be used in this way, for example by introduction into allogeneic T lymphocytes used as donor lymphocyte infusions following stem cell transplantation (Greco, et al., Improving the safety of cell therapy with the TK-suicide gene. Front. Pharmacol. 2015; 6:

95). In such cells, administration of a nucleoside prodrug such as ganciclovir or acyclovir causes cell death. Alternative safety switch constructs include inducible caspase 9, for example triggered by administration of a small-molecule dimerizer that brings together two nonfunctional icasp9 molecules to form the active enzyme. A wide variety of alternative approaches to implementing cellular proliferation controls have been described (see U.S. Patent Publication No. 20130071414; PCT Patent Publication WO2011146862; PCT Patent Publication WO2014011987; PCT Patent Publication WO2013040371; Zhou et al. BLOOD, 2014, 123/25:3895 – 3905; Di Stasi et al., The New England Journal of Medicine 2011; 365:1673-1683; Sadelain M, The New England Journal of Medicine 2011; 365:1735-173; Ramos et al., Stem Cells 28(6):1107-15 (2010)).

[00379] In a further refinement of adoptive therapies, genome editing may be used to tailor immunoresponsive cells to alternative implementations, for example providing edited CAR T cells (see Poirot et al., 2015, Multiplex genome edited T-cell manufacturing platform for "off-the-shelf" adoptive T-cell immunotherapies, Cancer Res 75 (18): 3853). Cells may be edited using any DNA targeting protein, including, but not limited to a CRISPR system, Zinc Finger binding protein, TALE or TALEN as known in the art. DNA targeting proteins may be delivered to an immune cell by any method known in the art. In preferred embodiments, cells are edited *ex vivo* and transferred to a subject in need thereof. Immunoresponsive cells, CAR T cells or any cells used for adoptive cell transfer may be edited. Editing may be performed to eliminate potential alloreactive T-cell receptors (TCR), disrupt the target of a chemotherapeutic agent, block an immune checkpoint, activate a T cell, and/or increase the differentiation and/or proliferation of functionally exhausted or dysfunctional CD8+ T-cells (see PCT Patent Publications: WO2013176915, WO2014059173, WO2014172606, WO2014184744, and WO2014191128). Editing may result in inactivation of a gene.

[00380] By inactivating a gene it is intended that the gene of interest is not expressed in a functional protein form. In a particular embodiment, the CRISPR system specifically catalyzes cleavage in one targeted gene thereby inactivating said targeted gene. The nucleic acid strand breaks caused are commonly repaired through the distinct mechanisms of homologous recombination or non-homologous end joining (NHEJ). However, NHEJ is an imperfect repair process that often results in changes to the DNA sequence at the site of the cleavage. Repair via non-homologous end joining (NHEJ) often results in small insertions or deletions (Indel) and can

be used for the creation of specific gene knockouts. Cells in which a cleavage induced mutagenesis event has occurred can be identified and/or selected by well-known methods in the art.

[00381] T cell receptors (TCR) are cell surface receptors that participate in the activation of T cells in response to the presentation of antigen. The TCR is generally made from two chains, α and β, which assemble to form a heterodimer and associates with the CD3-transducing subunits to form the T cell receptor complex present on the cell surface. Each α and β chain of the TCR consists of an immunoglobulin-like N-terminal variable (V) and constant (C) region, a hydrophobic transmembrane domain, and a short cytoplasmic region. As for immunoglobulin molecules, the variable region of the α and β chains are generated by V(D)J recombination, creating a large diversity of antigen specificities within the population of T cells. However, in contrast to immunoglobulins that recognize intact antigen, T cells are activated by processed peptide fragments in association with an MHC molecule, introducing an extra dimension to antigen recognition by T cells, known as MHC restriction. Recognition of MHC disparities between the donor and recipient through the T cell receptor leads to T cell proliferation and the potential development of graft versus host disease (GVHD). The inactivation of TCRα or TCRβ can result in the elimination of the TCR from the surface of T cells preventing recognition of alloantigen and thus GVHD. However, TCR disruption generally results in the elimination of the CD3 signaling component and alters the means of further T cell expansion.

[00382] Allogeneic cells are rapidly rejected by the host immune system. It has been demonstrated that, allogeneic leukocytes present in non-irradiated blood products will persist for no more than 5 to 6 days (Boni, Muranski et al. 2008 Blood 1;112(12):4746-54). Thus, to prevent rejection of allogeneic cells, the host's immune system usually has to be suppressed to some extent. However, in the case of adoptive cell transfer the use of immunosuppressive drugs also have a detrimental effect on the introduced therapeutic T cells. Therefore, to effectively use an adoptive immunotherapy approach in these conditions, the introduced cells would need to be resistant to the immunosuppressive treatment. Thus, in a particular embodiment, the present invention further comprises a step of modifying T cells to make them resistant to an immunosuppressive agent, preferably by inactivating at least one gene encoding a target for an immunosuppressive agent. An immunosuppressive agent is an agent that suppresses immune function by one of several mechanisms of action. An immunosuppressive agent can be, but is not

limited to a calcineurin inhibitor, a target of rapamycin, an interleukin-2 receptor α-chain blocker, an inhibitor of inosine monophosphate dehydrogenase, an inhibitor of dihydrofolic acid reductase, a corticosteroid or an immunosuppressive antimetabolite. The present invention allows conferring immunosuppressive resistance to T cells for immunotherapy by inactivating the target of the immunosuppressive agent in T cells. As non-limiting examples, targets for an immunosuppressive agent can be a receptor for an immunosuppressive agent such as: CD52, glucocorticoid receptor (GR), a FKBP family gene member and a cyclophilin family gene member.

[00383] Immune checkpoints are inhibitory pathways that slow down or stop immune reactions and prevent excessive tissue damage from uncontrolled activity of immune cells. In certain embodiments, the immune checkpoint targeted is the programmed death-1 (PD-1 or CD279) gene (*PDCD1*). In other embodiments, the immune checkpoint targeted is cytotoxic T-lymphocyte-associated antigen (CTLA-4). In additional embodiments, the immune checkpoint targeted is another member of the CD28 and CTLA4 Ig superfamily such as BTLA, LAG3, ICOS, PDL1 or KIR. In further additional embodiments, the immune checkpoint targeted is a member of the TNFR superfamily such as CD40, OX40, CD137, GITR, CD27 or TIM-3.

[00384] Additional immune checkpoints include Src homology 2 domain-containing protein tyrosine phosphatase 1 (SHP-1) (Watson HA, et al., SHP-1: the next checkpoint target for cancer immunotherapy? Biochem Soc Trans. 2016 Apr 15;44(2):356-62). SHP-1 is a widely expressed inhibitory protein tyrosine phosphatase (PTP). In T-cells, it is a negative regulator of antigen-dependent activation and proliferation. It is a cytosolic protein, and therefore not amenable to antibody-mediated therapies, but its role in activation and proliferation makes it an attractive target for genetic manipulation in adoptive transfer strategies, such as chimeric antigen receptor (CAR) T cells. Immune checkpoints may also include T cell immunoreceptor with Ig and ITIM domains (TIGIT/Vstm3/WUCAM/VSIG9) and VISTA (Le Mercier I, et al., (2015) Beyond CTLA-4 and PD-1, the generation Z of negative checkpoint regulators. Front. Immunol. 6:418).

[00385] WO2014172606 relates to the use of MT1 and/or MT1 inhibitors to increase proliferation and/or activity of exhausted CD8+ T-cells and to decrease CD8+ T-cell exhaustion (e.g., decrease functionally exhausted or unresponsive CD8+ immune cells). In certain embodiments, metallothioneins are targeted by gene editing in adoptively transferred T cells.

[00386] In certain embodiments, targets of gene editing may be at least one targeted locus involved in the expression of an immune checkpoint protein. Such targets may include, but are not limited to CTLA4, PPP2CA, PPP2CB, PTPN6, PTPN22, PDCD1, ICOS (CD278), PDL1, KIR, LAG3, HAVCR2, BTLA, CD160, TIGIT, CD96, CRTAM, LAIR1, SIGLEC7, SIGLEC9, CD244 (2B4), TNFRSF10B, TNFRSF10A, CASP8, CASP10, CASP3, CASP6, CASP7, FADD, FAS, TGFBRII, TGFRBRI, SMAD2, SMAD3, SMAD4, SMAD10, SKI, SKIL, TGIF1, IL10RA, IL10RB, HMOX2, IL6R, IL6ST, EIF2AK4, CSK, PAG1, SIT1, FOXP3, PRDM1, BATF, VISTA, GUCY1A2, GUCY1A3, GUCY1B2, GUCY1B3, MT1, MT2, CD40, OX40, CD137, GITR, CD27, SHP-1 or TIM-3. In preferred embodiments, the gene locus involved in the expression of PD-1 or CTLA-4 genes is targeted. In other preferred embodiments, combinations of genes are targeted, such as but not limited to PD-1 and TIGIT.

[00387] In other embodiments, at least two genes are edited. Pairs of genes may include, but are not limited to PD1 and TCRα, PD1 and TCRβ, CTLA-4 and TCRα, CTLA-4 and TCRβ, LAG3 and TCRα, LAG3 and TCRβ, Tim3 and TCRα, Tim3 and TCRβ, BTLA and TCRα, BTLA and TCRβ, BY55 and TCRα, BY55 and TCRβ, TIGIT and TCRα, TIGIT and TCRβ, B7H5 and TCRα, B7H5 and TCRβ, LAIR1 and TCRα, LAIR1 and TCRβ, SIGLEC10 and TCRα, SIGLEC10 and TCRβ, 2B4 and TCRα, 2B4 and TCRβ.

[00388] Whether prior to or after genetic modification of the T cells, the T cells can be activated and expanded generally using methods as described, for example, in U.S. Patents 6,352,694; 6,534,055; 6,905,680; 5,858,358; 6,887,466; 6,905,681; 7,144,575; 7,232,566; 7,175,843; 5,883,223; 6,905,874; 6,797,514; 6,867,041; and 7,572,631. T cells can be expanded *in vitro* or *in vivo*.

Selecting the patient population most likely to benefit from the therapy

[00389] In another aspect, the invention provides selecting for the patients in need thereof most likely to benefit from the therapy of the present invention. Although the compositions and methods of the present invention are typically applicable in a high proportion of subjects suffering from cancer, the method may still comprise one or more steps of selecting patients from the patient population who are likely to benefit. For instance, the method may comprise selecting subjects whose tumors contain one or more of the mutations represented in the neoantigenic peptides in the composition. In another embodiment, the method may comprise

selecting subjects having at least one HLA allele which binds to one or more neoepitopes represented in the neoantigenic peptides in the composition.

Vaccine or Immunogenic Composition Kits and Co-Packaging

[00390] In an aspect, the invention provides kits containing any one or more of the elements discussed herein to allow administration of the therapy. Elements may be provided individually or in combinations, and may be provided in any suitable container, such as a vial, a bottle, or a tube. In some embodiments, the kit includes instructions in one or more languages, for example in more than one language. In some embodiments, a kit comprises one or more reagents for use in a process utilizing one or more of the elements described herein. Reagents may be provided in any suitable container. For example, a kit may provide one or more delivery or storage buffers. Reagents may be provided in a form that is usable in a particular process, or in a form that requires addition of one or more other components before use (e.g. in concentrate or lyophilized form). A buffer can be any buffer, including but not limited to a sodium carbonate buffer, a sodium bicarbonate buffer, a borate buffer, a Tris buffer, a MOPS buffer, a HEPES buffer, and combinations thereof. In some embodiments, the buffer is alkaline. In some embodiments, the buffer has a pH from about 7 to about 10. In some embodiments, the kit comprises one or more of the vectors, proteins and/or one or more of the polynucleotides described herein. The kit may advantageously allow the provision of all elements of the systems of the invention. Kits can involve vector(s) and/or particle(s) and/or nanoparticle(s) containing or encoding RNA(s) for 1-50 or more neoantigen mutations to be administered to an animal, mammal, primate, rodent, etc., with such a kit including instructions for administering to such a eukaryote; and such a kit can optionally include any of the anti-cancer agents described herein. The kit may include any of the components above (e.g. vector(s) and/or particle(s) and/or nanoparticle(s) containing or encoding RNA(s) for 1-50 or more neoantigen mutations, neoantigen proteins or peptides) as well as instructions for use with any of the methods of the present invention.

[00391] In one embodiment the kit contains at least one vial with an immunogenic composition or vaccine. In one embodiment the kit contains at least one vial with an immunogenic composition or vaccine and at least one vial with an anticancer agent. In one embodiment kits may comprise ready to use components that are mixed and ready to administer.

In one aspect a kit contains a ready to use immunogenic or vaccine composition and a ready to use anti-cancer agent. The ready to use immunogenic or vaccine composition may comprise separate vials containing different pools of immunogenic compositions. The immunogenic compositions may comprise one vial containing a viral vector or DNA plasmid and the other vial may comprise immunogenic protein. The ready to use anticancer agent may comprise a cocktail of anticancer agents or a single anticancer agent. Separate vials may contain different anti-cancer agents. In another embodiment a kit may contain a ready to use anti-cancer agent and an immunogenic composition or vaccine in a ready to be reconstituted form. The immunogenic or vaccine composition may be freeze dried or lyophilized. The kit may comprise a separate vial with a reconstitution buffer that can be added to the lyophilized composition so that it is ready to administer. The buffer may advantageously comprise an adjuvant or emulsion according to the present invention. In another embodiment the kit may comprise a ready to reconstitute anti-cancer agent and a ready to reconstitute immunogenic composition or vaccine. In this aspect both may be lyophilized. In this aspect separate reconstitution buffers for each may be included in the kit. The buffer may advantageously comprise an adjuvant or emulsion according to the present invention. In another embodiment the kit may comprise single vials containing a dose of immunogenic composition and anti-cancer agent that are administered together. In another aspect multiple vials are included so that one vial is administered according to a treatment timeline. One vial may only contain the anti-cancer agent for one dose of treatment, another may contain both the anti-cancer agent and immunogenic composition for another dose of treatment, and one vial may only contain the immunogenic composition for yet another dose. In a further aspect the vials are labeled for their proper administration to a patient in need thereof. The immunogen or anti-cancer agents of any embodiment may be in a lyophilized form, a dried form or in aqueous solution as described herein. The immunogen may be a live attenuated virus, protein, or nucleic acid as described herein.

[00392] In one embodiment the anticancer agent is one that enhances the immune system to enhance the effectiveness of the immunogenic composition or vaccine. In a preferred embodiment the anti-cancer agent is a checkpoint inhibitor. In another embodiment the kit contains multiple vials of immunogenic compositions and anti-cancer agents to be administered at different time intervals along a treatment plan. In another embodiment the kit may comprise separate vials for an immunogenic composition for use in priming an immune response and

another immunogenic composition to be used for boosting. In one aspect the priming immunogenic composition could be DNA or a viral vector and the boosting immunogenic composition may be protein. Either composition may be lyophilized or ready for administering. In another embodiment different cocktails of anti-cancer agents containing at least one anti-cancer agent are included in different vials for administration in a treatment plan.

[00393] Although the present invention and its advantages have been described in detail, it should be understood that various changes, substitutions and alterations can be made herein without departing from the spirit and scope of the invention as defined in the appended claims.

[00394] The present invention will be further illustrated in the following Examples which are given for illustration purposes only and are not intended to limit the invention in any way.

Examples

Example 1

[00395] **sPDL1 generates immunogenic epitopes across a variety of HLA alleles.** PDL1 (CD274) is a trans- membrane protein which interacts with PD1 (CD279; *PDCD1*) on T cells and may be involved in multiple forms of natural immune suppression (such as during gestation). Expression of PDL1is also utilized by tumor cells as a way to evade host immune response. sPDL1 is an alternate spliced form of the PDL1 gene. This alternate spliced form is caused by a lack of splicing at the end of Exon 4, reading into the 4^{th} intron. The transcript terminates within intron 4. The translation product is in frame for 18 amino acids before a stop codon is encountered.

[00396] The translated product lacks the transmembrane domain typically found in PDL1 and thus is secreted. It also contains a cysteine within the neoORF translated from the intron and appears to dimerize in the media. The secreted form appears to block binding between PDL1 and PD1.

[00397] Applicants analyzed the predicted binding possibilities for 9 and 10mer peptides containing the neoORF region encoded by the intron. The analysis is shown for predicted 9mer peptides Table 1. The values highlighted in yellow are alleles that are present at a frequency >5% in the indicated population. Notably, the common HLA allele A0210 in the Caucasian population is predicted to have a reasonably tight binding peptide. A similar analysis shows that 10mer peptides are also predicted to be potentially immunogenic, including for the A0201 allele

(85 nM). Tumor cells expressing the alternate form of the PDL1 message would be thus rendered as targets of the immune system.

[00398] These peptides could be utilized across multiple patients (either HLA-restricted or more broadly if the patient is expected to have some probability to contain a relevant HLA allele) as a "Shared Neoantigen". Note that given the relatively short size of the neoORF region of sPDL1, two or three long overlapping peptides could be used as a mixture, allowing targeting of any HLA allele, even rare alleles, and reducing the need to prepare a different product for each patient based on their HLA type.

[00399] This neoORF may also contain a CD4 epitope although prediction algorithms for CD4 epitopes are not highly accurate. The presence of a CD4 epitope could be assessed in vitro with naive T cells or in patient samples.

Table 1

HLA	peptide 9mers	affinity(nM)	Caucasian	Black	Asian	Hispanic	ENHTAELVIPGNILNVSIKICLTLSPST
A0201	VIPGNILNV	182	28.3%	11.4%	9.7%	19.7%	
B4001	AELVIPGNI	144	4.0%	1.0%	12.0%	1.3%	
A3201	NILNVSIKI	491	3.2%	1.6%	0.3%	2.6%	
A3201	VSIKICLTL	224	3.2%	1.6%	0.3%	2.6%	
A2301	VSIKICLTL	468	2.3%	11.6%	0.2%	3.5%	
B4002	AELVIPGNI	53	1.6%	0.3%	7.6%	5.0%	
B4901	AELVIPGNI	108	1.4%	3.1%	0.0%	2.3%	
B4102	AELVIPGNI	192	1.0%	0.6%	0.0%	0.5%	
A0205	VIPGNILNV	170	0.8%	2.3%	0.1%	1.4%	
B5801	VSIKICLTL	373	0.8%	4.3%	4.5%	1.3%	
A6802	HTAELVIPG	170	0.7%	6.4%	0.0%	2.4%	
B4405	AELVIPGNI	219	0.6%	0.0%	0.0%	0.2%	
B4101	AELVIPGNI	92	0.5%	0.6%	0.0%	1.1%	
B4501	AELVIPGNI	302	0.4%	5.3%	0.0%	1.5%	
B1517	VSIKICLTL	23	0.3%	0.5%	0.1%	0.6%	
A0206	VIPGNILNV	85	0.2%	0.0%	4.7%	4.1%	
A0202	VIPGNILNV	90	0.1%	4.4%	0.0%	0.7%	
A6901	HTAELVIPG	283	0.1%	0.1%	0.0%	0.5%	
A6901	NILNVSIKI	162	0.1%	0.1%	0.0%	0.5%	
B1503	IKICLTLSP	408	0.1%	6.5%	0.1%	1.5%	
B1503	VSIKICLTL	138	0.1%	6.5%	0.1%	1.5%	
A0203	VIPGNILNV	98	0.0%	0.0%	5.2%	0.0%	

Example 2

[00400] Androgen Receptor generates immunogenic epitopes across a variety of HLA alleles. The androgen receptor was identified as another alternate spliced form of a message that results in a neoORF which may be specifically expressed in tumor cells. Alternate splicing results in at least two isoforms that bring in cryptic exons that are.neoORFs.

[00401] Of these alternate transcripts, AR-V1 and AR-V7 were consistently seen in hormone resistant prostate cancer samples.

[00402] The immunogenic potential of these neoORFs was unknown and thus Applicants conducted predicted binding analysis across a number of common HLA alleles. These are shown for HLA A alleles (Table 2).

Table 2

	A0201			A0202			A3101			A3301		
Caucasian		28.30%			13.70%			6.00%			1.60%	
Asian		9.70%			0.90%			22.40%			1.40%	
Hispanic		19.65%			7.59%			4.88%			2.20%	
Black		11.40%			7.10%			1.00%			6.50%	
	RVFGVSEWL	SEQ2	233	RVGNCKHLK	SEQ1	122	RVGNCKHLK	SEQ1	33	RVGNCKHLK	SEQ1	30
	GMTLGAVVV	SEQ2	282				VVVSERILR	SEQ2	359	KFRVGNCKH	SEQ1	103
	MTLGEKFRV	SEQ1	400							KFRVGNCKHL	SEQ1	190

A3302			A3303			A3304			A6801			A	B	
	2.40%			3.20%			0.70%			3.40%		30.30%	6.80%	Caucasian
	3.40%			0.30%			0.60%			0.30%		28.70%	19.70%	Asian
	4.72%			2.62%			1.97%			4.46%		26.46%	7.86%	Hispanic
	1.00%			1.60%			1.70%			3.20%		20.40%	2.10%	Black
RVGNCKHL	SEQ1	70	RVFGVSEWL	SEQ2	41	NCKHLKMSE	Q1	385	VVVSERILI	SEQ2	47			
TLGAVVVSI	SEQ2	131	ILRVFGVSI	SEQ2	255	TLGAVVVSI	SEQ2	417	TLGAVVVSI	SEQ2	84			
VVVSERILI	SEQ2	127							EAGMTLGEI	SEQ1	230			
GMTLGEKFI	SEQ1	199							LGAVVVSEI	SEQ2	268			
AVVVSERIS	SEQ2	230							AVVVSERIS	SEQ2	339			
AGMTLGEI	SEQ1	284												
GNCKHLKI	SEQ1	466												
LGAVVVSI	SEQ2	488												

[00403] Again, as for sPDL1, a number of peptides are predicted to be immunogenic binders and these can be applied across a large subset of patients. These immunogenic peptides can be used across multiple patients.

Example 3

[00404] **Drug Resistant Mutations.** Treatment with various chemotherapeutic agents, particularly with targeted therapies such as tyrosine kinase inhibitors, frequently leads to new mutations in the target molecules that resist the activity of the therapeutic. Multiple strategies to overcome this resistance are being evaluated, including development of second generation therapies that are not affected by these mutations and treatment with multiple agents including those that act downstream of the resistance mutation.

[00405] Applicants have evaluated the immunogenic potential of the mutated peptides created by these resistance mutations and have found that for some, predicted immunogenic peptides are created that can bind to a range of HLA alleles. Two specific examples are provided below as well as data for a range of resistance variants.

BTK/C481S

[00406] A very common mutation to ibrutinib, a molecule targeting Bruton's Tyrosine Kinase (BTK) and used for CLL and certain lymphomas, is a Cysteine to Serine change at position 481. This change produces a number of binding peptides which bind to a range of HLA molecules.

[00407] Shown are results of binding predictions for 9mer peptides. Similar binding peptides can be found for 10mer peptides (Table 3). Only peptides with mutant predicted affinity below

150 nM are included. Expanding the range of peptides up to 500 nM would also significantly increase the number of HLA range.

Table 3

HLA	peptide	affinity(nM) MUT	affinity (nM) NAT	Caucasian	Black	Asian	Hispanic
A0201	SLLNYLREM	97	278	28.3%	11.4%	9.7%	19.7%
A2402	EYMANGSLL	95	120	9.3%	2.0%	23.1%	12.4%
B1801	TEYMANGSL	80	252	6.1%	3.5%	0.4%	4.1%
B1501	MANGSLLNY	91	158	5.8%	0.8%	12.1%	2.6%
B3501	MANGSLLNY	17	17	5.6%	6.1%	2.4%	6.0%
B4001	TEYMANGSL	10	24	4.0%	1.0%	12.0%	1.3%
A3101	LLNYLREMR	43	206	2.4%	1.0%	3.4%	4.7%
A2301	EYMANGSLL	122	133	2.3%	11.6%	0.2%	3.5%
A2902	MANGSLLNY	17	10	2.0%	4.4%	0.0%	4.1%
B4002	TEYMANGSL	45	110	1.6%	0.3%	7.6%	5.0%
B4102	TEYMANGSL	133	341	1.0%	0.6%	0.0%	0.5%
B5801	MANGSLLNY	40	35	0.8%	4.3%	4.5%	1.3%
A3301	LLNYLREMR	91	188	0.7%	1.7%	0.6%	2.0%
A3002	MANGSLLNY	16	15	0.5%	6.6%	0.0%	2.8%
A6804	EYMANGSLL	47	448	0.0%	0.0%	0.0%	0.0%
B1801	TEYMANGSL	44	252	6.1%	3.5%	0.4%	4.1%
B1501	MANGSLLNY	42	158	5.8%	0.8%	12.1%	2.6%
B3501	MANGSLLNY	40	17	5.6%	6.1%	2.4%	6.0%
B4001	TEYMANGSL	38	24	4.0%	1.0%	12.0%	1.3%
A3101	LLNYLREMR	36	206	2.4%	1.0%	3.4%	4.7%
A2301	EYMANGSLL	34	133	2.3%	11.6%	0.2%	3.5%
A2902	MANGSLLNY	32	10	2.0%	4.4%	0.0%	4.1%
B4002	TEYMANGSL	30	110	1.6%	0.3%	7.6%	5.0%

[00408] Such peptide immunogens are preferably utilized prophylactically (prior to detection of resistant disease) to induce an immunogenic response capable of killing any pre-existing or newly mutated cells or could also be used at the time of detection of disease recurrence following or during therapy. These peptides could be utilized across multiple patients (either HLA-restricted or more broadly if the patient is expected with some probability to contain a relevant HLA allele).

EGFR/T790M

[00409] Erlotinib, which targets the tyrosine kinase domain of the Epidermal Growth Factor Receptor (EGFR), is commonly used in the treatment of lung cancer and resistant tumors invariably develop following therapy. A common mutation found in resistant clones is a Threonine to methionine mutation at position 790. This change produces a number of binding peptides which bind to a range of HLA molecules (Table 4).

Table 4

																							SUM
Caucasian	2.3%			3.9%			4.0%			3.2%			3.2%										17%
Black	11.6%			0.3%			1.5%			1.6%			1.6%										17%
Asian	0.2%			0.0%			3.9%			0.3%			0.3%										5%
Hispanic	3.5%			0.9%			2.8%			2.6%			2.6%										12%
	A2301			A2501			A2601			A3201			A3201										
	VQLIMQLMPF		366	STVQLIMQLM		125	STVQLIMQLM		67	QLIMQLMPF		155	QLIMQLMPF		155								
										VQLIMQLMPF		426	VQLIMQLMPF		426								
Caucasian	4.2%			5.8%			2.9%			1.4%			0.4%			1.6%							16%
Black	1.2%			0.8%			0.1%			0.3%			0.1%			0.3%							3%
Asian	1.2%			12.1%			0.2%			2.4%			0.0%			7.6%							24%
Hispanic	1.2%			2.6%			1.8%			1.0%			2.2%			5.0%							14%
	B1302			B1501			B3801			B3901			B3906			B4002							
	MQLMPFGCLL		125	MQLMPFGCLL		488	MQLMPFGCLL		400	MQLMPFGCLL		213	MQLMPFGCLL		400	MQLMPFGCL		221					
				QLIMQLMPF		23										MQLMPFGCLL		103					
				VQLIMQLMPF		73										VQLIMQLMPF		365					

[00410] As stated herein, such peptide immunogens are ideally utilized prophylactically (prior to detection of resistant disease) to induce an immunogenic response capable of killing any pre-existing or newly mutated cells or are also used at the time of detection of disease recurrence following or during therapy. These peptides could be utilized across multiple patients (either HLA-restricted or more broadly if the patient is expected with some probability to contain a relevant HLA allele).

[00411] Note that as an immunogen, only a single long peptide containing the mutated amino acid and at least 10 amino acids on either side of the mutated amino acid would be sufficient to contain all the epitopes listed. Thus, all the HLA alleles shown, as well as any additional alleles that have not been shown in this analysis would be covered. For the Caucasian population, the HLA A alleles shown represent 17% of the population distribution of alleles and the HLA B alleles represent 16% of the population distribution of alleles. As each individual has two HLA A alleles and two HLA B alleles, approximately 50% of Caucasian patients will be expected to have at least one of the alleles shown and thus benefit from immune therapy with a vaccine targeting this molecule. This rationale also applies to any other single amino acid mutation discussed herein.

Other Resistance Variants

[00412] In addition to the specific resistance cases discussed herein, there are many other observed resistance mutations to targeted therapy. Each of these are also used to define immunogenic epitopes that could be utilized as vaccine for immunotherapy targeting those cells containing the resistance mutations (Table 5).

Table 5

Drug	Gene	Resistance m	Sensitive	Refs
Imatinib	BCR-Abl	T315I		http://www.mycancergenome.org/content/disease/chronic-myeloid-leukemia/
Imatinib	BCR-Abl	Y253H		http://www.mycancergenome.org/content/disease/chronic-myeloid-leukemia/
Imatinib	BCR-Abl	E255K		http://www.mycancergenome.org/content/disease/chronic-myeloid-leukemia/
Imatinib	BCR-Abl	E255V		http://www.mycancergenome.org/content/disease/chronic-myeloid-leukemia/
Imatinib	c-kit	T670I		http://www.mycancergenome.org/content/disease/gist/kit/50/
Erlotinib/gefitinib	PIK3CA	E545K		PMC1570180; PMC3132801
Erlotinib/gefitinib	HER2	G776(YVMA)		PMID 16843263; 15753357
Erlotinib/gefitinib	EML4-ALK	G1269A		http://www.ncbi.nlm.nih.gov/pubmed/22235099?dopt=Abstract
Crizotinib	KRAS	G12V/D		http://www.ncbi.nlm.nih.gov/pubmed/22235099?dopt=Abstract
Crizotinib	ALK	L1196M		http://stm.sciencemag.org/content/4/120/120ra17
Crizotinib	ALK	G1202R		http://stm.sciencemag.org/content/4/120/120ra17
Crizotinib	ALK	S1206Y		http://stm.sciencemag.org/content/4/120/120ra17
Crizotinib	ALK	1151T(ins)		http://stm.sciencemag.org/content/4/120/120ra17
Crizotinib	ALK	F1174C		http://cancerdiscovery.aacrjournals.org/content/4/6/662
Crizotinib	ROS1	G2032R		http://www.nejm.org/doi/full/10.1056/NEJMoa1215530
Crizotinib	PIK3CA	E542K		http://www.mycancergenome.org/content/disease/breast-cancer/
Trastuzumab	Her2	E545K		http://www.mycancergenome.org/content/disease/breast-cancer/
Trastuzumab	Hwe2	H1047R		http://www.mycancergenome.org/content/disease/breast-cancer/
Trastuzumab	AKT1	E17K		http://www.ncbi.nlm.nih.gov/pmc/articles/PMC2834432/
Trastuzumab	BRAF		V600E	
Vemurafenib	MEK1	Q56P		http://www.ncbi.nlm.nih.gov/pubmed/23569304
Vemurafenib	MEK1	E203K		http://www.ncbi.nlm.nih.gov/pubmed/23569304
Vemurafenib	MEK1	C121S		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
Vemurafenib	NRAS	Q61K/L		http://www.ncbi.nlm.nih.gov/pubmed/23569304
Vemurafenib	NRAS	Q61R		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
Vemurafenib	NRAS	T58I		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
Vemurafenib	MEK2	C125S		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
Vemurafenib	MEK1	V60E		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
RAF/MEK	MEK1	G128V		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
RAF/MEK	MEK1	V154I		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
RAF/MEK	MEK1	P124S		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
RAF/MEK	MEK1	P124L		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
RAF/MEK	RAC1	P29S		http://cancerdiscovery.aacrjournals.org/content/4/1/94.long
RAF/MEK	ESR1	S463P		http://www.mycancergenome.org/content/disease/breast-cancer/er/314/
Antiestrogen therapy	AR	V534E		http://www.mycancergenome.org/content/disease/breast-cancer/er/314/
Antiestrogen therapy	AR	P535H		http://www.mycancergenome.org/content/disease/breast-cancer/er/314/
Antiestrogen therapy	AR	L536Q		http://www.mycancergenome.org/content/disease/breast-cancer/er/314/
Antiestrogen therapy	AR	L536R		http://www.mycancergenome.org/content/disease/breast-cancer/er/314/
Antiestrogen therapy	AR	Y537C		http://www.mycancergenome.org/content/disease/breast-cancer/er/314/
Antiestrogen therapy	AR	Y537S		http://www.mycancergenome.org/content/disease/breast-cancer/er/314/
Antiestrogen therapy	AR	Y537N		http://www.mycancergenome.org/content/disease/breast-cancer/er/314/
Antiestrogen therapy	AR	D538G		http://www.mycancergenome.org/content/disease/breast-cancer/er/314/
Antiestrogen therapy	AR	F876L		http://cancerdiscovery.aacrjournals.org/content/early/2013/06/18/2159-8290.CD-13-0226

[00413] A number of these examples have been used to predict immunogenic epitopes. These results are summarized in Table 6, in which for each resistance mutation, the number of potential binding peptides (with predicted affinity < 500 nM) for each mutation are shown for multiple Human HLA alleles.

Table 6

RES 500	Caucasian	Black	Asian	ABL1:p.T315i	ALK:p.F1174C	ALK:p.F1174L	ALK:p.G1202R	ALK:p.G1269A	ALK:p.L1196M	ALK:p.S1206Y	AR:p.F876L
				80	80	80	80	80	80	80	80
hla_a_01_01	0.143	0.047	0.012							1	
hla_a_02_01	0.283	0.114	0.097			1			2		
hla_a_02_03	0	0	0.052		1	2			2		
hla_a_02_07	0	0	0.08						1		
hla_a_03_01	0.137	0.071	0.009			1		1			
hla_a_11_01	0.06	0.01	0.224				1	1			2
hla_a_23_01	0.023	0.116	0.002	2							
hla_a_24_02	0.093	0.02	0.231	1							
hla_a_30_01	0.016	0.065	0.014		1	1	2		1	1	1
hla_a_30_02	0.005	0.066	0	2						2	
hla_a_33_03	0.004	0.041	0.072				3	1		3	
hla_a_68_02	0.007	0.064	0								
hla_a_74_01	0	0.051	0.001			1	1	1			
hla_b_07_02	0.118	0.062	0.015						2		1
hla_b_08_01	0.098	0.039	0.002						1		
hla_b_15_01	0.058	0.008	0.121	1			1			3	1
hla_b_15_02	0	0	0.066	1			2			3	1
hla_b_15_03	0.001	0.065	0.001	5		3	3	2	4	4	4
hla_b_18_01	0.061	0.035	0.004	2		1	1		1		
hla_b_35_01	0.056	0.061	0.024	3			1		1	2	2
hla_b_40_01	0.04	0.01	0.12	3		1	1		1		1
hla_b_40_02	0.016	0.003	0.076	3	1	1	1	1	1		2
hla_b_42_01	0	0.057	0						2		
hla_b_44_02	0.071	0.014	0.002			1					1
hla_b_45_01	0.004	0.053	0			1					1
hla_b_46_01	0	0	0.082								1
hla_b_51_01	0.051	0.021	0.04						2		
hla_b_53_01	0.003	0.11	0	1						1	

RES 500	Caucasian	Black	Asian	BTK:p.C481S	EGFR:p.T790M	KRAS p.G12D	MAP2K1:p.C121S	MAP2K1:p.E203K	MAP2K1 p.G128V	MAP2K1:p.P124L	MAP2K1:p.P124S
				80	80	80	80	80	80	80	80
hla_a_01_01	0.143	0.047	0.012	2	1					1	2
hla_a_02_01	0.283	0.114	0.097	1	2	1	1	3		2	1
hla_a_02_03	0	0	0.052	2	1	2	1	3		2	1
hla_a_02_07	0	0	0.08								
hla_a_03_01	0.137	0.071	0.009	1						1	
hla_a_11_01	0.06	0.01	0.224	2		2			1		
hla_a_23_01	0.023	0.116	0.002	1	2				1	1	2
hla_a_24_02	0.093	0.02	0.231	1					1	1	1
hla_a_30_01	0.016	0.065	0.014					1			1
hla_a_30_02	0.005	0.066	0	2			3	2	3	4	5
hla_a_33_03	0.004	0.041	0.072	2				1			
hla_a_68_02	0.007	0.064	0	1	2	1		1			1
hla_a_74_01	0	0.051	0.001	1							
hla_b_07_02	0.118	0.062	0.015					2			
hla_b_08_01	0.098	0.039	0.002								
hla_b_15_01	0.058	0.008	0.121	3	2		2	1	3	1	2
hla_b_15_02	0	0	0.066	3	2		2	1	3	3	3
hla_b_15_03	0.001	0.065	0.001	8	7		7	2	6	8	8
hla_b_18_01	0.061	0.035	0.004	2					1	1	1
hla_b_35_01	0.056	0.061	0.024	3	1		2	1	3		3
hla_b_40_01	0.04	0.01	0.12	2	1		2		1	1	1
hla_b_40_02	0.016	0.003	0.076	2	3		3		1	1	1
hla_b_42_01	0	0.057	0								
hla_b_44_02	0.071	0.014	0.002								
hla_b_45_01	0.004	0.053	0				2		1	1	1
hla_b_46_01	0	0	0.082	3	1		1	1	1		
hla_b_51_01	0.051	0.021	0.04					1	1		
hla_b_53_01	0.003	0.11	0	2				2			

RE5 500	Caucasian	Black	Asian	MAP2K1:p.Q56P	MAP2K1:p.V154I	MAP2K1:p.V60E	MAP2K2:p.C125S	MAP2K2:p.I46F	MAP2K2:p.N126D	MAP2K2:p.V35M	NRAS:p.Q61R
				80	80	80	80	80	80	80	80
hla_a_01_01	0.143	0.047	0.012								1
hla_a_02_01	0.283	0.114	0.097		1		1		1	1	
hla_a_02_03	0	0	0.052		1		1		1	1	
hla_a_02_07	0	0	0.08								
hla_a_03_01	0.137	0.071	0.009	1							
hla_a_11_01	0.06	0.01	0.224	1	1						
hla_a_23_01	0.023	0.116	0.002								
hla_a_24_02	0.093	0.02	0.231								
hla_a_30_01	0.016	0.065	0.014	2		1					1
hla_a_30_02	0.005	0.066	0				3		4		1
hla_a_33_03	0.004	0.041	0.072		1						
hla_a_68_02	0.007	0.064	0	1							1
hla_a_74_01	0	0.051	0.001								
hla_b_07_02	0.118	0.062	0.015	1							
hla_b_08_01	0.098	0.039	0.002	1							
hla_b_15_01	0.058	0.008	0.121				2	1	1		
hla_b_15_02	0	0	0.066				2		2		
hla_b_15_03	0.001	0.065	0.001		1		7	2	5	1	3
hla_b_18_01	0.061	0.035	0.004						1		
hla_b_35_01	0.056	0.061	0.024				2		2		
hla_b_40_01	0.04	0.01	0.12				2		1	1	
hla_b_40_02	0.016	0.003	0.076				3		1	1	
hla_b_42_01	0	0.057	0								
hla_b_44_02	0.071	0.014	0.002								
hla_b_45_01	0.004	0.053	0				2		1		
hla_b_46_01	0	0	0.082				1				
hla_b_51_01	0.051	0.021	0.04								
hla_b_53_01	0.003	0.11	0								

RES 500	Caucasian	Black	Asian	NRAS:p.T58I	PIK3CA:p.E545K	PLCG2:p.R665W	ROS1:p.G2032A
				80	80	80	80
hla_a_01_01	0.143	0.047	0.012	1			1
hla_a_02_01	0.283	0.114	0.097	1		2	3
hla_a_02_03	0	0	0.052	1		3	3
hla_a_02_07	0	0	0.08				
hla_a_03_01	0.137	0.071	0.009				
hla_a_11_01	0.06	0.01	0.224				2
hla_a_23_01	0.023	0.116	0.002				
hla_a_24_02	0.093	0.02	0.231				
hla_a_30_01	0.016	0.065	0.014			1	
hla_a_30_02	0.005	0.066	0	1		1	2
hla_a_33_03	0.004	0.041	0.072				1
hla_a_68_02	0.007	0.064	0			1	2
hla_a_74_01	0	0.051	0.001				
hla_b_07_02	0.118	0.062	0.015				
hla_b_08_01	0.098	0.039	0.002				
hla_b_15_01	0.058	0.008	0.121			1	2
hla_b_15_02	0	0	0.066			1	2
hla_b_15_03	0.001	0.065	0.001	3	2	4	5
hla_b_18_01	0.061	0.035	0.004			1	2
hla_b_35_01	0.056	0.061	0.024			1	1
hla_b_40_01	0.04	0.01	0.12				3
hla_b_40_02	0.016	0.003	0.076			1	3
hla_b_42_01	0	0.057	0				
hla_b_44_02	0.071	0.014	0.002		1	2	2
hla_b_45_01	0.004	0.053	0				
hla_b_46_01	0	0	0.082			1	
hla_b_51_01	0.051	0.021	0.04			1	
hla_b_53_01	0.003	0.11	0			1	

[00414] In all of the above examples, predictions are only shown for a subset of HLA alleles. These are often but not exclusively the most abundant alleles in each ethnic population. Additional alleles are readily predicted.

[00415] Moreover, for a given immunization designed to attack resistant variants for a given resistance mutation, multiple peptides, each targeting a separate possible resistance variant that may arise, are utilized to benefit the broadest set of patients.

Example 4

[00416] **Cancer Subtype Specific Immunogenic compositions**. Table 7 shows a data summary for the number of mutations found within a population of samples specific to a cancer subtype. Each mutation found within the data set for each disease leads to at least one predicted binder to any one of 33 HLA alleles selected based on being found in at least 5% of any one of the three ethnic populations (Caucasian, Black, Asian). A combination of neoantigenic peptides

derived from polypeptides resulting from these mutations can be used in an immunogenic composition. Based on the number of peptides from the mutations selected, a larger percentage of patients may receive a benefit from the vaccine. Table 7 shows the number of mutations that are recurrent in each cancer specific data set. Also shown are the percentage of subjects in each data set that will have at least a single mutation when selecting recurrent mutations. For example, an immunogenic composition for SKCM that includes neoantigenic peptides derived from 64 recurrent mutations described herein covers 90.91% of patients in this population, whereby each subject will contain at least one of the neoantigenic mutations.

Table 7

Exemplary disease	recurrence (muts that occur in >= given # samples)	# unique muts in the set	# samples that have at least one mutation in the set	total # samples	percentage
SKCM	5	64	230	253	90.91
SKCM	4	200	241	253	95.26
SKCM	3	707	247	253	97.63
SKCM	2	4437	250	253	98.81
SKCM	1	103732	253	253	100
ACC	5	161	90	90	100
ACC	4	219	90	90	100
ACC	3	299	90	90	100
ACC	2	546	90	90	100
ACC	1	10310	90	90	100
BLCA	5	6	35	130	26.92
BLCA	4	9	47	130	36.15
BLCA	3	26	77	130	59.23
BLCA	2	181	121	130	93.08
BLCA	1	25605	130	130	100
BRCA	5	18	320	888	36.04
BRCA	4	25	337	888	37.95
BRCA	3	35	357	888	40.2
BRCA	2	148	475	888	53.49
BRCA	1	31457	886	888	99.77
CESC	5	4	46	194	23.71

Exemplary disease	recurrence (muts that occur in >= given # samples)	# unique muts in the set	# samples that have at least one mutation in the set	total # samples	percentage
CESC	4	7	55	194	28.35
CESC	3	12	65	194	33.51
CESC	2	145	133	194	68.56
CESC	1	25585	194	194	100
CRC	5	15	132	233	56.65
CRC	4	22	142	233	60.94
CRC	3	53	160	233	68.67
CRC	2	711	209	233	89.7
CRC	1	55287	233	233	100
DLBCL	5	0	0	58	0
DLBCL	4	2	8	58	13.79
DLBCL	3	4	13	58	22.41
DLBCL	2	30	38	58	65.52
DLBCL	1	7435	57	58	98.28
HNSC	5	10	83	384	21.61
HNSC	4	15	97	384	25.26
HNSC	3	27	123	384	32.03
HNSC	2	154	227	384	59.11
HNSC	1	43143	384	384	100
KICH	5	0	0	66	0
KICH	4	0	0	66	0
KICH	3	0	0	66	0
KICH	2	24	33	66	50
KICH	1	2576	66	66	100
KIRP	5	9	68	161	42.24
KIRP	4	18	86	161	53.42
KIRP	3	35	104	161	64.6
KIRP	2	117	139	161	86.34
KIRP	1	10482	161	161	100
LIHC	5	2	13	198	6.57
LIHC	4	5	25	198	12.63

Exemplary disease	recurrence (muts that occur in >= given # samples)	# unique muts in the set	# samples that have at least one mutation in the set	total # samples	percentage
LIHC	3	10	38	198	19.19
LIHC	2	33	73	198	36.87
LIHC	1	18574	198	198	100
LUAD	5	11	134	401	33.42
LUAD	4	17	152	401	37.91
LUAD	3	35	185	401	46.13
LUAD	2	611	330	401	82.29
LUAD	1	101222	399	401	99.5
MM	5	6	49	205	23.9
MM	4	8	55	205	26.83
MM	3	16	71	205	34.63
MM	2	51	101	205	49.27
MM	1	7116	204	205	99.51
PRAD	5	24	104	261	39.85
PRAD	4	38	133	261	50.96
PRAD	3	83	174	261	66.67
PRAD	2	205	213	261	81.61
PRAD	1	10174	261	261	100
STAD	5	150	141	289	48.79
STAD	4	245	156	289	53.98
STAD	3	613	201	289	69.55
STAD	2	2729	269	289	93.08
STAD	1	97578	289	289	100
TGCT	5	14	80	155	51.61
TGCT	4	25	99	155	63.87
TGCT	3	64	124	155	80
TGCT	2	338	149	155	96.13
TGCT	1	7632	155	155	100
THCA	5	5	283	405	69.88
THCA	4	5	283	405	69.88
THCA	3	7	287	405	70.86

Exemplary disease	recurrence (muts that occur in >= given # samples)	# unique muts in the set	# samples that have at least one mutation in the set	total # samples	percentage
THCA	2	31	300	405	74.07
THCA	1	4439	405	405	100
UCS	5	2	9	56	16.07
UCS	4	10	31	56	55.36
UCS	3	19	41	56	73.21
UCS	2	55	53	56	94.64
UCS	1	3805	56	56	100
CLL	5	6	46	263	17.49
CLL	4	19	74	263	28.14
CLL	3	38	100	263	38.02
CLL	2	157	167	263	63.5
CLL	1	7870	263	263	100
GBM	5	14	100	291	34.36
GBM	4	24	125	291	42.96
GBM	3	45	153	291	52.58
GBM	2	221	252	291	86.6
GBM	1	14142	291	291	100
KIRC	5	4	25	417	6
KIRC	4	8	41	417	9.83
KIRC	3	23	78	417	18.71
KIRC	2	291	292	417	70.02
KIRC	1	17725	417	417	100
LAML	5	11	93	196	47.45
LAML	4	12	95	196	48.47
LAML	3	16	101	196	51.53
LAML	2	27	114	196	58.16
LAML	1	1458	195	196	99.49
LUSC	5	2	14	178	7.87
LUSC	4	4	22	178	12.36
LUSC	3	15	50	178	28.09
LUSC	2	130	138	178	77.53

Exemplary disease	recurrence (muts that occur in >= given # samples)	# unique muts in the set	# samples that have at least one mutation in the set	total # samples	percentage
LUSC	1	42062	178	178	100
OV	5	10	72	316	22.78
OV	4	12	80	316	25.32
OV	3	14	86	316	27.22
OV	2	56	151	316	47.78
OV	1	12840	316	316	100
PAAD	5	53	146	146	100
PAAD	4	69	146	146	100
PAAD	3	123	146	146	100
PAAD	2	398	146	146	100
PAAD	1	23715	146	146	100
UCEC	5	30	168	248	67.74
UCEC	4	81	196	248	79.03
UCEC	3	302	217	248	87.5
UCEC	2	2797	237	248	95.56
UCEC	1	112636	248	248	100
COAD	5	3	19	70	27.14%
COAD	4	7	20	70	28.57%
COAD	3	11	25	70	35.71%
COAD	2	84	44	70	62.86%
COAD	1	16670	70	70	100.00%
READ	5	0	0	39	0.00%
READ	4	2	8	39	20.51%
READ	3	5	16	39	41.03%
READ	2	33	29	39	74.36%
READ	1	12132	39	39	100.00%

[00417] Table 8 shows the specific recurrent mutations for each cancer subtype, as well as the peptides that each mutation generates and the flanking peptide that includes the peptides ("ACC", "BLCA", "BRCA", "CESC", "COAD", "CLL", "CRC", "DLBCL", "GBM", "HNSC", "KICH", "KIRC", "KIRP", "LAML", "LIHC", "LUAD", "LUSC", "MM", "OV", "PAAD",

"PRAD", "READ", "SKCM", "STAD", "TGCT", "THCA", "UCEC", and "UCS"). Frameshift muations are denoted with a "fs". "Del" and "Ins" indicate deletions and inserts. The number of peptides that are generated from each mutation that binds to a specific HLA allele are shown. The recurrent mutations include frameshift mutations and create HLA binders across many alleles.

Table 8

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
A2M	c.2195G>A	p.R732Q	FYESDVMGRGHARLVHVEEPHTETV[p.R732Q]QKYFPETWIWDLVVVNSAGVAEVGVT	VQKYFPETW,QKYFPETWI,ETVQKYFPET,VQKYFPETWI,QKYFPETWIW,EPHTETVQKY	CRC
A2ML1	c.1960_1961insC	p.S654fs	YDQCPVSGPWDFPQPLIDPMPQGHS[p.S654fs]EPAFHYLEALVL*	HSEPAFHYL,MPQGHSEPA,PQGHSEPAF,GHSEPAFHY,FHYLEALVL,EPAFHYLEA,QGHSEPAFHY,EPAFHYLEAL,MPQGHSEPAF,SEPAFHYLEA	LUAD
AADACL4	c.796G>A	p.A266T	VPLLSRKFMVTSLCNYLAIDLSWRD[p.A266T]TILNGTCVPPDVWRKYEKWLSPDNIP	IDLSWRDTI,SWRDTILNG,DTILNGTCV,IDLSWRDTIL	CRC
AASS	c.2634_2635insC	p.T878fs	KTIDLVAYGDINGFSAMAKTVGLPT[p.T878fs]RHGSQNVA*	MAKTVGLPTR,LPTRHGSQNV	GBM
ABCA11P	c.1154G>T	p.R385I	TGEKPYTCGECGKTFRQSANLYVHR[p.R385I]IIHTGEKPYKCEDCGKAFGRYTALNQ	VHRIIHTGEK,QSANLYVHRI	UCEC
ABCA3	c.285G>C	p.E95D	TFPPPGDTWELAYIPSHSDAAKTVT[p.E95D]DTVRRALVINMRVRGFPSEKDFEDYI	KTVTDTVRR,VTDTVRRALV,AAKTVTDTVR,DAAKTVTDTV,TVTDTVRRAL	KIRC
ABCA5	c.4427G>A	p.R1476Q	PQITLLDEPSTGMDPKAKQHMWRAI[p.R1476Q]QTAFKNRKRAAILTTHYMEEAEAVCD	HMWRAIQTA,IQTAFKNRK,MWRAIQTAF,AIQTAFKNR,QTAFKNRKR,MWRAIQTAFK,AIQTAFKNRK,HMWRAIQTAF,KQHMWRAIQT,RAIQTAFKNR,QHMWRAIQTA	UCEC
ABCA6	c.917delT	p.L306fs	FVTIIITFTQIIVMTGFMVIFILFF[p.L306fs]YMAYLW*	MVIFILFFY,VIFILFFYM,ILFFYMAYL,LFFYMAYLW,FILFFYMAY,MVIFILFFYM,VIFILFFYMA,FILFFYMAYL,ILFFYMAYLW,FMVIFILFFY,IFILFFYMAY	STAD
ABCA8	c.2086G>A	p.A696T	STQFMDEADILADRKVFLSQGKLKC[p.A696T]TGSSLFLKKKWGIGYHLSLQLNEICV	KLKCTGSSL,CTGSSLFLK,TGSSLFLKK,LKCTGSSLF,FLSQGKLKCT,CTGSSLFLKK,KCTGSSLFLK,KLKCTGSSLF,GKLKCTGSSL,LKCTGSSLFL	CRC
ABCA8	c.2525G>A	p.R842Q	RLVEMEQVLSSLNKMRKTIGGVALW[p.R842Q]QQQICAIARVRLLKLKHERKALLALL	ALWQQQICA,WQQQICAIA,ALWQQQICAI	CRC
ABCA8	c.3472G>A	p.E1158K	NSGIWSFCFYVVTVFSVAGFAFSIF[p.E1158K]KSDIPFIFTFLIPPATMIGCLFLSSH	AGFAFSIFK,IFKSDIPFI,SIFKSDIPF,FKSDIPFIF,SIFKSDIPFI,VAGFAFSIFK,IFKSDIPFIF,KSDIPFIFTF,FAFSIFKSDI,FSIFKSDIPF	CRC
ABCB1	c.1400G>T	p.R467L	RLYDPTEGMVSVDGQDIRTINVRFL[p.R467L]LEIIGVVSQEPVLFATTIAENIRYGR	RTINVRFLL,FLLEIIGVV,RFLLEIIGV,INVRFLLEI,FLLEIIGVVS,TINVRFLLEI,RFLLEIIGVV,RTINVRFLLE	LUAD
ABCB1	c.1581_1582delAG	p.R527fs	VKEANAYDFIMKLPHKFDTLVGERG[p.R527fs]PVEWWAEAEDRHCTCPGSQPQDPPAG*	TLVGERGPV,GERGPVEWW,AEAEDRHCT,DTLVGERGPV,GERGPVEWWA	STAD
ABCB6	c.953delG	p.G318fs	LTEKAPWNSLAWTVTSYVFLKFLQG[p.G318fs]VALAVQAS*	FLQGVALAV,FLKFLQGVA,LKFLQGVAL,YVFLKFLQGV,FLKFLQGVAL,KFLQGVALAV,LKFLQGVALA	STAD
ABCB8	c.1034G>A	p.R345H	SRQCQEQIARAMGVADEALGNVRTV[p.R345H]HAFAMEQREEERYGAELEACRCRAEE	NVRTVHAFA,GNVRTVHAF,VRTVHAFAM,ALGNVRTVHA,TVHAFAMEQR,NVRTVHAFAM,LGNVRTVHAF	CRC
ABCC10	c.1708C>T	p.R570W	RMLILPLNNFPWVINGLLEAKVSLD[p.R570W]WIQLFLDLPNHNPQAYYSPDPPAEPS	SLDWIQLFL,VSLDWIQLF,DWIQLFLDL,LEAKVSLDW,KVSLDWIQLF,AKVSLDWIQL,LEAKVSLDWI,LDWIQLFLDL	GBM
ABCC4	c.2648delT	p.L883fs	VAVIPWIAIPLVPLGIIFIFLRRYF[p.L883fs]WKRQEM*	IFLRRYFWK,FIFLRRYFW,RYFWKRQEM,FLRRYFWKR,FIFLRRYFWK,IFIFLRRYFW,IFLRRYFWKR,RRYFWKRQEM	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ABCC5	c.3269delT	p.L1090fs	HAYNKGQEFLHRYQELLDDNQAPFF[p.L1090fs]CLRVRCGGWLCGWTSSASPSSPPRG*	WLCGWTSSA,SASPSSPPR,RVRCGGWLC,NQAPFFCLR,QAPFFCLRV,NQAPFFCLRV,SSASPSSPPR,RVRCGGWLCG,DNQAPFFCLR,CLRVRCGGWL	KIRC
ABCC8	c.1535A>G	p.Y512C	STLEYSNERLKQTNEMLRGIKLLKL[p.Y512C]CAWENIFRTRVETTRRKEMTSLRAFA	IKLLKLCAW,LKLCAWENI,KLCAWENIF,LLKLCAWENI,KLCAWENIFR,CAWENIFRTR,LKLCAWENIF	TGCT
ABCC9	c.1397T>C	p.L466P	IIMGVILLYNLLGSSALVGAAVIVL[p.L466P]PAPIQYFIATKLAEAQKSTLDYSTER	AVIVLPAPI,IVLPAPIQY,VLPAPIQYF,LPAPIQYFI,VLPAPIQYFI,IVLPAPIQYF,AAVIVLPAPI,VIVLPAPIQY,LPAPIQYFIA	TGCT
ABCD1	c.1816T>C	p.S606P	DVVHLHHILQREGGWEAMCDWKDVL[p.S606P]PGGEKQRIGMARMFYHRPKYALLDEC	LPGGEKQRI,DVLPGGEKQR	CESC
ABCD1	c.507C>A	p.H169Q	ATFVNSAIRYLEGQLALSFRSRLVA[p.H169Q]QAYRLYFSQQTYYRVSNMDGRLRNPD	RLVAQAYRL,VAQAYRLYF,RSRLVAQAY,LVAQAYRLY,RLVAQAYRLY,RSRLVAQAYR,LVAQAYRLYF,SFRSRLVAQA,FRSRLVAQAY,SRLVAQAYRL	TGCT
ABI1	c.1335G>T	p.K445N	DYEDEEAAVVQYNDPYADGDPAWAP[p.K445N]NNYIEKVVAIYDYTKDKDDELSFMEG	DPAWAPNNY,AWAPNNYIEK,WAPNNYIEKV,DPAWAPNNYI	UCEC
ABL2	c.55C>A	p.P19T	MGQQVGRVGEAPGLQQPQ[p.P19T]TRGIRGSSAARPSGRRRDPAGRTTET	LQQPQTRGI,QTRGIRGSSA	TGCT
ABTB1	c.747_748insC	p.L249fs	TIEPPPADPRLREDMALLADCALPP[p.L249fs]RAPR*	CALPPRAPR,LLADCALPPR,DCALPPRAPR	LAML
ACACA	c.5191C>T	p.R1731C	ARAEGIPRIYVSANSGARIGLAEEI[p.R1731C]CHMFHVAWVDPEDPYKGYRYLYLTPQ	GLAEEICHM,EICHMFHVA,LAEEICHMF,ICHMFHVAW,EEICHMFHV,GLAEEICHMF,IGLAEEICHM,EEICHMFHVA,AEEICHMFHV	CRC
ACACB	c.6952G>C	p.E2318Q	VAVQFADFHDTPGRMLEKGVISDIL[p.E2318Q]QWKTARTFLYWRLRRLLLEDQVKQEI	ILQWKTART,VISDILQWK,QWKTARTFL,DILQWKTAR,LQWKTARTF,GVISDILQWK,ILQWKTARTF,QWKTARTFLY,LQWKTARTFL	BLCA
ACACB	c.763delG	p.G255fs	EHKKLDLHRDFTVASPAEFVTRFGG[p.G255fs]IGSSRRCLLPTTGLPP*	SSRRCLLPT,RFGGIGSSR,RCLLPTTGL,SSRRCLLPTT,AEFVTRFGGI,RRCLLPTTGL	STAD
ACADM	c.143T>G	p.F48C	QHTKANRQREPGLGFSFEFTEQQKE[p.F48C]CQATARKFAREEIIPVAAEYDKTGEY	QQKECQATA,QQKECQATAR,CQATARKFAR,KECQATARKF,TEQQKECQAT	CRC
ACADS	c.989G>A	p.R330H	TKLQVIQFKLADMALALESARLLTW[p.R330H]HAAMLKDNKKPFIKEAAMAKLAASEA	RLLTWHAAM,LLTWHAAML,LTWHAAMLK,HAAMLKDNK,SARLLTWHA,ARLLTWHAA,RLLTWHAAML,LLTWHAAMLK,SARLLTWHAA,HAAMLKDNKK,ESARLLTWHA,LESARLLTWH,ARLLTWHAAM	KIRC,PRAD
ACBD3	c.671G>T	p.R224L	REEEERERLQKEEEKRRREEEERLR[p.R224L]LEEEERRRIEEERLRLEQQKQQIMAA	REEEERLRL	LUAD
ACOT9	c.149G>A	p.R50Q	GPQNPKKQGIFHIHEACSSIHVNHV[p.R50Q]QDKLREIVGASTNWRDHVKAMEERKL	VQDKLREIV,SIHVNHVQDK,HVNHVQDKLR	CRC
ACP1	c.368delA	p.Q123fs	DLNRKSNQVKTCKAKIELLGSYDPQ[p.Q123fs]NNLLLKIPIMGMTLTLRRCTSSVSGAAERSWRRPTEAGSCPAAASLTRPHPEVLHFSVGV*	SLTRPHPEV,LLKIPIMGM,TLRRCTSSV,IMGMTLTLR,MGMTLTLRR,SSVSGAAER,RSWRRPTEA,LTRPHPEVL,GAAERSWRR,CTSSVSGAA,EVLHFSVGV,RPHPEVLHF,HPEVLHFSV,NLLLKIPIM,GSYDPQNNL,TEAGSCPAA,GSCPAAASL,AAASLTRPH,AERSWRRPT,LLLKIPIMGM,LTLRRCTSSV,SLTRPHPEVL,IMGMTLTLRR,SYDPQNNLLL,ASLTRPHPEV,LTRPHPEVLH,PIMGMTLTLR,SGAAERSWRR,IPIMGMTLTL,RPTEAGSCPA,GSYDPQNNLL,LKIPIMGMTL,TEAGSCPAAA,PEVLHFSVGV,DPQNNLLLKI	STAD
ACP6	c.86T>G	p.V29G	GVFSMRLWTPVGVLTSLAYCLHQRR[p.V29G]GALAELQEADGQCPVDRSLLKLKMVQ	CLHQRRGAL,HQRRGALAE,QRRGALAEL,CLHQRRGALA,HQRRGALAEL,YCLHQRRGAL	KIRP
ACPP	c.127C>T	p.R43W	FLFLLFFWLDRSVLAKELKFVTLVF[p.R43W]WHGDRSPIDTFPTDPIKESSWPQGFG	TLVFWHGDR,LKFVTLVFW,FWHGDRSPI,VTLVFWHGDR,VFWHGDRSPI	BRCA
ACPP	c.314G>A	p.R105Q	ELGEYIRKRYRKFLNESYKHEQVYI[p.R105Q]QSTDVDRTLMSAMTNLAALFPPEGVS	HEQVYIQST,IQSTDVDRTL	CRC

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ACPP	c.961G>A	p.E321K	LQMALDVYNGLLPPYASCHLTELYF[p.E321K]KKGEYFVEMYYRNETQHEPYPLMLPG	HLTELYFKK,LYFKKGEYF,ELYFKKGEY,KKGEYFVEM,LYFKKGEYFV,SCHLTELYFK,ELYFKKGEYF,TELYFKKGEY,FKKGEYFVEM,KKGEYFVEMY	BLCA
ACR	c.837G>T	p.W279C	YVVVGITSWGVGCARAKRPGIYTAT[p.W279C]CPYLNWIASKIGSNALRMIQSATPPP	GIYTATCPY,IYTATCPYL,CPYLNWIAS,TATCPYLNW,GIYTATCPYL,YTATCPYLNW,TATCPYLNWI	KICH
ACSBG2	c.750T>G	p.I250M	AVLIYTSGTTGIPKGVMLSHDNITW[p.I250M]MAGAVTKDFKLTDKHETVVSYLPLSH	NITWMAGAV,TWMAGAVTK,MAGAVTKDF,LSHDNITWM,MLSHDNITWM,ITWMAGAVTK,MAGAVTKDFK,DNITWMAGAV,WMAGAVTKDF	KIRP
ACSL3	c.562A>T	p.T188S	AIFCETRAEWMIAAQACFMYNFQLV[p.T188S]SLYATLGGPAIVHALNETEVTNIITS	FMYNFQLVS,FQLVSLYAT,QLVSLYATL,MYNFQLVSL,YNFQLVSLY,FMYNFQLVSL,FQLVSLYATL,SLYATLGGPA,MYNFQLVSLY,YNFQLVSLYA	CLL
ACSM2A	c.1206_1207insC	p.L402fs	PGYMGTAASCYDVQIIDDKGNVLPP[p.L402fs]RHRRRHWHQGQTHQAYRHLLWLCGQSRQDSSQHSRRLLAPWRPGNQR*	HQAYRHLLW,AYRHLLWLC,SSQHSRRLL,SQHSRRLLA,HSRRLLAPW,RLLAPWRPG,HQGQTHQAY,NVLPPRHRR,VLPPRHRRR,QGQTHQAYR,RHWHQGQTH,QAYRHLLWL,HQAYRHLLWL,THQAYRHLLW,QTHQAYRHLL,SSQHSRRLLA,HSRRLLAPWR,WHQGQTHQAY,NVLPPRHRRR,HQGQTHQAYR,HLLWLCGQSR,LAPWRPGNQR,GQTHQAYRHL,GQSRQDSSQH,SQHSRRLLAP,QHSRRLLAPW	KIRC
ACSM2B	c.585G>T	p.K195N	VASECPSLRIKLLVSEKSCDGWLNF[p.K195N]NKLLNEASTTHHCVETGSQEASAIYF	GWLNFNKLL	UCEC
ACTA1	c.823G>T	p.G275C	ITIGNERFRCPETLFQPSFIGMESA[p.G275C]CIHETTYNSIMKCDIDIRKDLYANNV	FIGMESACI,SACIHETTY,ESACIHETT,MESACIHET,ESACIHETTY,CIHETTYNSI,SFIGMESACI,MESACIHETT	LUAD
ACTG1	c.64G>C	p.A22P	MEEEIAALVIDNGSGMCKAGF[p.A22P]PGDDAPRAVFPSIVGRPRHQGVMVGM	FPGDDAPRA,FPGDDAPRAV	MM
ACTL6A	c.264delA	p.L88fs	GPTYYIDTNALRVPRENMEAISPLK[p.L88fs]MGWLKTGIVSKLFWIIPTKCMSNQKPVSILFSCQRHRGILEQRERN*	KMGWLKTGI,GIVSKLFWI,WLKTGIVSK,KLFWIIPTK,ILFSCQRHR,VSILFSCQR,IVSKLFWII,NQKPVSILF,PTKCMSNQK,MEAISPLKM,LKTGIVSKL,SKLFWIIPT,MSNQKPVSI,KMGWLKTGIV,WLKTGIVSKL,GIVSKLFWII,KLFWIIPTKC,AISPLKMGWL,CMSNQKPVSI,ISPLKMGWLK,GWLKTGIVSK,SILFSCQRHR,NMEAISPLKM,LKMGWLKTGI,LKTGIVSKLF,MSNQKPVSIL,SNQKPVSILF,FSCQRHRGIL,EAISPLKMGW	STAD
ACTL7B	c.1061G>A	p.R354H	TGFKEEMAANVLLCGGCTMLDGFPE[p.R354H]HFQRELSLLCPGDSPAVAAAPERKTS	HFQRELSLL,DGFPEHFQR,FPEHFQREL,TMLDGFPEH,MLDGFPEHF,EHFQRELSL,TMLDGFPEHF	CRC
ACTL7B	c.631G>A	p.E211K	IYSYGKTSGLVVESGHGVSHVVPIS[p.E211K]KGDVLPGLTSRADYAGGDLTNYLMQL	VSHVVPISK,VPISKGDVL,GVSHVVPISK,HVVPISKGDV	CESC
ACTL9	c.992G>A	p.R331H	EVPGLSPVGLSTMAKQSLRKLSLEM[p.R331H]HADLAQNVLLCGGSSLFTGFEGRFRA	LEMHADLAQ,HADLAQNVL,KLSLEMHADL,EMHADLAQNV,MHADLAQNVL	CRC
ACTN2	c.2677G>T	p.D893Y	AYSGPGSVPGALDYAAFSSALYGES[p.D893Y]YL*	SSALYGESY,SALYGESYL,FSSALYGESY,SSALYGESYL	LUAD
ACVR1	c.617G>A	p.R206H	ADLLDHSCTSGSGSGLPFLVQRTVA[p.R206H]HQITLLECVGKGRYGEVWRGSWQGEN	HQITLLECV,TVAHQITLL,RTVAHQITL,FLVQRTVAH,VQRTVAHQI,RTVAHQITLL,VQRTVAHQIT,QRTVAHQITL,HQITLLECVG	UCEC
ACVR1	c.869C>T	p.S290L	FIASDMTSRHSSTQLWLITHYHEMG[p.S290L]LLYDYLQLTTLDTVSCLRIVLSIASG	GLLYDYLQL,LLYDYLQLT,ITHYHEMGL,HYHEMGLLY,HEMGLLYDY,GLLYDYLQLT,LLYDYLQLTT,ITHYHEMGLL,THYHEMGLLY,YHEMGLLYDY,HEMGLLYDYL,MGLLYDYLQL	CRC
ADAD1	c.32C>T	p.S11L	MASNNHWFQS[p.S11L]LQVPSFAQMLKKNLPVQPATKTITTP	SNNHWFQSL,FQSLQVPSF,LQVPSFAQM,FQSLQVPSFA,SLQVPSFAQM,LQVPSFAQML,WFQSLQVPSF,ASNNHWFQSL	UCEC
ADAD2	c.131G>A	p.G44E	LAASLQISPQPRPWRPLPAQAQSAW[p.G44E]EPAPAPATYRAEGGWPQVSVLRDSGP	QSAWEPAPA,EPAPAPATY,AQAQSAWEP,AQSAWEPAP,WEPAPAPAT,AQSAWEPAPA,AQAQSAWEPA,SAWEPAPAPA,WEPAPAPATY	ACC
ADAM23	c.1139A>T	p.K380M	EKDQIDITTNPVQMLHEFSKYRQRI[p.K380M]MQHADAVHLISRVTFHYKRSSLSYFG	RIMQHADAV,MQHADAVHL,KYRQRIMQH,FSKYRQRIM,IMQHADAVH,IMQHADAVHL,MQHADAVHLI,KYRQRIMQHA,RQRIMQHADA,SKYRQRIMQH,RIMQHADAVH	KIRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ADAM28	c.217_218insA	p.K73fs	QEQFETELKYKMTINGKIAVLYLKK[p.K73fs]KQEPPCTRLHGNIL*	CTRLHGNIL,KQEPPCTRL,KIAVLYLKKK,YLKKKQEPPC,KKQEPPCTRL,KQEPPCTRLH	STAD
ADAM29	c.613G>A	p.V205I	IDNSTQKQSSYVGWWIHFRIVEIVV[p.V205I]IIDNYLYIRYERNDSKLLEDLYVIVN	RIVEIVVII,VIIDNYLYI,VVIIDNYLY,IVVIIDNYL,FRIVEIVVI,IIDNYLYIRY,VVIIDNYLYI,VIIDNYLYIR,HFRIVEIVVI,IVVIIDNYLY,EIVVIIDNYL,VEIVVIIDNY	GBM
ADAM30	c.2223G>T	p.Q741H	LKPKQEKMPLSKAKTEQEESKTKTV[p.Q741H]HEESKTKTGQEESEAKTGQEESKAKT	KTKTVHEES,KTKTVHEESK,KTVHEESKTK	LUAD
ADAM30	c.289_290GG>TT	p.G97L	KHVLHLWPKRLLLPRHLRVFSFTEH[p.G97L]LELLEDHPYIPKDCNYMGSVKESLDSK	RVFSFTEHL,SFTEHLELL,FSFTEHLEL,LELLEDHPY,HLELLEDHPY,VFSFTEHLEL,LRVFSFTEHL,FSFTEHLELL,LELLEDHPYI	SKCM
ADAM30	c.941C>A	p.S314Y	SSDWAHLYLQRKYNDALAWSFGKVC[p.S314Y]YLEYAGSVSTLLDTNILAPATWSAHE	WSFGKVCYL,CYLEYAGSV,AWSFGKVCY,FGKVCYLEY,SFGKVCYLEY,LAWSFGKVCY	CRC
ADAM32	c.1676G>A	p.R559Q	DRNNKYVFCGWRNLICGRLVCTYPT[p.R559Q]QKPFHQENGDVIYAFVRDSVCITVDY	LVCTYPTQK,CTYPTQKPF,RLVCTYPTQK,CTYPTQKPFH,VCTYPTQKPF	CRC
ADAM9	c.767G>A	p.R256Q	NQTAVREEMILLANYLDSMYIMLNI[p.R256Q]QIVLVGLEIWTNGNLINIVGGAGDVL	YIMLNIQIV,IMLNIQIVL,MLNIQIVLV,MYIMLNIQI,SMYIMLNIQI,YIMLNIQIVL,IMLNIQIVLV,MYIMLNIQIV,IQIVLVGLEI	UCEC
ADAMTS12	c.1075G>A	p.E359K	LNPVHHDVAVLLTRKDICAGFNRPC[p.E359K]KTLGLSHLSGMCQPHRSCNINEDSGL	CAGFNRPCK,CKTLGLSHL,KTLGLSHLSG,FNRPCKTLGL,AGFNRPCKTL	UCS
ADAMTS12	c.3157C>G	p.P1053A	RPRMLTTPTGPESMSTSTPAISSPS[p.P1053A]ATTASKEGDLGGKQWQDSSTQPELSS	TPAISSPSA,ISSPSATTA,AISSPSATTA,SSPSATTASK,STPAISSPSA,TPAISSPSAT	CESC
ADAMTS14	c.712G>T	p.G238C	QQEWAEPDGDLHNEAFGLGDLPNLL[p.G238C]CLVGDQLGDTERKRRHAKPGSYSIEV	DLPNLLCLV,NLLCLVGDQL	LUAD
ADAMTS16	c.2449G>A	p.D817N	LRRYYLNGHWTVDWPGRYKFSGTTF[p.D817N]NYRRSYNEPENLIATGPTNETLIVEL	FSGTTFNYR,KFSGTTFNY,TTFNYRRSY,SGTTFNYRR,FSGTTFNYRR,KFSGTTFNYR,YKFSGTTFNY,GTTFNYRRSY	CRC
ADAMTS17	c.1715A>C	p.N572T	SPWGAWSMCSRTCGTGARFRQRKCD[p.N572T]TPPPGPGGTHCPGASVEHAVCENLPC	RQRKCDTPP,RQRKCDTPPP	TGCT
ADAMTS2	c.2842G>A	p.D948N	WEPCSQTCGRTGMQVRSVRCIQPLH[p.D948N]NNTTRSVHAKHCNDARPESRRACSRE	LHNNTTRSV,SVRCIQPLHN,LHNNTTRSVH	CLL
ADAMTS20	c.1622G>T	p.R541L	KLHKGCFTQHVPPADGTDCGPGMHC[p.R541L]LHGLCVNKETETRPVNGEWGPWEPYS	CLHGLCVNK,GMHCLHGLCV,GPGMHCLHGL	LUAD
ADAMTS20	c.3751C>A	p.R1251S	GKTTRQVLCMNYHQPIDENYCDPEV[p.R1251S]SPLMEQECSLAACPPAHSHFPSSPVQ	SPLMEQECSL	LUAD
ADAMTS4	c.466C>T	p.R156W	TINGDPESVASLHWDGGALLGVLQY[p.R156W]WGAELHLQPLEGGTPNSAGGPGAHIL	VLQYWGAEL,ALLGVLQYW,QYWGAELHL,LQYWGAELH,LLGVLQYWGA,LQYWGAELHL,GALLGVLQYW,WGAELHLQPL	CRC
ADAMTS5	c.1645C>A	p.L549M	QGQMVCLTKKLPAVEGTPCGKGRIC[p.L549M]MQGKCVDKTKKKYYSTSSHGNWGSWG	KGRICMQGK,TPCGKGRICM	LUAD
ADAMTS8	c.1570G>A	p.V524M	TPCGPGHLCSEGSCLPEEEVERPKP[p.V524M]MADGGWAPWGPWGECSRTCGGGVQFS	KPMADGGWA,EEVERPKPM,MADGGWAPW,PMADGGWAPW,EEEVERPKPM	GBM
ADAMTS9	c.1975G>T	p.G659W	FKSCNTEPCLKQKRDFRDEQCAHFD[p.G659W]WKHFNINGLLPNVRWVPKYSGILMKD	HFDWKHFNI,CAHFDWKHF,WKHFNINGL,DEQCAHFDW,AHFDWKHFNI,WKHFNINGLL	LUAD

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ADAMTSL4	c.2332_2333insG	p.G778fs	TSCSRSCGPGTQHRQLQCRQEFGGG[p.G778fs]WLLGAPGALWTSPPAQHHPVLPAAPLWPLGSWLSLEPVLRAVRPGPEKPAGSLCWEQW*	WLLGAPGAL,GSWLSLEPV,SLEPVLRAV,RAVRPGPEK,SWLSLEPVL,HPVLPAAPL,LPAAPLWPL,SPPAQHHPV,PPAQHHPVL,WPLGSWLSL,GPEKPAGSL,RQEFGGGWL,QEFGGGWLL,LLGAPGALW,AQHHPVLPA,QHHPVLPAA,APLWPLGSW,VLPAAPLWPL,AQHHPVLPAA,WLSLEPVLRA,LWPLGSWLSL,AVRPGPEKPA,SWLSLEPVLR,SLEPVLRAVR,TSPPAQHHPV,SPPAQHHPVL,APLWPLGSWL,RQEFGGGWLL,WLLGAPGALW,GSWLSLEPVL,QEFGGGWLLG,HPVLPAAPLW	STAD
ADCY2	c.260C>T	p.A87V	LAVFFALGLEVEDHVAFLITVPTAL[p.A87V]VIFFAIFILVCIESVFKKLLRLFSLV	LVIFFAIFI,VIFFAIFIL,LITVPTALV,TVPTALVIF,TALVIFFAI,PTALVIFFA,ALVIFFAIF,ITVPTALVI,VPTALVIFF,FLITVPTALV,ALVIFFAIFI,VIFFAIFILV,ITVPTALVIF,TVPTALVIFF,TALVIFFAIF,PTALVIFFAI,LVIFFAIFIL,VPTALVIFFA	DLBCL
ADCY2	c.2662G>A	p.V888I	HVAEHFLARSLKNEELYHQSYDCVC[p.V888I]IMFASIPDFKEFYTESDVNKEGLECL	SYDCVCIMF,IMFASIPDF,QSYDCVCIM,HQSYDCVCI,IMFASIPDFK,CIMFASIPDF,HQSYDCVCIM,QSYDCVCIMF	OV
ADCY2	c.3046C>A	p.P1016T	SFNDFKLRVGINHGPVIAGVIGAQK[p.P1016T]TQYDIWGNTVNVASRMDSTGVLDKIQ	AQKTQYDIW,TQYDIWGNTV,GVIGAQKTQY	LUAD
ADCY5	c.1982G>A	p.R661H	SIETFLILRCTQKRKEEKAMIAKMN[p.R661H]HQRTNSIGHNPPHWGAERPFYNHLGG	MIAKMNHQR,KAMIAKMNH,KMNHQRTNS,HQRTNSIGH,MNHQRTNSI,KMNHQRTNSI,AMIAKMNHQR	CRC
ADD3	c.1708G>A	p.E570K	HGPPAPPNPFSHLTEGELEEYKRTI[p.E570K]KRKQQGLEDAEQELLSDDASSVSQIQ	TIKRKQQGL,RTIKRKQQGL	UCEC
ADGB	c.3371C>T	p.S1124L	PCNSFAIKEIRDYYIPNDKKILFRY[p.S1124L]LVKVLTPQPATIQVRTSKPDAFIKLQ	ILFRYLVKV,KILFRYLVK,LFRYLVKVL,KKILFRYLV,KILFRYLVKV,ILFRYLVKVL,KKILFRYLVK,LVKVLTPQPA	UCEC
ADH1A	c.461A>T	p.D154V	SRFTCRRKPIHHFLGISTFSQYTVV[p.D154V]VENAVAKIDAASPLEKVCLIGCGFST	YTVVVENAV,VVVENAVAK,TFSQYTVVV,SQYTVVVEN,STFSQYTVVV,SQYTVVVENA,VVVENAVAKI,TVVVENAVAK,YTVVVENAVA,VENAVAKIDA	KIRC
ADNP2	c.965delC	p.S322fs	NSPSPAAGQPVTVAQGAPGSLTHSP[p.S322fs]LLLANPT*	SLTHSPLLL,GSLTHSPLL,LTHSPLLLA,SLTHSPLLLA,APGSLTHSPL	STAD
AFF2	c.1790G>A	p.R597H	VKTNASQVPAEPKERPLLSLIREKA[p.R597H]HPRPTQKIPETKALKHKLSTTSETVS	KAHPRPTQK,LIREKAHPR,REKAHPRPT,KAHPRPTQKI,SLIREKAHPR	PRAD
AFF3	c.2755G>A	p.E919K	INKNEKMLRSPISPLSDASKHKYTS[p.E919K]KDLTSSSRPNGNSLFTSASSSKKPKA	ASKHKYTSK,TSKDLTSSSR,SKHKYTSKDL	BLCA
AFP	c.545C>G	p.A182G	TFMNKFIYEIARRHPFLYAPTILLW[p.A182G]GARYDKIIPSCCKAENAVECFQTKAA	LLWGARYDK,LWGARYDKI,TILLWGARY,PTILLWGAR,PTILLWGARY,YAPTILLWGA,LLWGARYDKI,ILLWGARYDK,LYAPTILLWG	LUAD
AGAP1	c.381delC	p.G127fs	GGRFKKEIVVDGQSYLLLIRDEGGP[p.G127fs]RRRSLPCGWTLLYLSSAWRMK*	LPCGWTLLY,SLPCGWTLL,LLYLSSAWR,YLSSAWRMK,RSLPCGWTL,LYLSSAWRM,WTLLYLSSA,GPRRRSLPC,TLLYLSSAW,LLYLSSAWRM,RSLPCGWTLL,LIRDEGGPRR,LYLSSAWRMK,SLPCGWTLLY,TLLYLSSAWR,RRSLPCGWTL,WTLLYLSSAW,LPCGWTLLYL	STAD
AGAP3	c.2296C>T	p.R766W	VWEGALGGYSKPGPDACREEKERWI[p.R766W]WAKYEQKLFLAPLPSSDVPLGQQLLR	WIWAKYEQK,IWAKYEQKL,KERWIWAKY,WAKYEQKLF,EEKERWIWA,WIWAKYEQKL,IWAKYEQKLF,RWIWAKYEQK,REEKERWIWA	GBM
AGAP6	c.207delC	p.D69fs	MAAAVQPAEVTVEVGEDLHMHHVRD[p.D69fs]GRCLKLWSLTFLPIQSQAQYSRGTLKQKLWSLTLLPIQRQAQYSRGTLKQML*	TLKQKLWSL,HVRDGRCLK,CLKLWSLTF,LWSLTFLPI,YSRGTLKQK,KQKLWSLTL,HMHHVRDGR,LPIQSQAQY,LKLWSLTFL,SQAQYSRGT,QKLWSLTLL,KLWSLTFLPI,KLWSLTLLPI,CLKLWSLTFL,KQKLWSLTLL,RCLKLWSLTF,HVRDGRCLKL,FLPIQSQAQY,LTFLPIQSQA,DGRCLKLWSL,SQAQYSRGTL,LKQKLWSLTL,YSRGTLKQML	KIRC
AGAP6	c.380G>T	p.S127I	NPSANPEASTIFQRNSQTDVVEIRR[p.S127I]INCTNHVSAVRFSQQYSLCSTIFLDD	RRINCTNHV,RINCTNHVSA	CLL,PRAD
AGAP7	c.211delG	p.E71fs	AAAVQPAEVTVEVGEDLHMHHVRDR[p.E71fs]RCLKLWSLTLLPIQRQAQYSRGTLKQML*	HMHHVRDRR,HVRDRRCLK,CLKLWSLTL,RRCLKLWSL,LKLWSLTLL,KLWSLTLLPI,CLKLWSLTLL,HVRDRRCLKL,DRRCLKLWSL,RCLKLWSLTL,YSRGTLKQML	KIRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
AGAP9	c.742A>G	p.M248V	STSQEDPQFSVPPTANTPTPVCKLS[p.M248V]VRWSNLFTSEKGSDPDKERKAPENHA	KLSVRWSNL,LSVRWSNLF,SVRWSNLFT,KLSVRWSNLF,SVRWSNLFTS,TPTPVCKLSV,CKLSVRWSNL,TPVCKLSVRW	SKCM
AGBL5	c.1260_1261insC	p.I420fs	KLNSVWIMPQQSAGLEESAPDTIPP[p.I420fs]QREWRCLLCGPAWTCFQKGLLHVRKQL*	CFQKGLLHV,TIPPQREWR,FQKGLLHVR,RCLLCGPAW,LCGPAWTCF,REWRCLLCG,CGPAWTCFQK,DTIPPQREWR,CFQKGLLHVR,LLCGPAWTCF,WRCLLCGPAW,REWRCLLCGP	STAD
AGMAT	c.937G>A	p.V313M	TGTPEIAGLTPSQALEIIRGCQGLN[p.V313M]MMGCDLVEVSPPYDLSGNTALLAANL	MMGCDLVEV,IRGCQGLNM,RGCQGLNMM,GLNMMGCDLV,NMMGCDLVEV,IIRGCQGLNM,IRGCQGLNMM	CRC
AGPAT4	c.634G>A	p.A212T	ISMQVARAKGLPRLKHHLLPRTKGF[p.A212T]TITVRSLRNVVSAVYDCTLNFRNNEN	RTKGFTITV,FTITVRSLR,LPRTKGFTI,LLPRTKGFTI,RTKGFTITVR,KGFTITVRSL,GFTITVRSLR,LPRTKGFTIT	CRC
AGRN	c.3851_3853delTGA	p.1284_1285VT>A	GATSGAIAAGATARATTASRLPSSA[p.1284_1285VT>A]APRAPHPSHTSQPVAKTTAAPTTRRPPT	ASRLPSSAA,RLPSSAAPR,SSAAPRAPH,APRAPHPSH,LPSSAAPRA,RLPSSAAPRA,APRAPHPSHT	KICH
AGXT2	c.1504C>T	p.R502C	FSQTFRIAPSMCITKPEVDFAVEVF[p.R502C]CSALTQHMERRAK*	FAVEVFCSA,FCSALTQHM,VEVFCSALT,FAVEVFCSAL,CSALTQHMER,VFCSALTQHM	UCEC
AHI1	c.909_910insA	p.K303fs	DDEISSMEQSTEDSMQDDTKPKPKK[p.K303fs]NKKED*	KPKPKKNKK	STAD
AHNAK	c.12449C>T	p.S4150F	KAPKISMPEVDLNLKGPKMKGDVDV[p.S4150F]FLPKVEGDLKGPEVDIKGPKVDIDVP	KMKGDVDVF,KMKGDVDVFL,KGDVDVFLPK,PKMKGDVDVF	BLCA
AHNAK	c.15_16insGAG	p.5_6insE	MEKEE[p.5_6insE]ETTRELLLPNWQGSGSHGLTIAQRDDGV	KEEETTREL,EEETTRELL,KEEETTRELL,EEETTRELLL	KIRC
AHNAK	c.3658G>A	p.V1220I	ISMPDVDLHLKGPKVKGDVDVSVPK[p.V1220I]IEGEMKVPDVEIKGPKMDIDAPDVEV	IEGEMKVPDV,VPKIEGEMKV	CLL
AHNAK	c.6341C>G	p.A2114G	PDVSLEGPEGKLKGPKLKMPEMHFK[p.A2114G]GPKISMPDVDLHLKGPKVKGDVDVSL	HFKGPKISM,MHFKGPKISM,PEMHFKGPKI	CLL
AHNAK	c.8665G>C	p.D2889H	LKGPEVDLKGPKVDIDVPDVNVQGP[p.D2889H]HWHLKMPKMKMPKFSMPGFKAEGPEV	VQGPHWHLK,NVQGPHWHL,NVQGPHWHLK,HWHLKMPKMK,VQGPHWHLKM	BLCA
AHNAK2	c.3643C>T	p.P1215S	APKVEADVSLPSMQGDLKTTDLSIQ[p.P1215S]SPSADLEVHAGQVDVKLLEGHVPEGA	SPSADLEVH	KIRP
AHNAK2	c.4918C>A	p.L1640M	PDVKMSLSSMEVDVQAPRAKLDGAQ[p.L1640M]MEGDLSLADKAVTAKDSKFKMPKFKM	AQMEGDLSL,QMEGDLSLA,RAKLDGAQM,AQMEGDLSLA	TGCT
AHNAK2	c.6497C>T	p.S2166F	LANKDLTTKDSKFKMPKFKMPSFGV[p.S2166F]FAPGKSIEASVDVSPPKVEADMSLPS	KMPSFGVFA,SFGVFAPGK,FKMPSFGVF,GVFAPGKSI,MPSFGVFAP,PSFGVFAPGK,KFKMPSFGVF,MPSFGVFAPG,FKMPSFGVFA	KIRP
AICDA	c.391C>G	p.R131G	LRIFTARLYFCEDRKAEPEGLRRLH[p.R131G]GAGVQIAIMTFKDYFYCWNTFVENHE	RLHGAGVQI,GLRRLHGAGV,RLHGAGVQIA,RRLHGAGVQI,LHGAGVQIAI,HGAGVQIAIM	LUSC
AICDA	c.431A>T	p.Y144F	RKAEPEGLRRLHRAGVQIAIMTFKD[p.Y144F]FFYCWNTFVENHERTFKAWEGLHENS	IMTFKDFFY,MTFKDFFYC,FFYCWNTFV,TFKDFFYCW,DFFYCWNTF,IAIMTFKDF,AIMTFKDFF,KDFFYCWNT,AIMTFKDFFY,IAIMTFKDFF,MTFKDFFYCW,KDFFYCWNTF,DFFYCWNTFV	GBM
AIDA	c.740A>T	p.K247M	VDIELQKHVEKLTKGAAIFFEFKHY[p.K247M]MPKKRFTSTKCFAFMEMDEIKPGPIV	IFFEFKHYM,EFKHYMPKK,MPKKRFTST,FEFKHYMPK,KHYMPKKRF,YMPKKRFTST,MPKKRFTSTK,FFEFKHYMPK,EFKHYMPKKR,AIFFEFKHYM,FKHYMPKKRF	KIRC
AK302879	c.572A>G	p.Q191R	AVSTQQQEEDRSSSCREAVLQWRLQ[p.Q191R]RTIKEQALLNAHVTQVTESLKQVQLE	AVLQWRLQR,QWRLQRTIK,RTIKEQALL,LQWRLQRTI,VLQWRLQRTI,EAVLQWRLQR,LQRTIKEQAL	PRAD
AK7	c.476C>T	p.A159V	SALSEEVSHFEKRKLFILLSTVMTW[p.A159V]VRSKALDPEDSEVPFTEEDYRRRKSH	LLSTVMTWV,VMTWVRSKA,TVMTWVRSK,MTWVRSKAL,LSTVMTWVR,ILLSTVMTWV,TVMTWVRSKA,VMTWVRSKAL,STVMTWVRSK,LLSTVMTWVR	GBM
AK8	c.728A>C	p.D243A	KLLEYHRNIVRVIPSYPKILKVISA[p.D243A]AQPCVDVFYQALTYVQSNHRTNAPFT	KILKVISAA,VISAAQPCV,AQPCVDVFY,AAQPCVDVF,KVISAAQPCV,AAQPCVDVFY,SAAQPCVDVF	GBM

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
AKAP12	c.3844G>A	p.E1282K	ILSKTEGTQEADQYADEKTKDVPFF[p.E1282K]KGLEGSIDTGITVSREKVTEVALKGE	KTKDVPFFK,KDVPFFKGL,KTKDVPFFKG	CRC
AKAP13	c.8353delA	p.K2785fs	QAPASTSASTRLFGLTKPKEKKEKK[p.K2785fs]RRTKPAALSPVMVPRQKYQQRVKRSSADPLPLC*	ALSPVMVPR,KRRTKPAAL,RTKPAALSP,RQKYQQRVK,QQRVKRSSA,RVKRSSADP,RSSADPLPL,KPAALSPVM,EKKRRTKPA,YQQRVKRSS,VKRSSADPL,RTKPAALSPV,AALSPVMVPR,RQKYQQRVKR,RVKRSSADPL,MVPRQKYQQR,KPAALSPVMV,VPRQKYQQRV,KKRRTKPAAL,TKPAALSPVM,YQQRVKRSSA,KRSSADPLPL,SPVMVPRQKY	STAD
AKAP9	c.10444C>A	p.L3482I	RRILYQNLNEPTTWSLTSDRTRNWV[p.L3482I]IQQKIEGETKESNYAKLIEMNGGGTG	RTRNWVIQQ,SDRTRNWVI,RNWVIQQKI,RTRNWVIQQK	CRC
AKAP9	c.11229delG	p.M3743fs	YLLLLLGGFQECEDATLALLARMGG[p.M3743fs]SQLSRI*	RMGGSQLSR,LARMGGSQL,RMGGSQLSRI,LLARMGGSQL	STAD
AKD1	c.3625delA	p.R1209fs	DMKAKIRVDTIAKRRAELILERDKK[p.R1209fs]GGRMLLEMMKRLVRKNLKKTMMILKTSLKMSFQKMRKR*	MLLEMMKRL,TMMILKTSL,NLKKTMMIL,RMLLEMMKR,EMMKRLVRK,RLVRKNLKK,MMILKTSLK,TSLKMSFQK,KMSFQKMRK,MSFQKMRKR,KRLVRKNLK,KNLKKTMMI,LKKTMMILK,KTMMILKTS,KTSLKMSFQ,SLKMSFQKM,MKRLVRKNL,MILKTSLKM,KGGRMLLEM,RKNLKKTMM,LKTSLKMSF,MLLEMMKRLV,MMILKTSLKM,NLKKTMMILK,TMMILKTSLK,KTSLKMSFQK,KMSFQKMRKR,GGRMLLEMMK,MMKRLVRKNL,MKRLVRKNLK,KRLVRKNLKK,KTMMILKTSL,SLKMSFQKMR,ILKTSLKMSF,LERDKKGGRM,KKGGRMLLEM,RMLLEMMKRL,RKNLKKTMMI,TSLKMSFQKM	STAD
AKNAD1	c.1859A>G	p.K620R	AEMTAPSPSCAFCRRLLEWKQNVEK[p.K620R]RGHGRINCGRFSIVLHEKAPHSDSTP	NVEKRGHGR,RGHGRINCGR	HNSC
AKT1	c.49G>A	p.E17K	MSDVAIVKEGWLHKRG[p.E17K]KYIKTWRPRYFLLKNDGTFIGYKERP	WLHKRGKYI,LHKRGKYIK,RGKYIKTWR,KYIKTWRPR,GWLHKRGKY,WLHKRGKYIK,KYIKTWRPRY,HKRGKYIKTW	BRCA,CESC,THCA
AKT2	c.867C>G	p.I289M	EYLHSRDVVYRDIKLENLMLDKDGH[p.I289M]MKITDFGLCKEGISDGATMKTFCGTP	LMLDKDGHM,HMKITDFGL,MLDKDGHMK,MLDKDGHMKI,LMLDKDGHMK	BRCA
ALAS1	c.904G>C	p.G302R	PRVCGAVMDTLKQHGAGAGGTRNIS[p.G302R]RTSKFHVDLERELADLHGKDAALLFS	GTRNISRTS,ISRTSKFHV,RTSKFHVDL,RNISRTSKF,NISRTSKFHV,GTRNISRTSK,TRNISRTSKF	KIRC
ALB	c.881C>T	p.S294L	CCHGDLLECADDRADLAKYICENQD[p.S294L]LISSKLKECCEKPLLEKSHCIAEVEN	YICENQDLI,KYICENQDL,NQDLISSKL,CENQDLISS,KYICENQDLI,AKYICENQDL	CRC
ALDH1A2	c.253C>T	p.R85C	PATGEQVCEVQEADKADIDKAVQAA[p.R85C]CLAFSLGSVWRRMDASERGRLLDKLA	CLAFSLGSV,QAACLAFSL,AVQAACLAF,VQAACLAFSL,KAVQAACLAF,CLAFSLGSVW	PRAD
ALDH1L1	c.2608G>A	p.A870T	KALYVSDKLQAGTVFVNTYNKTDVA[p.A870T]TPFGGFKQSGFGKDLGEAALNEYLRV	VATPFGGFK,DVATPFGGF,NKTDVATPF,DVATPFGGFK,YNKTDVATPF,TDVATPFGGF	CRC
ALDH2	c.858delG	p.L286fs	TEIGRVIQVAAGSSNLKRVTLELGG[p.L286fs]RAPTSSCQMPIWIGPWNRPTSPCSSTRASAAVPAPGPSCRRTSMMSLWSGALPGPSLGWSGTPLIARPSRGRRWMKLSLRRSSATSTRGSKRGRSCCVVGALLLTVVTSSSPLCLEMCRMA*	SMMSLWSGA,MMSLWSGAL,SLGWSGTPL,VVGALLLTV,KLSLRRSSA,ATSTRGSKR,QMPIWIGPW,STRASAAVP,RTSMMSLWS,IARPSRGRR,PSRGRRWMK,RGRRWMKLS,RWMKLSLRR,SLRRSSATS,SATSTRGSK,STRGSKRGR,RGRSCCVVG,SSSPLCLEM,PIWIGPWNR,SSTRASAAV,TVVTSSSPL,RPTSPCSST,GPSCRRTSM,RPSRGRRWM,LELGGRAPT,RAPTSSCQM,CRRTSMMSL,RRTSMMSLW,SLWSGALPG,SGALPGPSL,LGWSGTPLI,GRRWMKLSL,RSCCVVGAL,MPIWIGPWN,SMMSLWSGAL,SLGWSGTPLI,CVVGALLLTV,VVGALLLTVV,SSATSTRGSK,CQMPIWIGPW,STRASAAVPA,RASAAVPAPG,SCRRTSMMSL,RTSMMSLWSG,TSMMSLWSGA,RPSRGRRWMK,RGRRWMKLSL,GSKRGRSCCV,RGRSCCVVGA,RSCCVVGALL,MPIWIGPWNR,LIARPSRGRR,SATSTRGSKR,CSSTRASAAV,LTVVTSSSPL,APTSSCQMPI,GPWNRPTSPC,SPCSSTRASA,GPSCRRTSMM,GRAPTSSCQM,CRRTSMMSLW,MSLWSGALPG,WSGALPGPSL,GALPGPSLGW,IARPSRGRRW,MKLSLRRSSA,GRSCCVVGAL,TSSSPLCLEM,LELGGRAPTS,SPLCLEMCRM	STAD

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ALDH3A1	c.1685delC	p.P562fs	ETFSHRRSCLVRPLMNDEGLKVRYP[p.P562fs]RARPR*	GLKVRYPRA,KVRYPRARP,EGLKVRYPR,GLKVRYPRAR,KVRYPRARPR	STAD
ALG2	c.905C>A	p.S302Y	NVEHYQELKKMVQQSDLGQYVTFLR[p.S302Y]YFSDKQKISLLHSCTCVLYTPSNEHF	TFLRYFSDK,QYVTFLRYF,RYFSDKQKI,GQYVTFLRY,YVTFLRYFS,LGQYVTFLRY,VTFLRYFSDK,FLRYFSDKQK,GQYVTFLRYF	CRC
ALKBH1	c.409A>G	p.K137E	WHWVKQCLKLYSQKPNVCNLDKHMS[p.K137E]EEETQDLWEQSKEFLRYKEATKRRPR	SEEETQDLW,HMSEEETQDL,MSEEETQDLW	LUAD
ALPK2	c.1067delT	p.L356fs	ECSDVMTDYSNAVWQRNLLGTEHVF[p.L356fs]Y*	LLGTEHVFY,NLLGTEHVFY	STAD
ALPK2	c.1568delA	p.K523fs	LLSGESENSGMSQCWETAADKRVGG[p.K523fs]RTYGARGVQGNLPG*	RVGGRTYGA,RTYGARGVQ,RVGGRTYGAR,RTYGARGVQG,TAADKRVGGR,ADKRVGGRTY	UCEC
ALPK2	c.157G>A	p.D53N	DAVLRCIISGQPKPEVTWYKNGQAI[p.D53N]NGSGIISNYEFFENQYIHVLHLSCCT	NGSGIISNY,GQAINGSGI,INGSGIISNY,GQAINGSGII	LUSC
ALPPL2	c.92G>C	p.W31S	VLLLLGLRLQLSLGIIPVEEENPDF[p.W31S]SNRQAAEALGAAKKLQPAQTAAKNLI	SNRQAAEAL,FSNRQAAEAL	TGCT
ALX4	c.377G>A	p.R126Q	PPPQPQPQQQQPQPQPPAQPHLYLQ[p.R126Q]QGACKTPPDGSLKLQEGSSGHSAALQ	YLQQGACKT,HLYLQQGACK,LQQGACKTPP	BLCA
AMBN	c.674C>A	p.S225Y	QGPSLPGLDFADPQGSTIFQIARLI[p.S225Y]YHGPMPQNKQSPLYPGMLYVPFGANQ	IFQIARLIY,FQIARLIYH,ARLIYHGPM,TIFQIARLIY,IARLIYHGPM,IYHGPMPQNK,FQIARLIYHG	UCEC
AMDHD1	c.7A>G	p.S3G	MA[p.S3G]GGHSLLLENAQQVVLVCARGERFLAR	MAGGHSLLL	ACC
AMPH	c.874C>T	p.R292W	PSPLPSPTASPNHTLAPASPAPARP[p.R292W]WSPSQTRKGPPVPPLPKVTPTKELQQ	APARPWSPS,RPWSPSQTRK	CRC
ANAPC1	c.1609A>G	p.T537A	PGLPAPSLTMSNTMPRPSTPLDGVS[p.T537A]APKPLSKLLGSLDEVVLLSPVPELRD	VSAPKPLSK,APKPLSKLL,GVSAPKPLSK	PAAD,PRAD
ANK2	c.1358A>G	p.N453S	TESGLTPIHVAAFMGHLNIVLLLLQ[p.N453S]SGASPDVTNIRGETALHMAARAGQVE	VLLLLQSGA,LQSGASPDV,LLQSGASPDV,LQSGASPDVT	KIRC
ANK2	c.9227A>T	p.Q3076L	DDEAFEARVKEEEQKIFGLMVDRQS[p.Q3076L]LGTTPDTTPARTPTEEGTPTSEQNPF	GLMVDRQSL,RQSLGTTPD,LMVDRQSLGT,FGLMVDRQSL,RQSLGTTPDT	LUAD
ANK3	c.3966T>A	p.D1322E	LATQLYRELICVPYMAKFVVFAKMN[p.D1322E]EPVESSLRCFCMTDDKVDKTLEQQEN	KMNEPVESS,VVFAKMNEPV,KMNEPVESSL,EPVESSLRCF	TGCT
ANKDD1A	c.71G>A	p.R24H	MQEELAWETDGLLPLERQLHEAA[p.R24H]HQNNVGRMQELIGRRVNTRARNHVGR	HEAAHQNNV,AHQNNVGRM,EAAHQNNVGR,LERQLHEAAH,RQLHEAAHQN,AAHQNNVGRM	UCEC
ANKFN1	c.840G>T	p.M280I	YRLYRRMKTGFEHARAPEMPTNVCL[p.M280I]IVTSSTSLTVSFQEPLSVNAAVVTRY	EMPTNVCLI,LIVTSSTSL,MPTNVCLIV,CLIVTSSTSL,EMPTNVCLIV,IVTSSTSLTV,MPTNVCLIVT,PEMPTNVCLI	LUSC
ANKLE1	c.1930_1933delTGTT	p.C644fs	TAAPISGFRRGVCVCVCVCVCVCVC[p.C644fs]VCVCVCREHPGRSPPG*	CVCREHPGR,REHPGRSPP,CVCVCVCVCR,REHPGRSPPG	TGCT
ANKLE1	c.1932_1933delTT	p.C644fs	TAAPISGFRRGVCVCVCVCVCVCVC[p.C644fs]VCVCVCVGSTQADLPQAERGLCYRWYCWRGSK*	RWYCWRGSK,CYRWYCWRG,QAERGLCYR,LCYRWYCWR,PQAERGLCY,AERGLCYRW,RGLCYRWYCW,GLCYRWYCWR,LPQAERGLCY,AERGLCYRWY	TGCT
ANKMY1	c.905A>T	p.N302I	KELDARIFLNEIPPFVEDGEPWFII[p.N302I]IETPLLVKIQKQTYKFRNKPAHTSWN	FIIIETPLL,IIIETPLLV,IIETPLLVK,IETPLLVKI,FIIIETPLLV,IIIETPLLVK,WFIIIETPLL,GEPWFIIIET	THCA
ANKRD11	c.1106A>G	p.K369R	KDEYEFDEDDEQDRVPPVDDKHLLK[p.K369R]RDYRKETKSNSFISIPKMEVKSYTKN	HLLKRDYRK,KHLLKRDYR,KHLLKRDYRK	TGCT
ANKRD11	c.6044A>C	p.Y2015S	SPKRFCPADPLHSAAPGPFSASEAP[p.Y2015S]SPAPPASPAPYALPVAEPGLEDVKDG	SASEAPSPA,EAPSPAPPA,SPAPPASPA,FSASEAPSPA,SPAPPASPAP,SEAPSPAPPA	TGCT

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ANKRD12	c.1879G>A	p.E627K	HKEKSKHQKDFHLEFGEKSNAKIKD[p.E627K]KDHSPTFENSDCTLKKMDKEGKTLKK	KSNAKIKDK,KDKDHSPTF,IKDKDHSPTF	BLCA
ANKRD12	c.2161G>C	p.E721Q	WKENFFKSDETEDLFLNMEHESLTL[p.E721Q]QKKSKLEKNIKDDKSTKEKHVSKERN	LQKKSKLEK,TLQKKSKLEK	CESC
ANKRD32	c.2996C>A	p.T999N	SEFILASKGLTHLNELLMACKSHKE[p.T999N]NTSVHTDWLLDLYAGNIKTLQKLPHI	KSHKENTSV,NTSVHTDWL,NTSVHTDWLL,KSHKENTSVH,KENTSVHTDW	BLCA
ANKRD36	c.1010C>G	p.P337R	TSDKDDSVSNTATEIKDEQKSGTVL[p.P337R]RAVEQCLNRSLYRPDAVAQPVTENEF	KSGTVLRAV,EQKSGTVLR,QKSGTVLRAV	CLL
ANKRD36	c.1133A>G	p.K378R	VAQPVTENEFSLESEIISKLYIPKR[p.K378R]RIISPRSIKDVLPPVEEAVDRCLYLL	RIISPRSIK,LYIPKRRII,KLYIPKRRI,KRRIISPRS,IPKRRIISP,RRIISPRSI,ISKLYIPKRR,KLYIPKRRII,KRRIISPRSI,IPKRRIISPR	KIRC
ANKRD36	c.3040G>T	p.D1014Y	SEKPPGLKATSDEKDSVLNIARGKK[p.D1014Y]YGEKTRTVSSQKPPTLKATSDEEDSV	RGKKYGEKTR,KKYGEKTRTV	CLL
ANKRD36	c.3431T>C	p.M1144T	KSRTVSSPKQPALKAICDKEDSVPN[p.M1144T]TATEKKDEQISGTVSCQKQPALKATS	SVPNTATEK,KEDSVPNTA,SVPNTATEKK,KEDSVPNTAT	CESC
ANKRD36C	c.1313A>G	p.H438R	LEKDTIKNQNLEKKYLKDFEIVKRK[p.H438R]REDLQKA	IVKRKREDL	PAAD,PRAD
ANKRD50	c.1909G>A	p.V637M	WTALRSAAWGGHTEVVSALLYAGVK[p.V637M]MDCADADSRTALRAAAWGGHEDIVLN	ALLYAGVKM,SALLYAGVKM	TGCT
ANKRD6	c.1435C>T	p.R479C	TQHQMRVLDKLMVERLSAERTECLN[p.R479C]CLQQHSDTEKHEGEKRQISLVDELKT	CLQQHSDTEK,AERTECLNCL	CRC
ANO2	c.1000C>T	p.R334C	PLHDGEYDSPEDDMNDRKLLYQEWA[p.R334C]CYGVFYKFQPIDLIRKYFGEKIGLYF	YQEWACYGV,WACYGVFYK,ACYGVFYKF,LLYQEWACY,EWACYGVFY,QEWACYGVF,LYQEWACYGV,YQEWACYGVF,WACYGVFYKF,KLLYQEWACY,EWACYGVFYK,QEWACYGVFY	GBM
ANO3	c.121G>T	p.A41S	GMNISKSEITKETSLKPSRRSLPCL[p.A41S]SQSYAYSKSLSQSTSLFQSTESESQA	LSQSYAYSK,SLPCLSQSY,SLPCLSQSYA,CLSQSYAYSK,RSLPCLSQSY,SQSYAYSKSL,LPCLSQSYAY	LUAD
ANO3	c.2868G>T	p.M956I	IAYLIPDVPKGLHDRIRREKYLVQE[p.M956I]IMYEAELEHLQQQRRKSGQPVHHEWP	LVQEIMYEA,KYLVQEIMY,IMYEAELEH,REKYLVQEI,EKYLVQEIM,QEIMYEAEL,YLVQEIMYEA,IMYEAELEHL,RREKYLVQEI,REKYLVQEIM,EKYLVQEIMY,VQEIMYEAEL	CESC
ANXA6	c.692G>A	p.R231Q	RSKQHLRLVFDEYLKTTGKPIEASI[p.R231Q]QGELSGDFEKLMLAVVKCIRSTPEYF	IQGELSGDF,IEASIQGEL	HNSC
AOC3	c.237_238insG	p.L79fs	QSQLFADLSREELTAVMRFLTQRLG[p.L79fs]ARAGGCSPGPALGQLCLLSGVAAASQGCSPGSLGQGEPPTCPGGTGHRLLWQATPAQRE*	GQLCLLSGV,CLLSGVAAA,RLLWQATPA,RFLTQRLGA,FLTQRLGAR,LWQATPAQR,SPGPALGQL,GPALGQLCL,CPGGTGHRL,TQRLGARAG,SQGCSPGSL,FLTQRLGARA,RFLTQRLGAR,LLWQATPAQR,GPALGQLCLL,CPGGTGHRLL,MRFLTQRLGA,GQLCLLSGVA,HRLLWQATPA	STAD
AOX1	c.1520C>T	p.A507V	GRHWNEQMLDIACRLILNEVSLLGS[p.A507V]VPGGKVEFKRTLIISFLFKFYLEVSQ	LLGSVPGGK,NEVSLLGSV,LLGSVPGGKV,SLLGSVPGGK,SVPGGKVEFK,GSVPGGKVEF	GBM
AP1G1	c.2168G>T	p.R723L	NDIAAGIPSITAYSKNGLKIEFTFE[p.R723L]LSNTNPSVTVITIQASNSTELDMTDF	ELSNTNPSV,LKIEFTFEL,FELSNTNPS,IEFTFELSN,GLKIEFTFEL,IEFTFELSNT,FELSNTNPSV	LUAD
AP1G2	c.727G>A	p.D243N	PQLVHILRTLVTMGYSTEHSISGVS[p.D243N]NPFLQVQILRLLRILGRNHEESSETM	GVSNPFLQV,NPFLQVQIL,SISGVSNPF,SISGVSNPFL,HSISGVSNPF,NPFLQVQILR,VSNPFLQVQI	HNSC
AP3S1	c.121_124delAAGA	p.K41fs	LSKFYQPYSEDTQQQIIRETFHLVS[p.K41fs]EMKMFVIS*	LVSEMKMFV,TFHLVSEMK,ETFHLVSEM,FHLVSEMKM,HLVSEMKMF,SEMKMFVIS,RETFHLVSE,HLVSEMKMFV,LVSEMKMFVI,ETFHLVSEMK,RETFHLVSEM,FHLVSEMKMF	PAAD
AP4B1	c.826C>T	p.R276W	VVMGATKLFLILAKMFPHVQTDVLV[p.R276W]WVKGPLLAACSSESRELCFVALCHVR	VQTDVLVWV,VLVWVKGPL,QTDVLVWVK,HVQTDVLVW,VLVWVKGPLL,HVQTDVLVWV,VQTDVLVWVK,DVLVWVKGPL	PRAD

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APBA1	c.1870G>A	p.E624K	LIAQSIGQAFSVAYQEFLRANGINP[p.E624K]KDLSQKEYSDLLNTQDMYNDDLIHFS	FLRANGINPK,GINPKDLSQK,NPKDLSQKEY	CRC
APBA1	c.2190G>T	p.K730N	QIMSINGTSLVGLPLSTCQSIIKGL[p.K730N]NNQSRVKLNIVRCPPVTTVLIRRPDL	GLNNQSRVK,KGLNNQSRVK,IIKGLNNQSR	CRC
APBB2	c.729_730insC	p.T243fs	EDGQVATVSSSPETKKDHPKTGAKT[p.T243fs]RLCTAPDPEPGTER*	GAKTRLCTA,KTRLCTAPD,KTRLCTAPDP,HPKTGAKTRL	LUAD
APC	c.2540delA	p.E847fs	PYLNTTVLPSSSSSRGSLDSSRSEK[p.E847fs]IEVWRENAELV*	SSRSEKIEV,EVWRENAEL,EVWRENAELV,SSRSEKIEVW,IEVWRENAEL	CRC
APC	c.4060delT	p.F1354fs	PRTKSSRLQGSSLSSESARHKAVEF[p.F1354fs]LQERNLPPKVVLRHPKVHLNTMFRRPHSCLADVLLSVHLIVLRVVRLPAPFRVNHAVEW*	CLADVLLSV,VLLSVHLIV,LLSVHLIVL,TMFRRPHSC,SVHLIVLRV,KVHLNTMFR,LSVHLIVLR,VVRLPAPFR,RVVRLPAPF,KVVLRHPKV,VLRHPKVHL,MFRRPHSCL,VLRVVRLPA,KAVEFLQER,NLPPKVVLR,HLIVLRVVR,DVLLSVHLI,HPKVHLNTM,RPHSCLADV,APFRVNHAV,ARHKAVEFL,RNLPPKVVL,FRVNHAVEW,LPAPFRVNH,VEFLQERNL,QERNLPPKV,ADVLLSVHL,TMFRRPHSCL,VLLSVHLIVL,SVHLIVLRVV,HLIVLRVVRL,FLQERNLPPK,KVHLNTMFRR,RVVRLPAPFR,SARHKAVEFL,RNLPPKVVLR,MFRRPHSCLA,VVRLPAPFRV,LLSVHLIVLR,DVLLSVHLIV,LSVHLIVLRV,HPKVHLNTMF,RPHSCLADVL,LPAPFRVNHA,NTMFRRPHSC,LQERNLPPKV,RHPKVHLNTM,HLNTMFRRPH,CLADVLLSVH,LRVVRLPAPF,ADVLLSVHLI	CRC
APOB	c.128C>T	p.A43V	LLLLLAGARAEEEMLENVSLVCPKD[p.A43V]VTRFKHLRKYTYNYEAESSSGVPGTA	VTRFKHLRK,LVCPKDVTR,DVTRFKHLR,VTRFKHLRKY,SLVCPKDVTR,DVTRFKHLRK,LVCPKDVTRF	CRC
APOB	c.2917C>A	p.L973M	TKTEVIPPLIENRQSWSVCKQVFPG[p.L973M]MNYCTSGAYSNASSTDSASYYPLTGD	GMNYCTSGA,KQVFPGMNY,MNYCTSGAY,GMNYCTSGAY,SVCKQVFPGM,CKQVFPGMNY,KQVFPGMNYC	LUAD
APOB	c.9306C>A	p.F3102L	FLSPSAQQASWQVSARFNQYKYNQN[p.F3102L]LSAGNNENIMEAHVGINGEANLDFLN	NQYKYNQNL,YKYNQNLSA,NLSAGNNENI,QYKYNQNLSA,FNQYKYNQNL,NQYKYNQNLS,YKYNQNLSAG,LSAGNNENIM	UCEC
APOB	c.9406C>T	p.R3136C	MEAHVGINGEANLDFLNIPLTIPEM[p.R3136C]CLPYTIITTPPLKDFSLWEKTGLKEF	TIPEMCLPY,PEMCLPYTI,LTIPEMCLPY,PEMCLPYTII,IPLTIPEMCL,IPEMCLPYTI	CRC
APOBR	c.2519G>T	p.R840L	SQVEAFESREGGPWGGRVEAEESAG[p.R840L]VEDSCGLDPAGSQTARAEGMGAMVEA	VEAEESAGV,VEDSCGLDPA	LUAD
APOD	c.344C>T	p.S115L	IEGEATPVNLTEPAKLEVKFSWFMP[p.S115L]LAPYWILATDYENYALVYSCTCIIQL	FMPLAPYWI,WFMPLAPYW,KFSWFMPLA,SWFMPLAPY,MPLAPYWIL,VKFSWFMPL,FSWFMPLAPY,FMPLAPYWIL,SWFMPLAPYW,WFMPLAPYWI,EVKFSWFMPL,VKFSWFMPLA,MPLAPYWILA	CESC
APOE	c.388T>C	p.C130R	EETRARLSKELQAAQARLGADMEDV[p.C130R]RGRLVQYRGEVQAMLGQSTEELRVRL	RGRLVQYRG,MEDVRGRLV,DVRGRLVQYR	ACC
APOOL	c.412A>C	p.I138L	PKMGVITVSGLAGLVSARKGSKFKK[p.I138L]LTYPLGLATLGATVCYPVQSVIIAKV	KLTYPLGLA,KFKKLTYPL,GSKFKKLTY,KKLTYPLGL,LTYPLGLATL,KFKKLTYPLG,KGSKFKKLTY,SKFKKLTYPL,FKKLTYPLGL	CLL
APPL1	c.2002C>T	p.R668W	ERVKEKQQKELNKQKQIEKDLEEQS[p.R668W]WLIAASSRPNQASSEGQFVVLSSSQS	SWLIAASSR,LEEQSWLIA,EEQSWLIAA,QSWLIAASSR,IEKDLEEQSW,LEEQSWLIAA,EEQSWLIAAS,KDLEEQSWLI	CRC
AQP10	c.782A>T	p.Q261L	SAGNGWWWVPVVAPLVGATVGTATY[p.Q261L]LLLVALHHPEGPEPAQDLVSAQHKAS	GTATYLLLV,ATYLLLVAL,ATVGTATYL,TVGTATYLL,GTATYLLLVA,ATYLLLVALH,ATVGTATYLL	LUAD
AQP2	c.203A>C	p.N68T	QIAMAFGLGIGTLVQALGHISGAHI[p.N68T]TPAVTVACLVGCHVSVLRAAFYVAAQ	HITPAVTVA,SGAHITPAV,TPAVTVACL,AHITPAVTV,HISGAHITPA,ITPAVTVACL,TPAVTVACLV,AHITPAVTVA	KIRP
AQPEP	c.925G>A	p.A309T	KEDVNGSKWTVTTFSTTPHMPTYLV[p.A309T]TFVICDYDHVNRTERGKEIRIWARKD	HMPTYLVTF,PTYLVTFVI,TYLVTFVIC,LVTFVICDY,MPTYLVTFV,HMPTYLVTFV,PHMPTYLVTF,YLVTFVICDY,MPTYLVTFVI	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ARAP3	c.3677G>T	p.R1226L	ASLLLKKVPLAQAGCLFTGIRRESP[p.R1226L]LVGLLRCREEPPRLLGSRFQERFFLL	GIRRESPLV,TGIRRESPL,RRESPLVGL,RESPLVGLL,FTGIRRESPL,IRRESPLVGL	LUAD
ARF4	c.446G>A	p.R149H	FANKQDLPNAMAISEMTDKLGLQSL[p.R149H]HNRTWYVQATCATQGTGLYEGLDWLS	SLHNRTWYV,HNRTWYVQA,QSLHNRTWY,LQSLHNRTW,QSLHNRTWYV,LQSLHNRTWY,KLGLQSLHNR,GLQSLHNRTW	CRC
ARFGAP2	c.113G>A	p.S38N	LFKRLRAVPTNKACFDCGAKNPSWA[p.S38N]NITYGVFLCIDCSGVHRSLGVHLSFI	SWANITYGV,NPSWANITY,WANITYGVF,AKNPSWANI,ANITYGVFL,SWANITYGVF,GAKNPSWANI,KNPSWANITY,NITYGVFLCI,WANITYGVFL	PRAD
ARFGAP3	c.896delA	p.N299fs	SLRLAYKDLEIQMKKDEKMNISGKK[p.N299fs]MLTQTDSAWDLEIAEVLFHIQ*	KMLTQTDSA,EIAEVLFHI,KMNISGKKM,DSAWDLEIA,MLTQTDSAW,TQTDSAWDL,LEIAEVLFH,WDLEIAEVL,QTDSAWDLEI,SAWDLEIAEV,KMNISGKKML,EKMNISGKKM,KKMLTQTDSA,KMLTQTDSAW,LEIAEVLFHI,WDLEIAEVLF	PRAD
ARFGEF1	c.4654_4655insC	p.P1552fs	LDIFKTTIPHALLTWRPNSGETAPP[p.P1552fs]TSISCK*	ETAPPTSIS,GETAPPTSI,ETAPPTSISC	STAD
ARFGEF1	c.4894G>A	p.D1632N	KFPEQKLFAALLIKCVVQLELIQTI[p.D1632N]NNIVFFPATSKKEDAENLAAAQRDAV	ELIQTINNI,LIQTINNIV,QTINNIVFF,IQTINNIVF,TINNIVFFPA,ELIQTINNIV,IQTINNIVFF,LIQTINNIVF,LELIQTINNI	CRC
ARFIP2	c.257G>T	p.R86L	GLIPTGSGRHPSHSTTPSGPGDEVA[p.R86L]LGIAGEKFDIVKKWGINTYKCTKQLL	VALGIAGEK,ALGIAGEKF,DEVALGIAG,VALGIAGEKF,DEVALGIAGE	LUAD
ARHGAP24	c.103A>G	p.T35A	NPQQGQGRQNAIKCGWLRKQGGFVK[p.T35A]AWHTRWFVLKGDQLYYFKDEDETKPL	KAWHTRWFV,AWHTRWFVL,GFVKAWHTR,RKQGGFVKA,KQGGFVKAW,FVKAWHTRW,VKAWHTRWF,AWHTRWFVLK,GFVKAWHTRW,KAWHTRWFVL,FVKAWHTRWF,RKQGGFVKAW	TGCT
ARHGAP32	c.3757G>A	p.E1253K	LEFADKSPTPPNLPSDKIYPPSGSP[p.E1253K]KENTSTATMTYMTTTPATAQMSTKEA	SPKENTSTA,KENTSTATM,KIYPPSGSPK,SPKENTSTAT,KENTSTATMT	CRC
ARHGAP36	c.382C>T	p.R128C	GQQRAVSHKTFGISLEEVLVNEFTR[p.R128C]CKHLELTATMQVEEATGQAAGRRRGN	LVNEFTRCK,FTRCKHLEL,CKHLELTAT,NEFTRCKHL,VLVNEFTRCK,CKHLELTATM	CRC
ARHGAP36	c.440C>T	p.A147V	VNEFTRRKHLELTATMQVEEATGQA[p.A147V]VGRRRGNVVRRVFGRIRRFFSRRRNE	VGRRRGNVV,VEEATGQAV,VGRRRGNVVR	CRC
ARHGAP36	c.47C>A	p.P16H	MGGCIPFLKAARALC[p.P16H]HRIMPPLLLLSAFIFLVSVLGGAPGH	KAARALCHR,AARALCHRI,RALCHRIMP,LKAARALCH,ARALCHRIM,HRIMPPLLL,ALCHRIMPPL,KAARALCHRI,AARALCHRIM,RALCHRIMPP,HRIMPPLLLL	LUAD
ARHGAP5	c.2071A>T	p.M691L	ESLSFIGEFIGKIRTEASQIRKDKY[p.M691L]LANLPFTLILANQRDSISKNLPILRH	YLANLPFTL,KYLANLPFT,QIRKDKYLA,LANLPFTLI,DKYLANLPF,SQIRKDKYL,RKDKYLANL,YLANLPFTLI,KYLANLPFTL,KDKYLANLPF,LANLPFTLIL	GBM
ARHGAP5	c.2670delT	p.D890fs	RAFLSEVQDTIPVQLVAVTDSQADF[p.D890fs]LKMRLSKS*	VTDSQADFL,FLKMRLSKS,DFLKMRLSK,VTDSQADFLK,SQADFLKMRL,DSQADFLKMR	CRC,STAD
ARHGAP9	c.409C>T	p.R137C	QQVSLAEGDRFLLLRKTNSDWWLAR[p.R137C]CLEAPSTSRPIFVPAAYMIEESIPSQ	SDWWLARCL,WLARCLEAPS	BRCA
ARHGEF17	c.1844delC	p.A615fs	VQEARQVFEKIQRMGAQQDDGSDAP[p.A615fs]LEALTGQGM*	LEALTGQGM,QQDDGSDAPL	STAD
ARHGEF5	c.1460A>G	p.E487G	PISLLGSFLTEESPDKEIDQNSQQE[p.E487G]GSRLRKGTVSSQGTEVVFASASVTPP	GSRLRKGTV,SQQEGSRLRK	KIRC
ARHGEF5	c.4535delC	p.S1512fs	EKLRWISALAMPREELDLLECYNSP[p.S1512fs]RYSAFEPTSPERMMNWHWRKPTW*	RMMNWHWRK,NWHWRKPTW,CYNSPRYSA,LLECYNSPR,YNSPRYSAF,LECYNSPRY,LLECYNSPRY,MMNWHWRKPT,SAFEPTSPER,CYNSPRYSAF,RMMNWHWRKP,DLLECYNSPR,SPRYSAFEPT,MNWHWRKPTW,FEPTSPERMM,SPERMMNWHW	STAD
ARID1A	c.1841C>T	p.S614L	QTAYSQQRFPPPQELSQDSFGSQAS[p.S614L]LAPSMTSSKGGQEDMNLSLQSRPSSL	SLAPSMTSS,LAPSMTSSK,DSFGSQASL,SQASLAPSM,SLAPSMTSSK,DSFGSQASLA,GSQASLAPSM,SQASLAPSMT	BLCA
ARID1A	c.3211delA	p.K1071fs	KPLDLYRLYVSVKEIGGLTQVNKNK[p.K1071fs]NGGNLQPTSMWAHQAVLPAP*	SMWAHQAVL,NLQPTSMWA,TSMWAHQAV,WAHQAVLPA,LQPTSMWAH,TSMWAHQAVL,SMWAHQAVLP,MWAHQAVLPA	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ARID1A	c.3972delC	p.Y1324fs	STGAPQPNLMPSNPDSGMYSPSRYP[p.Y1324fs]RSSSSSSSNDMIPMAISSPPKAPLLAAPSPASRLQCINSNSRITSGQWMAHMALLPSGTKGRCTACHTALGRGSLSSSSCPQPSPSLPASNKLPSLPLSKMYTTSMAMPILPLPQLLLSADQQAAPRTNFHSSLAETVSLHPLAPMPSKTCHHK*	GQWMAHMAL,KMYTTSMAM,YTTSMAMPI,SMAMPILPL,HMALLPSGT,LLSADQQAA,MALLPSGTK,KLPSLPLSK,PMAISSPPK,QWMAHMALL,MYSPSRYPR,KGRCTACHT,LSKMYTTSM,RTNFHSSLA,HPLAPMPSK,LAAPSPASR,TACHTALGR,HTALGRGSL,TTSMAMPIL,ETVSLHPLA,YPRSSSSSS,IPMAISSPP,SPASRLQCI,LPASNKLPS,LPSLPLSKM,MPILPLPQL,APRTNFHSS,QQAAPRTNF,SSSNDMIPM,VSLHPLAPM,SSSSSSNDM,ISSPPKAPL,SRITSGQWM,MAHMALLPS,AHMALLPSG,RCTACHTAL,SNKLPSLPL,SKMYTTSMA,FHSSLAETV,SSLAETVSL,AETVSLHPL,LPLPQLLLS,GQWMAHMALL,AMPILPLPQL,LLLSADQQAA,WMAHMALLPS,KLPSLPLSKM,GMYSPSRYPR,HMALLPSGTK,CTACHTALGR,MYTTSMAMPI,IPMAISSPPK,RLQCINSNSR,KGRCTACHTA,ASNKLPSLPL,LSKMYTTSMA,TSMAMPILPL,RTNFHSSLAE,ITSGQWMAHM,LLAAPSPASR,LSADQQAAPR,SSNDMIPMAI,YTTSMAMPIL,TVSLHPLAPM,YPRSSSSSSS,SPPKAPLLAA,APLLAAPSPA,CPQPSPSLPA,SPSLPASNKL,LPASNKLPSL,MPILPLPQLL,APRTNFHSSL,SKMYTTSMAM,LPSLPLSKMY,SSSSSSSNDM,SSSSNDMIPM,ISSPPKAPLL,LAAPSPASRL,LQCINSNSRI,SGQWMAHMAL,GRCTACHTAL,SSCPQPSPSL,KMYTTSMAMP,DQQAAPRTNF,QQAAPRTNFH,HSSLAETVSL,LAETVSLHPL,LPLPQLLLSA,AETVSLHPLA	STAD
ARID1A	c.5542delG	p.G1848fs	VDCSDKLGRVQEFDSGLLHWRIGGG[p.G1848fs]TPLSISRPTSRARQSCCLPGLTHPAHQPLGSM*	RQSCCLPGL,CLPGLTHPA,LSISRPTSR,ISRPTSRAR,RARQSCCLP,LTHPAHQPL,RPTSRARQS,WRIGGGTPL,LPGLTHPAH,GLTHPAHQPL,LLHWRIGGGT,SISRPTSRAR,HWRIGGGTPL,TSRARQSCCL,RARQSCCLPG,RPTSRARQSC,HPAHQPLGSM,RIGGGTPLSI,ARQSCCLPGL,RQSCCLPGLT	STAD
ARID1A	c.6415delC	p.P2139fs	RLVLETLSKLSIQDNNVDLILATPP[p.P2139fs]SAAWRSCIALWCASSVTERTRCAGRWLWYCWPTWLRGTAWQLVPLQCRRAVSATSWAS*	IALWCASSV,ALWCASSVT,WLRGTAWQL,GTAWQLVPL,ILATPPSAA,AWRSCIALW,RWLWYCWPT,WLWYCWPTW,LWYCWPTWL,RTRCAGRWL,RAVSATSWA,RCAGRWLWY,WYCWPTWLR,QLVPLQCRR,WPTWLRGTA,VPLQCRRAV,SAAWRSCIA,LATPPSAAW,AAWRSCIAL,LQCRRAVSA,RRAVSATSW,CIALWCASSV,WLWYCWPTWL,WLRGTAWQLV,CAGRWLWYCW,RWLWYCWPTW,TWLRGTAWQL,RTRCAGRWLW,LATPPSAAWR,LWCASSVTER,VTERTRCAGR,LWYCWPTWLR,SAAWRSCIAL,WPTWLRGTAW,ILATPPSAAW,AAWRSCIALW,TERTRCAGRW,RGTAWQLVPL,LQCRRAVSAT,CRRAVSATSW,RAVSATSWAS	STAD
ARID3A	c.1649_1650delGA	p.G550fs	NGIMYTGVLFAQPPAPTPTSAPNKG[p.G550fs]RRRRRQQQQRRRPGRKHRNQRRPGWASGAVHTLHIYLK*	QQRRRPGRK,AVHTLHIYL,GAVHTLHIY,WASGAVHTL,RPGWASGAV,NQRRPGWAS,AVHTLHIYLK,GWASGAVHTL,QQQRRRPGRK,SGAVHTLHIY,RQQQQRRRPG	CLL
ARID4A	c.3462T>A	p.D1154E	LNVSKPQKLARSPARISPHIKDGEK[p.D1154E]EKHREKHPNSSPRTYKWSFQLNELDN	HIKDGEKEK	CLL
ARL13B	c.1073G>T	p.R358L	ETDRPSLESANGKKKTKKLRMKRNH[p.R358L]LVEPLNIDDCAPESPTPPPPPPPVGW	KLRMKRNHL,RMKRNHLVE,LRMKRNHLV,KRNHLVEPL,KLRMKRNHLV,RMKRNHLVEP,MKRNHLVEPL,KKLRMKRNHL	LUAD
ARL16	c.16G>A	p.G6R	MRVAG[p.G6R]RRALSRGAELRVPGGAKHGMCLLLGA	RVAGRRALS,MRVAGRRAL,RVAGRRALSR,AGRRALSRGA,RRALSRGAEL	SKCM
ARL6IP1	c.223A>T	p.M75L	GVVSLVFLIIYYLDPSVLSGVSCFV[p.M75L]LFLCLADYLVPILAPRIFGSNKWTTE	GVSCFVLFL,SGVSCFVLF,VLFLCLADY,LSGVSCFVL,VLSGVSCFVL,VLFLCLADYL,LSGVSCFVLF,FVLFLCLADY	MM
ARMC3	c.1540G>A	p.A514T	LRSKNDEVRKHASWAVMVCAGDELT[p.A514T]TNELCRLGALDILEEVNVSGTRKNKF	TTNELCRLGA	TGCT
ARMC4	c.64G>A	p.E22K	MGVALRKLTQWTAAGHGTGIL[p.E22K]KITPLNEAILKEIIVFVESFIYKHPQ	KITPLNEAI,AGHGTGILK,TGILKITPL,LKITPLNEA,ILKITPLNEA,AAGHGTGILK,LKITPLNEAI	SKCM
ARNTL	c.1184C>T	p.T395M	GTSCYEYFHQDDIGHLAECHRQVLQ[p.T395M]MREKITTNCYKFKIKDGSFITLRSRW	RQVLQMREK,LQMREKITT,AECHRQVLQM,RQVLQMREKI,LQMREKITTN,MREKITTNCY	CRC
ARPC1A	c.636C>A	p.F212L	SKMPFGQLMSEFGGSGTGGWVHGVS[p.F212L]LSASGSRLAWVSHDSTVSVADASKSV	WVHGVSLSA,SLSASGSRL,GGWVHGVSL,SLSASGSRLA,GVSLSASGSR,VSLSASGSRL,LSASGSRLAW	LUSC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ARPP21	c.1013G>A	p.R338H	SSSENELKWSDHQRAWSSTDSDSSN[p.R338H]HNLKPAMTKTASFGGITVLTRGDSTS	HNLKPAMTK,SNHNLKPAM,SSNHNLKPAM	CRC
ARPP21	c.388delA	p.I130fs	HNVEKQDIATYYCALWEVHSKLGKK[p.I130fs]SRYLVPEQSLSLQINNLMQMFPPSPLFFFLQLLKQSSRRLEHTFVFLRNFSLMLLRYIGKKRRATRFWDPRRGTP*	SLSLQINNL,MQMFPPSPL,RLEHTFVFL,FVFLRNFSL,FLRNFSLML,LQINNLMQM,LFFFLQLLK,LMLLRYIGK,MLLRYIGKK,RNFSLMLLR,RATRFWDPR,RYLVPEQSL,QMFPPSPLF,MFPPSPLFF,RRLEHTFVF,VFLRNFSLM,HSKLGKKSR,KLGKKSRYL,LGKKSRYLV,KSRYLVPEQ,KQSSRRLEH,SSRRLEHTF,RYIGKKRRA,IGKKRRATR,ATRFWDPRR,NFSLMLLRY,LLRYIGKKR,SPLFFFLQL,LLKQSSRRL,YIGKKRRAT,QINNLMQMF,HTFVFLRNF,SKLGKKSRY,LSLQINNLM,LRNFSLMLL,GKKRRATRF,KKRRATRFW,FPPSPLFFF,PPSPLFFFL,KLGKKSRYLV,YLVPEQSLSL,LMQMFPPSPL,FVFLRNFSLM,FLRNFSLMLL,SLSLQINNLM,PLFFFLQLLK,RLEHTFVFLR,SLMLLRYIGK,LMLLRYIGKK,LQINNLMQMF,MQMFPPSPLF,QMFPPSPLFF,MFPPSPLFFF,RRLEHTFVFL,TFVFLRNFSL,VFLRNFSLML,KSRYLVPEQS,SSRRLEHTFV,HTFVFLRNFS,RATRFWDPRR,ATRFWDPRRG,HSKLGKKSRY,RNFSLMLLRY,FLQLLKQSSR,MLLRYIGKKR,LLRYIGKKRR,YIGKKRRATR,FPPSPLFFFL,SPLFFFLQLL,SRYLVPEQSL,SLQINNLMQM,LKQSSRRLEH,KQSSRRLEHT,QSSRRLEHTF,SRRLEHTFVF,VPEQSLSLQI	STAD
ARRB2	c.295A>C	p.T99P	LSFRKDLFIATYQAFPPVPNPPRPP[p.T99P]PRLQDRLLRKLGQHAHPFFFTVRMPL	RPPPRLQDRL	TGCT
ARRDC4	c.235A>G	p.T79A	ALRLEAQGRATAAWGPSTCPRASAS[p.T79A]AAALAVFSEVEYLNVRLSLREPPAGE	RASASAAAL,ASASAAALA,SASAAALAV,CPRASASAA,ASAAALAVF,AAALAVFSEV,STCPRASASA,RASASAAALA,ASASAAALAV,CPRASASAAA,SASAAALAVF	ACC
ARSD	c.701C>G	p.A234G	LGILTLAAGQTCGFFSVSARAVTGM[p.A234G]GGVGCLFFISWYSSFGFVRRWNCILM	MGGVGCLFF,SARAVTGMG,GMGGVGCLF,GMGGVGCLFF,SARAVTGMGG,TGMGGVGCLF	KIRC
ARSD	c.701_709delCCGGCGTGG	p.AGV234del	LGILTLAAGQTCGFFSVSARAVTGM[p.AGV234del]GCLFFISWYSSFGFVRRWNCILMRNHDVTEQPMV	TGMGCLFFI,VTGMGCLFF,SARAVTGMG,AVTGMGCLF,GMGCLFFISW,MGCLFFISWY,RAVTGMGCLF,AVTGMGCLFF	KIRC
ARSG	c.391G>A	p.V131I	FAVTSVGGLPLNETTLAEVLQQAGY[p.V131I]ITGIIGKWHLGHHGSYHPNFRGFDYY	QQAGYITGI,EVLQQAGYI,LQQAGYITG,LQQAGYITGI,QQAGYITGII,AGYITGIIGK,GYITGIIGKW,AEVLQQAGYI	CRC
ART1	c.729delC	p.I243fs	IWTCLGAPIKGYSFFPGEEEVLIPP[p.I243fs]LRPSK*	LIPPLRPSK,EEEVLIPPL,VLIPPLRPSK,GEEEVLIPPL	STAD
ASB16	c.745A>G	p.T249A	QHVALYLEHGADVGLRTSQGETALN[p.T249A]AACAGAEGPGSCRRHQAAARRLLEAG	ALNAACAGA,ETALNAACA,SQGETALNA,GETALNAAC,SQGETALNAA,GETALNAACA	ACC
ASCC1	c.619C>T	p.H207Y	QEEVLAKCSMDHGVDSSIFQNPKKL[p.H207Y]YLTIGMLVLLSEEEIQQTCEMLQQCK	YLTIGMLVL,FQNPKKLYL,KLYLTIGML,LYLTIGMLV,IFQNPKKLY,NPKKLYLTI,KKLYLTIGM,KLYLTIGMLV,YLTIGMLVLL,IFQNPKKLYL,LYLTIGMLVL,SIFQNPKKLY,KKLYLTIGML	CESC
ASCC2	c.1094G>T	p.R365L	CDNIQGFIEEFLQIFSSLLQEKRFL[p.R365L]LDYDALFPVAEDISLLQQASSVLDET	LLQEKRFLL,FLLDYDALF,RFLLDYDAL,QEKRFLLDY,LDYDALFPV,SLLQEKRFLL,FLLDYDALFP,LLDYDALFPV,RFLLDYDALF,LQEKRFLLDY,KRFLLDYDAL,LDYDALFPVA	LUAD
ASCC3	c.3590G>A	p.R1197Q	VKQCVHQIPSVMMEASIQPITRTVL[p.R1197Q]QVTLSIYADFTWNDQVHGTVGEPWWI	TVLQVTLSI,VLQVTLSIY,LQVTLSIYA,VLQVTLSIYA,ITRTVLQVTL,RTVLQVTLSI,TVLQVTLSIY,QPITRTVLQV	CRC
ASCC3	c.407G>A	p.R136Q	ETKAIKQMFGPFPSSSATAACNATN[p.R136Q]QIISHFSQDDLTALVQMTEKEHGDRV	ATNQIISHF,TAACNATNQI,NATNQIISHF	UCEC
ASCL4	c.105delC	p.D35fs	ALPYSLRTAPLGVPGTLPGLPRRDP[p.D35fs]SGSPCVWTPRAGSGRAAAAHGDGSTCPCRWTAPSSPPSSASATSASGSGCAA*	RAGSGRAAA,STCPCRWTA,WTAPSSPPS,TPRAGSGRA,APSSPPSSA,DPSGSPCVW,RAGSGRAAAA,RWTAPSSPPS,SGSPCVWTPR,TPRAGSGRAA	STAD
ASIC2	c.137G>T	p.R46L	RMAREEPAPAALAAAGQPGGGRGGE[p.R46L]LALQGPGVARRGRPSLSRAKLHGLRH	ELALQGPGV,GELALQGPG,QPGGGRGGEL,GELALQGPGV	KIRP

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ASPDH	c.797A>G	p.Q266R	AVHTRRENPAEPGAVTGSATVTAFW[p.Q266R]RSLLACCQLPSRPGIHLC*	SATVTAFWR,TAFWRSLLA,RSLLACCQL,TVTAFWRSL,VTAFWRSLL,GSATVTAFWR,ATVTAFWRSL,TVTAFWRSLL,VTAFWRSLLA,WRSLLACCQL	ACC
ASPM	c.719C>T	p.S240F	EENKIPISPISPAFNECHGATCLPL[p.S240F]FVRRSTTYSSLHASENRELLNVHSAN	ATCLPLFVR,HGATCLPLF,FVRRSTTYS,LFVRRSTTY,TCLPLFVRR,LPLFVRRST,ATCLPLFVRR,LPLFVRRSTT,PLFVRRSTTY,CHGATCLPLF	LUAD
ASPN	c.201delT	p.F67fs	DDDDDDDDDEDNSLFPTREPRSHFF[p.F67fs]HLICFQCVHLDVSAIHELYIAQI*	DVSAIHELY,SHFFHLICF,CFQCVHLDV,RSHFFHLIC,EPRSHFFHL,HLICFQCVH,LDVSAIHEL,HLICFQCVHL,HLDVSAIHEL,AIHELYIAQI,RSHFFHLICF,DVSAIHELYI,EPRSHFFHLI,REPRSHFFHL,FQCVHLDVSA,LDVSAIHELY	STAD
ASTN2	c.661_663delCTG	p.L221del	EIVEEQMHILHISVMGGLIALLLLL[p.L221del]VFTVALYAQRRWQKRRRIPQKSASTEAT	LIALLLLLV,ALLLLLVFT,IALLLLLVF,GLIALLLLLV,ALLLLLVFTV,LIALLLLLVF	PRAD
ASXL2	c.3242C>T	p.S1081L	EGLSKATQDQILQTLIQRVRRQNLL[p.S1081L]LVVPPSQFNFAHSGFQLEDISTSQRF	RVRRQNLLL,LLVVPPSQF,RRQNLLLVV,RQNLLLVVP,RVRRQNLLLV,LLLVVPPSQF,LVVPPSQFNF,RQNLLLVVPP	LUSC
ASXL3	c.2618delA	p.E873fs	SIPELASTEMIKVKNHSVLQRTEKK[p.E873fs]CYLHHWNYLSFLKGQIIREMSFHLLNYRTSNISHQWIRLHFQKALEIKHISKGVHRVG*	EMSFHLLNY,YLHHWNYLS,IIREMSFHL,YLSFLKGQI,LLNYRTSNI,HISKGVHRV,MSFHLLNYR,ALEIKHISK,HWNYLSFLK,QWIRLHFQK,CYLHHWNYL,LHHWNYLSF,SHQWIRLHF,WIRLHFQKA,KCYLHHWNY,RTSNISHQW,SFLKGQIIR,SNISHQWIR,EIKHISKGV,GQIIREMSF,LQRTEKKCY,HHWNYLSFL,LSFLKGQII,LKGQIIREM,REMSFHLLN,IRLHFQKAL,LHFQKALEI,FQKALEIKH,YLHHWNYLSF,HLLNYRTSNI,YLSFLKGQI,FLKGQIIREM,QIIREMSFHL,IIREMSFHLL,RLHFQKALEI,HQWIRLHFQK,KALEIKHISK,HHWNYLSFLK,LSFLKGQIIR,CYLHHWNYLS,NYLSFLKGQI,ISHQWIRLHF,KCYLHHWNYL,RTSNISHQWI,KKCYLHHWNY,REMSFHLLNY,EMSFHLLNYR,TSNISHQWIR,MSFHLLNYRT,WIRLHFQKAL,LQRTEKKCYL,LHHWNYLSFL,KGQIIREMSF,LNYRTSNISH,YRTSNISHQW,FQKALEIKHI,LEIKHISKGV,KHISKGVHRV,TEKKCYLHHW	STAD
ASXL3	c.4409C>A	p.P1470Q	NRADNSGKPQQPPGGFAPAAINRSI[p.P1470Q]QCKVIVDHSTTLTSSLSLTVSVESSE	AINRSIQCK,RSIQCKVIV,AINRSIQCKV,AAINRSIQCK	LUAD
ATAD5	c.913A>G	p.I305V	EIPDSTMSICVPSETVDEIVKSGYI[p.I305V]GESENSEISQQVRFKTVTVLAQVHPI	YIGESENSEI	TGCT
ATM	c.2399C>T	p.S800F	SLRNMMQLCTRCLSNCTKKSPNKIA[p.S800F]FGFFLRLLTSKLMNDIADICKSLASF	KIAFGFFLR,AFGFFLRLL,SPNKIAFGF,KKSPNKIAF,NKIAFGFFL,IAFGFFLRL,KIAFGFFLRL,KSPNKIAFGF,NKIAFGFFLR,SPNKIAFGFF,TKKSPNKIAF,IAFGFFLRLL	CESC
ATP10B	c.3910C>A	p.L1304I	CNSPTNPYWVMEGQLSNPTFYLVCF[p.L1304I]ITPVVALLPRYFFLSLQGTCGKSLIS	YLVCFITPV,LVCFITPVV,FITPVVALL,CFITPVVAL,YLVCFITPVV,FYLVCFITPV,CFITPVVALL,ITPVVALLPR,NPTFYLVCFI	UCEC
ATP10D	c.932G>A	p.R311H	AVVGIVVYAGHETKAMLNNSGPRYK[p.R311H]HSKLERRANTDVLWCVMLLVIMCLTG	SGPRYKHSK,RYKHSKLER,GPRYKHSKL,NSGPRYKHSK	CRC
ATP12A	c.2572C>T	p.R858C	LGTDIIPSIALAYEKAESDIMNRKP[p.R858C]CHKNKDRLVNQPLAVYSYLHIGLMQA	IMNRKPCHK,MNRKPCHKNK,DIMNRKPCHK	BLCA
ATP2A1	c.2110G>T	p.G704C	VEPSHKSKIVEYLQSYDEITAMTGD[p.G704C]CVNDAPALKKAEIGIAMGSGTAVAKT	CVNDAPALK,ITAMTGDCV,AMTGDCVNDA,CVNDAPALKK,EITAMTGDCV	KIRC
ATP2A1	c.2457_2458insC	p.R819fs	LVTDGLPATALGFNPPDLDIMDRPP[p.R819fs]PEPQGAPHQWLALLPLHGNRGLCGCSHRGSSCLVVPVR*	HQWLALLPL,GSSCLVVPV,RGLCGCSHR,ALLPLHGNR,SSCLVVPVR,APHQWLALL,LPLHGNRGL,CSHRGSSCL,EPQGAPHQW,LLPLHGNRGL,GSSCLVVPVR,CSHRGSSCLV,LALLPLHGNR,HQWLALLPLH,SHRGSSCLVV,RGSSCLVVPV	STAD
ATP2B4	c.548G>A	p.R183H	SVIIVVLVTAFNDWSKEKQFRGLQC[p.R183H]HIEQEQKFSIIRNGQLIQLPVAEIVV	KQFRGLQCH,CHIEQEQKF,KQFRGLQCHI	CLL
ATP2C1	c.2170G>A	p.E724K	GTDVCKEAADMILVDDDFQTIMSAI[p.E724K]KEGKGIYNNIKNFVRFQLSTSIAALT	IMSAIKEGK,AIKEGKGIY,TIMSAIKEGK,SAIKEGKGIY,DFQTIMSAIK,KEGKGIYNNI	UCEC

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ATP6AP2	c.355G>C	p.E119Q	ISYPLENAVPFSLDSVANSIHSLFS[p.E119Q]QETPVVLQLAPSEERVYMVGKANSVF	SLFSQETPV,FSQETPVVL,QETPVVLQL,SLFSQETPVV,HSLFSQETPV,LFSQETPVVL,SQETPVVLQL,QETPVVLQLA	HNSC
ATP6V0A4	c.572G>A	p.R191Q	MTGKLGFIAGVINRERMASFERLLW[p.R191Q]QICRGNVYLKFSEMDAPLEDPVTKEE	SFERLLWQI,WQICRGNVY,FERLLWQIC,LLWQICRGNV,WQICRGNVYL,QICRGNVYLK,LWQICRGNVY,ASFERLLWQI	CRC
ATP6V1A	c.710T>C	p.L237P	RQVRPVTEKLPANHPLLTGQRVLDA[p.L237P]PFPCVQGGTTAIPGAFGCGKTVISQS	VLDAPFPCV,GQRVLDAPF,RVLDAPFPCV,TGQRVLDAPF	THCA
ATP6V1B1	c.1149delC	p.Y383fs	DLTGFITEGQIYVDRQLHNRQIYPP[p.Y383fs]STCSLPCRG*	IYPPSTCSL,RQIYPPSTC,QIYPPSTCSL,RQIYPPSTCS	STAD
ATP6V1C2	c.934_935insAG	p.R312fs	STFPDHKVKVTPLGNPDRPAAGQTD[p.R312fs]KERERVRARVRAPCCAGSR*	KERERVRAR,RERVRARVR,RVRARVRAP,RARVRAPCC,RVRAPCCAG,RAPCCAGSR,RVRARVRAPC,RARVRAPCCA,RVRAPCCAGS,KERERVRARV,RERVRARVRA	STAD
ATP7A	c.2968_2969insA	p.Q990fs	IVETYFPGYNRSISRTETIIRFAFQ[p.Q990fs]SLYHSSVYCMSLFTGTGHSNCCDGGYRSRCSKWHTNKRWRAIGDGS*	HSNCCDGGY,FQSLYHSSV,SLYHSSVYC,LYHSSVYCM,IIRFAFQSL,RFAFQSLYH,GGYRSRCSK,RSRCSKWHT,RCSKWHTNK,CSKWHTNKR,KWHTNKRWR,HTNKRWRAI,RWRAIGDGS,IRFAFQSLY,QSLYHSSVY,SSVYCMSLF,FAFQSLYHS,HSSVYCMSL,MSLFTGTGH,SKWHTNKRW,SLYHSSVYCM,TIIRFAFQSL,HSNCCDGGYR,IIRFAFQSLY,RSRCSKWHTN,KWHTNKRWRA,HTNKRWRAIG,FQSLYHSSVY,HSSVYCMSLF,GHSNCCDGGY,ETIIRFAFQS,FAFQSLYHSS,YHSSVYCMSL,GGYRSRCSKW	KIRC
ATP9A	c.1556G>A	p.R519Q	VYQASSPDEVALVQWTESVGLTLVG[p.R519Q]QDQSSMQLRTPGDQILNFTILQIFPF	LVGQDQSSM,GQDQSSMQL,TLVGQDQSSM	BLCA
ATP9A	c.869G>A	p.R290Q	ASGTVVGVVLYTGRELRSVMNTSNP[p.R290Q]QSKIGLFDLEVNCLTKILFGALVVVS	NTSNPQSKI,NPQSKIGLF,VMNTSNPQSK	UCEC
ATP9B	c.115A>G	p.S39G	AAAAANRKRAAYYSAAGPRPGADRH[p.S39G]GRYQLEDESAHLDEMPLMMSEEGFEN	RPGADRHGRY	ACC
ATR	c.5440delA	p.R1814fs	NYLAADGKSTTWSVRLGQLLLSAKK[p.R1814fs]EISQLFMTH*	AKKEISQLF,KKEISQLFM,KEISQLFMT,SAKKEISQLF,AKKEISQLFM,KEISQLFMTH	UCEC
ATRN	c.590C>A	p.P197Q	LRFNHFATECSWDHLYVYDGDSIYA[p.P197Q]QLVAAFSGLIVPERDGNETVPEVVAT	SIYAQLVAA,QLVAAFSGL,IYAQLVAAF,AQLVAAFSG,AQLVAAFSGL,QLVAAFSGLI,SIYAQLVAAF,DSIYAQLVAA	LUAD
ATRNL1	c.3732A>T	p.L1244F	IAFSQHNTIMDLVQFFVTFFSCFLS[p.L1244F]FLLVAAVVWKIKQTCWASRRREQLLR	FSCFLSFLL,FLSFLLVAA,FFSCFLSFL,LSFLLVAAV,TFFSCFLSF,FLLVAAVVW,FSCFLSFLLV,FFSCFLSFLL,FLSFLLVAAV,VTFFSCFLSF,TFFSCFLSFL,SFLLVAAVVW,LSFLLVAAVV	CLL
ATRX	c.5807A>G	p.K1936R	IASDSDETSMSLSSDDYTKKKKKGK[p.K1936R]RGKKDSSSSGSGSDNDVEVIKVWNSR	YTKKKKKGKR	TGCT
ATXN1	c.651G>T	p.Q217H	GHKAEQQQQQQQQQQQQHQHQQQQQ[p.Q217H]HQQQQQQQQHLSRAPGLITPGSPPPA	HQHQQQQQH,HQQQQQQQQH	LIHC
AURKA	c.1160C>T	p.S387L	RLLKHNPSQRPMLREVLEHPWITAN[p.S387L]LSKPSNCQNKESASKQS*	HPWITANLS,LSKPSNCQNK,LEHPWITANL	CESC
AVIL	c.190G>T	p.G64W	EGDCYVILSTRRVASLLSQDIHFWI[p.G64W]WKDSSQDEQSCAAIYTTQLDDYLGGS	SQDIHFWIW,SQDIHFWIWK,LSQDIHFWIW	LUAD
AVIL	c.896_897insG	p.G299fs	DLLNHDDCYILDQSGTKIYVWKGKG[p.G299fs]SHKG*	VWKGKGSHK,YVWKGKGSHK	KIRC
AVL9	c.102C>A	p.F34L	DGVPRGPVLHIVVVGFHHKKGCQVE[p.F34L]LSYPPLIPGDGHDSHTLPEEWKYLPF	KGCQVELSY,HKKGCQVEL,CQVELSYPP,VELSYPPLI,CQVELSYPPL,KKGCQVELSY	UCEC
AVL9	c.21_22insG	p.G7fs	MEKARRGG[p.G7fs]GWRPPGARTAHRGGRISPQEGLPG*	KARRGGGWR,RTAHRGGRI,RPPGARTAH,GRISPQEGL,KARRGGGWRP,GWRPPGARTA,GARTAHRGGR,MEKARRGGGW	ACC

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AVPR1A	c.1053delT	p.F351fs	ENPTITITALLGSLNSCCNPWIYMF[p.F351fs]LVAISFKTVFKASHAAKT*	WIYMFLVAI,YMFLVAISF,FLVAISFKT,LVAISFKTV,TVFKASHAA,MFLVAISFK,AISFKTVFK,IYMFLVAIS,KTVFKASHA,VFKASHAAK,VAISFKTVF,ISFKTVFKA,FKTVFKASH,NPWIYMFLV,FLVAISFKTV,AISFKTVFKA,YMFLVAISFK,VAISFKTVFK,TVFKASHAAK,PWIYMFLVAI,IYMFLVAISF,SFKTVFKASH,KTVFKASHAA,LVAISFKTVF,NPWIYMFLVA	STAD
AVPR1B	c.115G>A	p.G39R	RGTLSAPNATTPWLGRDEELAKVEI[p.G39R]RVLATVLVLATGGNLAVLLTLGQLGR	RVLATVLVL,ELAKVEIRV,EIRVLATVL,VEIRVLATV,RVLATVLVLA,KVEIRVLATV,EIRVLATVLV,AKVEIRVLAT,VEIRVLATVL,IRVLATVLVL,EELAKVEIRV	TGCT
AXDND1	c.2790G>T	p.E930D	WRESAKQGTLAQKYLEAMAVIEHMQ[p.E930D]DKLLEVENRARQAEEKFEDAYEKLHH	HMQDKLLEV,AVIEHMQDK,IEHMQDKLL,AVIEHMQDKL	CRC
AXDND1	c.301T>C	p.W101R	CPENLLPPKKIKTPKGTLPRLVDHV[p.W101R]RHHPVRRNKFKYLIDHPVSLTGAGRD	HVRHHPVRR,RHHPVRRNK,RLVDHVRHH,LVDHVRHHPV,HVRHHPVRRN,RHHPVRRNKF	LUAD
AXIN2	c.1988_1994delGGGGGGG	p.W663fs	QSTKKAYPLESARSSPGERASRHHL[p.W663fs]STAGTPAPPPVPTCSPRTLRCLP*	HLSTAGTPA,RASRHHLST,ASRHHLSTA,PTCSPRTLR,TPAPPPVPT,VPTCSPRTL,RASRHHLSTA,ASRHHLSTAG,HHLSTAGTPA	CRC
AXIN2	c.1993_1994insG	p.G665fs	KKAYPLESARSSPGERASRHHLWGG[p.G665fs]QQRAPPHHPPCPPVHPGPCDASPDPTQHAGSAGGGLSQAS*	HLWGGQQRA,GQQRAPPHH	CRC
AXIN2	c.1994delG	p.G665fs	TKKAYPLESARSSPGERASRHHLWG[p.G665fs]ATAGTPAPPPVPTCSPRTLRCLP*	HLWGATAGT,ASRHHLWGA,PTCSPRTLR,TPAPPPVPT,VPTCSPRTL,RHHLWGATA,WGATAGTPA,RASRHHLWGA,ASRHHLWGAT,RHHLWGATAG	STAD
B2M	c.1A>G	p.M1V	[p.M1V]VSRSVALAVLALLSLSGLEAIQRTPK	VSRSVALAV,VSRSVALAVL	OV
B2M	c.37_38delCT	p.L13fs	MSRSVALAVLALLS[p.L13fs]FWPGGYPAYSKDSGLLTSSSREWKVKFPELLCVWVSSIRH*	LLSFWPGGY,LLCVWVSSI,LTSSSREWK,SSSREWKVK,KFPELLCVW,KVKFPELLC,FWPGGYPAY,TSSSREWKV,EWKVKFPEL,LAVLALLSF,SFWPGGYPA,LLTSSSREW,SSREWKVKF,WKVKFPELL,VKFPELLCV,REWKVKFPE,FPELLCVWV,ELLCVWVSSI,ALLSFWPGGY,LLTSSSREWK,TSSSREWKVK,SFWPGGYPAY,KFPELLCVWV,KVKFPELLCV,DSGLLTSSSR,LLCVWVSSIR,LSFWPGGYPA,LTSSSREWKV,YPAYSKDSGL,ALAVLALLSF,LAVLALLSFW,GLLTSSSREW,SSSREWKVKF,REWKVKFPEL,VKFPELLCVW	CRC,STAD
B2M	c.3G>A	p.M1I	[p.M1I]ISRSVALAVLALLSLSGLEAIQRTPK	ISRSVALAV,ISRSVALAVL	HNSC
B3GALNT1	c.434G>A	p.R145Q	QEAEKEDKMLALSLEDEHLLYGDII[p.R145Q]QQDFLDTYNNLTLKTIMAFRWVTEFC	IQQDFLDTY,LYGDIIQQDF,IIQQDFLDTY	CRC
B3GAT1	c.374G>T	p.R125L	AELTRMANTLLHVPNLHWLVVEDAP[p.R125L]LRTPLTARLLRDTGLNYTHLHVETPR	WLVVEDAPL,VEDAPLRTPL	LUAD
B3GNT5	c.88delT	p.F30fs	GRRVKKWQLIIQLFATCFLASLMFF[p.F30fs]GNQSIITL*	FLASLMFFG,LMFFGNQSI,MFFGNQSII,FGNQSIITL,FLASLMFFGN,SLMFFGNQSI,LMFFGNQSII,FFGNQSIITL	STAD
B4GALNT1	c.263_264insG	p.G88fs	PVRIKEQVVGLLAWNNCSCESSGGG[p.G88fs]PPPPLPETSPSY*	PLPETSPSY,PPLPETSPSY	PRAD
BACH1	c.1613G>A	p.R538Q	ESCSAREQECEVKLPFNAQRIISLS[p.R538Q]QNDFQSLLKMHKLTPEQLDCIHDIRR	SQNDFQSLL,AQRIISLSQ,IISLSQNDF,LSQNDFQSL,SLSQNDFQSL,SQNDFQSLLK,RIISLSQNDF,LSQNDFQSLL	CRC
BAG1	c.133G>C	p.G45R	RLRALRPGREPRQSEPPAQRGPPPS[p.G45R]RRPPARSTASGHDRPTRGAAAGARRP	AQRGPPPSR,AQRGPPPSRR,GPPPSRRPPA	ACC
BAI2	c.692C>G	p.A231G	EECGRAAGRACGFAQPGCSCPGEAG[p.A231G]GGSTTTTSPGPPAAHTLSNALVPGGP	GEAGGGSTT,GEAGGGSTTT	TGCT
BAIAP2L2	c.1186G>A	p.V396M	SSASGWFPEAYVKALEEGPVNPMTP[p.V396M]MTPMTSMTSMSPMTPMNPGNELPSRS	NPMTPMTPM,GPVNPMTPM,TPMTPMTSM,MTPMTPMTSM,MTPMTSMTSM,TPMTPMTSMT	KIRP

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BAP1	c.233A>G	p.N78S	IEERRSRRKVSTLVDDTSVIDDDIV[p.N78S]SNMFFAHQLIPNSCATHALLSVLLNC	IVSNMFFAH,DIVSNMFFA,SNMFFAHQL,SNMFFAHQLI,VSNMFFAHQL	KIRC
BAP1	c.679C>T	p.R227C	WTDKARRVIMERIGLATAGEPYHDI[p.R227C]CFNLMAVVPDRRIKYEARLHVLKVNR	PYHDICFNL,DICFNLMAV,YHDICFNLM,GEPYHDICF,HDICFNLMA,PYHDICFNLM,DICFNLMAVV,EPYHDICFNL,HDICFNLMAV	OV
BARX2	c.203G>C	p.R68P	SLYSVCPSLVVRPKPLHSCTGSPSL[p.R68P]PAYPLLSVITRQPTVISHLVPATPGI	TGSPSLPAY,LPAYPLLSV,SPSLPAYPL,CTGSPSLPAY,SLPAYPLLSV,SPSLPAYPLL,LPAYPLLSVI	LUAD
BAX	c.114_115insG	p.M38fs	SEQIMKTGALLLQGFIQDRAGRMGG[p.M38fs]GGTRAGPGPGASGCVHQEAERVSQAHRGRTGQ*	RMGGGGTRA,GTRAGPGPG,RVSQAHRGR,QEAERVSQA,AGRMGGGGTR,GTRAGPGPGA,RMGGGGTRAG,HQEAERVSQA,QEAERVSQAH	STAD
BBOX1	c.526T>G	p.F176V	RLTGASDKPGEVSKLGKRMGFLYLT[p.F176V]VYGHTWQVQDKIDANNVAYTTGKLSF	RMGFLYLTV,TVYGHTWQV,YLTVYGHTW,MGFLYLTVY,FLYLTVYGHT,LTVYGHTWQV,RMGFLYLTVY,LYLTVYGHTW,KRMGFLYLTV	CRC
BBS9	c.802delT	p.F268fs	ALDICIVSFNQSASSVFVLGERNFF[p.F268fs]ALRIMDKFDS*	VLGERNFFA,FALRIMDKF,RNFFALRIM,FVLGERNFFA,VLGERNFFAL,NFFALRIMDK,FFALRIMDKF,GERNFFALRI,ERNFFALRIM	PRAD
BC139719	c.398T>G	p.L133R	SSKSRNAPRSSCGNCGARAPEHPPV[p.L133R]RRVESLNLPLLNGLREEGPGVFSRSV	PPVRRVESL,HPPVRRVESL,RRVESLNLPL	PRAD
BCAS3	c.641C>T	p.T214M	DLHCNKRILVVVLQEKIAAFDSCTF[p.T214M]MKKFFVTSCYPCPGPNMNPIALGSRW	CTFMKKFFV,AFDSCTFMK,TFMKKFFVT,AAFDSCTFM,FMKKFFVTS,MKKFFVTSC,FMKKFFVTSC,AAFDSCTFMK,AFDSCTFMKK,MKKFFVTSCY,IAAFDSCTFM,FDSCTFMKKF	BLCA
BCKDHA	c.111delC	p.H37fs	RGLSQAALLLLRQPGARGLARSHPP[p.H37fs]GSSSSFHLWMTSPSSQGPRRSL*	SSSSFHLWM,RSHPPGSSS,HPPGSSSSF,SSQGPRRSL,GSSSSFHLW,FHLWMTSPS,WMTSPSSQG,MTSPSSQGPR,RGLARSHPPG,RSHPPGSSSS,SHPPGSSSSF,GSSSSFHLWM,FHLWMTSPSS	STAD
BCKDHA	c.385_395delGGGGACTGGGC	p.G129fs	LCCFWPVGIAAFCLAQKVSLCVGLG[p.G129fs]IKEKNAPQKQRAIYLRREGGR*	SLCVGLGIK,CVGLGIKEK,KQRAIYLRR,IYLRREGGR,APQKQRAIY,KVSLCVGLGI,VSLCVGLGIK,GIKEKNAPQK,KQRAIYLRRE,AIYLRREGGR,APQKQRAIYL	PAAD
BCL11A	c.1735G>A	p.E579K	SMQHFSEAFHQVLGEKHKRGHLAEA[p.E579K]KGHRDTCDEDSVAGESDRIDDGTVNG	HLAEAKGHR,AEAKGHRDT	HNSC
BCL2	c.515A>G	p.N172S	IVAFFEFGGVMCVESVNREMSPLVD[p.N172S]SIALWMTEYLNRHLHTWIQDNGGWDA	LVDSIALWM,SIALWMTEY,EMSPLVDSI,MSPLVDSIA,SPLVDSIAL,REMSPLVDS,DSIALWMTEY,SIALWMTEYL,MSPLVDSIAL,REMSPLVDSI,SPLVDSIALW	DLBCL
BCL2	c.60T>G	p.H20Q	MAHAGRTGYDNREIVMKYI[p.H20Q]QYKLSQRGYEWDAGDVGAAPPGAAPA	VMKYIQYKL,IVMKYIQYK,YIQYKLSQR,IQYKLSQRG,REIVMKYIQ,IVMKYIQYKL,EIVMKYIQYK,IQYKLSQRGY,KYIQYKLSQR,REIVMKYIQY	DLBCL
BCL2	c.97G>A	p.G33R	GYDNREIVMKYIHYKLSQRGYEWDA[p.G33R]RDVGAAPPGAAPAPGIFSSQPGHTPH	YEWDARDVG,SQRGYEWDAR,YEWDARDVGA	DLBCL
BCL2L11	c.272G>A	p.R91Q	PPASPGPFATRSPLFIFMRRSSLLS[p.R91Q]QSSSGYFSFDTDRSPAPMSCDKSTQT	QSSSGYFSF,LLSQSSSGY,LSQSSSGYF,SQSSSGYFS,SQSSSGYFSF,SLLSQSSSGY,LLSQSSSGYF,FMRRSSLLSQ	CRC
BCL2L11	c.560_561insA	p.L187fs	YARRVFLNNYQAAEDHPRMVILRLL[p.L187fs]TLHCPPGVENALTGSLRSRDTMQTFCLFKPTRPSTAVSWCHYYAASGSLVEGAGDVSEDTELDGTTFLFITTQQNF*	STAVSWCHY,TAVSWCHYY,ELDGTTFLF,LTLHCPPGV,AVSWCHYYA,SLVEGAGDV,MVILRLLTL,TMQTFCLFK,DTMQTFCLF,HYYAASGSL,YYAASGSLV,LFITTQQNF,RSRDTMQTF,LFKPTRPST,VSWCHYYAA,TFCLFKPTR,CPPGVENAL,KPTRPSTAV,RMVILRLLT,VENALTGSL,GSLRSRDTM,TELDGTTFL,STAVSWCHYY,ELDGTTFLFI,RMVILRLLTL,LLTLHCPPGV,AVSWCHYYAA,FLFITTQQNF,DTMQTFCLFK,QTFCLFKPTR,HYYAASGSLV,TELDGTTFLF,RSRDTMQTFC,LFKPTRPSTA,PSTAVSWCHY,NALTGSLRSR,TAVSWCHYYA,LRSRDTMQTF,RDTMQTFCLF,MQTFCLFKPT,CHYYAASGSL	UCS
BCL7A	c.155C>T	p.T52M	KVRKWEKKWVTVGDTSLRIYKWVPV[p.T52M]MEPKVDDKNKNKKKGKDEKCGSEVTT	RIYKWVPVM,KWVPVMEPK,LRIYKWVPVM	CRC
BCL9L	c.2938G>T	p.G980C	PQTPSQMVPLPSANPPGPLKSPQVL[p.G980C]CSSLSVRSPTGSPSRLKSPSMAVPSP	QVLCSSLSV,SPQVLCSSL,QVLCSSLSVR	LUAD

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BCL9L	c.3379_3380insC	p.P1127fs	YHNAIKTIATSDDELLPDRPLLPPP[p.P1127fs]TTTAGLRARDQQQPAQPDAPELSRCPEPYGHEPARPAAPVP*	LLPPPTTTA,RARDQQQPA,LSRCPEPYG,ELSRCPEPY,TTTAGLRAR,EPARPAAPV,RPLLPPPTTT,LPPPTTTAGL,QPAQPDAPEL,YGHEPARPAA,HEPARPAAPV	STAD
BCLAF1	c.109_110insCA	p.R37fs	RSKSRSQSSSRSRSRSHSRKKRYSS[p.R37fs]TGLVPEHIQGLVVEIVCILEIIVAITEIIEE*	LVVEIVCIL,CILEIIVAI,IIVAITEII,LVPEHIQGL,HIQGLVVEI,GLVVEIVCI,EIVCILEII,EIIVAITEI,SRKKRYSST,KKRYSSTGL,KRYSSTGLV,VEIVCILEI,VPEHIQGLV,GLVPEHIQGL,LVPEHIQGLV,HIQGLVVEIV,GLVVEIVCIL,HSRKKRYSST,KKRYSSTGLV,EIVCILEIIV,EIIVAITEII,VPEHIQGLVV,RKKRYSSTGL,LEIIVAITEI,VEIVCILEII	CRC
BCOR	c.4376A>G	p.N1459S	LPCSSSPQETTQSRPMPPEARRLIV[p.N1459S]SKNAGETLLQRAARLGYEEVVLYCLE	EARRLIVSK,VSKNAGETL,SKNAGETLL	LUAD
BEND2	c.1607C>A	p.P536Q	RILFSKEILISSSVDIHLKDSQSLD[p.P536Q]QNKMAALREYLATTFPTCDLHEHGKD	DQNKMAALR,SQSLDQNKM,SLDQNKMAAL	LUAD
BEND2	c.1888G>A	p.E630K	NDQRGRDGGEGCSWMFQPMNNSKMR[p.E630K]KKRNLQPNSNAIPEGMREPSTDNPEE	PMNNSKMRK,MNNSKMRKK,KMRKKRNLQ,SKMRKKRNL,KMRKKRNLQP,MNNSKMRKKR,NSKMRKKRNL	MM
BEND3	c.793delG	p.D265fs	FQPPPEYQLTAAELKQIVDQSLSGG[p.D265fs]TWPAACWCSSSPSSSATWTSPGAAVPVALRPSASWSRCTCSSSATMWRSTTPR*	SLSGGTWPA,TMWRSTTPR,GAAVPVALR,CSSSATMWR,TSPGAAVPV,VPVALRPSA,RPSASWSRC,CTCSSSATM,DQSLSGGTW,VALRPSASW,WPAACWCSS,SLSGGTWPAA,ATWTSPGAAV,WTSPGAAVPV,ALRPSASWSR,ATMWRSTTPR,WSRCTCSSSA,SSATWTSPGA,SPGAAVPVAL,RPSASWSRCT,SSSPSSSATW,RCTCSSSATM,WPAACWCSSS	STAD
BEND5	c.592C>T	p.R198C	LEDAVVPRALYEELLRNYQQQQEEM[p.R198C]CHLQQELERTRRQLVQQAKKLKEYGA	QQQEEMCHL,YQQQQEEMCH,QQQQEEMCHL,EEMCHLQQEL	CRC
BEST3	c.1148C>T	p.P383L	SFLGSTVQMGKQMPKNEWKMEDIKI[p.P383L]LLPQPQFQCAKSDPGG*	KMEDIKILL,WKMEDIKIL,KILLPQPQF,LLPQPQFQCA,WKMEDIKILL,IKILLPQPQF	TGCT
BEST3	c.1331_1332insC	p.P444fs	SSMFLPRDDLSPARDLLDVPSRNPP[p.P444fs]QGLTHLEEILLPRRKPHAALQHGRAVHHQGDQPDKHFTEPDPTVQCENFPHQNATGT*	HLEEILLPR,LPRRKPHAA,AALQHGRAV,FPHQNATGT,LQHGRAVHH,CENFPHQNA,LLPRRKPHAA,HLEEILLPRR,HAALQHGRAV,VPSRNPPQGL,LPRRKPHAAL,AALQHGRAVH,LQHGRAVHHQ,HQGDQPDKHF,KHFTEPDPTV,CENFPHQNAT	STAD
BHLHE22	c.185T>A	p.L62Q	STPPGMDLSLAPPPRERPASSSSSP[p.L62Q]QGCFEPADPEGAGLLLPPPGGGGGGS	SPQGCFEPA,SSSSPQGCF,RPASSSSSPQ,SSSSSPQGCF	ACC
BICD2	c.485G>A	p.R162H	SENERLASVAQELKEINQNVEIQRG[p.R162H]HLRDDIKEYKFREARLLQDYSELEEE	RGHLRDDIK,HLRDDIKEY,HLRDDIKEYK,NVEIQRGHLR,IQRGHLRDDI,GHLRDDIKEY	CRC
BIRC6	c.1240G>C	p.V414L	SCFGSGSCPHFLAAATKRGKICIWD[p.V414L]LSKLMKVHLKFEINAYDPAIVQQLIL	KICIWDLSK,CIWDLSKLMK,LSKLMKVHLK,ICIWDLSKLM	TGCT
BIRC8	c.673_674GC>AT	p.A225M	VFIPCGHLVTCKQCAEAVDRCPMCS[p.A225M]MVIDFKQRVFMS*	MVIDFKQRV,MCSMVIDFK,VDRCPMCSM,PMCSMVIDF,SMVIDFKQRV,PMCSMVIDFK,CSMVIDFKQR,CPMCSMVIDF,MVIDFKQRVF	TGCT
BLM	c.1980T>A	p.H660Q	ASRNLKHERFQSLSFPHTKEMMKIF[p.H660Q]QKKFGLHNFRTNQLEAINAALLGEDC	KIFQKKFGL,EMMKIFQKK,KEMMKIFQK,MMKIFQKKF,FQKKFGLHN,QKKFGLHNF,KIFQKKFGLH,EMMKIFQKKF,FQKKFGLHNF,KEMMKIFQKK,MMKIFQKKFG,MKIFQKKFGL	KIRC
BLVRA	c.131C>T	p.S44L	AGSVRMRDLRNPHPSSAFLNLIGFV[p.S44L]LRRELGSIDGVQQISLEDALSSQEVE	FLNLIGFVL,VLRRELGSI,NLIGFVLRR,IGFVLRREL,FVLRRELGSI,AFLNLIGFVL,FLNLIGFVLR	CRC
BMP2K	c.1461C>G	p.H487Q	QQQQQQQQQQQQQQQQQQQQQQQQQQQ[p.H487Q]QHHHHHHHLLQDAYMQQYQHATQQQQ	QQHHHHHHHL,QHHHHHHHLL	TGCT
BMP3	c.1030C>T	p.R344W	KPYKTLQAQAPEKSKNKKKQRKGPH[p.R344W]WKSQTLQFDEQTLKKARRKQWIEPRN	HWKSQTLQF,KQRKGPHWK,GPHWKSQTL,KKQRKGPHW,KKQRKGPHWK,KQRKGPHWKS,KKKQRKGPHW,PHWKSQTLQF	CRC
BMP6	c.353A>T	p.Q118L	PRPLHGLQQPQPPALRQQEEQQQQQ[p.Q118L]LLPRGEPPPGRLKSAPLFMLDLYNAL	QEEQQQQQL,QQEEQQQQQL,QEEQQQQQLL	KIRP

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BMPER	c.1329_1340delGCGCATCGCGCT	p.RIAL444del	KSVELVLGESRVSLQQHLTVRWNGS[p.RIAL444del]PCRAPHFHIDLDGYLLKVTTKAGLEISWDGDSFVEVM	RWNGSPCRA,TVRWNGSPCR,NGSPCRAPHF,SPCRAPHFHI	KIRC
BMPER	c.722G>A	p.R241Q	PPGQCCPKCLGQRKVFDLPFGSCLF[p.R241Q]QSDVYDNGSSFLYDNCTACTCRDSTV	SCLFQSDVY,GSCLFQSDVY,LPFGSCLFQS	UCEC
BMS1	c.1364G>T	p.G455V	KAIFGDEDESGDSDDEEDDEMSEDD[p.G455V]VLENGSSDEEAEEEENAEMTDQYMAV	DEMSEDDVL	LUAD
BMS1	c.2634G>T	p.E878D	GEMQKQAQLNRAEFEDQDDEARVQY[p.E878D]DGFRPGMYVRIEIENVPCEFVQNFDP	YDGFRPGMY,DGFRPGMYV,VQYDGFRPG,QYDGFRPGMY,EARVQYDGFR,DGFRPGMYVR,VQYDGFRPGM,DEARVQYDGF	KIRP
BNC1	c.2809T>A	p.Y937N	MEKADQSLASLPSGLPITCHLCQKT[p.Y937N]NSNKGTFRAHYKTVHLRQLHKCKVPG	KTNSNKGTF,TNSNKGTFR,HLCQKTNSNK,KTNSNKGTFR,QKTNSNKGTF	CLL
BNC2	c.1534C>T	p.R512W	NRHSANPNPRLHMPMLRNNRDKDLI[p.R512W]WATSGAATPVIASTKSNLALTSPGRP	LIWATSGAA,DLIWATSGA,DLIWATSGAA,WATSGAATPV	CRC
BNC2	c.1723A>C	p.S575R	LQNPLPSQLVFSGLKTVQPVPPFYR[p.S575R]RLLTPGEMVSPPTSLPTSPIIPTSGT	RLLTPGEMV,QPVPPFYRR,VPPFYRRLL,RRLLTPGEM,QPVPPFYRRL,YRRLLTPGEM	STAD
BPI	c.765G>T	p.M255I	IDSVAGINYGLVAPPATTAETLDVQ[p.M255I]IKGEFYSENHHNPPPFAPPVMEFPAA	LDVQIKGEF,TTAETLDVQI,LDVQIKGEFY	BLCA
BRAF	c.1208delC	p.P403fs	NIDDLIRDQGFRGDGGSTTGLSATP[p.P403fs]LPHYLAH*	LSATPLPHY,SATPLPHYL,GLSATPLPH,TPLPHYLAH,GLSATPLPHY,STTGLSATPL,LSATPLPHYL	STAD
BRAF	c.1397G>T	p.G466V	LGRRDSSDDWEIPDGQITVGQRIGS[p.G466V]VSFGTVYKGKWHGDVAVKMLNVTAPT	SVSFGTVYK,GSVSFGTVY,GQRIGSVSF,RIGSVSFGTV,GSVSFGTVYK,VSFGTVYKGK,IGSVSFGTVY,ITVGQRIGSV,VGQRIGSVSF	LUAD
BRAF	c.1406G>C	p.G469A	RDSSDDWEIPDGQITVGQRIGSGSF[p.G469A]ATVYKGKWHGDVAVKMLNVTAPTPQQ	GSGSFATVY,SGSFATVYK,SFATVYKGK,FATVYKGKW,RIGSGSFATV,GSGSFATVYK,GSFATVYKGK,SFATVYKGKW,GQRIGSGSFA,IGSGSFATVY	MM,PRAD
BRAF	c.1406G>T	p.G469V	RDSSDDWEIPDGQITVGQRIGSGSF[p.G469V]VTVYKGKWHGDVAVKMLNVTAPTPQQ	SGSFVTVYK,SFVTVYKGK,GSGSFVTVY,RIGSGSFVTV,GSGSFVTVYK,GSFVTVYKGK,SFVTVYKGKW,GQRIGSGSFV,IGSGSFVTVY	LUAD
BRAF	c.1798_1799GT>AA	p.V600K	RDLKSNNIFLHEDLTVKIGDFGLAT[p.V600K]KKSRWSGSHQFEQLSGSILWMAPEVIR	ATKKSRWSG,KKSRWSGSH,ATKKSRWSGS,DFGLATKKSR,FGLATKKSRW	SKCM
BRAF	c.1799T>A	p.V600E	RDLKSNNIFLHEDLTVKIGDFGLAT[p.V600E]EKSRWSGSHQFEQLSGSILWMAPEVI	DFGLATEKSR,FGLATEKSRW	CRC,GBM,LUAD,MM,SKCM,THCA
BRAF	c.1801A>G	p.K601E	DLKSNNIFLHEDLTVKIGDFGLATV[p.K601E]ESRWSGSHQFEQLSGSILWMAPEVIR	VESRWSGSH,DFGLATVESR,ESRWSGSHQF,FGLATVESRW	DLBCL,SKCM
BRAF	c.1803A>T	p.K601N	DLKSNNIFLHEDLTVKIGDFGLATV[p.K601N]NSRWSGSHQFEQLSGSILWMAPEVIR	GLATVNSRW,DFGLATVNSR,NSRWSGSHQF,FGLATVNSRW	CLL
BRD3	c.70_71insC	p.P24fs	MSTATTVAPAGIPATPGPVNPPPP[p.P24fs]GGLQPQQARPQDQPAAVHAECGGEDALETPVRLALLPARGRNQIEPAGLS*	RGRNQIEPA,ETPVRLALL,RPQDQPAAV,LPARGRNQI,AECGGEDAL,LETPVRLAL,GEDALETPV,LLPARGRNQI,PVRLALLPAR,RLALLPARGR,TPVRLALLPA,QQARPQDQPA,ALETPVRLAL,LETPVRLALL	STAD
BRD9	c.988G>T	p.G330W	HAADEARDRINRFLPGGKMGYLKRN[p.G330W]WDGSLLYSVVNTAEPDADEEETHPVD	RNWDGSLLY,KMGYLKRNW,LKRNWDGSL,KRNWDGSLL,WDGSLLYSV,YLKRNWDGSL,KRNWDGSLLY,GKMGYLKRNW,LKRNWDGSLL,WDGSLLYSVV	LUAD
BRF1	c.1405G>T	p.V469L	DGELDLSGIDDLEIDRYILNESEAR[p.V469L]LKAELWMRENAEYLREQREKEARIAK	ILNESEARL,RLKAELWMR,SEARLKAEL,ARLKAELWM,NESEARLKA,YILNESEARL,ILNESEARLK,SEARLKAELW	LUAD
BRK1	c.208A>C	p.K70Q	SRLATLNEKLTALERRIEYIEARVT[p.K70Q]QGETLT*	ARVTQGETL,IEARVTQGET	KIRC

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BRMS1	c.321delG	p.G107fs	LSQLRLRLEEVGAERAPEYTEPLGG[p.G107fs]CSGASRFAFRWQGSTRASVWM*	WQGSTRASV,SGASRFAFR,ASRFAFRWQ,AFRWQGSTR,GGCSGASRF,CSGASRFAF,FAFRWQGST,FRWQGSTRA,GASRFAFRW,CSGASRFAFR,FAFRWQGSTR,ASRFAFRWQG,RFAFRWQGST,AFRWQGSTRA,RWQGSTRASV,LGGCSGASRF,GCSGASRFAF,SGASRFAFRW,FRWQGSTRAS,WQGSTRASVW	STAD
BRPF1	c.196C>T	p.R66C	HLYHYDHDNPPPPQQTPLRKHKKKG[p.R66C]CQSRPANKQSPSPSEVSQSPGREVMS	GCQSRPANK,KHKKKGCQSR,KGCQSRPANK	CRC
BRWD1	c.3956A>G	p.K1319R	TSSGRRRVHDGKKSIRATNYVESNW[p.K1319R]RKQCKELVNLIFQCEDSEPFRQPVDL	NYVESNWRK,ATNYVESNWR,RKQCKELVNL	TGCT
BRWD3	c.2359C>T	p.R787C	TVEKKKKPSYTTQRNDYEPSCGRSL[p.R787C]CRTQRKRQHTYQTRSNIEHNSQASCQ	RSLCRTQRK,CGRSLCRTQR,RSLCRTQRKR	CRC
BRWD3	c.478C>A	p.H160N	VNYVKPPNVVNITSAROLTGCSRFG[p.H160N]NIFPSSAYQHIKMHKRILGHLSSVYC	CSRFGNIFP,RFGNIFPSS,GNIFPSSAY,GCSRFGNIF,SRFGNIFPS,CSRFGNIFPS,RFGNIFPSSA,FGNIFPSSAY,TGCSRFGNIF	LUAD
BST1	c.107G>C	p.G36A	LLQLLLQLLLLLLLLAAGGARARWR[p.G36A]AEGTSAHLRDIFLGRCAEYRALLSPE	RARWRAEGT,RWRAEGTSA,WRAEGTSAH,RAEGTSAHL,GARARWRAEG,RARWRAEGTS,RWRAEGTSAH,ARWRAEGTSA,WRAEGTSAHL	KIRP
BTBD11	c.1352delC	p.T451fs	LSDLVSRAMHHLQPLNAKHHGNGTP[p.T451fs]CTTSRGHCTGSPRPCTPFAISCTAHKWNGKTPTWSLPKSTSRWKGPSSCCRR*	CTAHKWNGK,KTPTWSLPK,FAISCTAHK,KWNGKTPTW,RGHCTGSPR,TSRWKGPSS,WSLPKSTSR,SPRPCTPFA,NGKTPTWSL,KHHGNGTPC,GSPRPCTPF,HKWNGKTPT,TPFAISCTA,SLPKSTSRWK,RWKGPSSCCR,TWSLPKSTSR,CTPFAISCTA,SPRPCTPFAI,AKHHGNGTPC,TGSPRPCTPF,FAISCTAHKW,HKWNGKTPTW,WSLPKSTSRW,TPFAISCTAH	STAD
BTBD11	c.1682C>T	p.A561V	LLPGVDCEPRQLRADDCFCASRKLD[p.A561V]VVAIEAKFKQDLGFRMLNCGRTDLVK	KLDVVAIEA,VVAIEAKFK,ASRKLDVVA,KLDVVAIEAK,ASRKLDVVAI,DVVAIEAKFK,RKLDVVAIEA,LDVVAIEAKF	STAD
BTBD11	c.794G>C	p.G265A	CMESLFRDIYSRVVASGVPRSCSGP[p.G265A]ASGSGSGPGPSSGPGAAPAADKEREA	VPRSCSGPA,VPRSCSGPAS	ACC
BTBD7	c.1307C>T	p.S436L	HPYGSKWVHRQALHFLCEEFSQVMT[p.S436L]LDVFYELSKDHLLTAIQSDYLQASEQ	MTLDVFYEL,QVMTLDVFY,SQVMTLDVF,EEFSQVMTL,VMTLDVFYEL,TLDVFYELSK,FSQVMTLDVF,SQVMTLDVFY,MTLDVFYELS,CEEFSQVMTL	CRC
BTG1	c.91C>T	p.L31F	TRAATMIGEIAAAVSFISKFLRTKG[p.L31F]FTSERQLQTFSQSLQELLAEHYKHHW	RTKGFTSER,FLRTKGFTS,SKFLRTKGF,KGFTSERQL,FLRTKGFTSE,FTSERQLQTF,ISKFLRTKGF	DLBCL
BTLA	c.256C>A	p.Q86K	KYCANRPHVTWCKLNGTTCVKLEDR[p.Q86K]KTSWKEEKNISFFILHFEPVLPNDNG	KLEDRKTSW,KLEDRKTSWK,TTCVKLEDRK,VKLEDRKTSW	CLL
BTN2A2	c.43C>T	p.L15F	MEPAAALHFSLPAS[p.L15F]FLLLLLLLLSLCALVSAQFTVVGPA	FSLPASFLL,SLPASFLLL,SFLLLLLLL,LPASFLLLL,LHFSLPASF,ASFLLLLLL,FSLPASFLLL,SLPASFLLLL,HFSLPASFLL,SFLLLLLLL,ALHFSLPASF,LPASFLLLLL,LHFSLPASFL,ASFLLLLLLL	TGCT
BTN3A2	c.457G>A	p.E153K	FQDGDFYEKALVELKVAALGSNLHV[p.E153K]KVKGYEDGGIHLECRSTGWYPQPQIQ	ALGSNLHVK,GSNLHVKVK,NLHVKVKGY,ALGSNLHVKV,AALGSNLHVK	UCEC
BTRC	c.1248T>G	p.I416M	FNNGMMVTCSKDRSIAVWDMASPTD[p.I416M]MTLRRVLVGHRAAVNVVDFDDKYIVS	MASPTDMTL,WDMASPTDM,MASPTDMTLR,MTLRRVLVGH,DMASPTDMTL,SPTDMTLRRV	KIRC
BTRC	c.778G>T	p.G260W	TDSLWRGLAERRGWGQYLFKNKPPD[p.G260W]WNAPPNSFYRALYPKIIQDIETIESN	KNKPPDWNA,WNAPPNSFY,YLFKNKPPDW,DWNAPPNSFY,WNAPPNSFYR	LUAD
BUB1B	c.2988C>A	p.F996L	VFWDGSFWKLSQNISELKDGELWNK[p.F996L]LFVRILNANDEATVSVLGELAAEMNG	KLFVRILNA,LWNKLFVRI,ELWNKLFVR,GELWNKLFV	CRC
BZRAP1	c.4248_4249insA	p.P1416fs	CLEDMPGLVGGSSRRRGGGSPEKPP[p.P1416fs]KPQAASRSPRTLQPTSQQQWAPGLWTTGPHTGEGWPPRN*	SQQQWAPGL,HTGEGWPPR,QQQWAPGLW,QWAPGLWTT,ASRSPRTLQ,AASRSPRTL,LQPTSQQQW,QQWAPGLWT,SQQQWAPGLW,ASRSPRTLQP,TLQPTSQQQW,QQWAPGLWTT	STAD

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BZRAP1	c.4879G>A	p.V1627I	VLRPSTAELVPARSPSETLAYQHLP[p.V1627I]IRIFVALFDYDPVSMSPNPDAGEEEL	TLAYQHLPI,HLPIRIFVA,AYQHLPIRI,LAYQHLPIR,LPIRIFVAL,YQHLPIRIF,YQHLPIRIFV,HLPIRIFVAL,AYQHLPIRIF,IRIFVALFDY,TLAYQHLPIR,ETLAYQHLPI,LPIRIFVALF,LAYQHLPIRI	CRC
C10orf95	c.253G>T	p.A85S	GRRRRSCSPAPTWPPLCCYPQSRPT[p.A85S]SSAAGPGACMRASGRPHGNTTASTAP	QSRPTSSAA,YPQSRPTSS,YPQSRPTSSA,SSAAGPGACM	ACC
C11orf30	c.3331C>T	p.R1111C	KQTASQVEQPIITQGSSVTKITFEG[p.R1111C]CQPPTVTKITGGSSVPKLTSPVTSIS	FEGCQPPTV	CRC
C11orf68	c.403G>T	p.V135L	PGSPNSEPVGWIAVYGQGYSPNSGD[p.V135L]LQGLQAAWEALQTSGRPITPGTLRQL	GDLQGLQAA,SPNSGDLQGL,GDLQGLQAAW	LUAD
C11orf9	c.782_783insC	p.S261fs	QLLQQHGAELPTHPSKKRKHSESPP[p.S261fs]QHPQCPDAEWNDQTGAWDRDSPASAPHSSPIATLASPGSALPGPWFLASQHCPCPDTALAPARCPLPRPPAGQ*	SALPGPWFL,ALPGPWFLA,FLASQHCPC,ALAPARCPL,TLASPGSAL,ASAPHSSPI,ATLASPGSA,HSSPIATLA,APHSSPIAT,AEWNDQTGA,RDSPASAPH,GSALPGPWF,HPQCPDAEW,LPGPWFLAS,CPDTALAPA,ASAPHSSPIA,ATLASPGSAL,SALPGPWFLA,LAPARCPLPR,APHSSPIATL,TALAPARCPL,RKHSESPPQH,AEWNDQTGAW,SQHCPCPDTA,SPIATLASPG,SPGSALPGPW	STAD
C12orf32	c.179A>T	p.D60V	LPITHTRQVPSKPIDHSTITSWVSP[p.D60V]VFDTAAGSLFPAYQKHQNRARHSSRK	TITSWVSPV,WVSPVFDTA,ITSWVSPVF,SPVFDTAAG,STITSWVSPV,WVSPVFDTAA,VFDTAAGSLF,TITSWVSPVF	TGCT
C12orf4	c.1004G>A	p.R335Q	KLHRLQTALSLYSTSLCGLVLLVDN[p.R335Q]QINSYSGIKRDFATVCQECTDFHFPR	LVDNQINSY,NQINSYSGI,QINSYSGIK,GLVLLVDNQI,LLVDNQINSY,QINSYSGIKR	UCEC
C12orf43	c.82G>C	p.E28Q	APSGTVSDSESSNSSSDAEELERCR[p.E28Q]QAAMPAWGLEQRPHVAGKPRAGAANS	RCRQAAMPA,QAAMPAWGL,LERCRQAAM,CRQAAMPAW,RQAAMPAWG,EELERCRQA,RQAAMPAWGL,ELERCRQAAM,RCRQAAMPAW,EELERCRQAA,AEELERCRQA	CESC
C12orf65	c.428A>C	p.K143T	VFYNGENSPVHKEKREAAKKKQERK[p.K143T]TRAKETLEKKKLLKELWESSKKVH*	KQERKTRAK,KTRAKETLE,RKTRAKETL,KTRAKETLEK,ERKTRAKETL	TGCT
C13orf33	c.200delG	p.R67fs	QPGAFQLSGDQLVVARPGEPAAARG[p.R67fs]ASTSSVTASCASTGSSTASAATSRGMWN*	STASAATSR,STGSSTASA,ASAATSRGM,SAATSRGMW,GEPAAARGA,SSTASAATSR,AARGASTSSV,STSSVTASCA,EPAAARGAST,RGASTSSVTA,TASAATSRGM,ASAATSRGMW	STAD
C14orf101	c.883G>A	p.E295K	FSLAKSEIGSSMSEILLSQVTNMRT[p.E295K]KLSFNIQALAVCANICLATKDRQNPS	KLSFNIQAL,RTKLSFNIQ,TNMRTKLSF,KLSFNIQALA,NMRTKLSFNI,LSQVTNMRTK,RTKLSFNIQA,SQVTNMRTKL,VTNMRTKLSF,TKLSFNIQAL	CRC
C14orf102	c.268delA	p.R90fs	SSDESDTNKKLKQTSRKKKKEKKKK[p.R90fs]GSISIIRKQRGSMGRRVAAGLRQTPILKRTNLPEALEAVKRNLRNRIKEIMLQLILDIALFGLRTFRL*	NLPEALEAV,IMLQLILDI,MLQLILDIA,ILDIALFGL,RIKEIMLQL,GLRQTPILK,ALFGLRTFR,KGSISIIRK,IALFGLRTF,LFGLRTFRL,IIRKQRGSM,KQRGSMGRR,RGSMGRRVA,GSMGRRVAA,MGRRVAAGL,AVKRNLRNR,KRNLRNRIK,RNRIKEIML,SISIIRKQR,TPILKRTNL,SMGRRVAAG,NLRNRIKEI,QLILDIALF,KKKKGSISI,KKKGSISII,KRTNLPEAL,LRNRIKEIM,KEIMLQLIL,LQLILDIAL,SMGRRVAAGL,IMLQLILDIA,MLQLILDIAL,LILDIALFGL,ALFGLRTFRL,ILKRTNLPEA,RIKEIMLQLI,AGLRQTPILK,IALFGLRTFR,KQRGSMGRRV,RGSMGRRVAA,MGRRVAAGLR,GLRQTPILKR,RTNLPEALEA,AVKRNLRNRI,EAVKRNLRNR,EIMLQLILDI,SIIRKQRGSM,NLRNRIKEIM,LQLILDIALF,DIALFGLRTF,KKKKGSISII,RRVAAGLRQT,VAAGLRQTPI,LKRTNLPEAL,IKEIMLQLIL	STAD
C14orf102	c.343G>A	p.D115N	RKHQHHKKTKRKHGPSSSSRSETDT[p.D115N]NSEKDKPSRGVGGSKKESEEPNQGNN	RSETDTNSEK	CRC
C14orf105	c.299G>T	p.R100I	ASRDMYFDIPLEHRETSIIKRHPPQ[p.R100I]ILQKLEPIDLPRVITSGRLLSQREAR	IIKRHPPQI,IKRHPPQIL,SIIKRHPPQI,IIKRHPPQIL,KRHPPQILQK	CRC
C14orf118	c.836G>T	p.R279I	GECVPGFTVPNLLPKWAPDHCSEVE[p.R279I]IMDSGLDKFSDSTFLLPSRPAQRGYH	EIMDSGLDK,IMDSGLDKF,EIMDSGLDKF,SEVEIMDSGL	UCEC
C14orf126	c.16C>T	p.R6W	MAEGS[p.R6W]WIPQARALLQQCLHARLQIRPADGDV	EGSWIPQAR,SWIPQARAL,AEGSWIPQA,SWIPQARALL,GSWIPQARAL	KIRP

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C14orf166B	c.690C>A	p.F230L	DSAALLCQALSTNYQIKKLDLSHNQ[p.F230L]LSDVGGEHLGQMLAINVGLTSLDLSW	KLDLSHNQL,QLSDVGGEHL,KKLDLSHNQL	UCEC
C14orf177	c.269G>T	p.G90V	CCGECSTCFCTEEKSECQRHEETSP[p.G90V]VSCNHQIMSASTISAFCATPRFKQLF	SPVSCNHQI,CQRHEETSPV,SPVSCNHQIM	CLL
C14orf43	c.939delC	p.P313fs	GLQPAGPLGQSHLAHHSMAPYPFPP[p.P313fs]TQI*	PYPFPPTQI,MAPYPFPPT,SMAPYPFPPT,APYPFPPTQI	STAD
C15orf2	c.1462G>A	p.V488I	LALPADLVPILGDQSNEKGGSYNSV[p.V488I]IGAAPLTSDPPTPPSSTPSFKPPVTR	NSVIGAAPL,KGGSYNSVI,GSYNSVIGAA,YNSVIGAAPL	CRC
C15orf2	c.2257G>T	p.V753F	PGSGNTQPSGNTASVQGSTSLPAQS[p.V753F]FRAPATASNHPLNPGATPQPKFGAPD	SLPAQSFRA,TSLPAQSFR,QSFRAPATA,LPAQSFRAP,STSLPAQSF,AQSFRAPAT,STSLPAQSFR,SFRAPATASN,LPAQSFRAPA,GSTSLPAQSF,AQSFRAPATA	LUAD
C15orf2	c.2716G>T	p.G906W	RRPTTTSSHPLNTGSISHSTLGATD[p.G906W]WQQKSDSSFILGNPATPAPVIGLTSP	WQQKSDSSF,TLGATDWQQK,WQQKSDSSFI	LUAD
C15orf23	c.71C>T	p.S24F	MAAPEAPPLDRVFRTTWLSTECD[p.S24F]FHPLPPSYRKFLFETQAADLAGGTTV	TWLSTECDF,DFHPLPPSY,STECDFHPL,DFHPLPPSYR,LSTECDFHPL,CDFHPLPPSY	SKCM
C15orf33	c.1018G>A	p.D340N	GSKKAPAKSVKERIADSQEHISTSI[p.D340N]NFNIIKILNNPRAYTLPISKEESRLS	SINFNIIKI,TSINFNIIK,ISTSINFNI,STSINFNII,EHISTSINF,INFNIIKIL,HISTSINFNI,STSINFNIIK,TSINFNIIKI,QEHISTSINF,ISTSINFNII	CRC
C15orf52	c.294delG	p.G98fs	RKKNQALLRRYQEIQEDRRQAEQGG[p.G98fs]WL*	RQAEQGGWL	STAD
C16orf3	c.193G>A	p.G65S	RACPVACPVGCPIACPVSCPVACPV[p.G65S]SCPVGSMATAPQGLSPQEWEADRETG	VACPVSCPV,PVACPVSCPV,CPVSCPVGSM	CESC
C16orf55	c.353A>C	p.D118A	RASNETLVSCSSSGSDQQRTIREPE[p.D118A]AWGPYRRHRNPSTADAYNSHLKE*	REPEAWGPY,RTIREPEAW,EAWGPYRRHR,IREPEAWGPY	KIRC
C16orf62	c.730C>A	p.L244I	SDTSVIQFYPSKFVLITDILDTFGK[p.L244I]IVYERIFSMCVDSRSVLPDHFSPENA	IVYERIFSM,TFGKIVYER,DILDTFGKI,LDTFGKIVY,GKIVYERIF,ILDTFGKIVY,TFGKIVYERI,KIVYERIFSM,DTFGKIVYER,FGKIVYERIF	TGCT
C16orf74	c.61_63delAGC	p.S21del	MGLKMSCLKGFQMCVSSSSS[p.S21del]HDEAPVLNDKHLDVPDIIITPPTPTGMM	MCVSSSSSH,QMCVSSSSSH	PRAD
C16orf87	c.452G>T	p.R151I	ANLSDEKAFVFSVALAEINRKIINQ[p.R151I]ILIL*	KIINQILIL,NRKIINQIL,RKIINQILI,EINRKIINQI,RKIINQILIL	CRC
C17orf96	c.187C>G	p.L63V	LCLRALAFCALAKPRASSLGPGPGE[p.L63V]VAARSPVLRGPQAPLRPGGWAPDGLK	SLGPGPGEV,VAARSPVLR,EVAARSPVL,GEVAARSPV,EVAARSPVLR,GEVAARSPVL	ACC
C19orf10	c.34G>C	p.G12R	MAAPSGGWNGV[p.G12R]RASLWAALLLGAVALRPAEAVSEPTT	GVRASLWAA,RASLWAALL,VRASLWAAL,GVRASLWAAL,GWNGVRASLW,RASLWAALLL,GGWNGVRASL,VRASLWAALL	ACC
C19orf21	c.784C>T	p.R262C	PHLANGHVVPIKPQVKGVVREENKV[p.R262C]CAVPTWASVQVVDDPGSLASVESPGT	CAVPTWASV,REENKVCAV,NKVCAVPTW,EENKVCAVPT	STAD
C19orf70	c.150delC	p.P50fs	YDQELLGPSDKSQAALQKAGEVVPP[p.P50fs]PCTSSASTCVSRQACRYPSSQPLQRFTFPSVTPGMQAS*	CVSRQACRY,LQRFTFPSV,SSASTCVSR,SQPLQRFTF,TFPSVTPGM,RQACRYPSS,CTSSASTCV,FTFPSVTPG,VPPPCTSSA,CRYPSSQPL,GEVVPPPCT,PLQRFTFPSV,FTFPSVTPGM,TSSASTCVSR,STCVSRQACR,SSQPLQRFTF,YPSSQPLQRF,FPSVTPGMQA,RQACRYPSSQ,LQRFTFPSVT	STAD
C1QBP	c.674C>T	p.T225I	ESDIFSIREVSFQSTGESEWKDTNY[p.T225I]ILNTDSLDWALYDHLMDFLADRGVDN	NYILNTDSL,SEWKDTNYI,ILNTDSLDW,ILNTDSLDWA,SEWKDTNYIL,YILNTDSLDW	TGCT
C1QTNF5	c.582_583insG	p.G194fs	CVWHIQVATDHAIQLKIEALSIESV[p.G194fs]GLLPF*	ALSIESVGL,IESVGLLPF,LSIESVGLL,ALSIESVGLL,EALSIESVGL,SIESVGLLPF	STAD
C1QTNF5	c.924delC	p.P308fs	NCADGSDETNCSAKFSGSVEQSHPP[p.P308fs]PRLLAP*	QSHPPPRLLA,VEQSHPPPRL	STAD

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C1R	c.647delC	p.P216fs	AECSSELYTEASGYISSLEYPRSYP[p.P216fs]LTCAATTASGWSGASPCTSSSWSLLILMTTSKYTAPMTSYRSMPTGRTLASSVGSKGPPTSTPAAMLWICCSSQMSRGTAGAGSCATPPRSSSAPSPRP*	TSSSWSLLI,ILMTTSKYT,SMPTGRTLA,QMSRGTAGA,LLILMTTSK,TLASSVGSK,YTAPMTSYR,RSSSAPSPR,RSYPLTCAA,TTSKYTAPM,MTSYRSMPT,SYRSMPTGR,RSMPTGRTL,RTLASSVGS,SSQMSRGTA,AGSCATPPR,ATPPRSSSA,LILMTTSKY,KYTAPMTSY,TTASGWSGA,CTSSSWSLL,STPAAMLWI,YPRSYPLTC,APMTSYRSM,MPTGRTLAS,LEYPRSYPL,CAATTASGW,SSSWSLLIL,SSWSLLILM,LMTTSKYTA,SKYTAPMTS,LWICCSSQM,SQMSRGTAG,YPLTCAATT,PPTSTPAAM,TSTPAAMLW,TPAAMLWIC,CTSSSWSLLI,SLEYPRSYPL,ILMTTSKYTA,MLWICCSSQM,SQMSRGTAGA,SLLILMTTSK,RTLASSVGSK,TSYRSMPTGR,RSYPLTCAAT,MTTSKYTAPM,KYTAPMTSYR,RSMPTGRTLA,LLILMTTSKY,SKYTAPMTSY,WICCSSQMSR,TTASGWSGAS,YTAPMTSYRS,YPRSYPLTCA,YPLTCAATTA,SPCTSSSWSL,MPTGRTLASS,GPPTSTPAAM,LEYPRSYPLT,GASPCTSSSW,TSSSWSLLIL,SSSWSLLILM,YRSMPTGRTL,SKGPPTSTPA	STAD
C1RL	c.1051delC	p.L351fs	PDYRQNESHNFSGDIALLELQHSIP[p.L351fs]WAPTSSRSVCPIMRPSTAAACWATSVGLAWRWAG*	AAACWATSV,ELQHSIPWA,IMRPSTAAA,ATSVGLAWR,SSRSVCPIM,IPWAPTSSR,STAAACWAT,APTSSRSVC,CPIMRPSTA,LELQHSIPW,LQHSIPWAP,WATSVGLAW,RPSTAAACW,TSVGLAWRW,TAAACWATSV,CWATSVGLAW,SSRSVCPIMR,IMRPSTAAAC,SIPWAPTSSR,WATSVGLAWR,STAAACWATS,CPIMRPSTAA,RPSTAAACWA,LLELQHSIPW,LELQHSIPWA,LQHSIPWAPT,TSSRSVCPIM,AACWATSVGL	CRC
C1orf106	c.1612C>T	p.R538C	PPGYFPAGRYVVVAESPLPPGEWEL[p.R538C]CRAAPGPAYEEEGTPLRYQRLVPSRS	GEWELCRAA,CRAAPGPAY,WELCRAAPG,LCRAAPGPAY,WELCRAAPGP,GEWELCRAAP	ACC
C1orf167	c.367A>G	p.S123G	WWHLRALGPDATSSCTKTPSALEPL[p.S123G]GSSTLQDSLEKVPRAPTLPDTLQGSL	LEPLGSSTL,ALEPLGSSTL	TGCT
C1orf173	c.2063C>A	p.S688Y	ESFENVLKEGTEKGTQEIAEGLSEK[p.S688Y]YGKHVSAEEKEKDKSKLWEESTAQVK	IAEGLSEKY,GLSEKYGKHV,YGKHVSAEEK,EIAEGLSEKY,SEKYGKHVSA	LUAD
C1orf173	c.4360G>A	p.G1454S	AGVGTPGALERKTSGLGQEQEEGSE[p.G1454S]SQEAATGSGDGRQETGAAEKFRLGLS	EEGSESQEA,QEEGSESQEA,EEGSESQEAA	LUAD
C1orf74	c.760G>A	p.D254N	PGLRDILNTWEKDLRTRFRTQNDFA[p.D254N]NLSISSEIVTLPAVAL*	NLSISSEIV,RTQNDFANL,FANLSISSEI,RFRTQNDFAN,FRTQNDFANL,TQNDFANLSI	LUSC
C1orf87	c.1622G>T	p.R541L	LSPQKIDQALRRFRSGENMLLEPAL[p.R541L]LYLKEL*	MLLEPALLY,NMLLEPALL,LLEPALLYL,MLLEPALLYL,LLEPALLYLK,NMLLEPALLY,EPALLYLKEL	LUAD
C20orf132	c.1146A>C	p.E382D	LKLPLRFQRLGHLVALMALLCGDPQ[p.E382D]DKVAEEAAEGIHSLLHITLRLKYITH	LLCGDPQDKV	KIRC
C20orf160	c.136delC	p.P46fs	KAGRRAACRSSVSRRPLHSMPLYPP[p.P46fs]TTSSTPRFCCVTTWRKRSSSWATLPG*	HSMPLYPPT,SSTPRFCCV,RFCCVTTWR,RKRSSSWAT,KRSSSWATL,MPLYPPTTS,RFCCVTTWRK,TWRKRSSSWA,RKRSSSWATL,RSSSWATLPG,TSSTPRFCCV,MPLYPPTTSS,HSMPLYPPTT,TTWRKRSSSW,TPRFCCVTTW	STAD
C20orf26	c.3263G>A	p.R1088Q	LEVQMAQPNYGLELVTGSAKNGTYF[p.R1088Q]QIHINKYKMVETITCLSREPFPASNY	TYFQIHINK,FQIHINKYK,YFQIHINKY,AKNGTYFQI,GTYFQIHINK,TYFQIHINKY,SAKNGTYFQI,YFQIHINKYK,FQIHINKYKM,AKNGTYFQIH	CRC
C22orf26	c.83C>T	p.P28L	ASATAAWHCPPLCLPPLPASAPTSP[p.P28L]LNPATRPAPGPGRRARCPQSAHPAPT	APTSPLNPA,LPASAPTSPL,SPLNPATRPA	ACC

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C22orf40	c.96_97insC	p.P32fs	RPLGVFECELCTLTAPYSYVGQKPP[p.P32fs]QHPVDGPPGGKLCHEGSLHLRQGQIPGPRLVLQFVQQAGVCGPGMQFILLQEILPPLCPGEHQCFSSGNSARLGEKESSIKEDPQPARFSDVSATGARSSGGTLHRAPGPACARDAAELGAAMPGLVSGPLGAALQPRGAGVQLGAATGPGSCSKRVVQRQMPDKTQPGTRPGPPTCPSGPRPE*	LQFVQQAGV,MQFILLQEI,LLQEILPPL,RLGEKESSI,ALQPRGAGV,GQIPGPRLV,TLHRAPGPA,GLVSGPLGA,LVSGPLGAA,ATGPGSCSK,RSSGGTLHR,VVQRQMPDK,GQKPPQHPV,HLRQGQIPG,GNSARLGEK,KTQPGTRPG,GTRPGPPTC,CFSSGNSAR,FSSGNSARL,DAAELGAAM,GPRLVLQFV,GARSSGGTL,GPACARDAA,MPGLVSGPL,QPRGAGVQL,SLHLRQGQI,GKLCHEGSL,LCHEGSLHL,GVCGPGMQF,GEHQCFSSG,KEDPQPARF,ARFSDVSAT,LHRAPGPAC,VSGPLGAAL,SKRVVQRQM,RQMPDKTQP,AELGAAMPG,KLCHEGSLHL,VLQFVQQAGV,GMQFILLQEI,MQFILLQEIL,ILLQEILPPL,LLQEILPPLC,AMPGLVSGPL,RLVLQFVQQA,ELGAAMPGLV,GLVSGPLGAA,LVSGPLGAAL,RLGEKESSIK,RVVQRQMPDK,AATGPGSCSK,SGNSARLGEK,SIKEDPQPAR,RSSGGTLHRA,GTLHRAPGPA,IPGPRLVLQF,QQAGVCGPGM,RQGQIPGPRL,GQIPGPRLVL,LQFVQQAGVC,AGVCGPGMQF,HQCFSSGNSA,IKEDPQPARF,RDAAELGAAM,AELGAAMPGL,LQPRGAGVQL,VQLGAATGPG,CSKRVVQRQM,RQMPDKTQPG,GEHQCFSSGN	CRC
C22orf43	c.55A>G	p.K19E	MGNILTCCINSHCGWPRG[p.K19E]EDAPCYESDTDIYETVAAATSESTTV	WPRGEDAPC,GEDAPCYES,WPRGEDAPCY	TGCT
C2orf44	c.1368T>A	p.N456K	IMLEEEPSITSGESQTTYSTFSAPL[p.N456K]KKANRKKLIESLSPDFCHQNKGLLLT	YSTFSAPLK,STFSAPLKK,PLKKANRKK,SAPLKKANR,TYSTFSAPLK,YSTFSAPLKK,STFSAPLKKA,SAPLKKANRK,FSAPLKKANR	CLL
C2orf53	c.815C>A	p.P272H	VEYPICLVCLRPRSPSCPLPRYRTG[p.P272H]HRLLAFPQLLPCVQGQESGPLRIGIG	RYRTGHRLL,RTGHRLLAF,HRLLAFPQL,RYRTGHRLLA,LPRYRTGHRL,YRTGHRLLAF,GHRLLAFPQL,HRLLAFPQLL	LUAD
C2orf71	c.3675_3676insAGC	p.1225_1226insS	GRPQPPTLDPTSTSYESQLGQNSSS[p.1225_1226insS]SEESPKKDTEPGSSPCSPELQGGTRRAS	SSSSEESPK,SSSSEESPKK,SQLGQNSSSS	KIRC
C2orf81	c.943A>C	p.T315P	LELRSEGVPCIASGVLVSYPSVGGA[p.T315P]PRPSASCQQQRAGHSDVRLSAHHHRM	YPSVGGAPR,SYPSVGGAPR	ACC
C3	c.2670delC	p.P890fs	LLHNPAFCSLATTKRRHQQTVTIPP[p.P890fs]SPRCPFHMSSCR*	TVTIPPSPR,IPPSPRCPF,QTVTIPPSPR,SPRCPFHMSS,HQQTVTIPPS	STAD
C3orf15	c.1655G>A	p.R552Q	RTCHALQEDEKLVKKAEKQVTLALQ[p.R552Q]QQRNLHEHKVSLVENHLAGLEGRALA	VTLALQQQR,QQRNLHEHK,KQVTLALQQ,QQQRNLHEH,QVTLALQQQR,KQVTLALQQQ,LQQQRNLHEH,QQRNLHEHKV	CLL
C3orf20	c.2219G>T	p.R740L	IISSQNYTSTGQLQWLLNTLYNHQQ[p.R740L]LGRGSPCIQCRYDSYRLLQYDLDSPL	LYNHQQLGR,QQLGRGSPC,TLYNHQQLGR,HQQLGRGSPC,QQLGRGSPCI	LUAD
C3orf23	c.649C>T	p.R217C	SWLDNNGKSAVKKLKNSLPLRKELD[p.R217C]CLKDELSHQLQLSDIRWQRSWGIAHR	CLKDELSHQL,KELDCLKDEL,LPLRKELDCL	UCEC
C3orf30	c.681C>A	p.D227E	AERRTSEQITHRLSKLSERRPSVQI[p.D227E]ESGSSVPSDQSPSVQIDSGSSVPSDQ	VQIESGSSV,IESGSSVPS,SVQIESGSSV,VQIESGSSVP	LUSC
C3orf39	c.997C>T	p.R333W	LALAQEFQMKTVTVSLEDHTFADVV[p.R333W]WLVSNASMLVSMHGAQLVTTLFLPRG	TFADVVWLV,WLVSNASML,HTFADVVWL,DVVWLVSNA,VWLVSNASM,HTFADVVWLV,WLVSNASMLV,VWLVSNASML,VVWLVSNASM	CRC
C3orf62	c.554G>A	p.R185Q	SNMPLNNSSQEVTKDLLDMIDHTSI[p.R185Q]QTIEELAGKIEFENELNHMCGHCQDS	QTIEELAGK,IDHTSIQTI,TSIQTIEEL,MIDHTSIQTI,HTSIQTIEEL,QTIEELAGKI	UCEC
C3orf70	c.17C>T	p.S6L	MSAAA[p.S6L]LPASERGWKSEKLDEAQALARSCAAR	AAALPASER,SAAALPASER,AALPASERGW	BLCA,CESC
C4orf21	c.2398G>C	p.E800Q	SKDTEAHISEPEDLGKIRSPPPDHV[p.E800Q]QVETAREGKQYWNPRNSSELSGLVNT	VQVETAREG	CESC
C5orf30	c.10G>A	p.D4N	MEV[p.D4N]NINGESRSTLTTLPFPGAEANSPGKA	EVNINGESR	CRC

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C5orf4	c.341G>A	p.R114Q	LFFWSFNGLLLVVDTTGKPNFISRY[p.R114Q]QIQVGKNEPVDPVKLRQSIRTVLFNQ	FISRYQIQV,ISRYQIQVGK,KPNFISRYQI,YQIQVGKNEP	CRC
C5orf65	c.734A>G	p.Q245R	PRAAGAPRPRLLLRTGSLDESLGPL[p.Q245R]RAAAGFVQTALARKLSPEAPAPSSAT	SLGPLRAAA,GPLRAAAGF,RAAAGFVQTA,ESLGPLRAAA,DESLGPLRAA	ACC
C6orf170	c.2171A>C	p.K724T	RTGAINECVTFIFNRYAKKLQVSRH[p.K724T]TKFGYGVLVTRVASTAAGGIALKKSG	KLQVSRHTK,VSRHTKFGY,HTKFGYGVL,LQVSRHTKF,RHTKFGYGV,TKFGYGVLV,KLQVSRHTKF,KKLQVSRHTK,VSRHTKFGYG,HTKFGYGVLV,QVSRHTKFGY,RHTKFGYGVL,TKFGYGVLVT	CRC
C6orf89	c.172_173insC	p.P58fs	GMSEKAIEKFIRQLLEKNEPQRPPP[p.P58fs]AVSSPYSCV*	AVSSPYSCV,EPQRPPPAV,PPPAVSSPY,RPPPAVSSPY	STAD
C7	c.2059C>A	p.R687S	GMSLEGPSAFLCGSSLKWSPEMKNA[p.R687S]SCVQKENPLTQAVPKCQRWEKLQNSR	EMKNASCVQK,SPEMKNASCV	LUAD
C7orf49	c.389delG	p.G130fs	GSSSEEEDSGKQALAPGLSPSQRPG[p.G130fs]VPALPVAGALRRRRKRMC*	SQRPGVPAL,AGALRRRRK,GALRRRRKR,ALRRRRKRM,RPGVPALPV,GLSPSQRPGV,VAGALRRRRK,SPSQRPGVPA,RPGVPALPVA,VPALPVAGAL,ALRRRRKRMC,SQRPGVPALP	STAD
C7orf50	c.535delC	p.L179fs	RARELTVQKAEALMRELDEEGSDPP[p.L179fs]CRGGPSASDRCCSCSPSGFSAGRGRCPVQGCLRPHRVQLLRRWGPGSPAGQRLSKGFQLLRWWGPGSPAPEPRKGPFPPPDPPWPVTAVTVMAGSVPSAQSVDALESPGPLALEGPSSPRNLLWREMSIFLPGIF*	RLSKGFQLL,VMAGSVPSA,NLLWREMSI,CLRPHRVQL,EMSIFLPGI,LSKGFQLLR,MSIFLPGIF,RPHRVQLLR,RVQLLRRWG,RWWGPGSPA,LWREMSIFL,TVMAGSVPS,APEPRKGPF,WPVTAVTVM,GPSSPRNLL,LLWREMSIF,RRWGPGSPA,QRLSKGFQL,SKGFQLLRW,KGFQLLRWW,LESPGPLAL,REMSIFLPG,DPPWPVTAV,TVMAGSVPSA,LLWREMSIFL,FSAGRGRCPV,CLRPHRVQLL,RLSKGFQLLR,REMSIFLPGI,RGRCPVQGCL,RPHRVQLLRR,GSPAGQRLSK,CSPSGFSAGR,LALEGPSSPR,FPPPDPPWPV,TAVTVMAGSV,GPGSPAGQRL,VPSAQSVDAL,SPRNLLWREM,EMSIFLPGIF,RCCSCSPSGF,LRRWGPGSPA,RRWGPGSPAG,GQRLSKGFQL,QRLSKGFQLL,LSKGFQLLRW,FQLLRWWGPG,LRWWGPGSPA,ALESPGPLAL,LEGPSSPRNL,RNLLWREMSI,NLLWREMSIF,CPVQGCLRPH,WPVTAVTVMA,PPWPVTAVTV,GPFPPPDPPW,GPSSPRNLLW	STAD
C7orf57	c.88G>A	p.E30K	SKELQGATHRYAPCDWYYHVPVKRS[p.E30K]KKAVDAPPASQIPGLSNLGDSHSENL	HVPVKRSKK,KKAVDAPPA,YYHVPVKRSK,RSKKAVDAPP,VPVKRSKKAV	HNSC
C7orf58	c.418G>T	p.G140W	HQHILTQHGYTVVIAEERLNAGLGP[p.G140W]WLLEQGDLGSWDLLICLSSKKAEGTP	RLNAGLGPW,RLNAGLGPWL	LUAD
C7orf58	c.713G>T	p.R238L	PSVCLDQGMQLKPSTSSHLLKTVKP[p.R238L]LVWKPGDWSREQLNETTVLAPHETIF	LLKTVKPLV,KTVKPLVWK,HLLKTVKPL,LKTVKPLVW,HLLKTVKPLV,LVWKPGDWSR,SHLLKTVKPL,LLKTVKPLVW	LUAD
C7orf63	c.28G>A	p.A10T	MWTEEAGAT[p.A10T]TEAQESGIRNKSSSSSQIPVVGVVTE	EEAGATTEA,TEEAGATTEA	CRC
C9orf131	c.1024delC	p.P342fs	GYETHLETTGHKKMPQAFEPPMPPP[p.P342fs]ANPQLLCQNPEKLALKEDLLYLRTSGEPWDTERNLRPLSLQCQSLALP*	LALKEDLLY,ALKEDLLYL,SLQCQSLAL,KLALKEDLL,QLLCQNPEK,MPPPANPQL,ERNLRPLSL,YLRTSGEPW,CQNPEKLAL,FEPPMPPPA,QLLCQNPEKL,KLALKEDLLY,CQNPEKLALK,LYLRTSGEPW,ALKEDLLYLR,MPPPANPQLL,RPLSLQCQSL,LALKEDLLYL,TERNLRPLSL,LSLQCQSLAL,GEPWDTERNL	STAD
C9orf174	c.406C>T	p.R136W	ITNHREKKLQQSTKYWCLNQSAESL[p.R136W]WICAMRGGENRPPARVQSSSEELELR	ESLWICAMR,NQSAESLWI,AESLWICAM,QSAESLWICA,CLNQSAESLW,SAESLWICAM	BRCA
CABP5	c.433delC	p.R145fs	NGDGEITLVELQQAMQRLLGERLTP[p.R145fs]GRSLRLSGRLMLMETAQLTLKSL*	RLSGRLMLM,LMLMETAQL,MLMETAQLT,RLTPGRSLR,RSLRLSGRL,SLRLSGRLM,ERLTPGRSL,LRLSGRLML,LMETAQLTL,RLMLMETAQL,MLMETAQLTL,RLTPGRSLRL,LMETAQLTLK,RSLRLSGRLM,SLRLSGRLML,SGRLMLMETA,ETAQLTLKSL,GERLTPGRSL,LRLSGRLMLM	STAD
CACHD1	c.2159C>A	p.S720Y	SLMDKAFDPTRRQWYLHAVANPGLI[p.S720Y]YLTGPYLDVGGAGYVVTISHTIHSSS	AVANPGLIY,LIYLTGPYL,YLTGPYLDV,GLIYLTGPY,VANPGLIYL,AVANPGLIYL,GLIYLTGPYL,IYLTGPYLDV,HAVANPGLIY	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
CACNA1A	c.1994C>T	p.T665M	NFDEGTPPTNFDTFPAAIMTVFQIL[p.T665M]MGEDWNEVMYDGIKSQGGVQGGMVFS	LMGEDWNEV,IMTVFQILM,FQILMGEDW,MGEDWNEVM,MGEDWNEVMY,ILMGEDWNEV,LMGEDWNEVM,VFQILMGEDW,AIMTVFQILM	CRC
CACNA1A	c.2315C>A	p.S772Y	EVSPLSAANMSIAVKEQQKNQKPAK[p.S772Y]YVWEQRTSEMRKQNLLASREALYNEM	PAKYVWEQR,NQKPAKYVW,YVWEQRTSEM,QQKNQKPAKY	LUAD
CACNA1C	c.2129C>T	p.S710L	RRSTFDNFPQSLLTVFQILTGEDWN[p.S710L]LVMYDGIMAYGGPSFPGMLVCIYFII	ILTGEDWNL,LTGEDWNLV,GEDWNLVMY,NLVMYDGIM,TGEDWNLVMY,ILTGEDWNLV,LVMYDGIMAY,LTGEDWNLVM	UCEC
CACNA1D	c.3218G>T	p.R1073L	AKSNPEECRGLFILYKDGDVDSPVV[p.R1073L]LERIWQNSDFNFDNVLSAMMALFTVS	SPVVLERIW,DVDSPVVLER,LERIWQNSDF	LUAD
CACNA2D1	c.1055C>A	p.A352E	AKGITDYKKGFSFAFEQLLNYNVSR[p.A352E]ENCNKIIMLFTDGGEERAQEIFNKYN	RENCNKIIM,RENCNKIIML	LUAD
CACNA2D3	c.994G>A	p.A332T	CLNGTLVQADRTNKEHFREHLDKLF[p.A332T]TKGIGMLDIALNEAFNILSDFNHTGQ	KLFTKGIGM,REHLDKLFT,KLFTKGIGML	CRC
CACNB2	c.1823G>A	p.R608H	ASHRDHNHRDETHGSSDHRHRESRH[p.R608H]HSRDVDREQDHNECNKQRSRHKSKDR	RHRESRHHSR,RESRHHSRDV	CRC
CACNG3	c.400G>A	p.V134I	ILSVTLLFFGGLCVAASEFHRSRHN[p.V134I]IILSAGIFFVSAGLSNIIGIIVYISA	RSRHNIILS,FHRSRHNII,HRSRHNIIL,SRHNIILSA,RSRHNIILSA,EFHRSRHNII,FHRSRHNIIL,SEFHRSRHNI	CRC
CACNG3	c.413C>T	p.A138V	TLLFFGGLCVAASEFHRSRHNVILS[p.A138V]VGIFFVSAGLSNIIGIIVYISANAGD	ILSVGIFFV,VILSVGIFF,NVILSVGIF,SRHNVILSV,VILSVGIFFV,RSRHNVILSV,LSVGIFFVSA,NVILSVGIFF,RHNVILSVGI,HNVILSVGIF	CRC
CACNG3	c.694C>T	p.R232W	LRAKSHSEFLKKSTFARLPPYRYRF[p.R232W]WRRSSSRSTEPRSRDLSPISKGFHTI	RYRFWRRSS,RFWRRSSSR,PPYRYRFWR,PYRYRFWRR,YRFWRRSSS,LPPYRYRFW,RLPPYRYRFW,RYRFWRRSSS,RFWRRSSSRS,LPPYRYRFWR,PPYRYRFWRR,YRYRFWRRSS	LUAD
CACNG5	c.361G>A	p.G121R	MIRSATPFPLVSLFFMFIGFILNNI[p.G121R]RHIRPHRTILAFVSGIFFILSGLSLV	FILNNIRHI,NIRHIRPHR,ILNNIRHIR,RHIRPHRTI,GFILNNIRHI,FIGFILNNIR,FILNNIRHIR,NNIRHIRPHR,RHIRPHRTIL	CRC
CACNG8	c.437T>G	p.V146G	LRVVRASSIFPILSAILLLLGGVCV[p.V146G]GASRVYKSKRNIILGAGILFVAAGLS	LLGGVCVGA,CVGASRVYK,GASRVYKSK,VCVGASRVY,LLLGGVCVGA,VGASRVYKSK,GVCVGASRVY	BLCA
CADM1	c.569C>T	p.S190L	NCTAMASKPATTIRWFKGNTELKGK[p.S190L]LEVEEWSDMYTVTSQLMLKVHKEDDG	LEVEEWSDM,TELKGKLEV,LEVEEWSDMY	CRC
CADPS	c.2875C>A	p.R959S	DAALEVQPPDTWDSFPLFQLLNDFL[p.R959S]STDYNLCNGKFHKHLQDLFAPLVVRY	LNDFLSTDY,FLSTDYNLC,DFLSTDYNL,LLNDFLSTDY,STDYNLCNGK,FQLLNDFLST,NDFLSTDYNL	LUAD
CADPS	c.3217G>A	p.A1073T	PSWMAAIYDADNGSGTSEDLFWKLD[p.A1073T]TLQTFIRDLHWPEEEFGKHLEQRLKL	KLDTLQTFI,WKLDTLQTF,KLDTLQTFIR,FWKLDTLQTF,WKLDTLQTFI	CRC
CALB2	c.180G>C	p.K60N	YIEGKELENFFQELEKARKGSGMMS[p.K60N]NSDNFGEKMKEFMQKYDKNSDGKIEM	NSDNFGEKM,GMMSNSDNF,SNSDNFGEK,MSNSDNFGEK,SGMMSNSDNF	CESC
CALB2	c.772C>T	p.R258C	KEMNIQQLTNYRKSVMSLAEAGKLY[p.R258C]CKDLEIVLCSEPPM*	KLYCKDLEI,KLYCKDLEIV,LYCKDLEIVL	LUAD
CALCB	c.242G>C	p.R81T	DYVQMKASELKQEQETQGSSSAAQK[p.R81T]TACNTATCVTHRLAGLLSRSGGMVKS	AQKTACNTA,KTACNTATCV,AQKTACNTAT	CESC
CALD1	c.1018G>A	p.E340K	ERMREEEKRAAEERQRIKEEEKRAA[p.E340K]KERQRIKEEEKRAAEERQRIKEEEKR	AAKERQRIK,RAAKERQRI,RAAKERQRIK	CLL
CALN1	c.691G>A	p.V231I	LNETSGNCQTEFEGVHSQKQNRQTC[p.V231I]IRKSLICAFAMAFIISVMLIAANQIL	KQNRQTCIR,QNRQTCIRK,CIRKSLICA,RQTCIRKSL,IRKSLICAF,KQNRQTCIRK,SQKQNRQTCI,CIRKSLICAF,RQTCIRKSLI	GBM
CAMK2B	c.392G>T	p.G131V	EYYSEADASHCIQQILEAVLHCHQM[p.G131V]VVVHRDLKPENLLLASKCKGAAVKLA	AVLHCHQMV,VLHCHQMVV,MVVVHRDLK,AVLHCHQMVV,VLHCHQMVVV,QMVVVHRDLK,EAVLHCHQMV,HQMVVVHRDL	LUAD
CAMSAP1	c.1396_1397insA	p.T466fs	RHRSNSLTRVDGQPRGAAIAWPEKK[p.T466fs]NQACVPANTFCSTSRCEL*	VPANTFCST,QACVPANTF,KKNQACVPA,WPEKKNQACV,NQACVPANTF	BLCA

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CAMSAP1	c.1396delA	p.T466fs	RHRSNSLTRVDGQPRGAAIAWPEKK[p.T466fs]PGLRPSQHLLLYITLRVVKWIPALATASAWPAPSAKTVWHPTLLI*	LLLYITLRV,LLYITLRVV,RVVKWIPAL,GLRPSQHLL,VVKWIPALA,SAWPAPSAK,HLLLYITLR,KWIPALATA,LYITLRVVK,ASAWPAPSA,SAKTVWHPT,KTVWHPTLL,RPSQHLLLY,LATASAWPA,TVWHPTLLI,IPALATASA,WPAPSAKTV,SQHLLLYIT,VKWIPALAT,AKTVWHPTL,HLLLYITLRV,LLLYITLRVV,ALATASAWPA,GLRPSQHLLL,YITLRVVKWI,RVVKWIPALA,WIPALATASA,LLYITLRVVK,ASAWPAPSAK,LYITLRVVKW,TLRVVKWIPA,SAKTVWHPTL,KTVWHPTLLI,LRPSQHLLLY,TASAWPAPSA,KPGLRPSQHL,RPSQHLLLYI,IPALATASAW,WPAPSAKTVW,SQHLLLYITL,LRVVKWIPAL,VKWIPALATA,AKTVWHPTLL	KICH
CANT1	c.392A>G	p.K131R	RIAVIADLDTESRAQEENTWFSYLK[p.K131R]RGYLTLSDSGDKVAVEWDKDHGVLES	YLKRGYLTL,NTWFSYLKR,SYLKRGYLT,WFSYLKRGY,FSYLKRGYL,YLKRGYLTLS,SYLKRGYLTL,TWFSYLKRGY,ENTWFSYLKR	PRAD
CAPNS1	c.906_911delGCTGGT	p.LV303del	LHTSSELQSPSSYFASRPWVRAKGL[p.LV303del]LGFPVLTLHPPLPSGCS*	GLLGFPVLT,WVRAKGLLG,VRAKGLLGF,AKGLLGFPV,KGLLGFPVL,GLLGFPVLTL,RAKGLLGFPV,WVRAKGLLGF,RPWVRAKGLL,AKGLLGFPVL	TGCT
CAPRIN2	c.37G>A	p.E13K	MEVQVSQASLGF[p.E13K]KLTSVEKSLREWSRLSREVIAWLCPS	SLGFKLTSV,VSQASLGFK,GFKLTSVEK,SQASLGFKL,QVSQASLGFK,LGFKLTSVEK,KLTSVEKSLR,SQASLGFKLT,FKLTSVEKSL	CRC
CARD11	c.1268G>A	p.R423Q	IEKDKYRKQIRELEEKNDEMRIEMV[p.R423Q]QREACIVNLESKLRRLSKDSNNLDQS	EMRIEMVQR,DEMRIEMVQ,IEMVQREAC,MRIEMVQREA,IEMVQREACI,VQREACIVNL	CRC
CARD11	c.1876G>A	p.E626K	LDDDSHERYSFGPSSIHSSSSSHQS[p.E626K]KGLDAYDLEQVNLMFRKFSLERPFRP	SSSSSHQSK,HQSKGLDAY,HSSSSSHQSK,SHQSKGLDAY	DLBCL
CARD11	c.279G>C	p.E93D	SKINRAGRLLDILHTKGQRGYVVFL[p.E93D]DSLEFYYPELYKLVTGKEPTRRFSTI	FLDSLEFYY,GYVVFLDSL,VVFLDSLEF,VFLDSLEFY,FLDSLEFYYP,VVFLDSLEFY,YVVFLDSLEF,RGYVVFLDSL,VFLDSLEFYY,DSLEFYYPEL	DLBCL
CARD11	c.3195C>G	p.I1065M	ANIEAVAAKNKHCLLEAGIGCTRDL[p.I1065M]MKSNIYPIVLFIRVCEKNIKRFRKLL	LMKSNIYPI,RDLMKSNIY,MKSNIYPIV,DLMKSNIYPI,LMKSNIYPIV,GIGCTRDLMK,CTRDLMKSNI,MKSNIYPIVL	LUAD
CARM1	c.605C>T	p.A202V	LQNHTDFKDKIVLDVGCGSGILSFF[p.A202V]VAQAGARKIYAVEASTMAQHAEVLVK	ILSFFVAQA,FVAQAGARK,SFFVAQAGA,FFVAQAGAR,LSFFVAQAG,GILSFFVAQA,FVAQAGARKI,SFFVAQAGAR,VAQAGARKIY,CGSGILSFFV,LSFFVAQAGA	GBM
CASC1	c.161G>A	p.R54Q	ERRLKEEEEARLKYEKEEMERLEIQ[p.R54Q]QIEKEKWHRLEAKDLERRNEELEELY	RLEIQQIEK,MERLEIQQI	CRC
CASC3	c.1808C>T	p.P603L	MNLPHPGLHPHQTPAPLPNPGLYPP[p.P603L]LVSMSPGQPPPQQLLAPTYFSAPGVM	GLYPPLVSM,NPGLYPPLV,GLYPPLVSMS,LPNPGLYPPL	STAD
CASC3	c.1934C>T	p.P645L	TYFSAPGVMNFGNPSYPYAPGALPP[p.P645L]LPPPHLYPNTQAPSQVYGGVTYYNPA	YAPGALPPL,LPPLPPPHL,ALPPLPPPHL,PYAPGALPPL,LPPLPPPHLY	STAD
CASC3	c.1973C>T	p.S658L	PSYPYAPGALPPPPPHLYPNTQAP[p.S658L]LQVYGGVTYYNPAQQQVQPKPSPPRR	NTQAPLQVY,LYPNTQAPL,LQVYGGVTY,APLQVYGGV,HLYPNTQAPL,LQVYGGVTYY,QAPLQVYGGV,YPNTQAPLQV	STAD
CASC3	c.695C>T	p.S232F	RQRKLWKDEGRWEHDKFREDEQAPK[p.S232F]FRQELIALYGYDIRSAHNPDDIKPRR	KFRQELIAL,APKFRQELI,REDEQAPKF,FRQELIALY,KFRQELIALY,EQAPKFRQEL	STAD
CASD1	c.2341delT	p.F781fs	DLAQIIIPKDNSSLLKRLACIAAFF[p.F781fs]VDSSSYHPFKINQNIRFQKF*	DSSSYHPFK,INQNIRFQK,AFFVDSSSY,LACIAAFFV,HPFKINQNI,VDSSSYHPF,FKINQNIRF,NQNIRFQKF,FVDSSSYHPF,RLACIAAFFV,KINQNIRFQK,INQNIRFQKF,AAFFVDSSSY,HPFKINQNIR,DSSSYHPFKI	STAD
CASP14	c.13C>T	p.R5W	MSNP[p.R5W]WSLEEEKYDMSGARLALILCVTKARE	NPWSLEEEKY	CRC
CASP5	c.67delA	p.R23fs	MAAVPRVEGVFIFLIEDSGKKK[p.R23fs]GVRILKLCSKVSFRVDWITS*	RILKLCSKV,KVSFRVDWI,KLCSKVSFR,KKKGVRILK,GKKKGVRIL,KKGVRILKL,LKLCSKVSF,SKVSFRVDW,KLCSKVSFRV,GVRILKLCSK,SGKKKGVRIL,ILKLCSKVSF,KKKGVRILKL,SKVSFRVDWI	KIRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
CASP8	c.1413delA	p.R471fs	YEVSNKDDKKNMGKQMPQPTFTLRK[p.R471fs]NLSSLLIDGAILFVLFCFVFLRQNLALSPRLECSGVISAHRKLRLPGSGHSPASASRVAGTTGARHHTWLIF*	LLIDGAILF,LIDGAILFV,ILFVLFCFV,FVLFCFVFL,TLRKNLSSL,FVFLRQNLA,VLFCFVFLR,CSGVISAHR,SGVISAHRK,RVAGTTGAR,DGAILFVLF,AILFVLFCF,LFVLFCFVF,CFVFLRQNL,VFLRQNLAL,RQNLALSPR,VISAHRKLR,KLRLPGSGH,GARHHTWLI,LPGSGHSPA,LRKNLSSLL,RKNLSSLLI,ARHHTWLIF,IDGAILFVL,FTLRKNLSSL,NLSSLLIDGA,LLIDGAILFV,LIDGAILFVL,AILFVLFCFV,FVFLRQNLAL,TLRKNLSSLL,RLECSGVISA,RLPGSGHSPA,FVLFCFVFLR,CSGVISAHRK,IDGAILFVLF,GAILFVLFCF,ILFVLFCFVF,RQNLALSPRL,KLRLPGSGHS,SGHSPASASR,ASRVAGTTGA,GARHHTWLIF,RVAGTTGARH,ECSGVISAHR,GVISAHRKLR,QPTFTLRKNL,SLLIDGAILF	STAD
CAST	c.1917T>A	p.D639E	DDALDKLSDSLGQRQPDPDENKPME[p.D639E]EKVKEKAKAEHRDKLGERDDTIPPEY	MEEKVKEKA	CLL
CATSPER4	c.1274C>T	p.T425M	MIVEEVRAIRFNQEQESEVLNRRSS[p.T425M]MSGSLETTSSKDIRQMSQQQDLLSAL	SMSGSLETT,EVLNRRSSM,RRSSMSGSL,NRRSSMSGSL,SEVLNRRSSM	KIRC
CBFB	c.454G>A	p.E152K	FDEERAQQEDALAQQAFEEARRRTR[p.E152K]KFEDRDRSHREEMEVRVSQLLAVTGK	EARRRTRKF,RTRKFEDRDR,RKFEDRDRSH,EEARRRTRKF	CRC
CBLL1	c.413delA	p.E138fs	PIKIYGRMIPCKHVFCYDCAILHEK[p.E138fs]REIRCVQAVVILCSELSSVHEVLSSCVALFKGAREHICLRETYRLISTIAI*	ILCSELSSV,VLSSCVALF,CLRETYRLI,LSSCVALFK,CVALFKGAR,HICLRETYR,GAREHICLR,TYRLISTIA,ILHEKREIR,EIRCVQAVV,ELSSVHEVL,EVLSSCVAL,ETYRLISTI,REIRCVQAV,RCVQAVVIL,SELSSVHEV,HEVLSSCVA,ALFKGAREH,EHICLRETY,RETYRLIST,YRLISTIAI,REHICLRET,HEKREIRCV,VILCSELSSV,SVHEVLSSCV,ALFKGAREHI,VLSSCVALFK,TYRLISTIAI,EHICLRETYR,ETYRLISTIA,EVLSSCVALF,REIRCVQAVV,SELSSVHEVL,HEVLSSCVAL,REHICLRETY,RETYRLISTI	STAD
CBLN3	c.206delC	p.P69fs	ECLVVCEPGRAAAGGPGGAALGEAP[p.P69fs]LGEWHLLRSEATTMSQQGKPAMAPVGPSTSTRSW*	AMAPVGPST,ATTMSQQGK,QGKPAMAPV,APLGEWHLL,MSQQGKPAM,APVGPSTST,LLRSEATTM,GAALGEAPL,GEWHLLRSE,GPSTSTRSW,EAPLGEWHLL,TTMSQQGKPA,KPAMAPVGPS,TMSQQGKPAM,HLLRSEATTM,GEAPLGEWHL,GEWHLLRSEA,QQGKPAMAPV,AMAPVGPSTS	STAD
CBWD6	c.304_305insG	p.E102fs	ESGEGSALEKSLAVSQGGELYEEWL[p.E102fs]GT*	GELYEEWLGT	KICH
CC2D2A	c.3850C>T	p.R1284C	ESQEDEKLLQATEKFQAECALKFPN[p.R1284C]CQCLTTVIDISGKTVFITRYLKPLNP	LKFPNCQCL,FPNCQCLTT,ALKFPNCQCL,CQCLTTVID,FPNCQCLTTV,AECALKFPNC	CRC
CCDC108	c.3492delC	p.P1164fs	LERDPTPCELTYKVPTRHSMSQIPP[p.P1164fs]SSPL*	SQIPPSSPL,MSQIPPSSPL	STAD
CCDC111	c.1250G>T	p.R417L	GIKGGIRRWNYFFPEELLVYDICKY[p.R417L]LWCENIGRAHKSNNIMILVDLKNEVW	LVYDICKYL,VYDICKYLW,YLWCENIGR,CKYLWCENI,LLVYDICKYL,YLWCENIGRA,LVYDICKYLW	LUAD
CCDC120	c.22A>G	p.I8V	MEVKGQL[p.I8V]VSSPTFNAPAALFGEAAPQVKSERLR	LVSSPTFNA,GQLVSSPTF,MEVKGQLVS,QLVSSPTFNA,MEVKGQLVSS,KGQLVSSPTF	KIRC
CCDC121	c.1190G>T	p.W397L	IEQAQKLTATQSHLENRKQQLQQEQ[p.W397L]LYLESLIQARQRLQGSHNQCLNRQDV	QQLQQEQLY,KQQLQQEQL,QEQLYLESL,QLYLESLIQA,KQQLQQEQLY,LYLESLIQAR,RKQQLQQEQL,QQLQQEQLYL,QQEQLYLESL,QEQLYLESLI	LUSC
CCDC132	c.2512C>T	p.R838C	NIYVDALLKEFEQFNRRLNEVSKRV[p.R838C]CIPLPVSNILWEHCIRLANRTIVEGY	CIPLPVSNI,VSKRVCIPL,KRVCIPLPV,NEVSKRVCI,EVSKRVCIPL,SKRVCIPLPV	UCEC
CCDC135	c.937G>A	p.E313K	AEKAKPDALHGLRVHSWVLVLSGKR[p.E313K]KVPENFFIDPFTGHSYSTQDEHFLGI	GKRKVPENF,RKVPENFFI,WVLVLSGKRK,KRKVPENFF,GKRKVPENFF	HNSC
CCDC144A	c.3791C>T	p.S1264L	NTTSIKTQMELTIKDLESEISRIKT[p.S1264L]LQADFNKTELERYKELYLEEVKVRES	KTLQADFNK,ISRIKTLQA,RIKTLQADF,SEISRIKTL,LQADFNKTEL,RIKTLQADFN,EISRIKTLQA,SRIKTLQADF	UCEC
CCDC148	c.1260delA	p.K420fs	KEEEKEKLWKKKELLQRAEKKKKIK[p.K420fs]NTGPRKNRSGKKWK*	KIKNTGPRK,KNRSGKKWK,RKNRSGKKW	STAD

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CCDC15	c.1463C>A	p.P488H	ILPKYQDQNFLPKDQNFLSRDQHVL[p.P488H]HKDQDILPKYQDQNFLPKDQNFLSRD	LSRDQHVLH,LSRDQHVLHK	CLL
CCDC152	c.457G>C	p.E153Q	GYKKEISKLYQDMQRKVELNEEKHK[p.E153Q]QLIEKKEMEISELNAKLRSQEKEKQN	KHKQLIEKK,KQLIEKKEM,QLIEKKEMEI,HKQLIEKKEM	CESC
CCDC153	c.598_599insC	p.P200fs	QWDGAALRLHARHKEQQRQFGLTPP[p.P200fs]WIFEATSP*	LTPPWIFEA,RQFGLTPPW,QFGLTPPWI,FGLTPPWIF,RQFGLTPPWI,GLTPPWIFEA,QFGLTPPWIF,QRQFGLTPPW	STAD
CCDC153	c.599delC	p.P200fs	QQWDGAALRLHARHKEQQRQFGLTP[p.P200fs]LDL*	QRQFGLTPL,RQFGLTPLD,RQFGLTPLDL,QQRQFGLTPL	STAD
CCDC159	c.994G>T	p.A332S	KELSDIWSAVHVLQNSIDSLTLCSG[p.A332S]SCPKASSLRGHKGHQCLSPPLPSWDS	TLCSGSCPK,TLCSGSCPKA,LTLCSGSCPK,GSCPKASSLR	TGCT
CCDC168	c.15058G>T	p.D5020Y	GYTLSNSKGPVQPTAQGEEKGGLRI[p.D5020Y]YMEDKMLPKCTDLKAKQLLLSDILNT	YMEDKMLPK,GLRIYMEDK,EEKGGLRIY,LRIYMEDKM,RIYMEDKML,IYMEDKMLPK,GEEKGGLRIY,EEKGGLRIYM	UCEC
CCDC169-SOHLH2	c.485A>G	p.K162R	LDDCIFNMVLLKVPSSLSAEELEAI[p.K162R]RLIRFGKKKNTHSLFVFIIPENFKGC	AIRLIRFGK,RLIRFGKKK,ELEAIRLIR,LEAIRLIRF,EELEAIRLI,AEELEAIRL,AIRLIRFGKK,EAIRLIRFGK,EELEAIRLIR,AEELEAIRLI	STAD
CCDC19	c.620G>T	p.R207L	KLRMEQEEELKDMSKIILNAKCHAI[p.R207L]LDAQILEKQQIQKELDTEEKRLDQMM	ILDAQILEK,LNAKCHAIL,HAILDAQIL,ILNAKCHAIL,AILDAQILEK	LUAD
CCDC19	c.836G>T	p.R279L	RIRGRRQIVEQMEKNQEERSLLAEQ[p.R279L]LEQEKEQMLEYMEQLQEEDLKDMERR	LEQEKEQML,EERSLLAEQL	LUAD
CCDC36	c.626G>T	p.R209I	AQNDLVFEAVQDKGNMEQAILEMKK[p.R209I]IFEARQGEFIEMKSNLKHLEVLVAQQ	IFEARQGEF,EMKKIFEAR,AILEMKKIF,LEMKKIFEA,KIFEARQGEF,QAILEMKKIF	UCEC
CCDC53	c.172C>T	p.R58C	FVVHTVQFLNRFSTVCEEKLADLSL[p.R58C]CIQQIETTLNILDAKLSSIPGLDDVT	KLADLSLCI,ADLSLCIQQI	CESC
CCDC60	c.689G>A	p.R230H	GQKWEHFITAPKTKKFKIPTMRVTN[p.R230H]HKPSRRGSTLSLSRASGGSSPQSSMI	PTMRVTNHK,RVTNHKPSR,VTNHKPSRR,RVTNHKPSRR	CRC
CCDC79	c.1319A>C	p.N440T	IEQLEREGNEEEIQRENYQDNISSM[p.N440T]TISIQNTWKHLHADRIGRGSKAEDED	NISSMTISI,TISIQNTWK,MTISIQNTW,YQDNISSMT,YQDNISSMTI,MTISIQNTWK,SMTISIQNTW	CLL
CCDC81	c.776G>T	p.R259I	NRERKCKLKDQSDKEEGTRDISSPK[p.R259I]ILRDRQALFPAKVTNVSLLEKFERSE	ILRDRQALF,DISSPKILR,RDISSPKIL,KILRDRQAL,GTRDISSPKI,KILRDRQALF	CRC
CCDC88A	c.2031_2032insA	p.K677fs	ITCEKIEALEQENSELERENRKLKK[p.K677fs]NIG*	RENRKLKKNI	STAD
CCDC88C	c.5553_5554insC	p.P1851fs	QKLGAPEALGGRETGSHTLQSPAPP[p.P1851fs]QLP*	LQSPAPPQL,TLQSPAPPQL	CRC
CCKAR	c.811C>A	p.L271M	QKKSAKERKPSTTSSGKYEDSDGCY[p.L271M]MQKTRPPRKLELRQLSTGSSSRANRI	YMQKTRPPR,MQKTRPPRK,YEDSDGCYM,YMQKTRPPRK,MQKTRPPRKL,CYMQKTRPPR	LUAD
CCKBR	c.706G>A	p.V236M	SARVRQTWSVLLLLLLFFIPGVVMA[p.V236M]MAYGLISRELYLGLRFDGDSDSDSQS	FIPGVVMAM,VVMAMAYGL,VMAMAYGLI,AMAYGLISR,MAMAYGLIS,FIPGVVMAMA,VVMAMAYGLI,MAMAYGLISR,FFIPGVVMAM,MAYGLISREL,IPGVVMAMAY	CRC
CCNB3	c.2794G>A	p.A932T	ETLLKKPLALKMSTINEAVLFEDMI[p.A932T]TLNEKPTTGKELSFKEPLALQESPTY	VLFEDMITL	CLL
CCR5	c.554G>T	p.S185I	SLPGIIFTRSQKEGLHYTCSSHFPY[p.S185I]IQYQFWKNFQTLKIVILGLVLPLLVM	SSHFPYIQY,HFPYIQYQF,IQYQFWKNF,FPYIQYQFW,CSSHFPYIQY,YTCSSHFPYI,SHFPYIQYQF,HFPYIQYQFW,YIQYQFWKNF	KIRC
CCZ1	c.642G>C	p.E214D	IFGGISFFPLDKMTYLKIQSFINRM[p.E214D]DESLNIVKYTAFLYNDQLIWSGLEQD	FINRMDESL,RMDESLNIV,DESLNIVKY,RMDESLNIVK,SFINRMDESL,MDESLNIVKY	KIRC
CD101	c.1781G>A	p.R594Q	SDLKVPLTVTWQFQPASSHIFHQLI[p.R594Q]QITHNGTIEWGNFLSRFQKKTKVSQS	HIFHQLIQI,IQITHNGTI,SHIFHQLIQI	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
CD101	c.847G>T	p.D283Y	PDETWMFITKKQTDQTTLRIQPAVK[p.D283Y]YFQVNITADSLFAEGKPLELVCLVVS	RIQPAVKYF,KYFQVNITA,AVKYFQVNI,LRIQPAVKY,QPAVKYFQV,IQPAVKYFQV,TLRIQPAVKY,LRIQPAVKYF,VKYFQVNITA	CRC
CD109	c.1409T>A	p.L470Q	AYFLGSKSSMAVHSLFKSPSKTYIQ[p.L470Q]QKTRDENIKVGSPFELVVSGNKRLKE	KTYIQQKTR,PSKTYIQQK,QQKTRDENIK,IQQKTRDENI	CLL
CD163L1	c.2161G>A	p.V721M	SDMELRLVGGSSRCAGKVEVNVQGA[p.V721M]MGILCANGWGMNIAEVVCRQLECGSA	VEVNVQGAM,MGILCANGW,EVNVQGAMGI,KVEVNVQGAM,VQGAMGILCA,AMGILCANGW	GBM
CD180	c.683A>C	p.N228T	SLNFNGNNVKGIELGAFDSTIFQSL[p.N228T]TFGGTPNLSVIFNGLQNSTTQSLWLG	LTFGGTPNL,STIFQSLTF,SLTFGGTPNL,FQSLTFGGTP	CRC
CD1B	c.122G>T	p.W41L	GNSEHAFQGPTSFHVIQTSSFTNST[p.W41L]LAQTQGSGWLDDLQIHGWDSDSGTAI	FTNSTLAQT,SSFTNSTLA,TSSFTNSTL,LAQTQGSGW,QTSSFTNSTL,TSSFTNSTLA,TLAQTQGSGW	LUAD
CD1C	c.265C>T	p.R89C	TIIFLHNWSKGNFSNEELSDLELLF[p.R89C]CFYLFGLTREIQDHASQDYSKYPFEV	LSDLELLFC,ELLFCFYLF,LFCFYLFGL,CFYLFGLTR,SDLELLFCF,LELLFCFYL,LSDLELLFCF,LLFCFYLFGL,SDLELLFCFY,FCFYLFGLTR,LELLFCFYLF	SKCM
CD1D	c.74delT	p.L25fs	MGCLLFLLLWALLQAWGSAEVPQRL[p.L25fs]SPSAASRSRPSPIAAGRAPTAWRGWGSCRRTAGATTRTPSAL*	RLSPSAASR,ASRSRPSPI,RSRPSPIAA,AGRAPTAWR,VPQRLSPSA,SPIAAGRAP,AAGRAPTAW,AASRSRPSPI,ASRSRPSPIA,RSRPSPIAAG,AWRGWGSCRR,TAWRGWGSCR,EVPQRLSPSA,VPQRLSPSAA,RPSPIAAGRA,SPIAAGRAPT,AEVPQRLSPS,IAAGRAPTAW	GBM
CD1E	c.253T>G	p.F85V	GDLQTHGWDTVLGTIRFLKPWSHGN[p.F85V]VSKQELKNLQSLFQLYFHSFIQIVQA	KPWSHGNVS,FLKPWSHGNV,KPWSHGNVSK,HGNVSKQELK	STAD
CD209	c.847G>A	p.A283T	WEWTFFQGNCYFMSNSQRNWHDSIT[p.A283T]TCKEVGAQLVVIKSAEEQNFLQLQSS	DSITTCKEV	GBM
CD4	c.492delG	p.Q164fs	TLESPPGSSPSVQCRSPRGKNIQGG[p.Q164fs]RPSPCLSWSSRIVAPGHALSCRTRRRWSSK*	CLSWSSRIV,RIVAPGHAL,RTRRRWSSK,RGKNIQGGR,SSRIVAPGH,HALSCRTRR,LSWSSRIVA,SSRIVAPGHA,HALSCRTRRR,IQGGRPSPCL,GGRPSPCLSW,SRIVAPGHAL,SPCLSWSSRI	STAD
CD55	c.466G>A	p.E156K	PGYRREPSLSPKLTCLQNLKWSTAV[p.E156K]KFCKKKSCPNPGEIRNGQIDVPGGIL	NLKWSTAVK,STAVKFCKK,WSTAVKFCK,TAVKFCKKK,LKWSTAVKF,KWSTAVKFCK,WSTAVKFCKK,STAVKFCKKK,NLKWSTAVKF	UCEC
CD7	c.521delC	p.P174fs	ASALPAPPTGSALPDPQTASALPDP[p.P174fs]QQPLPSLRPWR*	ALPDPQQPL,DPQQPLPSL,QPLPSLRPW,SALPDPQQPL,QQPLPSLRPW	KIRC
CD79B	c.589T>C	p.Y197H	LFIIVPIFLLLDKDDSKAGMEEDHT[p.Y197H]HEGLDIDQTATYEDIVTLRTGEVKWS	EEDHTHEGL,MEEDHTHEGL,HEGLDIDQTA	DLBCL
CD79B	c.589T>G	p.Y197D	LFIIVPIFLLLDKDDSKAGMEEDHT[p.Y197D]DEGLDIDQTATYEDIVTLRTGEVKWS	MEEDHTDEGL	DLBCL
CD93	c.838delG	p.D280fs	PLCVSPKYGCNFNNGGCHQDCFEGG[p.D280fs]MAPSSAAADQDSGCWMTW*	GMAPSSAAA,HQDCFEGGM,FEGGMAPSS,FEGGMAPSSA	STAD
CDAN1	c.1936_1937insC	p.L646fs	GERKQFAVVLLSLRLLAKFLGFVAF[p.L646fs]PAIPGA*	FLGFVAFPA,FVAFPAIPG,LGFVAFPAI,FLGFVAFPAI,FVAFPAIPGA,KFLGFVAFPA	KIRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
CDC14A	c.369delC	p.N123fs	AYAVIYLKKTPEEAYRALLSGSNPP[p.N123fs]IFHSGMLPLEIALTISPFSTVCRESERDYNMDFLTLRHLMWMNMNIMSELKMVTSTGLFQENF*	NMDFLTLRH,LLSGSNPPI,GMLPLEIAL,MLPLEIALT,LTISPFSTV,HLMWMNMNI,NIMSELKMV,IMSELKMVT,STVCRESER,NMNIMSELK,IFHSGMLPL,DYNMDFLTL,KMVTSTGLF,YNMDFLTLR,EIALTISPF,MNMNIMSEL,PPIFHSGML,LPLEIALTI,LMWMNMNIM,LSGSNPPIF,LEIALTISP,RESERDYNM,SERDYNMDF,MDFLTLRHL,LRHLMWMNM,MNIMSELKM,SELKMVTST,LKMVTSTGL,RDYNMDFLT,ALLSGSNPPI,MLPLEIALTI,ALTISPFSTV,NMDFLTLRHL,FLTLRHLMWM,HLMWMNMNIM,WMNMNIMSEL,TISPFSTVCR,MNMNIMSELK,DFLTLRHLMW,RHLMWMNMNI,TLRHLMWMNM,FSTVCRESER,DYNMDFLTLR,EIALTISPFS,NPPIFHSGML,ELKMVTSTGL,LLSGSNPPIF,LEIALTISPF,LKMVTSTGLF,FHSGMLPLEI,SGMLPLEIAL,SERDYNMDFL,RDYNMDFLTL,YNMDFLTLRH,MDFLTLRHLM,NMNIMSELKM,TSTGLFQENF,LPLEIALTIS	STAD
CDC14B	c.1123C>T	p.R375C	GSVIGPQQQFLVMKQTNLWLEGDYF[p.R375C]CQKLKGQENGQHRAAFSKLLSGVDDI	LEGDYFCQKL	CRC
CDC25C	c.965delA	p.K322fs	ENLNRPRLKQVEKFKDNTIPDKVKK[p.K322fs]SIFLAKESSGRAYV*	KVKKSIFLA,IPDKVKKSI,AKESSGRAY,KESSGRAYV,FLAKESSGRA,KVKKSIFLAK,LAKESSGRAY,IFLAKESSGR,IPDKVKKSIF	STAD
CDC27	c.1379delT	p.L460fs	ITKLDSSIISEGKISTITPQIQAFN[p.L460fs]HKKQQQKV*	QIQAFNHKK,AFNHKKQQQK	UCS
CDC27	c.1665T>G	p.D555E	EVRRIENYRVEGMEIYSTTLWHLQK[p.D555E]EVALSVLSKDLTDMDKNSPEAWCAAG	TLWHLQKEV,LQKEVALSV,EVALSVLSK,WHLQKEVAL,QKEVALSVL,KEVALSVLS,HLQKEVALSV,LQKEVALSVL,TTLWHLQKEV,KEVALSVLSK	CRC
CDC27	c.1712A>T	p.N571I	STTLWHLQKDVALSVLSKDLTDMDK[p.N571I]ISPEAWCAAGNCFSLQREHDIAIKFF	MDKISPEAW,KISPEAWCAA	TGCT
CDC27	c.271delA	p.I91fs	CTTPQCKYLLAKCCVDLSKLAEGEQ[p.I91fs]SYLVECLISRKAMMILLLSLVIQLALLFHCWDMYIARQIGLPKDQNVTKRALV*	AMMILLLSL,MMILLLSLV,LLLSLVIQL,LLSLVIQLA,SLVIQLALL,ALLFHCWDM,CLISRKAMM,LISRKAMMI,LVECLISRK,IARQIGLPK,LVIQLALLF,LFHCWDMYI,MYIARQIGL,ISRKAMMIL,KLAEGEQSY,LLFHCWDMY,YLVECLISR,HCWDMYIAR,SRKAMMILL,RKAMMILLL,MILLLSLVI,LSLVIQLAL,DQNVTKRAL,AEGEQSYLV,GEQSYLVEC,VECLISRKA,WDMYIARQI,KLAEGEQSYL,CLISRKAMMI,KAMMILLLSL,AMMILLLSLV,MMILLLSLVI,ILLLSLVIQL,LLLSLVIQLA,LLSLVIQLAL,LLFHCWDMYI,YIARQIGLPK,YLVECLISRK,SLVIQLALLF,IQLALLFHCW,ISRKAMMILL,ALLFHCWDMY,SKLAEGEQSY,GEQSYLVECL,VECLISRKAM,SRKAMMILLL,LALLFHCWDM	BLCA
CDC27	c.724C>T	p.P242S	LESSNSKYSLNTDSSVSYIDSAVIS[p.P242S]SDTVPLGTGTSILSKQVQNKPKTGRS	VISSDTVPL,AVISSDTVPL,DSAVISSDTV	CESC,TGCT
CDC42BPA	c.2023C>A	p.P675T	EQSEHYSKQLENELEGLKQKQISYS[p.P675T]TGVCSIEHQQEITKLKTDLEKKSIFY	KQISYSTGV,SYSTGVCSI,KQKQISYST,KQKQISYSTG,KQISYSTGVC,ISYSTGVCSI	BRCA
CDCA7L	c.1215delC	p.P405fs	GPCLRNRYGEDVRSALLDPDWVCPP[p.P405fs]VVGSAIAATVGSVTAAVPQESSFIWPSFMVMTMLRNIWRAYKRSW*	AIAATVGSV,FIWPSFMVM,MVMTMLRNI,TMLRNIWRA,ATVGSVTAA,TVGSVTAAV,MTMLRNIWR,SSFIWPSFM,SFMVMTMLR,SFIWPSFMV,MLRNIWRAY,LRNIWRAYK,RNIWRAYKR,CPPVVGSAI,WPSFMVMTM,AAVPQESSF,ESSFIWPSF,VMTMLRNIW,QESSFIWPS,VPQESSFIW,DPDWVCPPV,VVGSAIAATV,ATVGSVTAAV,SSFIWPSFMV,FIWPSFMVMT,FMVMTMLRNI,MTMLRNIWRA,SAIAATVGSV,MLRNIWRAYK,PSFMVMTMLR,SFIWPSFMVM,IWPSFMVMTM,MVMTMLRNIW,TMLRNIWRAY,VMTMLRNIWR,WVCPPVVGSA,ESSFIWPSFM,WPSFMVMTML,TAAVPQESSF,IAATVGSVTA,QESSFIWPSF,DPDWVCPPVV,CPPVVGSAIA	CRC
CDH1	c.727G>A	p.E243K	EPLDRERIATYTLFSHAVSSNGNAV[p.E243K]KDPMEILITVTDQNDNKPEFTQEVFK	VSSNGNAVK,AVSSNGNAVK,AVKDPMEILI	BRCA

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CDH1	c.760G>T	p.D254Y	TLFSHAVSSNGNAVEDPMEILITVT[p.D254Y]YQNDNKPEFTQEVFKGSVMEGALPGT	TVTYQNDNK,MEILITVTY,YQNDNKPEF,ITVTYQNDNK,TYQNDNKPEF	STAD
CDH10	c.1045G>A	p.E349K	DTQEGIITVKKPLDYESRRLYTLKV[p.E349K]KAENTHVDPRFYYLGPFKDTTIVKIS	RLYTLKVKA,KVKAENTHV,LKVKAENTH,LKVKAENTHV	CRC
CDH10	c.1414C>T	p.R472C	LDRELSQWHNLTVIAAEINNPKETT[p.R472C]CVAVFVRILDVNDNAPQFAVFYDTFV	TTCVAVFVR,ETTCVAVFV,KETTCVAVF,ETTCVAVFVR,TTCVAVFVRI,NPKETTCVAV,KETTCVAVFV	LUAD
CDH10	c.1731C>G	p.S577R	NGFNRHEISTYLLPVVISDNDYPIQ[p.S577R]RSTGTLTIRVCACDSQGNMQSCSAEA	YPIQRSTGT,IQRSTGTLT,QRSTGTLTI,IQRSTGTLTI,YPIQRSTGTL	LUAD
CDH10	c.382C>A	p.R128S	IIDEKTGDIHATRRIDREEKAFYTL[p.R128S]SAQAINRRTLRPVEPESEFVIKIHDI	TLSAQAINR,FYTLSAQAI,EKAFYTLSA,KAFYTLSAQ,YTLSAQAINR,AFYTLSAQAI,KAFYTLSAQA,TLSAQAINRR,SAQAINRRTL,EEKAFYTLSA,REEKAFYTLS	LUAD
CDH11	c.1070A>C	p.K357T	KKPVDFETKRAYSLKVEAANVHIDP[p.K357T]TFISNGPFKDTVTVKISVEDADEPPM	TFISNGPFK,NVHIDPTFI,ANVHIDPTF,PTFISNGPF,PTFISNGPFK,EAANVHIDPT,AANVHIDPTF,DPTFISNGPF	STAD
CDH12	c.2020G>A	p.D674N	SKEDIRDNVIHYDDEGGGEEDTQAF[p.D674N]NIGALRNPKVIEENKIRRDIKPDSLC	TQAFNIGAL,QAFNIGALR,NIGALRNPK,DTQAFNIGA,EEDTQAFNI,TQAFNIGALR,DTQAFNIGAL,GEEDTQAFNI	CRC
CDH12	c.2116C>A	p.P706T	PKVIEENKIRRDIKPDSLCLPRQRP[p.P706T]TMEDNTDIRDFIHQRLQENDVDPTAP	LCLPRQRPTM,RQRPTMEDNT	HNSC
CDH18	c.2161G>T	p.A721S	KLTPRHQTSSTLESIDVQEFIKQRL[p.A721S]SEADLDPSVPPYDSLQTYAYEGQRSE	FIKQRLSEA,KQRLSEADL,SEADLDPSV	LUAD
CDH18	c.583G>A	p.A195T	EMSDMGTSVLQVTATDADDPTYGNS[p.A195T]TRVVYSILQGQPYFSVDPKTGVIRTA	STRVVYSIL,YGNSTRVVY,NSTRVVYSI,STRVVYSILQ	GBM
CDH2	c.1639G>T	p.D547Y	QDPDRYMQQNIRYTKLSDPANWLKI[p.D547Y]YPVNGQITTIAVLDRESPNVKNNIYN	KIYPVNGQI,DPANWLKIY,YPVNGQITT,YPVNGQITTI,LKIYPVNGQI	CRC
CDH20	c.1298C>A	p.P433H	IQIISAKDPDVTNNSIRYSIDRSSD[p.P433H]HGRFFYVDITTGALMTARPLDREEFS	SSDHGRFFY,RSSDHGRFF,HGRFFYVDI,RSSDHGRFFY,SSDHGRFFYV,IDRSSDHGRF	LUAD
CDH20	c.401C>T	p.A134V	IDDTTGDIHAIQRLDREERAQYTLR[p.A134V]VQALDRRTGRPMEPESEFIIKIQDIN	QYTLRVQAL,AQYTLRVQA,AQYTLRVQAL,YTLRVQALDR,RAQYTLRVQA,TLRVQALDRR	CRC
CDH23	c.1207G>A	p.V403I	EGLNSMFEVYLVGNNSHHFIISPTS[p.V403I]IQGKADIRIRVAIPLDYETVDRYDFD	HFIISPTSI,IQGKADIRI,IISPTSIQGK,HHFIISPTSI	STAD
CDH23	c.3395T>A	p.F1132Y	ASVPEDIPEGHSILQLKATDADEGE[p.F1132Y]YGRVWYRILHGNHGNNFRIHVSNGLL	ATDADEGEY,EYGRVWYRI,YGRVWYRIL,DEGEYGRVW,EYGRVWYRIL,KATDADEGEY,EGEYGRVWYR,GEYGRVWYRI,DEGEYGRVWY	KIRC
CDH23	c.531C>A	p.F177L	FIVNATDPDLGAGGSVLYSFQPPSQ[p.F177L]LFAIDSARGIVTVIRELDYETTQAYQ	FQPPSQLFA,SFQPPSQLF,QLFAIDSAR,YSFQPPSQL,SQLFAIDSA,QPPSQLFAI,FQPPSQLFAI,LYSFQPPSQL,YSFQPPSQLF,SFQPPSQLFA,SQLFAIDSAR	CRC
CDH6	c.709C>A	p.Q237K	SETGIIKTALLNMDRENREQYQVVI[p.Q237K]KAKDMGGQMGGLSGTTTVNITLTDVN	KAKDMGGQM,REQYQVVIKA,YQVVIKAKDM,IKAKDMGGQM	LUAD
CDH7	c.673C>A	p.Q225K	PYFSVEPKTGVIKTALPNMDREAKD[p.Q225K]KYLLVIQAKDMVGQNGGLSGTTSVTV	KYLLVIQAK,EAKDKYLLV,REAKDKYLL,AKDKYLLVI,NMDREAKDKY,EAKDKYLLVI,REAKDKYLLV	HNSC
CDH9	c.1569C>A	p.F523L	ENAKPGQLIQTVSVMDKDDPPRGHK[p.F523L]LFFEPVPEFTLNPNFTIVDNKDNTAG	LFFEPVPEF,KLFFEPVPEF,RGHKLFFEPV	CRC
CDHR1	c.652A>G	p.R218G	QAGATLDYERSRTHYITVVAKDGGG[p.R218G]GLHGADVVFSATTTVTVNVEDVQDMA	GLHGADVVF,GGLHGADVVF	MM

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CDK11B	c.237_239delAGA	p.E79del	SPYRREDSMEDRGEEDDSLAIKPPQ[p.E79del]MSRKEKVHHRKDEKRKEKCRHHSHSAEG	SLAIKPPQM,AIKPPQMSR,AIKPPQMSRK,LAIKPPQMSR	HNSC
CDK13	c.2638C>A	p.R880S	DFGLARLYSSEESRPYTNKVITLWY[p.R880S]SPPELLLGEERYTPAIDVWSCGCILG	TLWYSPPEL,LWYSPPELL,WYSPPELLL,ITLWYSPPEL,TLWYSPPELL,LWYSPPELLL	LUAD
CDK16	c.322C>T	p.R108C	GSDGESDQASATSSDEVQSPVRVRM[p.R108C]CNHPPRKISTEDNKRLSLPADIRLP	RMCNHPPRK,RVRMCNHPP,RVRMCNHPPR,RMCNHPPRKI	CRC
CDK5RAP2	c.4776C>G	p.H1592Q	LDEEHRRLREASGEGWKGQDPFRDL[p.H1592Q]QSLLMEIQALRLQLERSIETSSTLQS	RDLQSLLMEI,LQSLLMEIQA,DPFRDLQSLL	KIRC
CDKAL1	c.1226_1227CA>TG	p.P409L	YKFPSLFINQFYPRPGTPAAKMEQV[p.P409L]LAQVKKQRTKDLSRVFHSYSPYDHKIG	KMEQVLAQV,AAKMEQVLA,AKMEQVLAQ,MEQVLAQVK,KMEQVLAQVK,LAQVKKQRTK,QVLAQVKKQR,TPAAKMEQVL,AKMEQVLAQV	TGCT
CDKN2A	c.247C>T	p.H83Y	RVAELLLLHGAEPNCADPATLTRPV[p.H83Y]YDAAREGFLDTLVVLHRAGARLDVRD	VYDAAREGF,LTRPVYDAA,TLTRPVYDAA,LTRPVYDAAR,DPATLTRPVY	HNSC
CDKN2A	c.322G>T	p.D108Y	HDAAREGFLDTLVVLHRAGARLDVR[p.D108Y]YAWGRLPVDLAEELGHRDVARYLRAA	RYAWGRLPV,GARLDVRYA,AGARLDVRY,ARLDVRYAW,RAGARLDVRY,RLDVRYAWGR,GARLDVRYAW,VRYAWGRLPV,YAWGRLPVDL	LUSC
CDR1	c.92T>C	p.V31A	DVDFLEDVPLLEDIPLLEDVPLLED[p.V31A]APLLEDTSRLEDINLMEDMALLEDVD	PLLEDAPLL,VPLLEDAPL,APLLEDTSRL,LEDVPLLEDA,VPLLEDAPLL	KIRP
CDYL	c.179C>G	p.A60G	VSAPDGPSDPSISVSSEQSGAQQPP[p.A60G]GLQVERIVDKRKNKKGKTEYLVRWKG	AQQPPGLQV,AQQPPGLQVE	TGCT
CEACAM5	c.1918C>A	p.L640I	CHSASNPSPQYSWRINGIPQQHTQV[p.L640I]IFIAKITPNNNGTYACFVSNLATGRN	HTQVIFIAK,IPQQHTQVI,PQQHTQVIF,QQHTQVIFI,TQVIFIAKI,HTQVIFIAKI,IPQQHTQVIF,QQHTQVIFIA	CRC
CELF4	c.925G>C	p.A309P	YLNPMAAFAAAQMQQMAALNMNGLA[p.A309P]PAPMTPTSGGSTPPGITAPAVPSIPS	APAPMTPTS,LNMNGLAPA,MNGLAPAPM,ALNMNGLAPA,GLAPAPMTPT,NMNGLAPAPM	LUAD
CELSR1	c.1841delG	p.G614fs	AVDADSGENARLHYRLVDTASTFLG[p.G614fs]AAALGLRILPPPLTSPSRSTTAPVGSQCVPSWTARRWSTTASGWRRWTTARPP*	FLGAAALGL,STFLGAAAL,STTASGWRR,GLRILPPPL,PSRSTTAPV,TARRWSTTA,SGWRRWTTA,GWRRWTTAR,CVPSWTARR,DTASTFLGA,TASTFLGAA,GAAALGLRI,AAALGLRIL,VGSQCVPSW,SQCVPSWTA,RRWSTTASG,RWSTTASGW,RRWTTARPP,VPSWTARRW,ILPPPLTSPS,TFLGAAALGL,RWSTTASGWR,ASGWRRWTTA,SGWRRWTTAR,SQCVPSWTAR,DTASTFLGAA,TASTFLGAAA,TTAPVGSQCV,WTARRWSTTA,SPSRSTTAPV,ASTFLGAAAL,GAAALGLRIL,RRWSTTASGW	STAD
CELSR2	c.34_35insCGC	p.16_17insP	MRSPATGVPLPTPPPP[p.16_17insP]PLLLLLLLLLPPPLLGDQVGPCRSLGSR	LPTPPPPPL,TPPPPPLLL,LPTPPPPPLL,TPPPPPLLLL	ACC
CELSR2	c.50T>C	p.L17P	MRSPATGVPLPTPPPP[p.L17P]PLLLLLLLPPPLLGDQVGPCRSLGS	LPTPPPPPL,TPPPPPLLL,LPTPPPPPLL,TPPPPPLLLL	TGCT
CEP152	c.61G>A	p.E21K	MSLDFGSVALPVQNEDEEYD[p.E21K]KEDYEREKELQQLLTDLPHDMLDDDL	KEDYEREKEL	CRC
CEP192	c.6173C>T	p.S2058L	TEVYDLPQRPNDVQLFYGSMCKIIL[p.S2058L]LVIGEFRDCISSREFLQPSSKASLES	SMCKIILLV,ILLVIGEFR,IILLVIGEF,GSMCKIILLV,SMCKIILLVI,IILLVIGEFR,KIILLVIGEF	BLCA
CEP44	c.758C>T	p.S253L	VNVNPEITALQTMLAECQENLKKLT[p.S253L]LIEKRLDCLEQKMKGKVMVDENTWTN	QENLKKLTL,TLIEKRLDCL,NLKKLTLIEK,CQENLKKLTL,KKLTLIEKRL,QENLKKLTLI	UCEC

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CERCAM	c.254_260delCGGCTGT	p.A85fs	RARMALWCATDHNVDNTTEMLQEWL[p.A85fs]GAMTMLLWSGGLRASPGSTQMKRVPSTGPKKGTSF*	MLQEWLGAM,WLGAMTMLL,TMLLWSGGL,LLWSGGLRA,MLLWSGGLR,RVPSTGPKK,RASPGSTQM,STQMKRVPS,MTMLLWSGG,TQMKRVPST,LQEWLGAMT,QEWLGAMTM,LGAMTMLLW,MLQEWLGAMT,MTMLLWSGGL,MLLWSGGLRA,TMLLWSGGLR,RASPGSTQMK,EWLGAMTMLL,WLGAMTMLLW,MKRVPSTGPK,EMLQEWLGAM,LQEWLGAMTM,QEWLGAMTML,LRASPGSTQM,TQMKRVPSTG,TEMLQEWLGA	KIRC
CERS3	c.285G>T	p.E95D	FVASPLAKSFGIKETVRKVTPNTVL[p.E95D]DNFFKHSTRQPLQTDIYGLAKKCNLT	NTVLDNFFK,TVLDNFFKH,DNFFKHSTR,TPNTVLDNF,VTPNTVLDNF,TPNTVLDNFF	CRC
CETN3	c.189delA	p.K63fs	TDKDEAIDYHELKVAMRALGFDVKK[p.K63fs]LMY*	GFDVKKLMY,LGFDVKKLM,LGFDVKKLMY,RALGFDVKKL	STAD
CFB	c.940_941CG>AT	p.R314M	INVSVAIITFASEPKVLMSVLNDNS[p.R314M]MDMTEVISSLENANYKDHENGTGTNTY	VLNDNSMDM,NSMDMTEVI,MSVLNDNSM,LMSVLNDNSM,VLNDNSMDMT,MDMTEVISSL	SKCM
CFDP1	c.386_387insC	p.P129fs	ARKKKEDELWASFLNDVGPKSKVPP[p.P129fs]KYTS*	GPKSKVPPK,KSKVPPKYT,KSKVPPKYTS	LUAD
CFHR5	c.1322G>A	p.R441H	LCKENYLLPEAKEIVCKDGRWQSLP[p.R441H]HCVESTAYCGPPPSINNGDTTSFPLS	SLPHCVEST,RWQSLPHCV,LPHCVESTA,SLPHCVESTA,LPHCVESTAY,GRWQSLPHCV,WQSLPHCVES	CESC
CFI	c.111delA	p.K37fs	CFHLRFCKVTYTSQEDLVEKKCLAK[p.K37fs]NILTSPAIKSSASHGRDALRAPVFVNYRISAQRMALQCVQLTGEASQHTVNKRVWNVFIQGQSF*	RMALQCVQL,TVNKRVWNV,AQRMALQCV,NILTSPAIK,ASHGRDALR,RAPVFVNYR,RISAQRMAL,LRAPVFVNY,VNYRISAQR,DALRAPVFV,SPAIKSSAS,SASHGRDAL,APVFVNYRI,NVFIQGQSF,KKCLAKNIL,AKNILTSPA,KNILTSPAI,RDALRAPVF,YRISAQRMA,SQHTVNKRV,VNKRVWNVF,RMALQCVQLT,ALRAPVFVNY,FVNYRISAQR,RAPVFVNYRI,TVNKRVWNVF,LAKNILTSPA,KNILTSPAIK,AIKSSASHGR,KSSASHGRDA,HGRDALRAPV,SASHGRDALR,EASQHTVNKR,LTSPAIKSSA,LTGEASQHTV,HTVNKRVWNV,SPAIKSSASH,SSASHGRDAL,AKNILTSPAI,GRDALRAPVF,VNYRISAQRM,YRISAQRMAL,QRMALQCVQL,VQLTGEASQH,SQHTVNKRVW,WNVFIQGQSF,VEKKCLAKNI	STAD
CGB8	c.52A>G	p.T18A	MEMFQGLLLLLLLSMGG[p.T18A]AWASREMLRPRCRPINATLAVEKEGC	AWASREMLR,GGAWASREM,GAWASREML,GAWASREMLR,MGGAWASREM	BLCA
CHCHD4	c.236C>T	p.T79M	PCLGGMASGPCGEQFKSAFSCFHYS[p.T79M]MEEIKGSDCVDQFRAMQECMQKYPDL	AFSCFHYSM,SAFSCFHYSM,CFHYSMEEIK,MEEIKGSDCV	HNSC
CHD3	c.1789delC	p.P597fs	WRWGEPPVAVPAPQQADGNPDVPPP[p.P597fs]VLFKADQSESSLSSG*	NPDVPPPVL,KADQSESSL,VPPPVLFKA,DVPPPVLFKA,FKADQSESSL,NPDVPPPVLF	STAD
CHD4	c.2924G>A	p.R975H	LGPHMLRRLKADVFKNMPSKTELIV[p.R975H]HVELSPMQKKYYKYILTRNFEALNAR	HVELSPMQK,IVHVELSPM,TELIVHVEL,HVELSPMQKK,LIVHVELSPM,MPSKTELIVH,TELIVHVELS	CRC,UCEC
CHD5	c.2401G>A	p.A801T	YVVTYTGDKESRSVIRENEFSFEDN[p.A801T]TIRSGKKVFRMKKEVQIKFHVLLTSY	FSFEDNTIR,NTIRSGKKV,TIRSGKKVFR,EFSFEDNTIR,NTIRSGKKVF,NEFSFEDNTI	CRC
CHDH	c.119A>C	p.E40A	ARGALGQQQSLGARALASAGSESRD[p.E40A]AYSYVVVGAGSAGCVLAGRLTEDPAE	AGSESRDAY,SESRDAYSY,ESRDAYSYV,RDAYSYVVV,GSESRDAYSY,ESRDAYSYVV,DAYSYVVVGA,SAGSESRDAY,SESRDAYSYV	ACC
CHEK2	c.1116_1117CA>TG	p.K373E	LKPENVLLSSQEEDCLIKITDFGHS[p.K373E]EILGETSLMRTLCGTPTYLAPEVLSV	ITDFGHSEI,EILGETSLM,SEILGETSL,TDFGHSEIL,KITDFGHSEI,EILGETSLMR,SEILGETSLM	GBM
CHEK2	c.1117A>G	p.K373E	LKPENVLLSSQEEDCLIKITDFGHS[p.K373E]EILGETSLMRTLCGTPTYLAPEVLVS	ITDFGHSEI,EILGETSLM,SEILGETSL,TDFGHSEIL,KITDFGHSEI,EILGETSLMR,SEILGETSLM	KIRC,PRAD,UCS
CHIT1	c.851_852insC	p.P284fs	LILGMPTYGRSFTLASSSDTRVGAP[p.P284fs]SHRVWHSRPLHQGRRDAGLL*	RVWHSRPLH,RVGAPSHRV,HSRPLHQGR,PSHRVWHSR,HRVWHSRPL,VGAPSHRVW,HQGRRDAGL,RVWHSRPLHQ,HSRPLHQGRR,DTRVGAPSHR,RPLHQGRRDA,SHRVWHSRPL,RVGAPSHRVW,HQGRRDAGLL	KIRC
CHN1	c.792G>C	p.K264N	CGLNVHKQCSKMVPNDCKPDLKHVK[p.K264N]NVYSCDLTTLVKAHTTKRPMVVDMCI	DLKHVKNVY,VKNVYSCDL,NVYSCDLTTL,HVKNVYSCDL	LUAD

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CHN2	c.129C>G	p.I43M	AEEYQPPIWKSYLYQLQQEAPRPKR[p.I43M]MICPREVENRPKYYGREFHGIISREQ	RPKRMICPR,APRPKRMIC,QEAPRPKRM,KRMICPREV,RMICPREVE,MICPREVENR,QQEAPRPKRM	LUSC
CHRNA3	c.67_69delCTG	p.L23del	MGSGPLSLPLALSPPRLLLLLL[p.L23del]SLLPVARASEAEHRLFERLFEDYNEIIR	RLLLLLLSL,RLLLLLLSLL	BLCA
CHRNA4	c.1188C>G	p.S396R	LIESMHKMASAPRFWPEPEGEPPAT[p.S396R]RGTQSLHPPSPSFCVPLDVPAEPGPS	ATRGTQSLH,PPATRGTQSL	LUAD
CHRNA9	c.1082C>A	p.P361Q	WARVVILKYMSRVLFVYDVGESCLS[p.P361Q]QHHSRERDHLTKVYSKLPESNLKAAR	ESCLSQHHSR,CLSQHHSRER,SQHHSRERDH,GESCLSQHHS	LUAD
CIC	c.1521delC	p.R507fs	PEGNKGFGRKVFSPVIRSSFTHCRP[p.R507fs]HWTLSPQGPRILL*	TLSPQGPRI,WTLSPQGPR,SFTHCRPHW,SSFTHCRPH,RPHWTLSPQ,SPQGPRILL,FTHCRPHWTL,RSSFTHCRPH,HWTLSPQGPR,WTLSPQGPRI,SSFTHCRPHW	STAD
CIC	c.3341_3342insC	p.A1114fs	ITAFYSGSPAPTSSAPLAQPSQAPP[p.A1114fs]KPGLHCGHQHNPTCSHHSAQGPASPCHCHPSPD*	AQPSQAPPK,SQAPPKPGL,HQHNPTCSH,SHHSAQGPA,AQGPASPCH,NPTCSHHSA,LAQPSQAPPK,SQAPPKPGLH,HQHNPTCSHH	STAD
CIC	c.3341delC	p.A1114fs	VITAFYSGSPAPTSSAPLAQPSQAP[p.A1114fs]QAWSTLWPPAQPHLQPPFCPRARQPLPLPPQPRLALSPAPQQVP*	ALSPAPQQV,HLQPPFCPR,LWPPAQPHL,AWSTLWPPA,RARQPLPLP,LPLPPQPRL,LPPQPRLAL,QPRLALSPA,AQPHLQPPF,SQAPQAWST,TLWPPAQPH,QPSQAPQAW,APQAWSTLW,TLWPPAQPHL,SQAPQAWSTL,HLQPPFCPRA,RARQPLPLPP,CPRARQPLPL,AQPSQAPQAW,QAWSTLWPPA,LPLPPQPRLA,LALSPAPQQV	STAD
CIITA	c.2182G>A	p.E728K	AESELAFPSFLLQCFLGALWLALSG[p.E728K]KIKDKELPQYLALTPRKKRPYDNWLE	ALWLALSGK,LWLALSGKI,ALWLALSGKI,GALWLALSGK,LWLALSGKIK,KIKDKELPQY	UCEC
CILP2	c.1657G>A	p.V553M	VTFVDPSGEFMDAVRVLPFDPRGAG[p.V553M]MYHEVKAMRKKAPVILHTSQSNTIPL	GMYHEVKAM,MYHEVKAMR,RGAGMYHEVK,MYHEVKAMRK,GMYHEVKAMR,LPFDPRGAGM,AGMYHEVKAM	GBM
CIRH1A	c.749G>T	p.S250I	TGTLVKSHLIANADVQSIAVADQED[p.S250I]IFVVGTAEGTVFHFQLVPVTSNSSEK	AVADQEDIFV,IAVADQEDIF,QEDIFVVGTA	HNSC
CIZ1	c.2003T>C	p.V668A	SEPQHQQRLGEIQHMSQACLLSLLP[p.V668A]APRDVLETEDEEPPPRRWCNTCQLYY	SLLPAPRDV,LLSLLPAPR,CLLSLLPAPR,SLLPAPRDVL,LPAPRDVLET	CRC
CIZ1	c.266T>C	p.L89P	QLLQLQQLLQQSPPQAPLPMAVSRG[p.L89P]PPPQQPQQPLLNLQGTNSASLLNGSM	LPMAVSRGPP	GBM
CKAP2	c.2050T>A	p.*684K	GRETDAFVCRPNAALCRVYYEADTT[p.*684K]KEK*	RVYYEADTTK	CLL
CKAP5	c.1727G>C	p.G576A	AGGPPKKGKPAAPGGAGNTGTKNKK[p.G576A]ALETKEIVEPELSIEVCEEKASAVLP	KNKKALETK,KKALETKEI	TGCT
CLCN2	c.1934_1935insCCG	p.645_645R>RR	ILLGSIERSQVVALLGAQLSPARRR[p.645_645R>RR]RQHMQERRATQTSPLSDQEGPPTPEASV	QLSPARRRR,SPARRRRQH,RRRRQHMQER,SPARRRRQHM	KIRC
CLCNKA	c.371C>A	p.P124Q	YPVALVSFSSGFSQSITPSSGGSGI[p.P124Q]QELKTMLAGVILEDYLDIKNFGAKVV	SGIQELKTM,QELKTMLAG,QELKTMLAGV	LUAD
CLDN23	c.628G>A	p.V210M	CDERCRRRRKGPSAGPRRSSVSTIQ[p.V210M]MEWPEPDLAPAIKYYSDGQHRPPPAQ	RSSVSTIQM,IQMEWPEPD,MEWPEPDLA,IQMEWPEPDL,RRSSVSTIQM,SSVSTIQMEW,MEWPEPDLAP	ACC
CLDN7	c.514T>G	p.S172A	DFYNPLIPTNIKYEFGPAIFIGWAG[p.S172A]AALVILGGALLSCSCPGNESKAGYRV	AIFIGWAGA,FIGWAGAAL,GWAGAALVI,FIGWAGAALV,AIFIGWAGAA,IFIGWAGAAL,GWAGAALVIL,IGWAGAALVI	KIRP
CLEC12B	c.650G>T	p.W217L	MSQPLLMFSFFWLGLSWDSSGRSWF[p.W217L]LEDGSVPSPSLFSTKELDQINGSKGC	FLEDGSVPS,DSSGRSWFL,RSWFLEDGSV	LUAD
CLEC18A	c.1268G>A	p.R423H	GQPDNHGFGNCVELQASAAFNWNNQ[p.R423H]HCKTRNRYICQFAQEHISRWGPGS*	NQHCKTRNR,AAFNWNNQH,AFNWNNQHCK,NWNNQHCKTR,NQHCKTRNRY	CRC

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CLEC4A	c.626G>A	p.R209H	YNESSTFWHPREPSDPNERCVVLNF[p.R209H]HKSPKRWGWNDVNCLGPQRSVCEMMK	VLNFHKSPK,RCVVLNFHK,LNFHKSPKR,VVLNFHKSPK,VLNFHKSPKR,LNFHKSPKRW,NERCVVLNFH	PRAD
CLEC4C	c.536G>T	p.R179L	QWVDQTPYNENVTFWHSGEPNNLDE[p.R179L]LCAIINFRSSEEWGWNDIHCHVPQKS	NLDELCAII,ELCAIINFR,DELCAIINF,GEPNNLDEL	LUSC
CLIC6	c.892C>G	p.Q298E	EGPAGDSMDAEGPAGRARRVSGEPQ[p.Q298E]ESGDGSLSPQAEAIEVAAGESAGRSP	EPQESGDGSL	ACC
CLIP1	c.3052_3053insA	p.S1018fs	AAKKHEEEKKELERKLSDLEKKMET[p.S1018fs]KPQPVSGAESQV*	KMETKPQPV,METKPQPVS,ETKPQPVSGA,KKMETKPQPV	BLCA,KIRP
CLK4	c.203G>T	p.R68L	CKPHHQFKESDCHYLEARSLNERDY[p.R68L]LDRRYVDEYRNDYCEGYVPRHYHRDI	RSLNERDYL,LDRRYVDEY,RDYLDRRYV,YLDRRYVDEY,SLNERDYLDR,NERDYLDRRY	LUAD
CLN3	c.616G>A	p.G206S	ISWWSSGTGGAGLLGALSYLGLTQA[p.G206S]SLSPQQTLLSMLGIPALLLASYFLLL	YLGLTQASL,SLSPQQTLL,ASLSPQQTL,SYLGLTQASL,LSYLGLTQAS,ASLSPQQTLL	LUSC
CLSTN1	c.1844C>T	p.T615M	LEGEDLGELDKAMQHISYLNSRQFP[p.T615M]MPGIRRLKITSTIKCFNEATCISVPP	YLNSRQFPM,RQFPMPGIR,QFPMPGIRR,FPMPGIRRL,MPGIRRLKI,RQFPMPGIRR,SYLNSRQFPM,NSRQFPMPGI	STAD
CLSTN2	c.2276C>T	p.P759L	YSIYGVGSMSRYEQVLHHIRYRNWR[p.P759L]LASLEARRFRIKCSELNGRYTSNEFN	HIRYRNWRL,RYRNWRLAS,RLASLEARR,YRNWRLASL,LASLEARRF,RYRNWRLASL,HIRYRNWRLA,RLASLEARRF,NWRLASLEAR,LASLEARRFR,HHIRYRNWRL,RNWRLASLEA	HNSC
CLUL1	c.1387G>C	p.G463R	SELANQAPETEIIFNSIQVVPRIHE[p.G463R]RNISKQDETMMTDLSILPSSNFTLKI	RIHERNISK,QVVPRIHER,VPRIHERNI,RNISKQDETM	KIRC
CMA1	c.242T>A	p.I81K	IRRNFVLTAAHCAGRSITVTLGAHN[p.I81K]KTEEEDTWQKLEVIKQFRHPKYNTST	TVTLGAHNK,ITVTLGAHNK,KTEEEDTWQK	CLL
CMAS	c.329G>A	p.R110Q	FQSVWVSTDHDEIENVAKQFGAQVH[p.R110Q]QRSSEVSKDSSTSLDAIIEFLNYHNE	HQRSSEVSK,QFGAQVHQR,KQFGAQVHQ,AQVHQRSSEV,KQFGAQVHQR	CRC
CMIP	c.688G>A	p.A230T	EIVSKLLSENTNLTTQEHENIIVAI[p.A230T]TPLLENNHPPPDLCEFFCKHCRERPR	IIVAITPLL,NIIVAITPL,HENIIVAIT,NIIVAITPLL	CLL
CMTM8	c.77G>C	p.S26T	MEEPQRARSHTVTTTASSFAENFST[p.S26T]TSSSFAYDREFLRTLPGFLIVAEIVL	STTSSSFAY,TSSSFAYDR,FSTTSSSFA,AENFSTTSS,NFSTTSSSF,FSTTSSSFAY,TTSSSFAYDR,ENFSTTSSSF,SSFAENFSTT,AENFSTTSSS	TGCT
CNBD1	c.1187T>C	p.L396P	RSIIGFVKLRSNKVKRSQKLVYMGK[p.L396P]PKEKESFGEISVLLQVPFTCTIITKK	KLVYMGKPK,LVYMGKPKEK,MGKPKEKESF	STAD
CNGA4	c.1529A>C	p.K510T	AEIALQEATESRLRGLDQQLDDLQT[p.K510T]TFARLLAELESSALKIAYRIERLEWQ	TFARLLAEL,QLDDLQTTF,LQTTFARLL,QLDDLQTTFA,TTFARLLAEL,QQLDDLQTTF,LQTTFARLLA	STAD
CNKSR2	c.746C>T	p.P249L	SEGLGMYIKSTYDGLHVITGTTENS[p.P249L]LADRCKKIHAGDEVIQVNHQTVVGWQ	SLADRCKKI,NSLADRCKK	TGCT
CNOT3	c.58G>A	p.E20K	MADKRKLQGEIDRCLKKVS[p.E20K]KGVEQFEDIWQKLHNAANANQKEKYE	CLKKVSKGV,KVSKGVEQF,KKVSKGVEQF	PRAD
CNOT6	c.744delT	p.S248fs	QEILSCNADIVSLQEVETEQYYSFF[p.S248fs]W*	TEQYYSFFW	STAD
CNRIP1	c.304C>T	p.R102W	EPDGDRVVYTGTYDTEGVTPTKSGE[p.R102W]WQPIQITMPFTDIGTFETVWQVKFYN	EWQPIQITM,TKSGEWQPI,GEWQPIQIT,WQPIQITMPF,GEWQPIQITM	CRC
CNTFR	c.754G>T	p.D252Y	QTPSTWPDPESFPLKFFLRYRPLIL[p.D252Y]YQWQHVELSDGTAHTITDAYAGKEYI	LILYQWQHV,YRPLILYQW,LYQWQHVEL,RYRPLILYQ,LRYRPLILY,YQWQHVELS,ILYQWQHVEL,PLILYQWQHV,FLRYRPLILY,RYRPLILYQW,YQWQHVELSD	LUAD
CNTN5	c.1136C>T	p.S379F	LEIPNVQLDDAGIYECRAENSRGKN[p.S379F]FFRGQLQVYTYPHWVEKLNDTQLDSG	NSRGKNFFR,FFRGQLQVY,AENSRGKNF,GKNFFRGQL,RGKNFFRGQL,KNFFRGQLQV,NFFRGQLQVY,ENSRGKNFFR,RAENSRGKNF,AENSRGKNFF	SKCM
CNTN5	c.533C>A	p.T178N	IDGTFIISNPSEAKDSGHYQCLATN[p.T178N]NVGSILSREATLQFAYLGNFSGRTRS	YQCLATNNV,LATNNVGSI,CLATNNVGSI,HYQCLATNNV,YQCLATNNVG,LATNNVGSIL	LUSC

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CNTN6	c.2420G>T	p.R807M	NNEGEGSLSTVTIVYSGEDEPQLAP[p.R807M]MGTSLQSFSASEMEVSWNAIAWNRNT	QLAPMGTSL,PMGTSLQSF,APMGTSLQSF,GEDEPQLAPM,PQLAPMGTSL	LUAD
CNTNAP1	c.3086G>T	p.S1029I	EPGTWMRYNLQSALRSAAREFSHML[p.S1029I]IRPVPGYEPGYIPGYDTPGYVPGYHG	FSHMLIRPV,MLIRPVPGY,REFSHMLIR,AAREFSHMLI,HMLIRPVPGY,EFSHMLIRPV,REFSHMLIRP	PRAD
CNTNAP2	c.1185C>A	p.F395L	EPYTVPVFFNATSYLEVPGRLNQDL[p.F395L]LSVSFQFRTWNPNGLLVFSHFADNLG	RLNQDLLSV,LLSVSFQFR,DLLSVSFQF,NQDLLSVSF,LLSVSFQFRT,DLLSVSFQFR,LNQDLLSVSF,QDLLSVSFQF	LUAD
CNTNAP4	c.1307A>C	p.Y436S	LFSELQLISGGILLFLSDGKLKSNL[p.Y436S]SQPGKLPSDITAGVELNDGQWHSVSL	KSNLSQPGK,KLKSNLSQPG,KSNLSQPGKL	KIRC
CNTNAP4	c.34A>T	p.I12F	MLLFYLLVVLS[p.I12F]FDSTKASALTNPNVALFLLADDCDDP	VLSFDSTKA,VVLSFDSTK,FYLLVVLSF,FDSTKASAL,LVVLSFDSTK,LFYLLVVLSF,LSFDSTKASA	CLL
CNTRL	c.553C>T	p.P185S	SKIEGIENMCNLQKLNLAGNEIEHI[p.P185S]SVWLGKKLKSLRVLNLKGNKISSLQD	HISVWLGKK,SVWLGKKLK,EIEHISVWL,NEIEHISVW,ISVWLGKKL,ISVWLGKKLK,NEIEHISVWL	CESC
CNTROB	c.2759_2760insG	p.R920fs	PKTEKPPARKKSGHPAPSSMRSRGG[p.R920fs]SLEMSPPTLSPLCSLIVVILINAH*	TLSPLCSLI,SMRSRGGSL,MSPPTLSPL,RSRGGSLEM,SPLCSLIVV,SLEMSPPTL,LEMSPPTLS,TLSPLCSLIV,SLIVVILINA,EMSPPTLSPL,SSMRSRGGSL,SMRSRGGSLE,RSRGGSLEMS,SPLCSLIVVI,MRSRGGSLEM,GSLEMSPPTL,LEMSPPTLSP	STAD
COBLL1	c.2196A>C	p.K732N	DPLTVKDPICAHGNDDLLPPVDRID[p.K732N]NNSTASYLKNYPLYRQDYNPKPKPSN	IDNNSTASY,RIDNNSTASY,IDNNSTASYL	CRC
COG5	c.1850A>G	p.H617R	TKVVSSQSSFPLAAEQTIISALKAI[p.H617R]RALMENAVQPLLTSVGDAIEAIIITM	ALKAIRALM,AIRALMENA,IISALKAIR,SALKAIRAL,AIRALMENAV,SALKAIRALM,TIISALKAIR,ISALKAIRAL	TGCT
COL14A1	c.3245G>T	p.R1082I	STVGALNKIGTDGTQVAMVQFTDDP[p.R1082I]ITEFKLNAYKTKETLLDAIKHISYKG	FTDDPITEF,ITEFKLNAY,MVQFTDDPI,VQFTDDPIT,FTDDPITEFK,AMVQFTDDPI,ITEFKLNAYK,QFTDDPITEF	CRC
COL15A1	c.2123A>G	p.K708R	ARGPNGSVGEKGDPGNRGLPGPPGK[p.K708R]RGQAGPPGVMGPPGPPGPPGPPGPGC	RGQAGPPGVM	TGCT
COL18A1	c.2652delC	p.G884fs	DRGSRGEKGDPGKDGVGQPGLPGPP[p.G884fs]DPRDLWSTCRSRTDPS*	DLWSTCRSR	KIRP
COL19A1	c.1613C>A	p.P538Q	GPPGLIGSPGLKGQQGSAGSMGPRG[p.P538Q]QPGDVGLPGEHGIPGKQGIKGEKGDP	GPRGQPGDV	LUAD
COL4A6	c.1648C>A	p.L550I	GPAGAPGLVGPLGPSGPKGKKGEPI[p.L550I]ISTIQGMPGDRGDSGSQGFRGVIGEP	KGKKGEPII,KKGEPIISTI,EPIISTIQGM	CRC
COL5A2	c.1546G>T	p.G516W	QGPIGPPGEEGKRGPRGDPGTVGPP[p.G516W]WPVGERGAPGNRGFPGSDGLPGPKGA	GTVGPPWPV,DPGTVGPPW	LUAD
COL5A2	c.1834G>T	p.G612W	LGPLGAPGEDGRPGPPGSIGIRGQP[p.G612W]WSMGLPGPKGSSGDPGKPGEAGNAGV	WSMGLPGPK,SIGIRGQPW,RGQPWSMGL,QPWSMGLPG,GSIGIRGQPW,IGIRGQPWSM	LUAD
COL6A3	c.7133C>A	p.A2378D	GQKGDPGYPGPAGPKGNRGDSIDQC[p.A2378D]DLIQSIKDKCPCCYGPLECPVFPTEL	DSIDQCDLI	TGCT
COL6A3	c.8374G>A	p.D2792N	YFFVVLGIGRKVNIKEVYTFASEPN[p.D2792N]NVFFKLVDKSTELNEEPLMRFGRLLP	NVFFKLVDK,FASEPNNVF,ASEPNNVFF,EPNNVFFKL,YTFASEPNNV,ASEPNNVFFK,TFASEPNNVF,FASEPNNVFF,EPNNVFFKLV,SEPNNVFFKL	CRC
COL6A5	c.6671C>T	p.T2224M	QEDFLGGNGFIGQELNSGRESPFVK[p.T2224M]MEDNGSDYLVYLPSQMFEPQKLMINY	KMEDNGSDY,MEDNGSDYL,KMEDNGSDYL,SGRESPFVKM,VKMEDNGSDY,MEDNGSDYLV	GBM
COL9A1	c.632C>A	p.P211Q	GVERSSATLFVDCNRIESLPIKPRG[p.P211Q]QIDIDGFAVLGKLADNPQVSVPFELQ	QIDIDGFAV,GQIDIDGFA,LPIKPRGQI,GQIDIDGFAV	LUAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
COL9A1	c.848delC	p.P283fs	RITPSQTTDERGPPGEQGPPGPPGP[p.P283fs]LEFQASMASTVTEVLRAPRAPRVLQVNRESQELQASLAHLALMD*	FQASMASTV,SMASTVTEV,ELQASLAHL,LQASLAHLA,VLRAPRAPR,ASLAHLALM,VTEVLRAPR,MASTVTEVL,ESQELQASL,GPLEFQASM,LEFQASMAS,RESQELQAS,QELQASLAH,QASLAHLAL,TEVLRAPRA,ASMASTVTEV,SMASTVTEVL,LQASLAHLAL,FQASMASTVT,VLRAPRAPRV,ELQASLAHLA,MASTVTEVLR,TVTEVLRAPR,EVLRAPRAPR,ESQELQASLA,APRAPRVLQV,LEFQASMAST,LRAPRAPRVL,LQVNRESQEL,RESQELQASL,SQELQASLAH,QELQASLAHL,QASLAHLALM	STAD
COPB1	c.1273C>T	p.R425C	NVIPVLMEFLSDNNEAAAADVLEFV[p.R425C]CEAIQRFDNLRMLIVEKMLEVFHAIK	EFVCEAIQR,DVLEFVCEA,FVCEAIQRF,EFVCEAIQRF,DVLEFVCEAI,CEAIQRFDNL	CRC
COQ2	c.196G>T	p.V66L	SFALARAAGAPHGGDLQPPACPEPR[p.V66L]WRQLSLSAAAVVDSAPRPLQPYLRLM	RWRQLSLSA,CPEPRWRQL,EPRWRQLSL,WRQLSLSAA,RWRQLSLSAA,WRQLSLSAAA,QPPACPEPRW	ACC
CORO2A	c.1576T>A	p.*526R	LTQREVQAKQLELEIKNLRMGSEQL[p.*526R]RAETSALLTLRDTTRLHGEV*	QLRAETSAL,TLRDTTRLH,ETSALLTLR,LLTLRDTTR,DTTRLHGEV,LRAETSALL,AETSALLTL,SEQLRAETS,QLRAETSALL,LLTLRDTTRL,NLRMGSEQLR,SEQLRAETSA,EQLRAETSAL,RAETSALLTL	CRC
COX15	c.256C>A	p.L86I	PSKAAERVVGRWLLVCSGTVAGAVI[p.L86I]IGGVTRLTESGLSMVDWHLIKEMKPP	VIIGGVTRL	CRC
COX6A1	c.23C>T	p.S8L	MAVVGVS[p.S8L]LVSRLLGRSRPQLGRPMSSGAHGEEG	MAVVGVSLV,SLVSRLLGR,AVVGVSLVSR,VSLVSRLLGR,LVSRLLGRSR	BLCA
CPAMD8	c.2352delC	p.P784fs	TDEAVPAFQPHTGSLVAVAPSRHPP[p.P784fs]EQRREKGLSSPKHGFGIVSTSVTHLVRGHSV*	IVSTSVTHL,STSVTHLVR,REKGLSSPK,VSTSVTHLV,SPKHGFGIV,GLSSPKHGF,IVSTSVTHLV,GIVSTSVTHL,VSTSVTHLVR,VTHLVRGHSV,HGFGIVSTSV,KGLSSPKHGF,FGIVSTSVTH	STAD
CPE	c.869C>A	p.P290Q	SAHEYSSSPDDAIFQSLARAYSSFN[p.P290Q]QAMSDPNRPPCRKNDDDSSFVDGTTN	RAYSSFNQA,AYSSFNQAM,RAYSSFNQAM	LUAD
CPNE8	c.381G>T	p.Q127H	SKSPNLSKHDFLGQVFCTLGEIVGS[p.Q127H]HGSRLEKPIVGIPGKKCGTIILTAEE	GSHGSRLEK,EIVGSHGSR,GEIVGSHGS,VGSHGSRLEK,EIVGSHGSRL	LUAD
CPS1	c.2564C>A	p.T855K	TPRLPMNKEWPSNLDLRKELSEPSS[p.T855K]KRIYAIAKAIDDNMSLDEIEKLTYID	SSKRIYAIA,SKRIYAIAK,ELSEPSSKR,SEPSSKRIY,LSEPSSKRIY,SSKRIYAIAK,EPSSKRIYAI,KRIYAIAKAI	LUSC
CPSF4	c.656C>A	p.P219Q	NPPLQRSSSLIQLTSQNSSPNQQRT[p.P219Q]QQVIGVMQSQNSSAGNRGPRPLEQVT	RTQQVIGVM,NQQRTQQVI,SPNQQRTQQV,QQRTQQVIGV,QRTQQVIGVM	LUAD
CR1L	c.237delA	p.L79fs	PIGTYLNYECRPGYSGRPFSIICLK[p.L79fs]TQSGQVLRTSANVNHVVILQIL*	CLKTQSGQV,QVLRTSANV,RTSANVNHV,KTQSGQVLR,TSANVNHVV,LKTQSGQVL,SANVNHVVI,ANVNHVVIL,GQVLRTSANV,RTSANVNHVV,TSANVNHVVI,NVNHVVILQI,CLKTQSGQVL,SANVNHVVIL	STAD
CR2	c.618delC	p.V206fs	ESGYLLVGEKIINCLSSGKWSAVPP[p.V206fs]HVKRHAVNL*	WSAVPPHVK,KWSAVPPHV,HVKRHAVNL,SAVPPHVKR,PPHVKRHAV,GKWSAVPPH,SGKWSAVPPH,KWSAVPPHVK,WSAVPPHVKR,VPPHVKRHAV,GKWSAVPPHV	STAD
CRB1	c.1883delT	p.L628fs	SICAFQNSFLGGLPVGMTSNGVALL[p.L628fs]TSIICHPHLRL*	SIICHPHLR,SIICHPHLRL,TSIICHPHLR,MTSNGVALLT,LTSIICHPHL	HNSC
CRB1	c.1888T>G	p.F630V	ICAFQNSFLGGLPVGMTSNGVALLN[p.F630V]VYNMPSTPSFVGCLQDIKIDWNHITL	NGVALLNVY,VALLNVYNM,LLNVYNMPST,VYNMPSTPSF,SNGVALLNVY,TSNGVALLNV	STAD
CRB2	c.3329C>T	p.T1110M	GWEGPRCEAHVDPCHSAPCARGRCH[p.T1110M]MHPDGRFECRCPPGFGGPRCRLPVPS	RGRCHMHPD,CHMHPDGRF,RGRCHMHPDG,APCARGRCHM,RCHMHPDGRF,HMHPDGRFEC	ACC
CREBBP	c.4303G>C	p.D1435H	FGMHVQEYGSDCPPPNTRRVYISYL[p.D1435H]HSIHFFRPRCLRTAVYHEILIGYLEY	YLHSIHFFR,HSIHFFRPR,VYISYLHSI,ISYLHSIHF,SYLHSIHFF,RVYISYLHS,YISYLHSIH,RVYISYLHSI,SYLHSIHFFR,YISYLHSIHF,ISYLHSIHFF	BLCA
CREBBP	c.4337G>A	p.R1446H	CPPPNTRRVYISYLDSIHFFRPRCL[p.R1446H]HTAVYHEILIGYLEYVKKLGYVTGHI	HFFRPRCLH,HTAVYHEIL,RPRCLHTAV,FFRPRCLHT,CLHTAVYHEI,FFRPRCLHTA,RPRCLHTAVY,HTAVYHEILI	DLBCL

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CREBBP	c.6281C>T	p.P2094L	DLLRTLKSPSSPQQQQQVLNILKSN[p.P2094L]LQLMAAFIKQRTAKYVANQPGMQPQP	VLNILKSNL,ILKSNLQLM,NLQLMAAFI,LQLMAAFIK,KSNLQLMAA,SNLQLMAAF,LKSNLQLMA,ILKSNLQLMA,NLQLMAAFIK,KSNLQLMAAF,LKSNLQLMAA	UCEC
CRIPAK	c.142_143insCG	p.M48fs	PACSCAHVECPPAHTCRCGVPACSH[p.M48fs]TCPCGVPACSHVPMWSARLLTHVSMWSAHLLMCPCGVPTCSHVPMWSATCSHTCPCGVPACSRAHVECPPAHTCRCGVPACSHVPMRSARLLTRAHAECPPAHTCPCGVPACSHVPTWSARLLTRAHVECPPAHTCQRGVPA*	SMWSAHLLM,HLLMCPCGV,WSARLLTHV,HVSMWSAHL,RLLTHVSMW,LTHVSMWSA,HTCQRGVPA,MWSARLLTH,TWSARLLTR,VPTCSHVPM,VPACSRAHV,VPTWSARLL,ARLLTHVSM,THVSMWSAH,VSMWSAHLL,LMCPCGVPT,SHVPMWSAT,LLTHVSMWSA,SMWSAHLLMC,LLMCPCGVPT,HVSMWSAHLL,GVPACSRAHV,SARLLTHVSM,PTWSARLLTR,HVPTWSARLL,ARLLTHVSMW,LTHVSMWSAH,THVSMWSAHL,VSMWSAHLLM,VPTCSHVPMW,VPMWSATCSH	BLCA
CRIPAK	c.427T>C	p.C143R	SHVPMRSARLLTRAHAECPPAHTCP[p.C143R]RGVPACSHVPMRSARLLTRADVECPP	HTCPRGVPA,CPPAHTCPR,RGVPACSHV	ACC
CRIPAK	c.520T>C	p.C174R	SHVPMRSARLLTRADVECPPAHTCP[p.C174R]RGVPACSHVPTWSARLITRAHVECSP	HTCPRGVPA,CPPAHTCPR,RGVPACSHV	ACC
CRIPAK	c.538_568delTCACACGTGCCAACGTGGAGTGCCCGCCTGA	p.S180fs	LTRADVECPPAHTCPCGVPACSHVP[p.S180fs]MWSARLLTRADVECLPAHTCPCGVFACSHVPMRSARLLTRADAECPPAHTCPCGVPACSRADVECPPAHTCPCGVPACSRADVGCPPAHMCRCGVPACSHVPMWSARLLTRADVECPPAHVPIWSARLLTRAIVECPPAHTHADVECPPAHTCPCGVPACSHVPMWSARLLTHVPMWSARLLTRAHVECLPAHTRAHVECPPAHTKPWHGGSVGFLSCRPSQTLLPYILLMVAF*	FLSCRPSQT,TLLPYILLM,LLPYILLMV,CLPAHTCPC,HMCRCGVPA,WSARLLTHV,GSVGFLSCR,VFACSHVPM,RLLTHVPMW,PWHGGSVGF,PYILLMVAF,HTCPCGVFA,SARLLTRAI,LTRAHVECL,RAHVECLPA,MWSARLLTH,RPSQTLLPY,FACSHVPMR,IWSARLLTR,DVECPPAHV,HVPIWSARL,QTLLPYILL,VPACSRADV,VPIWSARLL,LPAHTRAHV,AHTCPCGVF,RAIVECPPA,ARLLTHVPM,AHVECLPAH,LSCRPSQTL,SQTLLPYIL,LPYILLMVA,CPPAHVPIW,CPPAHTKPW,LLTRAHVECL,CLPAHTRAHV,FLSCRPSQTL,TLLPYILLMV,LLPYILLMVA,LLTRADVECL,HVECPPAHTK,GVFACSHVPM,SARLLTRADA,SARLLTRAIV,SARLLTHVPM,HTKPWHGGSV,VFACSHVPMR,PAHVPIWSAR,PIWSARLLTR,HVECLPAHTR,HVPIWSARLL,WSARLLTRAI,KPWHGGSVGF,RPSQTLLPYI,LPYILLMVAF,SRADVGCPPA,ADVGCPPAHM,AHMCRCGVPA,VECPPAHVPI,AHVPIWSARL,RAIVECPPAH,ARLLTHVPMW,RAHVECLPAH,LSCRPSQTLL,CRPSQTLLPY,SQTLLPYILL,VECLPAHTRA,VECPPAHTHA,LPAHTCPCGV,CPPAHTHADV	LUAD
CRIPAK	c.568A>C	p.I190L	ECPPAHTCPCGVPACSHVPTWSARL[p.I190L]LTRAHVECSPAHTCRCGVPACSHVPM	TWSARLLTR,VPTWSARLL,PTWSARLLTR,HVPTWSARLL	ACC
CRISPLD1	c.664C>T	p.R222W	PKAVYLVCNYSPKGNWWGHAPYKHG[p.R222W]WPCSACPPSFGGGCRENLCYKEGSDR	APYKHGWPC,YKHGWPCSA,WPCSACPPS,WPCSACPPSF,YKHGWPCSAC	BRCA
CROCC	c.1063G>C	p.A355P	RTSRAVQEAGLGLSTGLRLAESRAE[p.A355P]PALEKQALLQAQLEEQLRDKVLREKD	EPALEKQAL,AESRAEPAL,RLAESRAEPA,ESRAEPALEK,AEPALEKQAL	KIRP
CROT	c.1740G>T	p.Q580H	DPLFSKSGGGGNFVLSTSLVGYLRV[p.Q580H]HGVVVPMVHNGYGFFYHIRDDRFVVA	YLRVHGVVV,GYLRVHGVV,RVHGVVVPM,RVHGVVVPMV,LVGYLRVHGV,GYLRVHGVVV,LRVHGVVVPM	LUAD
CROT	c.96delA	p.L32fs	TEERTFQYQDSLPSLPVPSLEESLK[p.L32fs]NTLNQSPEHATR*	LEESLKNTL	STAD
CRTC3	c.1088C>T	p.S363L	NKTVLSSSLNNHPQTSVPNASALHP[p.S363L]LLRLFSLSNPSLSTTNLSGPSRRRQP	ASALHPLLR,ALHPLLRLF,NASALHPLL,HPLLRLFSL,SALHPLLRLF,NASALHPLLR,VPNASALHPL	LUAD
CRYGB	c.427A>G	p.R143G	HLTEIHSLNVLEGSWILYEMPNYRG[p.R143G]GQYLLRPGEYRRFLDWGAPNAKVGSL	NYRGGQYLL,MPNYRGGQY,YEMPNYRGG,EMPNYRGGQY,GQYLLRPGEY,NYRGGQYLLR,MPNYRGGQYL	TGCT
CRYGD	c.476delG	p.G159fs	YEMPNYRGRQYLLRPGDYRRYHDWG[p.G159fs]VQMPKSAL*	RYHDWGVQM,GVQMPKSAL,RRYHDWGVQM,WGVQMPKSAL	STAD
CRYM	c.943T>A	p.*315K	FKSLGMAVEDTVAAKLIYDSWSSGK[p.*315K]KNKGT*	SWSSGKKNK	CLL

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
CSDE1	c.658C>T	p.R220C	NVQLETGDKINFVIDNNKHTGAVSA[p.R220C]CNIMLLKKKQARCQGVVCAMKEAFGF	SACNIMLLK,GAVSACNIM,AVSACNIMLL,VSACNIMLLK,SACNIMLLKK,HTGAVSACNI	UCEC
CSF2RB	c.892G>A	p.G298S	SFGLFYKPSPDAGEEECSPVLREGL[p.G298S]SSLHTRHHCQIPVPDPATHGQYIVSV	VLREGLSSL,EGLSSLHTR,REGLSSLHT	GBM
CSF3R	c.1404delC	p.P468fs	SLWVGWEPPNPWPQGYVIEWGLGPP[p.P468fs]ARAIATRPGGWNRMGEPRGFC*	ATRPGGWNR,RAIATRPGG,EWGLGPPAR,IEWGLGPPA,ATRPGGWNRM,IATRPGGWNR,RAIATRPGGW,IEWGLGPPAR	STAD
CSGALNACT2	c.1086G>T	p.L362F	VSLNEEFNRGRGLNVGARAWDKGEV[p.L362F]FMFFCDVDIYFSAEFLNSCRLNAEPG	FMFFCDVDI,EVFMFFCDV,RAWDKGEVF,GEVFMFFCD,AWDKGEVFMF,VFMFFCDVDI,RAWDKGEVFM,FMFFCDVDIY,ARAWDKGEVF,GEVFMFFCDV	ACC,KIRP,TGCT
CSHL1	c.350G>A	p.R117Q	SSNMEETQQKSNLELLHISLLLIES[p.R117Q]QLEPVRFLRSTFTNNLVYDTSDSDDY	SLLLIESQL,LIESQLEPV,SQLEPVRFL,QLEPVRFLR,LLIESQLEPV,SQLEPVRFLR,ISLLLIESQL,IESQLEPVRF	CESC
CSMD2	c.5564C>A	p.P1855Q	PTCVVPCGGNLTERRGTILSPGFPE[p.P1855Q]QYLNSLNCVWKIVVPEGAGIQIQVVS	QYLNSLNCV,FPEQYLNSL,GFPEQYLNSL,QYLNSLNCVW,ILSPGFPEQY,EQYLNSLNCV	LUAD
CSMD3	c.2071C>A	p.Q691K	DPGTPLYGIREGDGFSNRDVLRFEC[p.Q691K]KFGFELIGEKSIVCQENNQWSANIPI	LRFECKFGF,FECKFGFEL,RFECKFGFEL,VLRFECKFGF,RDVLRFECKF,FECKFGFELI	LUSC
CSMD3	c.2854C>T	p.H952Y	AEPGHSIKITFERFQTELNYDVLEV[p.H952Y]YDGPNLLSPLLGSYNGTQVPQFLFSS	LNYDVLEVY,EVYDGPNLL,LEVYDGPNL,ELNYDVLEVY,EVYDGPNLLS,LEVYDGPNLL,YDGPNLLSPL	CESC
CSMD3	c.3281C>A	p.T1094K	GDVRGPSGTILSPGYPEFYPNSLNC[p.T1094K]KWTVDVTHGKGVQFNFHTFHLEDHHD	NSLNCKWTV,YPNSLNCKW,SLNCKWTVDV,FYPNSLNCKW,KWTVDVTHGK,EFYPNSLNCK	LUSC
CSMD3	c.511G>A	p.E171K	STKSVFSLRLTSDFAVSAHGFKVYY[p.E171K]KELQSSSCGNPGVPPKGVLYGTRFDV	AHGFKVYYK,SAHGFKVYYK,HGFKVYYKEL	GBM
CSMD3	c.522G>T	p.Q174H	SVFSLRLTSDFAVSAHGFKVYYEEL[p.Q174H]HSSSCGNPGVPPKGVLYGTRFDVGDK	YEELHSSSC,HSSSCGNPGV	LUAD
CSMD3	c.7149_7150insT	p.F2383fs	LESVYSTSNQILIKFHSDFTTSGFF[p.F2383fs]CAQLSRLSTKGVPTSTTCAQC*	FTTSGFFCA,AQLSRLSTK,GFFCAQLSR,LSRLSTKGV,QLSRLSTKGV,SGFFCAQLSR,CAQLSRLSTK,TTSGFFCAQL,AQLSRLSTKG	LIHC
CSMD3	c.8179C>A	p.P2727T	LEHGRWRIVNGSHYEYKTKVVFSCD[p.P2727T]TGYHGLGPASIECLPNGTWSWRNERP	VVFSCDTGY,VVFSCDTGYH,KTKVVFSCDT,KVVFSCDTGY,FSCDTGYHGL,DTGYHGLGPA	LUAD
CSMD3	c.8429C>A	p.T2810N	CDLGFMLVGSAVRECLSSGLWSESE[p.T2810N]NRCLAGHCGIPELIVNGQVIGENYGY	SESENRCLA,SENRCLAGH	LUAD
CSPG5	c.355G>A	p.D119N	AVTGTAWLEADSPGLGGVTAEAGSG[p.D119N]NAQALPATLQAPHEVLGQSIMPPAIP	VTAEAGSGNA,AEAGSGNAQA	BLCA
CT47B1	c.702_728delGAAGCTCACAGAGGAGGCCACAGAGGA	p.234_243EKLTEEATEE>E	DLAEMAREPAEEAADEKPPEEAAEE[p.234_243EKLTEEATEE>E]PAAEEPTSEEAVAPEEVTKSQPEKWDEEAQDAAGEEEKEQEKEKDVENKVKN	EEAAEEPAA,AEEPAAEEPT	BRCA
CTAGE15P	c.1091C>T	p.A364V	IIQLSEVDKTKEELTEHIKNLQTQQ[p.A364V]VSLQSENIYFESENQKLQQKLKIMTE	VSLQSENIY,NLQTQQVSL,HIKNLQTQQV,QVSLQSENIY,KNLQTQQVSL,QQVSLQSENI,VSLQSENIYF	KIRP
CTCF	c.604_605insAA	p.K202fs	EQGELPPQEDPSWQKDPDYQPPAKK[p.K202fs]KQRKPKRANCVIQRRAKM*	RANCVIQRR,KPKRANCVI,KQRKPKRANC,RANCVIQRRA	STAD
CTCF	c.604delA	p.K202fs	EQGELPPQEDPSWQKDPDYQPPAKK[p.K202fs]QRKPKRANCVIQRRAKM*	RANCVIQRR,KPKRANCVI,KQRKPKRANC,RANCVIQRRA	STAD
CTCFL	c.1267G>A	p.E423K	YECHICHTRFTQSGTMKIHILQKHG[p.E423K]KNVPKYQCPHCATIIARKSDLRVHMR	ILQKHGKNV,KHGKNVPKY,KIHILQKHGK,LQKHGKNVPK,QKHGKNVPKY	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
CTDNEP1	c.376G>A	p.E126K	KHPVRFFVHKRPHVDFFLEVVSQWY[p.E126K]KLVVFTASMEIYGSAVADKLDNSRSI	KLVVFTASM,VVSQWYKLV,SQWYKLVVF,WYKLVVFTA,EVVSQWYKL,YKLVVFTAS,FLEVVSQWYK,VSQWYKLVVF,EVVSQWYKLV,YKLVVFTASM,LEVVSQWYKL,SQWYKLVVFT	CRC
CTNNA3	c.2567_2568insAA	p.K856fs	IIRIQSPAGPRHPVVMWRMKAPAKK[p.K856fs]NP*	RMKAPAKKNP	STAD
CTNNB1	c.1004A>T	p.K335I	ESKLIILASGGPQALVNIMRTYTYE[p.K335I]ILLWTTSRVLKVLSVCSSNKPAIVEA	IMRTYTYEI,YTYEILLWT,ILLWTTSRV,TYTYEILLW,TYEILLWTT,RTYTYEILL,EILLWTTSR,MRTYTYEIL,YEILLWTTS,NIMRTYTYEI,YTYEILLWTT,ILLWTTSRVL,IMRTYTYEIL,RTYTYEILLW,EILLWTTSRV,MRTYTYEILL,YEILLWTTSR	LIHC
CTNNB1	c.100G>A	p.G34R	ELDMAMEPDRKAAVSHWQQQSYLDS[p.G34R]RIHSGATTTAPSLSGKGNPEEEDVDT	QQSYLDSRI,RIHSGATTT,YLDSRIHSGA,RIHSGATTTA,QQQSYLDSRI,QQSYLDSRIH	UCEC
CTNNB1	c.101G>T	p.G34V	ELDMAMEPDRKAAVSHWQQQSYLDS[p.G34V]VIHSGATTTAPSLSGKGNPEEEDVDT	QQQSYLDSV,YLDSVIHSG,QQSYLDSVI,WQQQSYLDSV,YLDSVIHSGA,VIHSGATTTA,QQQSYLDSVI,QQSYLDSVIH	LIHC
CTNNB1	c.107A>C	p.H36P	DMAMEPDRKAAVSHWQQQSYLDSGI[p.H36P]PSGATTTAPSLSGKGNPEEEDVDTSQ	YLDSGIPSG,IPSGATTTA,YLDSGIPSGA	LIHC
CTNNB1	c.109T>G	p.S37A	MAMEPDRKAAVSHWQQQSYLDSGIH[p.S37A]AGATTTAPSLSGKGNPEEEDVDTSQV	YLDSGIHAG,IHAGATTTA,YLDSGIHAGA,GIHAGATTTA,AGATTTAPSL	UCEC
CTNNB1	c.110C>G	p.S37C	MAMEPDRKAAVSHWQQQSYLDSGIH[p.S37C]CGATTTAPSLSGKGNPEEEDVDTSQV	YLDSGIHCGA,GIHCGATTTA	UCEC
CTNNB1	c.110C>T	p.S37F	MAMEPDRKAAVSHWQQQSYLDSGIH[p.S37F]FGATTTAPSLSGKGNPEEEDVDTSQV	YLDSGIHFG,SYLDSGIHF,IHFGATTTA,YLDSGIHFGA,GIHFGATTTA,QSYLDSGIHF,IHFGATTTAP,FGATTTAPSL	LUAD,UCEC
CTNNB1	c.1161T>A	p.N387K	GMQALGLHLTDPSQRLVQNCLWTLR[p.N387K]KLSDAATKQEGMEGLLGTLVQLLGSD	VQNCLWTLRK	LIHC
CTNNB1	c.121A>G	p.T41A	PDRKAAVSHWQQQSYLDSGIHSGAT[p.T41A]ATAPSLSGKGNPEEEDVDTSQVLYEW	ATAPSLSGK,GATATAPSL,GIHSGATATA,TATAPSLSGK,SGATATAPSL	PRAD
CTNNB1	c.122C>T	p.T41I	PDRKAAVSHWQQQSYLDSGIHSGAT[p.T41I]ITAPSLSGKGNPEEEDVDTSQVLYEW	ITAPSLSGK,SGIHSGATI,TITAPSLSGK,SGATITAPSL	UCEC
CTNNB1	c.133T>C	p.S45P	AAVSHWQQQSYLDSGIHSGATTTAP[p.S45P]PLSGKGNPEEEDVDTSQVLYEWEQGF	TTAPPLSGK,GATTTAPPL,TTTAPPLSGK,SGATTTAPPL	ACC,LIHC
CTNNB1	c.94G>A	p.D32N	LMELDMAMEPDRKAAVSHWQQQSYL[p.D32N]NSGIHSGATTTAPSLSGKGNPEEEDV	YLNSGIHSG,QQSYLNSGI,WQQQSYLNS,QQQSYLNSG,YLNSGIHSGA,QQQSYLNSGI,WQQQSYLNSG,QQSYLNSGIH	LIHC,UCEC
CTNNB1	c.94G>T	p.D32Y	LMELDMAMEPDRKAAVSHWQQQSYL[p.D32Y]YSGIHSGATTTAPSLSGKGNPEEEDV	YLYSGIHSG,QQSYLYSGI,HWQQQSYLY,WQQQSYLYS,QQQSYLYSG,QSYLYSGIH,YLYSGIHSGA,QQQSYLYSGI,SHWQQQSYLY,WQQQSYLYSG,QQSYLYSGIH	UCEC
CTNNB1	c.95A>G	p.D32G	LMELDMAMEPDRKAAVSHWQQQSYL[p.D32G]GSGIHSGATTTAPSLSGKGNPEEEDV	YLGSGIHSG,WQQQSYLGS,QQQSYLGSG,QQSYLGSGI,QSYLGSGIH,YLGSGIHSGA,WQQQSYLGSG,QQQSYLGSGI,QQSYLGSGIH	CESC,LIHC
CTNNB1	c.95A>T	p.D32V	LMELDMAMEPDRKAAVSHWQQQSYL[p.D32V]VSGIHSGATTTAPSLSGKGNPEEEDV	QQSYLVSGI,YLVSGIHSG,LVSGIHSGA,HWQQQSYLV,WQQQSYLVS,QQQSYLVSG,QSYLVSGIH,YLVSGIHSGA,QQQSYLVSGI,SHWQQQSYLV,WQQQSYLVSG,QQSYLVSGIH	LIHC
CTNNB1	c.97T>C	p.S33P	MELDMAMEPDRKAAVSHWQQQSYLD[p.S33P]PGIHSGATTTAPSLSGKGNPEEEDVD	YLDPGIHSG,WQQQSYLDP,QQQSYLDPG,QQSYLDPGI,YLDPGIHSGA,WQQQSYLDPG,QQQSYLDPGI,QQSYLDPGIH	LIHC
CTNNB1	c.98C>A	p.S33Y	MELDMAMEPDRKAAVSHWQQQSYLD[p.S33Y]YGIHSGATTTAPSLSGKGNPEEEDVD	YLDYGIHSG,WQQQSYLDY,QQSYLDYGI,YLDYGIHSGA,HWQQQSYLDY,QQQSYLDYGI,QQSYLDYGIH	UCEC
CTNNB1	c.98C>G	p.S33C	MELDMAMEPDRKAAVSHWQQQSYLD[p.S33C]CGIHSGATTTAPSLSGKGNPEEEDVD	YLDCGIHSG,WQQQSYLDC,QQSYLDCGI,YLDCGIHSGA,QQQSYLDCGI,QQSYLDCGIH	LIHC,UCEC

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CTNNB1	c.98C>T	p.S33F	MELDMAMEPDRKAAVSHWQQQSYLD[p.S33F]FGIHSGATTTAPSLSGKGNPEEEDVD	YLDFGIHSG,WQQQSYLDF,QQSYLDFGI,QSYLDFGIH,YLDFGIHSGA,HWQQQSYLDF,QQQSYLDFGI,QQSYLDFGIH	UCEC
CTNND1	c.1341delA	p.I447fs	VHLGACGALKNISFGRDQDNKIAIK[p.I447fs]TVMVCLPLCDCFERLVIWTLLKLLPEPCGIFHPMTQSKWRLWTMHCMP*	KIAIKTVMV,KLLPEPCGI,AIKTVMVCL,LVIWTLLKL,RLVIWTLLK,KTVMVCLPL,IFHPMTQSK,QSKWRLWTM,KWRLWTMHC,EPCGIFHPM,NKIAIKTVM,FERLVIWTL,LLPEPCGIF,SKWRLWTMH,WRLWTMHCM,LPEPCGIFH,RLVIWTLLKL,LVIWTLLKLL,GIFHPMTQSK,CFERLVIWTL,KLLPEPCGIF,IFHPMTQSKW,KWRLWTMHCM,HPMTQSKWRL,TQSKWRLWTM,IAIKTVMVCL,IKTVMVCLPL,FERLVIWTLL,LPLCDCFERL,PEPCGIFHPM	STAD
CTSC	c.315delT	p.F105fs	NSGHFTIIYNQGFEIVLNDYKWFAF[p.F105fs]LSIKKRAAR*	FLSIKKRAA,KWFAFLSIK,WFAFLSIKK,LSIKKRAAR,FAFLSIKKR,YKWFAFLSI,NDYKWFAFL,KWFAFLSIKK,DYKWFAFLSI,WFAFLSIKKR,FLSIKKRAAR	STAD
CTSD	c.267_268insC	p.P89fs	GPIPEVLKNYMDAQYYGEIGIGTPP[p.P89fs]PVLHSRLRHGLLQPVGPLHPLQTAGHRLLDPPQVQQRQVQHLREEWYLV*	GLLQPVGPL,HLREEWYLV,HSRLRHGLL,RLRHGLLQP,QQRQVQHLR,VQHLREEWY,QPVGPLHPL,IGIGTPPPV,LRHGLLQPV,LQTAGHRLL,VQQRQVQHL,RQVQHLREE,RLRHGLLQPV,VLHSRLRHGL,HSRLRHGLLQ,QVQHLREEWY,EIGIGTPPPV,TPPPVLHSRL,HPLQTAGHRL,IGIGTPPPVL,LQPVGPLHPL,RQVQHLREEW,VQHLREEWYL,GEIGIGTPPP	STAD
CTTNBP2	c.1259C>T	p.S420L	TSSTPPLPSNAAPPTAQTPGIAPQN[p.S420L]LQAPPMHSLHSPCANTSLHPGLNPRI	LQAPPMHSL,PQNLQAPPM,NLQAPPMHSL,QTPGIAPQNL,APQNLQAPPM,LQAPPMHSLH	UCEC
CTTNBP2	c.490C>T	p.R164C	LEMEKLQLQALEQEHKKLAARLEEE[p.R164C]CGKNKQVVLMLVKECKQLSGKVIEEA	CGKNKQVVL,KLAARLEEEC,AARLEEECGK	CRC
CUBN	c.1786G>T	p.G596C	EHLRNGRGFTVRWETQQPECGGILT[p.G596C]CPYGSIKSPGYPGNYPPGRDCVWIVV	ILTCPYGSI,LTCPYGSIK,CGGILTCPY,ILTCPYGSIK	LUAD
CUBN	c.8448C>G	p.I2816M	GGGFYATWNTQTLGCGGIFHSDNGT[p.I2816M]MRSPHWPQNFPENSRCSWTAITHKSK	TMRSPHWPQ,IFHSDNGTM,TMRSPHWPQN,IFHSDNGTMR,GIFHSDNGTM,MRSPHWPQNF	KIRP
CUL1	c.1453G>A	p.E485K	DVFQKFYAKMLAKRLVHQNSASDDA[p.E485K]KASMISKLKQACGFEYTSKLQRMFQD	KASMISKLK,DAKASMISK,AKASMISKL,SASDDAKASM	BLCA
CUL7	c.1113G>C	p.L371F	QAQPSFRRSRRFRPRSEFASGNTYA[p.L371F]FYVRDTLQPGMRVRMLDDYEEISAGD	ASGNTYAFY,FASGNTYAF,YAFYVRDTL,FASGNTYAFY,EFASGNTYAF,TYAFYVRDTL,SGNTYAFYVR	LUAD
CUL9	c.5178T>G	p.D1726E	SPRCWPVSPLCYLYHPRKCLPTEFC[p.D1726E]EALDRFSSFYSQSQNHPVLDMGPHRR	CLPTEFCEA,LPTEFCEAL,EALDRFSSF,CEALDRFSS,CLPTEFCEAL,EALDRFSSFY,TEFCEALDRF,CEALDRFSSF	KIRC
CUX1	c.1316_1317insC	p.A439fs	LSGSARRKGKDQPESRRPGSLPAPP[p.A439fs]SFSVAPQPGGAGFQY*	LPAPPSFSV,APQPGGAGF,GSLPAPPSF,QPGGAGFQY,SLPAPPSFSV,FSVAPQPGGA,LPAPPSFSVA	STAD
CWC25	c.1090A>G	p.K364E	EELERKRQEMMENAKWREEERLNIL[p.K364E]ERHAKDEEREQRLEKLDSRDGKFIHR	RLNILERHAK	KIRC
CXCL9	c.366G>C	p.K122N	KKQKNGKKHQKKKVLKVRKSQRSRQ[p.K122N]NKTT*	KSQRSRQNK	LUAD
CXCR4	c.1033G>C	p.E345Q	VSRGSSLKILSKGKRGGHSSVSTES[p.E345Q]QSSSFHSS*	STESQSSSF,SQSSSFHSS,VSTESQSSSF	LUAD
CXXC1	c.468G>C	p.Q156H	MLARGSASPHKSSPQPLVATPSQHH[p.Q156H]HQQQQQIKRSARMCGECEACRRTEDC	HHHQQQQQI	TGCT
CXorf51B	c.127G>A	p.V43I	QTPSTSSTKGRKKGKTPRQRRSRSG[p.V43I]IKGLKTTRKAKRPLRGSSSQKAGETN	RQRRSRSGI,QRRSRSGIK,RSRSGIKGL,RSRSGIKGLK,RQRRSRSGIK,GIKGLKTTRK,RRSRSGIKGL	KIRC
CXorf59	c.593G>T	p.R198M	LLHLSGKMPPGINSSQSLPVDNHEK[p.R198M]MVIQLHLQHSSLLDFLNAQGGCISHV	LPVDNHEKM,HEKMVIQLH,HEKMVIQLHL,LPVDNHEKMV	LUAD

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CYP11B1	c.1492C>G	p.R498G	LVRVFLYSLGRNPALFPRPERYNPQ[p.R498G]GWLDIRGSGRNFYHVPFGFGMRQCLG	RYNPQGWLDI	LUAD
CYP19A1	c.1216T>C	p.F406L	DVIDGYPVKKGTNIILNIGRMHRLE[p.F406L]LFPKPNEFTLENFAKNVPYRYFQPFG	IGRMHRLEL,MHRLELFPK,ELFPKPNEF,GRMHRLELF,RMHRLELFPK,LFPKPNEFTL,NIGRMHRLEL,IGRMHRLELF,LELFPKPNEF	TGCT
CYP19A1	c.338G>T	p.S113I	WISGEETLIISKSSSMFHIMKHNHY[p.S113I]ISRFGSKLGLQCIGMHEKGIIFNNNP	HIMKHNHYI,YISRFGSKL,HYISRFGSK,ISRFGSKLG,KHNHYISRF,HYISRFGSKL,IMKHNHYISR,NHYISRFGSK,ISRFGSKLGL,MKHNHYISRF,FHIMKHNHYI	THCA
CYP1A2	c.1447G>A	p.V483M	CIGEVLAKWEIFLFLAILLQQLEFS[p.V483M]MPPGVKVDLTPIYGLTMKHARCEHVQ	LLQQLEFSM,FSMPPGVKV,MPPGVKVDL,QQLEFSMPP,LEFSMPPGV,ILLQQLEFSM,QLEFSMPPGV,SMPPGVKVDL,LQQLEFSMPP,QQLEFSMPPG	BRCA
CYP27A1	c.335C>A	p.P112Q	LYKAKYGPMWMSYLGPQMHVNLASA[p.P112Q]QLLEQVMRQEGKYPVRNDMELWKEHR	ASAQLLEQV,HVNLASAQL,VNLASAQLL,SAQLLEQVM,LASAQLLEQV,HVNLASAQLL,MHVNLASAQL,ASAQLLEQVM	LUAD
CYP2B6	c.1331C>A	p.A444E	ALKKTEAFIPFSLGKRICLGEGIAR[p.A444E]EELFLFFTTILQNFSMASPVAPEDID	IAREELFLF,AREELFLFF,EELFLFFTT,GEGIAREEL,REELFLFFT,GIAREELFLF,IAREELFLFF,EELFLFFTTI,GEGIAREELF,REELFLFFTT	LUAD
CYP2D6	c.1055A>G	p.H352R	VQRRVQQEIDDVIGQVRRPEMGDQA[p.H352R]RMPYTTAVIHEVQRFGDIVPLGVTHM	MGDQARMPY,RMPYTTAVI,QARMPYTTA,ARMPYTTAV,QARMPYTTAV,EMGDQARMPY,RPEMGDQARM,ARMPYTTAVI,RMPYTTAVIH	GBM
CYP4A11	c.553G>T	p.V185F	GLMADSVRVMLDKWEELLGQDSPLE[p.V185F]FFQHVSLMTLDTIMKCAFSHQGSIQV	LGQDSPLEF,GQDSPLEFF,LEFFQHVSL,EFFQHVSLM,SPLEFFQHV,FFQHVSLMTL,DSPLEFFQHV,LLGQDSPLEF,LEFFQHVSLM,LGQDSPLEFF	OV
CYP4B1	c.1302G>T	p.E434D	HIYALHRNSAVWPDPEVFDSLRFST[p.E434D]DNASKRHPFAFMPFSAGPRNCIGQQF	SLRFSTDNA,RFSTDNASK,TDNASKRHPF	CRC
CYP7B1	c.995A>C	p.K332T	YLLRHPEAMAAVRDEIDRLLQSTGQ[p.K332T]TKGSGFPIHLTREQLDSLICLESSIF	QTKGSGFPI,RLLQSTGQTK,GQTKGSGFPI,TKGSGFPIHL	STAD
DAB2IP	c.481G>A	p.E161K	ILGQDYCFEVTTSSGSKCFSCRSAA[p.E161K]KRDKWMENLRRAVHPNKDNSRRVEHI	CFSCRSAAK,FSCRSAAKR,RSAAKRDKW,KCFSCRSAAK,SCRSAAKRDK,CFSCRSAAKR,AKRDKWMENL	BRCA
DACH2	c.1615C>T	p.R539C	TMQKRLKKEKKTKRKLQEALEFESK[p.R539C]CREQVEQALKQATTSDSGLRMLKDTG	FESKCREQV,EALEFESKCR	CRC
DACH2	c.1616G>T	p.R539L	TMQKRLKKEKKTKRKLQEALEFESK[p.R539L]LREQVEQALKQATTSDSGLRMLKDTG	KLREQVEQA,EALEFESKL,FESKLREQV,KLREQVEQAL,EALEFESKLR,QEALEFESKL	LUAD
DBC1	c.646G>A	p.V216I	AIKVTETRTGPLGCNSYDNLDSVSS[p.V216I]ILLQSTESKLHLQGLQIIFPQYLQEK	NLDSVSSIL,ILLQSTESK,NLDSVSSILL,ILLQSTESKL,SILLQSTESK,YDNLDSVSSI	CRC
DBF4B	c.761C>A	p.S254Y	PFLKIEDESRKFRPFHHQFKSFPEI[p.S254Y]YFLGPKDASPFEAPTTLGSMHHTRES	KSFPEIYFL,SFPEIYFLG,QFKSFPEIY,FKSFPEIYF,QFKSFPEIYF,HQFKSFPEIY,FKSFPEIYFL	CRC
DCAF12L2	c.737G>A	p.R246H	RMDPDMFNGSIAWHSEVGLPVYAHI[p.R246H]HPRDVEAIPRASTNPSNRKVRALAFS	PVYAHIHPR,HIHPRDVEA,HIHPRDVEAI,VYAHIHPRDV,LPVYAHIHPR	GBM
DCC	c.1337G>A	p.R446H	AIPSSSVLPSAPRDVVPVLVSSRFV[p.R446H]HLSWRPPAEAKGNIQTFTVFFSREGD	LVSSRFVHL,SSRFVHLSW,VLVSSRFVH,VHLSWRPPA,VLVSSRFVHL,FVHLSWRPPA,HLSWRPPAEA,SSRFVHLSWR,VSSRFVHLSW	LUAD
DCHS1	c.703delC	p.R235fs	LDRENRSHYMLQLEAYDGGSPPRRA[p.R235fs]RPCWT*	SPPRRARPC	STAD
DCHS2	c.6447C>A	p.F2149L	TRENTYVEYSIISGNSQNNFHVETK[p.F2149L]LFHSEYPYKQVGYLVLLHSLDREASA	KLFHSEYPY,LFHSEYPYK,NFHVETKLF,ETKLFHSEY,KLFHSEYPYK,NNFHVETKLF,VETKLFHSEY,TKLFHSEYPY	CRC
DCLK2	c.1646C>A	p.S549Y	HGLSIVHRDIKPENLLVCEYPDGTK[p.S549Y]YLKLGDFGLATVVEGPLYTVCGTPTY	YLKLGDFGL,CEYPDGTKY,TKYLKLGDF,YLKLGDFGLA,KYLKLGDFGL,YPDGTKYLKL,CEYPDGTKYL	CRC
DCLRE1B	c.82T>A	p.F28I	GVLIPHTPIAVDFWSLRRAGTARLF[p.F28I]ILSHMHSDHTVGLSSTWARPLYCSPI	RLFILSHMH,RAGTARLFI,ARLFILSHM,ILSHMHSDHT,GTARLFILSH,RAGTARLFIL,TARLFILSHM,RRAGTARLFI	TGCT

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DCT	c.1595G>A	p.R532Q	LVVMGTLVALVGLFVLLAFLQYRRL[p.R532Q]QKGYTPLMETHLSSKRYTEEA*	RLQKGYTPL,FLQYRRLQK,LQKGYTPLM,QYRRLQKGY,LQYRRLQKG,RLQKGYTPLM,AFLQYRRLQK,LQYRRLQKGY,RRLQKGYTPL	UCEC
DCUN1D4	c.824T>C	p.L275P	EKDQRSLDINTAKCMLGLLLGKIWP[p.L275P]PFPVFHQFLEQSKYKVINKDQWCNVL	LLLGKIWPP,LLGKIWPPF,KIWPPFPVF,PFPVFHQFL,GKIWPPFPV,PPFPVFHQF,LLLGKIWPPF,LGKIWPPFPV,KIWPPFPVFH,GKIWPPFPVF,WPPFPVFHQF	THCA
DDC	c.1297delA	p.I433fs	LVCFRLKGSNKVNEALLQRINSAKK[p.I433fs]STWFHVTSGTSLSCALPSVLARWNLPMCSGPGNTSKSWRPTCCEQRGSRSEASCRNQKLKRDISENWNKKQINIILPSWNSAVCGFPCLSPKLSRGL*	SLSCALPSV,VLARWNLPM,ILPSWNSAV,CGFPCLSPK,CALPSVLAR,CSGPGNTSK,ASCRNQKLK,ALPSVLARW,SWNSAVCGF,SAKKSTWFH,GSRSEASCR,INSAKKSTW,AKKSTWFHV,KKSTWFHVT,FHVTSGTSL,SGTSLSCAL,LSCALPSVL,LKRDISENW,KQINIILPS,SAVCGFPCL,LPSWNSAVC,SLSCALPSVL,VLARWNLPMC,IILPSWNSAV,ILPSWNSAVC,CLSPKLSRGL,RSEASCRNQK,CALPSVLARW,KQINIILPSW,SAKKSTWFHV,SVLARWNLPM,SWRPTCCEQR,STWFHVTSGT,TSLSCALPSV,NIILPSWNSA,NSAVCGFPCL,LPSVLARWNL,WNKKQINIIL,RINSAKKSTW,INSAKKSTWF,WFHVTSGTSL,SEASCRNQKL,KLKRDISENW,CGFPCLSPKL,CEQRGSRSEA	STAD
DDI1	c.824G>A	p.R275Q	VNGHPLKAFVDSGAQMTIMSQACAE[p.R275Q]QCNIMRLVDRRWAGVAKGVGTQRIIG	AEQCNIMRL,SQACAEQCNI,AEQCNIMRLV	CRC
DDX11	c.1126G>A	p.A376T	PYYGSRLAIPAAQLVVLPYQMLLHA[p.A376T]TTRQAAGIRLQDQVVIIDEAHNLIDT	LLHATTRQA,TTRQAAGIR,QMLLHATTR,YQMLLHATT,LHATTRQAA,MLLHATTRQA,LLHATTRQAA,TTRQAAGIRL,YQMLLHATTR,LPYQMLLHAT	TGCT
DDX11	c.622delA	p.K208fs	AERLEQLESGEEELVLAEYESDEEK[p.K208fs]RWRAEWMRMRMTWRKNT*	MRMRMTWRK,RWRAEWMRM,EWMRMRMTW,RAEWMRMRM,WMRMRMTWR,RMRMTWRKN,EEKRWRAEW,AEWMRMRMT,WMRMRMTWRK,RWRAEWMRMR,RMRMTWRKNT,EWMRMRMTWR,KRWRAEWMRM,WRAEWMRMRM,AEWMRMRMTW,DEEKRWRAEW	TGCT
DDX11L2	c.382T>C	p.*128Q	CLFLSLEPPPPRDHISHCLLSAQFH[p.*128Q]QK*	LLSAQFHQK,CLLSAQFHQK	UCS
DDX17	c.488delG	p.G163fs	HPEVARLTPYEVDELRRKKEITVRG[p.G163fs]EMFVLNPCLPSIMLTSHNM*	VLNPCLPSI,SIMLTSHNM,ITVRGEMFV,KEITVRGEM,GEMFVLNPC,EMFVLNPCL,NPCLPSIML,LPSIMLTSH,FVLNPCLPSI,VLNPCLPSIM,EITVRGEMFV,KKEITVRGEM,KEITVRGEMF,GEMFVLNPCL	STAD
DDX39B	c.447_448insT	p.F149fs	LAFQISKEYERFSKYMPNVKVAVFF[p.F149fs]WWSVYQEG*	VAVFFWWSV,AVFFWWSVY,FWWSVYQEG,VKVAVFFWW,KVAVFFWWSV,VAVFFWWSVY	KIRC
DDX56	c.986G>T	p.R329L	FNQGFYDCVIATDAEVLGAPVKGKR[p.R329L]LGRGPKGDKASDPEAGVARGIDFHHV	LGRGPKGDK,KGKRLGRGPK,RLGRGPKGDK	LUAD
DEFA1	c.270G>T	p.W90C	DCYCRIPACIAGERRYGTCIYQGRL[p.W90C]CAFCC*	IYQGRLCAF,IYQGRLCAFC,CIYQGRLCAF	LUAD
DENND2A	c.1496G>T	p.R499L	GRKKRKIPKLVLRINAIYEVRRGKK[p.R499L]LVKRLSQSMESNSGKVTDENSESDSD	RGKKLVKRL,LVKRLSQSM,YEVRRGKKL,KLVKRLSQSM,EVRRGKKLVK,YEVRRGKKLV	LUAD
DENND2A	c.2063G>A	p.R688Q	EVYCIVSRLGCFSLFSRILDEVEKR[p.R688Q]QGISPALVQPLMRSVMEAPFPALGKT	KRQGISPAL,RQGISPALV,EKRQGISPAL,VEKRQGISPA	LUAD
DENND4A	c.1070C>A	p.P357H	LYRYSISGPHVLPIEKHISHFMHKV[p.P357H]HFPSPQRPRILVQLSPHDNLILSQPV	FMHKVHFPS,KVHFPSPQR,HFPSPQRPR,ISHFMHKVH,SHFMHKVHF,KVHFPSPQRP,ISHFMHKVHF,FMHKVHFPSP	CRC
DENND4C	c.3242G>A	p.R1081Q	ESEKSSPAVSRSKTFTGRFKQQTPS[p.R1081Q]QTHKERSTSLSALVRSSPHGSLGSVV	RFKQQTPSQ,KQQTPSQTH,RFKQQTPSQT,KQQTPSQTHK,FKQQTPSQTH	CRC
DENND5B	c.3068G>A	p.G1023E	GELGDTGVMQIPKNLLEMTFECQNL[p.G1023E]EKLTTVQIGHDNSGLLAKWLVDCVMV	FECQNLEKL,LEKLTTVQI,CQNLEKLTTV,MTFECQNLEK	HNSC
DGCR8	c.1552G>A	p.E518K	SVQDAPTKKEFVINPNGKSEVCILH[p.E518K]KYMQRVLKVRPVYNFFECENPSEPFG	ILHKYMQRV,KSEVCILHK,CILHKYMQR,KYMQRVLKV,HKYMQRVLK,SEVCILHKY,LHKYMQRVL,KSEVCILHKY,CILHKYMQRV,ILHKYMQRVL,LHKYMQRVLK,KYMQRVLKVR,SEVCILHKYM,HKYMQRVLKV	THCA

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DGKB	c.38C>T	p.S13L	MTNQEKWAHLSP[p.S13L]LEFSQLQK YAEYSTKKLKDVLEEFHG	EKWAHLSPL,WAHLSPLEF,LEFSQLQKY,HLSPLEFSQL,KW AHLSPLEF,QEKWAHLSPL,LEFSQLQKYA	BRCA
DHPS	c.147C>A	p.F49L	LPPESTQVRGYDFNRGVNYRALLEA[p.F 49L]LGTTGFQATNFGRAVQQVNAMIE KKL	ALLEALGTT,ALGTTGFQA,NYRALLEAL,LEALGTTGF,EALGT TGFQA,LLEALGTTGF,VNYRALLEAL	CESC
DHRS 4	c.653T>C	p.I218T	LGLNKTLAIELAPRNIRVNCLAPGL[p.I2 18T]TKTSFSRMLWMDKEKEESMKETL RIR	CLAPGLTKT,LTKTSFSRM,GLTKTSFSR,APGLTKTSF,TKTSFS RML,GLTKTSFSRM,LTKTSFSRML,LAPGLTKTSF,TKTSFSR MLW	LIHC
DHTK D1	c.1229G>A	p.R410 Q	DIGKLVGCAIIHVNGDSPEEVVRAT[p.R 410Q]QLAFEYQRQFRKDVIIDLLCYRQ WGH	TQLAFEYQR,VVRATQLAF,RATQLAFEY,EVVRATQLA,EEV VRATQL,ATQLAFEYQR,VVRATQLAFE,VRATQLAFEY,QLA FEYQRQF,EVVRATQLAF,EEVVRATQLA	CRC
DHX9	c.119T>G	p.V40G	RKMTPSYEIRAVGNKNRQKFMCEVQ[p .V40G]GEGYNYTGMGNSTNKKDAQS NAARDF	GEGYNYTGM,FMCEVQGEGY,CEVQGEGYNY	LUSC
DIAPH 2	c.361G>A	p.E121 K	ERSLNLSEKEVLDLFEKMMEDMNLN[p. E121K]KEKKAPLRNKDFTTKREMVVQY ISAT	MMEDMNLNK,LNKEKKAPL,KMMEDMNLNK,KEKKAPLR NK,NLNKEKKAPL	UCEC
DICER 1	c.5113G>A	p.E170 5K	KAYLLQAFTHASYHYNTITDCYQRL[p.E 1705K]KFLGDAILDYLITKHLYEDPRQH SPG	RLKFLGDAI,ITDCYQRLK,LKFLGDAIL,ITDCYQRLKF,RLKFLG DAIL,TITDCYQRLK,KFLGDAILDY,YQRLKFLGDA	CLL
DIRAS 1	c.235G>T	p.G79C	VCTLQITDTTGSHQFPAMQRLSISK[p.G 79C]CHAFILVFSVTSKQSLEELGPIYKLI	SISKCHAFI,RLSISKCHA,ISKCHAFIL,LSISKCHAF,MQRLSISK C,KCHAFILVF,SISKCHAFIL,ISKCHAFILV,LSISKCHAFI,RLSIS KCHAF,MQRLSISKCH,SKCHAFILVF	KIRC
DIS3	c.2339G>A	p.R780 K	CSGMDNDFHHYGLASPIYTHFTSPI[p.R 780K]KRYADVIVHRLLAVAIGADCTYPE LT	YTHFTSPIK,HFTSPIKRY,FTSPIKRYA,SPIKRYADV,IKRYADV IV,KRYADVIVH,YTHFTSPIKR,IYTHFTSPIK,SPIKRYADVI,TH FTSPIKRY,IKRYADVIVH	MM
DISP1	c.2194_219 5GG>TT	p.G732 L	EKVLPCIVIKFRYLWLFWFLALTVG[p.G 732L]LAYIVCINPKMKLPSLELSEFQVFR SS	FLALTVGLA,ALTVGLAYI,LTVGLAYIV,WFLALTVGL,LALTV GLAY,FLALTVGLAY,ALTVGLAYIV,LAYIVCINPK,FWFLALTV GL,LALTVGLAYI	SKCM
DISP1	c.2287C>T	p.R763 C	INPKMKLPSLELSEFQVFRSSHPFE[p.R7 63C]CYDAEYKKLFMFERVHHGEELHM PIT	RSSHPFECY,HPFECYDAE,CYDAEYKKLF,HPFECYDAEY,FRS SHPFECY	CRC
DISP2	c.3062T>C	p.F102 1S	VAGTVLLTVGLLVLLEWQLNTAEAL[p.F 1021S]SLSASVGLSVDFTVNYCISYHLCP HP	NTAEALSLS,EALSLSASV,LNTAEALSL,AEALSLSAS,LSLSAS VGL,ALSLSASVGL,SLSASVGLSV,QLNTAEALSL,NTAEALSL SA,WQLNTAEALS,AEALSLSASV	KIRC
DKK2	c.689G>A	p.R230 H	KPVLHQGEVCTKQRKKGSHGLEIFQ[p. R230H]HCDCAKGLSCKVWKDATYSSK ARLHV	EIFQHCDCA,FQHCDCAKGL,LEIFQHCDCA	CRC
DLC1	c.1049C>T	p.A350 V	LATQEPTDNQVRLRKRKEIREDRDR[p. A350V]VRLDSMVLLIMKLDQLDQDIEN ALST	RVRLDSMVL,RDRVRLDSM,VRLDSMVLL,REDRDRVRL,RV RLDSMVLL,EIREDRDRVR,KEIREDRDRV	CRC
DLC1	c.2222G>C	p.S741 T	ISALNGNRINVPMVRKRSVSNSTQT[p. S741T]TSSSSQSETSSAVSTPSPVTRTRS LS	RSVSNSTQTT	BLCA,PR AD,TGCT ,THCA
DLC1	c.666G>T	p.E222 D	ISLSEIKDAPKVNAVDTLNVKDIAP[p.E2 22D]DKQLLNSAVIAQQRRKPDPPKDE NER	NVKDIAPDK	CRC
DLEU7	c.248C>T	p.A83V	RARPGPGREERGGGVGTRSRRTAAR[p. A83V]VNSPEEEVVRGAEGGAELLPFPR DRG	RSRRTAARV,RTAARVNSP,RSRRTAARVN,RTAARVNSPE	ACC
DLG2	c.1871C>T	p.S624 L	KRRVERKERARLKTVKFNAKPGVID[p.S 624L]LKGSFNDKRKKSFIFSRKFPFYKNK E	GVIDLKGSF,NAKPGVIDLK,DLKGSFNDKR	UCEC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
DLGAP3	c.1130delG	p.G377fs	GLLGPETKAKARTYHYLQVPQDDWG[p.G377fs]VTPPVARMGRSPAAGCGAAATSKPWGMRRAETQTAAPRHLPKQSPDASPPVAPPAWTRPGSTAVSHPGSTPGAPSLATAVPSPLDSSAMS*	WTRPGSTAV,TAAPRHLPK,ATSKPWGMR,VARMGRSPA,TSKPWGMRR,PVAPPAWTR,QVPQDDWGV,QSPDASPPV,STPGAPSLA,SPAAGCGAA,KPWGMRRAE,VPSPLDSSA,ARMGRSPAA,RMGRSPAAG,GAAATSKPW,MRRAETQTA,RRAETQTAA,TQTAAPRHL,KQSPDASPP,GSTPGAPSL,LATAVPSPL,SPPVAPPAW,LQVPQDDWGV,KQSPDASPPV,SLATAVPSPL,QTAAPRHLPK,ATSKPWGMRR,VARMGRSPAA,TSKPWGMRRA,GMRRAETQTA,RAETQTAAPR,VSHPGSTPGA,DWGVTPPVAR,VTPPVARMGR,DASPPVAPPA,SPAAGCGAAA,KPWGMRRAET,VPSPLDSSAM,WGVTPPVARM,CGAAATSKPW,MRRAETQTAA	STAD
DLL3	c.952G>C	p.D318H	PRSFECTCPRGFYGLRCEVSGVTCA[p.D318H]HGPCFNGGLCVGGADPDSAYICHCPP	VTCAHGPCF,CEVSGVTCAH,GVTCAHGPCF	BLCA
DMBT1	c.4562G>T	p.R1521L	SRASTAGSESTLALRLVNGGDRCRG[p.R1521L]LVEVLYQGSWGTVCDDYWDTNDANVV	GLVEVLYQGS,RCRGLVEVLY	LUAD
DMD	c.5316G>C	p.K1772N	DHCRKLVEPQISELNHRFAAISHRI[p.K1772N]NTGKASIPLKELEQFNSDIQKLLEPL	ISHRINTGK,RINTGKASI,NTGKASIPL,AISHRINTGK,NTGKASIPLK,HRINTGKASI	BRCA
DMD	c.9584G>A	p.R3195H	NVPLCVDMCLNWLLNVYDTGRTGRI[p.R3195H]HVLSFKTGIISLCKAHLEDKYRYLFK	TGRTGRIHV,HVLSFKTGI,TGRIHVLSF,TGRIHVLSFK,RTGRIHVLSF,RIHVLSFKTG,IHVLSFKTGI	CRC
DMPK	c.131G>A	p.R44H	AGVGPGLPGAGAPARPSPGRPPGAG[p.R44H]HLRTGPGQVRGRLLAVGPKSRVFQSV	HLRTGPGQV,HLRTGPGQVR	CESC
DMRT1	c.133T>A	p.S45T	PGVPPQGRAGGFGKASGALVGAASG[p.S45T]TSAGGSSRGGGSGSGASDLGAGSKKS	ALVGAASGT,GTSAGGSSR	ACC
DMRT2	c.317C>G	p.T106S	RGGPQPRPPLAPQASPAGTGPRERC[p.T106S]SPAGGGAEPRKLSRTPKCARCRNHGV	GPRERCSPA,GPRERCSPAG	KIRP
DMXL2	c.7236C>A	p.D2412E	GGGVKLVVKPRRQSENISAPPVLSE[p.D2412E]EIDKHRRRFNMRMLVPGRPVKDATPP	EEIDKHRRRF	MM
DNAH10	c.5558G>T	p.C1853F	GAPAGPAGTGKTETTKDLAKALGLL[p.C1853F]FVVTNCGEGMDYRAVGKIFSGLAQCG	KALGLLFVV,LAKALGLLF,AKALGLLFV,LAKALGLLFV,FVVTNCGEGM,DLAKALGLLF,AKALGLLFVV	THCA
DNAH10	c.5663G>A	p.R1888Q	DYRAVGKIFSGLAQCGAWGCFDEFN[p.R1888Q]QIDASVLSVISSQIQTIRNALIHQLT	QIDASVLSV,EFNQIDASV,DEFNQIDAS,NQIDASVLSV,DEFNQIDASV	UCEC
DNAH14	c.4099C>T	p.R1367C	QDIGPPAVKMLISAEGEGLVLPKKI[p.R1367C]CVRSAVEQWLVNVEKSMFDVLKKERY	KKICVRSAV,CVRSAVEQW,CVRSAVEQWL,LVLPKKICVR,LPKKICVRSA	UCEC
DNAH3	c.10099G>C	p.E3367Q	LNLRIKYIIDHFTLSIYNNVCRSLF[p.E3367Q]QKDKLLFSLLLTIGIMKQKKEITEEV	SLFQKDKLL,NVCRSLFQK,LFQKDKLLF,QKDKLLFSL,FQKDKLLFSL,SLFQKDKLLF	CESC
DNAH5	c.11465G>T	p.R3822L	QKLEISAETEVQINSAREEYRPVAT[p.R3822L]LGSILYFLITEMRLVNEMYQTSLRQF	VATLGSILY,TLGSILYFL,ATLGSILYF,RPVATLGSI,EEYRPVATL,PVATLGSILY,ATLGSILYFL,TLGSILYFLI,RPVATLGSIL,REEYRPVATL,VATLGSILYF	LUAD
DNAH5	c.2225G>A	p.R742Q	LFRETECMAQMGLEVSPLATSLFQK[p.R742Q]QDRYKRNFSNMKMMLAEYQRVKSKIP	LFQKQDRYK,SLFQKQDRY,KQDRYKRNF,SLFQKQDRYK,TSLFQKQDRY,LFQKQDRYKR,QKQDRYKRNF	SKCM
DNAH5	c.2945G>A	p.R982H	ELLSHFNHQNMDALLKVTRNTLEAI[p.R982H]HKRIHSSHTINFRDSNSASNMKQNSL	NTLEAIHKR,AIHKRIHSSH,NTLEAIHKRI,HKRIHSSHTI	CRC
DNAH5	c.5389C>G	p.Q1797E	TIELDKPVMAEGNVEVWLNSLLEES[p.Q1797E]ESSLHLVIRQAAANIQETGFQLTEFL	ESESSLHLV,LLEESESSL,ESSLHLVIR,EESESSLHL,SESSLHLVI,SLLEESESSL,LEESESSLHL,EESESSLHLV	HNSC
DNAH5	c.671G>A	p.R224Q	FLSSLEGFVNVLSGAQESLKEKVNL[p.R224Q]QKCDILELKTLKEPTDYLTLANNPET	LQKCDILEL,NLQKCDILEL,SLKEKVNLQK,LQKCDILELK	CRC

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DNAH5	c.9590G>A	p.R3197Q	HVTPKSYLSFIQGYKFIYGEKHVEV[p.R3197Q]QTLANRMNTGLEKLKEASESVAALSK	EKHVEVQTL,HVEVQTLANR,GEKHVEVQTL,VEVQTLANRM	OV
DNAH5	c.9706G>A	p.D3236N	KEASESVAALSKELEAKEKELQVAN[p.D3236N]NKADMVLKEVTMKAQAAEKVKAEVQK	ANNKADMVLK,QVANNKADMV,LQVANNKADM,KELQVANNKA	SKCM
DNAH7	c.8882G>A	p.R2961Q	LCKGRDIPCSDDCSLMGTLGEAVTI[p.R2961Q]QTWNIAGLPSDSFSIDNGIIIMNARR	IQTWNIAGL,GEAVTIQTW,TIQTWNIAGL,EAVTIQTWNI	UCEC
DNAH9	c.4639G>A	p.D1547N	LESIFTGSEDIRAQLPQDSKRFEGI[p.D1547N]NIDFKELAYDAQKIPNVVQTTNKPGL	NIDFKELAY,RFEGINIDF,SKRFEGINI,RFEGINIDFK,INIDFKELAY,KRFEGINIDF	CRC
DNAH9	c.8979C>G	p.S2993R	KFPAIVNCTAIHWFHEWPQQALESV[p.S2993R]RLRFLQNTEGIEPTVKQSISKFMAFV	SVRLRFLQN,RLRFLQNTE,QALESVRLR,QQALESVRL,ALESVRLRF,LESVRLRFL,SVRLRFLQNT,RLRFLQNTEG,QALESVRLRF	LUAD
DNAI2	c.691G>T	p.V231L	PNKPELALKPSSPLVTLEFNPKDSH[p.V231L]LLLGGCYNGQIACWDTRKGSLVAELS	NPKDSHLLL,SHLLLGGCY,LEFNPKDSHL	LUAD
DNAJC1	c.578delA	p.K193fs	AVVWSIYLEKQLDELLSRKKREKKK[p.K193fs]RLAARVWMYQNSVLQKKMKDC*	RVWMYQNSV,RLAARVWMY,MYQNSVLQK,VWMYQNSVL,REKKKRLAA,KKRLAARVW,KRLAARVWM,WMYQNSVLQ,WMYQNSVLQK,KKRLAARVWM,RVWMYQNSVL,MYQNSVLQKK,KRLAARVWMY,YQNSVLQKKM,KKKRLAARVW,ARVWMYQNSV	STAD
DNAJC10	c.239T>A	p.I80K	FKKLALKLHPDKNPNNPNAHGDFLK[p.I80K]KNRAYEVLKDEDLRKKYDKYGEKGLE	NAHGDFLKK,KNRAYEVLK,LKKNRAYEV,KKNRAYEVL,FLKKNRAYEV,GDFLKKNRAY,LKKNRAYEVL	MM
DNAJC12	c.404G>A	p.R135K	DLMLEESDKTHTTKMENEECNEQRE[p.R135K]KKKEELASTAEKTEQKEPKPLEKSVS	EQREKKKEEL,KKKEELASTA	MM
DNAJC13	c.3742G>A	p.E1248K	TPRLQSNTRALYQYCPIPIINYPQL[p.E1248K]KNELFCNIYYLKQLCDTLRFPDWPIK	PIINYPQLK,KNELFCNIY,YPQLKNELF,LKNELFCNI,QLKNELFCNI,NYPQLKNELF,KNELFCNIYY,INYPQLKNEL,LKNELFCNIY	UCEC
DNAJC24	c.181G>A	p.E61K	LMYHPDKQSTDVPAGTVEECVQKFI[p.E61K]KIDQAWKILGNEETKREYDLQRCEDD	KFIKIDQAW,FIKIDQAWK,IKIDQAWKI,FIKIDQAWKI,KFIKIDQAWK,QKFIKIDQAW,IKIDQAWKIL	CRC
DNASE1L1	c.634G>A	p.D212N	CASLTKKRLDKLELRTEPGFHWVIA[p.D212N]NGEDTTVRASTHCTYDRVVLHGERCR	VIANGEDTTV	CESC
DNM2	c.1134G>C	p.E378D	TLELSGGARINRIFHERFPFELVKM[p.E378D]DFDEKDLRREISYAIKNIHGVRTGLF	LVKMDFDEK,FPFELVKMDF	LIHC
DNM2	c.2371_2372insC	p.P791fs	QRRPVSSIHPPGRPPAVRGPTPGPP[p.P791fs]PDSCSRGGSSLLLGAPNPIPAWTPERVCQQ*	LLLGAPNPI,CSRGGSSLL,SRGGSSLLL,NPIPAWTPE,IPAWTPERV,SLLLGAPNPI,LLGAPNPIPA,CSRGGSSLLL,NPIPAWTPER,LGAPNPIPAW	STAD
DNMBP	c.232A>C	p.T78P	SSFVEIVTIPSLKEGERLFVCICEF[p.T78P]PSQELDNLPLHRGDLVILDGIPTAGW	FPSQELDNL	KIRC
DNMT1	c.1294G>A	p.E432K	LTCFSVYCKHGHLCPIDTGLIEKNI[p.E432K]KLFFSGSAKPIYDDDPSLEGGVNGKN	GLIEKNIKL,KLFFSGSAK,IEKNIKLFF,IKLFFSGSA,NIKLFFSGSA,GLIEKNIKLF	CRC
DNMT1	c.151G>A	p.E51K	RRLKDLERDSLTEKECVKEKLNLLH[p.E51K]KFLQTEIKNQLCDLETKLRKEELSEE	KLNLLHKFL,KEKLNLLHK,EKLNLLHKF,LLHKFLQTEI,KEKLNLLHKF	UCEC
DNMT1	c.2984G>A	p.R995Q	PEHYRKYSDYIKGSNLDAPEPYRIG[p.R995Q]QIKEIFCPKKSNGRPNETDIKIRVNK	QIKEIFCPK,RIGQIKEIF,GQIKEIFCPK,QIKEIFCPKK,APEPYRIGQI,YRIGQIKEIF	TGCT
DNMT1	c.4591G>C	p.E1531Q	RHNHWAGLYGRLEWDGFFSTTVTNP[p.E1531Q]QPMGKQGRVLHPEQHRVVSVRECARS	VTNPQPMGK,TTVTNPQPM,QPMGKQGRV,TVTNPQPMGK,QPMGKQGRVL,STTVTNPQPM	CRC
DNMT3A	c.2207G>A	p.R736H	NDLSIVNPARKGLYEGTGRLFFEFY[p.R736H]HLLHDARPKEGDDRPFFWLFENVVAM	HLLHDARPK,FYHLLHDAR,FEFYHLLHD,EFYHLLHDAR,FEFYHLLHDA	LAML

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DNMT3A	c.2644C>T	p.R882C	DILWCTEMERVFGFPVHYTDVSNMS[p.R882C]CLARQRLLGRSWSVPVIRHLFAPLKE	VSNMSCLAR,NMSCLARQR,DVSNMSCLA,YTDVSNMSCL,NMSCLARQRL,CLARQRLLGR,DVSNMSCLAR,SNMSCLARQR	LAML
DNMT3A	c.2645G>A	p.R882H	DILWCTEMERVFGFPVHYTDVSNMS[p.R882H]HLARQRLLGRSWSVPVIRHLFAPLKE	YTDVSNMSH,VSNMSHLAR,MSHLARQRL,NMSHLARQR,DVSNMSHLA,YTDVSNMSHL,HLARQRLLGR,MSHLARQRLL,DVSNMSHLAR,SNMSHLARQR,NMSHLARQRL	LAML
DNMT3B	c.274C>T	p.R92W	TQDLTGDGDGEDGDGSDTPVMPKLF[p.R92W]WETRTRSESPAVRTRNNNSVSSRERH	VMPKLFWET,KLFWETRTR,MPKLFWETR,TPVMPKLFW,VMPKLFWETR	CRC
DOCK1	c.2590G>A	p.E864K	SKMFTEFILNVPMGLLTIQKLYCLI[p.E864K]KIVHSDLFTQHDCREILLPMMTDQLK	KLYCLIKIV,IQKLYCLIK,IKIVHSDLF,CLIKIVHSDL,TIQKLYCLIK,LIKIVHSDLF,IQKLYCLIKI	CRC
DOCK10	c.5489C>T	p.A1830V	NENILVEQLYMCVEFLWKSERYELI[p.A1830V]VDVNKPIIAVFEKQRDFKKLSDLYYD	LIVDVNKPI,ELIVDVNKPI,WKSERYELIV,SERYELIVDV	CRC
DOCK11	c.505C>G	p.Q169E	FEIDEDCEKDEDSSSLCSQKGGVIK[p.Q169E]EGWLHKANVNSTITVTMKVFKRRYFY	VIKEGWLHKA,GVIKEGWLHK,KEGWLHKANV	TGCT
DOCK3	c.3547C>T	p.R1183C	ELFSLLTQLFGPYPSLLEKVEQETW[p.R1183C]CETGISFVTSVTRLMERLLDYRDCMK	TWCETGISF,QETWCETGI,VEQETWCET,CETGISFVT,ETWCETGISF,CETGISFVTS	CRC
DOCK5	c.529G>A	p.E177K	IDHGNRMLGLDLVVRDDNGNILDPD[p.E177K]KTSTIALFKAHEVASKRIEEKIQEEK	KTSTIALFK,ILDPDKTSTI,KTSTIALFKA,DPDKTSTIAL	CRC
DOCK8	c.3332delT	p.L1111fs	TLISMRLEFLRILCSHEHYLNLNLF[p.L1111fs]L*	HYLNLNLFL	KICH
DOCK8	c.531_532insG	p.A177fs	HKTLPKQTFESETLECSEPAAQAGP[p.A177fs]PPLKRAVRRVWERPRHCL*	AQAGPPPLK,RAVRRVWER,GPPPLKRAV,AAQAGPPPL,LKRAVRRVW,AAQAGPPPLK,AVRRVWERPR,RVWERPRHCL	KIRC
DOK5	c.820C>T	p.R274W	KMSERAASLSTMVPLPRSAYWQHIT[p.R274W]WQHSTGQLYRLQDVSSPLKLHRTETF	SAYWQHITW,YWQHITWQH,WQHSTGQLY,WQHITWQHS,RSAYWQHITW,YWQHITWQHS,TWQHSTGQLY,WQHITWQHST,ITWQHSTGQL	CRC
DOK7	c.1382G>A	p.G461D	GQTSAGCPSGWLGTRRRGLVMEAPQ[p.G461D]DSEATLPGPAPGEPWEAGGPHAGPPP	APQDSEATL,MEAPQDSEA,MEAPQDSEAT	ACC
DOPEY2	c.3586G>A	p.E1196K	KAGAKLSLVRVDSDKTQASESFSSD[p.E1196K]KEADLELQALTTSRLLKQQRERQEAV	ASESFSSDK,KEADLELQA,QASESFSSDK,KEADLELQAL,SESFSSDKEA	BLCA
DOPEY2	c.6143A>C	p.Y2048S	FEQKAMLLKRQAFAVFSGELDQYHL[p.Y2048S]SLPLIQERLTDNLRVGQTSIVAAQMF	SLPLIQERL,QYHLSLPLI,LSLPLIQER,DQYHLSLPL,GELDQYHLS,HLSLPLIQER,GELDQYHLSL,LDQYHLSLPL,DQYHLSLPLI,LSLPLIQERL	KIRC
DPCR1	c.2302_2304delTTG	p.L768del	NRERTANENTTPSPAQPTENGDRTP[p.L768del]ANEKTTPSLAEPTENGKRTPFANEKTTS	TENGDRTPA	KIRC
DPEP1	c.31G>T	p.V11L	MWSGWWLWPL[p.V11L]LAVCTADFFRDEAERIMRDSPVIDGH	WLWPLLAVC,GWWLWPLLA,WWLWPLLAV,LLAVCTADF,SGWWLWPLL,LAVCTADFF,WPLLAVCTA,WLWPLLAVCT,WSGWWLWPLL,GWWLWPLLAV,LAVCTADFFR,LLAVCTADFF	BRCA
DPP10	c.547G>A	p.V183I	TASYVIYNIHTREVWELNPPEVEDS[p.V183I]ILQYAAWGVQGQQLIYIFENNIYYQP	EVEDSILQY,ILQYAAWGV,VEDSILQYA,NPPEVEDSI,SILQYAAWGV,EVEDSILQYA,PEVEDSILQY,VEDSILQYAA	GBM
DPP6	c.2271G>T	p.L757F	TFTCGSALSPITDFKLYASAFSERY[p.L757F]FGLHGLDNRAYEMTKVAHRVSALEEQ	FSERYFGLH,AFSERYFGL,ASAFSERYF,ERYFGLHGL,SAFSERYFGL,YASAFSERYF,SERYFGLHGL	LUAD
DPP8	c.493G>A	p.G165R	QATLDYGMYSREEELLRERKRIGTV[p.G165R]RIASYDYHQGSGTFLFQAGSGIYHVK	RKRIGTVRI,IGTVRIASY,TVRIASYDY,KRIGTVRIA,GTVRIASYDY,RERKRIGTVR,RIGTVRIASY,TVRIASYDYH,RKRIGTVRIA	CRC
DPY19L1	c.1134C>A	p.F378L	ILKYLTSKIFGIADDAHIGNLLTSK[p.F378L]LFSYKDFDTLLYTCAAEFDFMEKETP	LTSKLFSYK,LLTSKLFSY,GNLLTSKLF,SKLFSYKDF,KLFSYKDFDT,LLTSKLFSYK,NLLTSKLFSY,IGNLLTSKLF	CRC
DPY19L1	c.745G>T	p.V249L	MLLVTHILRATKLYRGSLIALCISN[p.V249L]LFFMLPWQFAQFVLLTQIASLFAVYV	LIALCISNL,CISNLFFML,IALCISNLF,LFFMLPWQF,ALCISNLFF,LCISNLFFM,SNLFFMLPW,SLIALCISNL,ALCISNLFFM,IALCISNLFF,NLFFMLPWQF,LIALCISNLF,ISNLFFMLPW	KIRP

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DPY19L2	c.628A>G	p.M210V	INAIKRFHLYPEVIIASWYCTFMGI[p.M210V]VNLFGLETKTCWNVTRIEPLNEVQSC	CTFMGIVNL,CTFMGIVNLF,SWYCTFMGIV	PRAD
DQX1	c.1514G>A	p.R505H	ASCEFDCVDEMLTLAAMLTAAPGFT[p.R505H]HPPLSAEEAALRRALEHTDGDHSSLI	APGFTHPPL,MLTAAPGFTH	GBM
DRD5	c.825C>A	p.S275R	RIAQVQIRRISSLERAAEHAQSCRS[p.S275R]RAACAPDTSLRASIKKETKVLKTLSV	HAQSCRSRA,RSRAACAPD,AQSCRSRAA,RSRAACAPDT,RAACAPDTSL,AQSCRSRAAC	GBM
DSG4	c.383G>T	p.R128L	NPRTGEINITSVVDREITPLFLIYC[p.R128L]LALNSRGEDLERPLELRVKVMDINDN	FLIYCLALN,IYCLALNSR,TPLFLIYCL,FLIYCLALNS,ITPLFLIYCL,LIYCLALNSR,TPLFLIYCLA	LUAD
DSP	c.478C>G	p.R160G	CDAYQKRLLQLQEQMRALYKAISVP[p.R160G]GVRRASSKGGGGYTCQSGSGWDEFTK	AISVPGVRR,KAISVPGVR,GVRRASSKG,YKAISVPGV,KAISVPGVRR,LYKAISVPGV	HNSC
DST	c.13228G>T	p.A4410S	TICGKSVERQNKLEEALLFSGQFTD[p.A4410S]SLQALIDWLYRVEPQLAEDQPVHGDI	FTDSLQALI,SLQALIDWL,FSGQFTDSL,GQFTDSLQA,FTDSLQALID,SLQALIDWLY,GQFTDSLQAL,QFTDSLQALI	LUAD
DST	c.5300C>A	p.S1767Y	ITLTRSLSVQDGLDEMLDWMGNVES[p.S1767Y]YLKEQGQVPLNSTALQDIISKNIMLE	WMGNVESYL,MGNVESYLK,YLKEQGQVPL,WMGNVESYLK,DWMGNVESYL,ESYLKEQGQV,LDWMGNVESY	UCEC
DSTN	c.301_302insT	p.F101fs	KDCRYALYDASFETKESRKEELMFF[p.F101fs]FVGTRTSTSEK*	LMFFFVGTR,GTRTSTSEK,ELMFFFVGT,RKEELMFFF,EELMFFFVG,KEELMFFFV,LMFFFVGTRT,ELMFFFVGTR,SRKEELMFFF,FFFVGTRTST,EELMFFFVGT,KEELMFFFVG	STAD
DUOX2	c.2640C>A	p.F880L	SPEDKSRLMFTMYDLDENGFLSKDE[p.F880L]LFTMMRSFIEISNNCLSKAQLAEVVE	FLSKDELFT,GFLSKDELF,LFTMMRSFI,ELFTMMRSF,LSKDELFTM,SKDELFTMM,DELFTMMRS,FLSKDELFTM,ELFTMMRSFI,NGFLSKDELF,LSKDELFTMM,DELFTMMRSF	CRC
DVL2	c.1801delG	p.A601fs	YGGGSASSQHSEGSRSSGSTRSDGG[p.A601fs]QGARGGPRSGPPSPSPAVAVSLSPPAEGAAFGGVGKQVGLAMGALLHPEAQLGVPLISEPTQGSIPMDRPLAWPSPTTP*	ALLHPEAQL,SLSPPAEGA,GAAFGGVGK,GPPSPSPAV,SPPAEGAAF,EPTQGSIPM,IPMDRPLAW,RPLAWPSPT,VGKQVGLAM,KQVGLAMGA,PEAQLGVPL,AQLGVPLIS,GSIPMDRPL,LAWPSPTTP,AEGAAFGGV,AMGALLHPEA,LLHPEAQLGV,AVAVSLSPPA,SLSPPAEGAA,KQVGLAMGAL,LISEPTQGSI,STRSDGGQGA,RSGPPSPSPA,SPSPAVAVSL,HPEAQLGVPL,RPLAWPSPTT,LSPPAEGAAF,GVGKQVGLAM,SEPTQGSIPM,PEAQLGVPLI,AEGAAFGGVG	CRC
DVL2	c.197T>G	p.V66G	GDFKSVLQRPAGAKYFFKSMDQDFG[p.V66G]GVKEEISDDNARLPCFNGRVVSWLVS	SMDQDFGGV,KSMDQDFGGV,SMDQDFGGVK	GBM
DYNC2H1	c.2649G>T	p.E883D	KEWIVIGQVDMEALVEKHLFTVHDW[p.E883D]DKNFKALKIKGKEVERLPSAVKVDCL	HLFTVHDWDK,TVHDWDKNFK,HDWDKNFKAL	UCEC
DYRK1B	c.1633delC	p.Q545fs	DVPHKTHQAPASASSLPGTGAQLPP[p.Q545fs]SPDTLVVPHHQPHHHPRS*	HHQPHHHPR,LVVPHHQPH,SPDTLVVPH,LPPSPDTLV,QLPPSPDTLV,AQLPPSPDTL,LPPSPDTLVV	STAD
DYRK4	c.1402delA	p.K468fs	TASRRQTFFDSKGFPKNITNNRGKK[p.K468fs]DTQIPRTSRWC*	TQIPRTSRW,DTQIPRTSR,RGKKDTQIPR	STAD
DZIP3	c.964A>C	p.M322L	NLKYPGENDQSFSGKKCLKEGCTGD[p.M322L]LVRMLQCDVPGIVKILFEVVRKDEYI	KEGCTGDLV,CLKEGCTGDL	LUAD
E2F7	c.272T>G	p.I91S	PITPVKFVDRQQAEPWTPTANLKML[p.I91S]SSAASPDIRDREKKKGLFRPIENKDD	NLKMLSSAA,LKMLSSAAS,KMLSSAASP,MLSSAASPDI,LKMLSSAASP	TGCT
EAF2	c.327delA	p.V109fs	CILIINHDTGECRLEKLSSNITVKK[p.V109fs]QELKEAVKFSIVKNNSNNKCGIQPGLPIL*	ITVKKQELK,IVKNNSNNK,KQELKEAVK,KKQELKEAV,QELKEAVKF,KEAVKFSIV,CGIQPGLPI,SIVKNNSNNK,ELKEAVKFSI,KQELKEAVKF,CGIQPGLPIL	STAD
EBAG9	c.559G>A	p.E187K	EEDAAWQAEEVLRQQKLADREKRAA[p.E187K]KQQRKKMEKEAQRLMKKEQNKIGVKL	RAAKQQRKK,KQQRKKMEK,RAAKQQRKKM	CRC
EBF1	c.1058A>G	p.D353G	SYKSKQFCKGTPGRFIYTALNEPTI[p.D353G]GYGFQRLQKVIPRHPGDPERLPKEVI	ALNEPTIGY,PTIGYGFQR,NEPTIGYGF,IGYGFQRLQK,GYGFQRLQKV,TALNEPTIGY,LNEPTIGYGF	TGCT

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
EBPL	c.565C>G	p.L189V	YCWLYLFFFNGVWVLIPGLLLWQSW[p.L189V]VELKKMHQKETSSVKKFQ*	GLLLWQSWV,LLWQSWVEL,WQSWVELKK,LLLWQSWVEL,LLWQSWVELK,WQSWVELKKM	KICH,KIRP,TGCT
EBPL	c.587A>C	p.Q196P	FFNGVWVLIPGLLLWQSWLELKKMH[p.Q196P]PKETSSVKKFQ*	KMHPKETSS,KMHPKETSSV	KICH
ECE2	c.760G>A	p.D254N	DRGVSPCEDFYQFSCGGWIRRNPLP[p.D254N]NGRSRWNTFNSLWDQNQAILKHLLEN	NGRSRWNTF,NPLPNGRSRW	CESC
ECI2	c.164A>G	p.K55R	HMNRTAMRASQKDFENSMNQVKLLK[p.K55R]RDPGNEVKLKLYALYKQATEGPCNMP	LLKRDPGNEV,SMNQVKLLKR	TGCT
ECM1	c.796G>A	p.E266K	EIGYSRCCHCRSHTNRLECAKLVWE[p.E266K]KAMSRFCEAEFSVKTRPHWCCTRQGE	KAMSRFCEA,VWEKAMSRF,LVWEKAMSR,AKLVWEKAM,WEKAMSRFC,KLVWEKAMSR,LVWEKAMSRF,CAKLVWEKAM	BLCA
EDA	c.174G>C	p.L58F	RAGEGNSCLLFLGFFGLSLALHLLT[p.L58F]FCCYLELRSELRRERGAESRLGGSGT	HLLTFCCYL,LTFCCYLEL,SLALHLLTF,TFCCYLELR,LHLLTFCCY,LLTFCCYLEL,SLALHLLTFC,LTFCCYLELR,LSLALHLLTF,ALHLLTFCCY	HNSC
EDNRB	c.1349T>G	p.L450R	SRILKLTLYNQNDPNRCELLSFLLV[p.L450R]WDYIGINMASLNSCINPIALYLVSKR	LSFLLVWDY,LLVWDYIGI,SFLLVWDYI,WDYIGINMA,FLLVWDYIGI,LLSFLLVWDY,CELLSFLLVW,LVWDYIGINM	CRC
EEA1	c.1709delA	p.N570fs	EREDLYAKIQAGEGETAVLNQLQEK[p.N570fs]TIHYRSK*	QLQEKTIHY,QLQEKTIHYR,NQLQEKTIHY	STAD
EEF1A1	c.1294_1295AC>TT	p.T432L	GKPMCVESFSDYPPLGRFAVRDMRQ[p.T432L]LVAVGVIKAVDKKAAGAGKVTKSAQKA	QLVAVGVIK,AVRDMRQLV,FAVRDMRQL,RDMRQLVAV,RQLVAVGVI,QLVAVGVIKA,LVAVGVIKAV,AVRDMRQLVA,RQLVAVGVIK,FAVRDMRQLV	LIHC
EEF1A2	c.1253A>C	p.Y418S	SLKSGDAAIVEMVPGKPMCVESFSQ[p.Y418S]SPPLGRFAVRDMRQTVAVGVIKNVEK	ESFSQSPPL,SPPLGRFAV,SQSPPLGRF,SFSQSPPLGR,VESFSQSPPL,FSQSPPLGRF,SQSPPLGRFA	BLCA,TGCT
EEF1B2	c.127A>G	p.S43G	YLADKSYIEGYVPSQADVAVFEAVS[p.S43G]GPPPADLCHALRWYNHIKSYEKEKAS	EAVSGPPPA,FEAVSGPPP,FEAVSGPPPA	KIRP,PRAD,SKCM
EEF2K	c.2017G>A	p.E673K	TDCDEGGEYDGMQDEPRYMMLAREA[p.E673K]KMLFTGGYGLEKDPQRSGDLYTQAAE	MMLAREAKM,MLAREAKML,YMMLAREAK,AKMLFTGGY,LAREAKMLF,REAKMLFTG,YMMLAREAKM,MMLAREAKML,KMLFTGGYGL,MLAREAKMLF,RYMMLAREAK,EAKMLFTGGY,REAKMLFTGG	BLCA
EFCAB4B	c.793G>C	p.E265Q	MEQQIKSEKEQFLLKDTERFQARSQ[p.E265Q]QLEQKLLCKEQELEQLTQKQKRLEGQ	RFQARSQQL,RSQQLEQKL,SQQLEQKLL,QARSQQLEQK,ERFQARSQQL,FQARSQQLEQ,RSQQLEQKLL	LUAD
EFCAB6	c.1136G>A	p.R379K	NWKQFLTSFHEPQGLQVSSKGPLTK[p.R379K]KNSINSRNESHKENIITKLFRHTEDH	SSKGPLTKK,GPLTKKNSI,VSSKGPLTKK,LTKKNSINSR	BLCA,GBM,PRAD
EFCAB6	c.3004G>A	p.E1002K	DQSKTNYISICKMQEVLEECGCSLT[p.E1002K]KGELTHLLNSWGVSRHDNAINYLDFL	SLTKGELTHL	HNSC
EGFR	c.1786C>T	p.P596S	CTGRGPDNCIQCAHYIDGPHCVKTC[p.P596S]SAGVMGENNTLVWKYADAGHVCHLCH	CVKTCSAGV,VKTCSAGVM,CVKTCSAGVM	GBM
EGFR	c.1787C>T	p.P596L	CTGRGPDNCIQCAHYIDGPHCVKTC[p.P596L]LAGVMGENNTLVWKYADAGHVCHLCH	CVKTCLAGV,GPHCVKTCL,VKTCLAGVM	GBM
EGFR	c.1793G>C	p.G598A	GRGPDNCIQCAHYIDGPHCVKTCPA[p.G598A]AVMGENNTLVWKYADAGHVCHLCHPN	CVKTCPAAV,VKTCPAAVM,AVMGENNTL,AVMGENNTLV,CVKTCPAAVM,AAVMGENNTL	GBM
EGFR	c.1793G>T	p.G598V	GRGPDNCIQCAHYIDGPHCVKTCPA[p.G598V]VVMGENNTLVWKYADAGHVCHLCHPN	CVKTCPAVV,VKTCPAVVM,VVMGENNTLV,CVKTCPAVVM	GBM
EGFR	c.185T>G	p.L62R	KLTQLGTFEDHFLSLQRMFNNCEVV[p.L62R]RGNLEITYVQRNYDLSFLKTIQEVAG	MFNNCEVVR,EVVRGNLEI,VRGNLEITY,RMFNNCEVVR,VVRGNLEITY,CEVVRGNLEI	GBM
EGFR	c.2125G>A	p.E709K	QERELVEPLTPSGEAPNQALLRILK[p.E709K]KTEFKKIKVLGSGAFGTVYKGLWIPE	RILKKTEFK,ILKKTEFKK,QALLRILKK,LRILKKTEF,RILKKTEFKK,NQALLRILKK,LLRILKKTEF	GBM

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
EGFR	c.2156G>C	p.G719A	PSGEAPNQALLRILKETEFKKIKVL[p.G719A]ASGAFGTVYKGLWIPEGEKVKIPVAI	ASGAFGTVY,VLASGAFGT,LASGAFGTV,KIKVLASGA,KVLASGAFG,IKVLASGAF,KKIKVLASG,VLASGAFGTV,ASGAFGTVYK,KIKVLASGAF,LASGAFGTVY,KKIKVLASGA,TEFKKIKVLA	LUAD
EGFR	c.2235_2249delGGAATTAAGAGAAGC	p.ELREA746del	GAFGTVYKGLWIPEGEKVKIPVAIK[p.ELREA746del]TSPKANKEILDEAYVMASVDNPHVCRLLGICLTSTVQLIT	AIKTSPKANK,KVKIPVAIKT,KTSPKANKEI	LUAD
EGFR	c.2303G>T	p.S768I	AIKELREATSPKANKEILDEAYVMA[p.S768I]IVDNPHVCRLLGICLTSTVQLITQLM	MAIVDNPHV,VMAIVDNPH,DEAYVMAIV,LDEAYVMAI,ILDEAYVMAI,VMAIVDNPHV,AIVDNPHVCR,YVMAIVDNPH,DEAYVMAIVD	LUAD
EGFR	c.2512C>A	p.L838M	YLLNWCVQIAKGMNYLEDRRLVHRD[p.L838M]MAARNVLVKTPQHVKITDFGLAKLLG	RLVHRDMAA,DMAARNVLV,MAARNVLVK,LVHRDMAAR,RDMAARNVL,RLVHRDMAAR,DMAARNVLVK,HRDMAARNVL,RDMAARNVLV	KIRC
EGFR	c.2573T>G	p.L858R	LVHRDLAARNVLVKTPQHVKITDFG[p.L858R]RAKLLGAEEKEYHAEGGKVPIKWMAL	KITDFGRAK,HVKITDFGR,FGRAKLLGA,HVKITDFGRA,RAKLLGAEEK	LUAD
EGFR	c.2582T>A	p.L861Q	RDLAARNVLVKTPQHVKITDFGLAK[p.L861Q]QLGAEEKEYHAEGGKVPIKWMALESI	LAKQLGAEEK,KQLGAEEKEY	LUSC
EGFR	c.323G>A	p.R108K	QEVAGYVLIALNTVERIPLENLQII[p.R108K]KGNMYYENSYALAVLSNYDANKTGLK	QIIKGNMYY,LQIIKGNMY,LQIIKGNMYY,KGNMYYENSY	GBM
EGFR	c.754C>T	p.R252C	SPSDCCHNQCAAGCTGPRESDCLVC[p.R252C]CKFRDEATCKDTCPPLMLYNPTTYQM	RESDCLVCC	GBM
EGFR	c.865G>A	p.A289T	CPPLMLYNPTTYQMDVNPEGKYSFG[p.A289T]TTCVKKCPRNYVVTDHGSCVRACGAD	YSFGTTCVK,TTCVKKCPR,GKYSFGTTC,YSFGTTCVKK,KYSFGTTCVK,GTTCVKKCPR,GKYSFGTTCV	GBM
EGFR	c.866C>A	p.A289D	CPPLMLYNPTTYQMDVNPEGKYSFG[p.A289D]DTCVKKCPRNYVVTDHGSCVRACGAD	YSFGDTCVK,DTCVKKCPR,GKYSFGDTC,YSFGDTCVKK,KYSFGDTCVK,GKYSFGDTCV	GBM
EGFR	c.866C>T	p.A289V	CPPLMLYNPTTYQMDVNPEGKYSFG[p.A289V]VTCVKKCPRNYVVTDHGSCVRACGAD	YSFGVTCVK,KYSFGVTCV,VTCVKKCPR,GKYSFGVTC,YSFGVTCVKK,KYSFGVTCVK,GVTCVKKCPR,GKYSFGVTCV	GBM
EGFR	c.910C>T	p.H304Y	VNPEGKYSFGATCVKKCPRNYVVTD[p.H304Y]YGSCVRACGADSYEMEEDGVRKCKKC	VVTDYGSCV,YVVTDYGSCV,VVTDYGSCVR,CPRNYVVTDY	GBM
EGR1	c.27G>C	p.Q9H	MAAAKAEM[p.Q9H]HLMSPLQISDPFGSFPHSPTMDNYPK	AAKAEMHLM,AEMHLMSPL,MHLMSPLQI,MAAAKAEMHL,AAAKAEMHLM,KAEMHLMSPL,EMHLMSPLQI,AEMHLMSPLQ	MM
EGR1	c.994delC	p.P332fs	TSYQSQLIKPSRMRKYPNRPSKTPP[p.P332fs]TNALTLAQWSPVIAASPAPTSSPATSASTQARSPSSAASACATSAAATTSPPTSAPTQAKSPSPATSVEESLPGAMNARGIPRSTCGRRTRKQTKVLWPLRPPPLSLPTRPRLLPLTRPRLLPLIHPRPPPHTHPLCPPPSPLPAPRPTHPLCTVASPPRRWPPRTPLFPLLSRPRSAASLPQLSPTPSAPPQGFRT*	LTLAQWSPV,TLAQWSPVI,AQWSPVIAA,KQTKVLWPL,VIAASPAPT,AMNARGIPR,RLLPLTRPR,RLLPLIHPR,ATSASTQAR,STCGRRTRK,CTVASPPRR,LWPLRPPPL,STQARSPSS,QARSPSSAA,RSPSSAASA,ASACATSAA,KSPSPATSV,RSTCGRRTR,RTRKQTKVL,QTKVLWPLR,PTRPRLLPL,RPRLLPLTR,LTRPRLLPL,LIHPRPPPH,SLPGAMNAR,ESLPGAMNA,SPVIAASPA,SPAPTSSPA,RPPPLSLPT,LPLTRPRLL,RPRLLPLIH,HPRPPPHTH,RPPPHTHPL,SPLPAPRPT,APRPTHPLC,RPTHPLCTV,SLPTRPRLL,SKTPPTNAL,TQARSPSSA,TQAKSPSPA,VEESLPGAM,LSLPTRPRL,CPPPSPLPA,ALTLAQWSPV,TLAQWSPVIA,VLWPLRPPPL,RLLPLTRPRL,GAMNARGIPR,RSTCGRRTRK,KTPPTNALTL,STQARSPSSA,ASACATSAAA,RGIPRSTCGR,CGRRTRKQTK,RTRKQTKVLW,KQTKVLWPLR,KVLWPLRPPP,LTRPRLLPLI,HTHPLCPPPS,ESLPGAMNAR,WSPVIAASPA,TTSPPTSAPT,RPSKTPPTNA,SPAPTSSPAT,APTSSPATSA,SPATSASTQA,SPATSVEESL,LPGAMNARGI,WPLRPPPLSL,LPTRPRLLPL,HPLCPPPSPL,LPAPRPTHPL,APRPTHPLCT,RPTHPLCTVA,LTLAQWSPVI,AQWSPVIAAS,TQARSPSSAA,TQAKSPSPAT,AKSPSPATSV,RKQTKVLWPL,LSLPTRPRLL,EESLPGAMNA	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
EGR2	c.1105G>A	p.E369K	SKTPVHERPYPCPAEGCDRRFSRSD[p.E369K]KLTRHIRIHTGHKPFQCRICMRNFSR	RRFSRSDKL	CLL
EGR2	c.1169G>A	p.R390H	SRSDELTRHIRIHTGHKPFQCRICM[p.R390H]HNFSRSDHLTTHIRTHTGEKPFACDY	RICMHNFSR,HNFSRSDHL,FQCRICMHNF,CMHNFSRSDH,MHNFSRSDHL	CRC
EGR2	c.1189C>A	p.H397N	RHIRIHTGHKPFQCRICMRNFSRSD[p.H397N]NLTTHIRTHTGEKPFACDYCGRKFAR	RNFSRSDNL,RSDNLTTHI,MRNFSRSDNL,FSRSDNLTTH,SRSDNLTTHI	CLL
EHD3	c.130G>A	p.E44K	QTVSEGLKKLYKSKLLPLEEHYRFH[p.E44K]KFHSPALEDADFDNKPMVLLVGQYST	HYRFHKFHS,RFHKFHSPA,FHKFHSPAL,EEHYRFHKF,YRFHKFHSP,RFHKFHSPAL,YRFHKFHSPA,LEEHYRFHKF,EEHYRFHKFH	CRC
EHHADH	c.2112G>T	p.Q704H	LQKYYRQNPDIPQLEPSDYLKKLAS[p.Q704H]HGNPPLKEWQSLAGSPSSKL*	ASHGNPPLK,LASHGNPPL,KLASHGNPPL,LASHGNPPLK	LUAD
EIF1AX	c.26G>A	p.G9D	MPKNKGKG[p.G9D]DKNRRRGKNENESEKRELVFKEDGQE	KGDKNRRRGK	THCA
EIF2C1	c.416G>A	p.R139Q	EVTIPGEGKDRIFKVSIKWLAIVSW[p.R139Q]QMLHEALVSGQIPVPLESVQALDVAM	WLAIVSWQM,WQMLHEALV,AIVSWQMLH,SWQMLHEAL,LAIVSWQML,WLAIVSWQML,IVSWQMLHEA,KWLAIVSWQM,SWQMLHEALV,VSWQMLHEAL,WQMLHEALVS	CRC
EIF3J	c.23C>G	p.A8G	MAAAAAA[p.A8G]GGDSDSWDADAFSVEDPVRKVGGGGT	AAAGGDSDSW	TGCT
EIF4G3	c.23G>A	p.R8H	MNSQPQT[p.R8H]HSPFFQRPQIQPPRATIPNSSPSIRP	QTHSPFFQR,SQPQTHSPF,QPQTHSPFF,SQPQTHSPFF,NSQPQTHSPF	CLL
ELAVL2	c.789G>T	p.L263F	RLDNLLNMAYGVKRFSPMTIDGMTS[p.L263F]FAGINIPGHPGTGWCIFVYNLAPDAD	MTIDGMTSF,TIDGMTSFA,DGMTSFAGI,MTSFAGINI,MTIDGMTSFA,GMTSFAGINI,PMTIDGMTSF	LUAD
ELF3	c.915delC	p.F305fs	DILIHPELNEGLMKWENRHEGVFKF[p.F305fs]CAPRLWPNYGAKRKRTAT*	GVFKFCAPR,RLWPNYGAK,VFKFCAPRL,CAPRLWPNY,YGAKRKRTA,FKFCAPRLW,HEGVFKFCA,RLWPNYGAKR,VFKFCAPRLW,FCAPRLWPNY,EGVFKFCAPR,APRLWPNYGA,GVFKFCAPRL	CRC
ELF4	c.1244C>T	p.S415L	KLTKAVSASSVPSNIHLGVAPVGSG[p.S415L]LALTLQTIPLTTVLTNGPPASTTAPT	GLALTLQTI,GVAPVGSGL,APVGSGLAL,VGSGLALTL,GVAPVGSGLA,LGVAPVGSGL,SGLALTLQTI,LALTLQTIPL	HNSC
ELMOD2	c.422C>T	p.T141M	RKRPYDSDNLQHEELLMKLWNLLMP[p.T141M]MKKLNARISKQWAEIGFQGDDPKTDF	KLWNLLMPM,LWNLLMPMK,MPMKKLNAR,LLMPMKKLNA,KLWNLLMPMK,LWNLLMPMKK,MKKLNARISK,LMPMKKLNAR,MPMKKLNARI,MKLWNLLMPM	CRC
EME1	c.1708G>C	p.D570H	IGPELSRRIYLQMTTLQPHLSLDSA[p.D570H]H*	QPHLSLDSAH	LUSC
EMILIN1	c.79C>G	p.R27G	APRTLWSCYLCCLLTAAAGAASYPP[p.R27G]GGFSLYTGSSGALSPGGPQAQIAPRP	SYPPGGFSL,YPPGGFSLY,AASYPPGGF,SYPPGGFSLY,ASYPPGGFSL,GAASYPPGGF	BLCA
EML6	c.2414A>G	p.K805R	FSADGKCLVSVGLDDFHSIVFWDWK[p.K805R]RGEKIATTRGHKDKIFVVKCNPHHVD	SIVFWDWKR,WDWKRGEKI,HSIVFWDWKR,VFWDWKRGEK	TGCT
EMR1	c.1478G>A	p.R493H	EESESTETTGVAFVSFVGMESVLNE[p.R493H]HFFKDHQAPLTTSEIKLKMNSRVVGG	SVLNEHFFK,MESVLNEHF,ESVLNEHFFK,HFFKDHQAPL,GMESVLNEHF,MESVLNEHFF,NEHFFKDHQA	LUAD
EMR1	c.1892G>A	p.R631Q	SHVGIIISLVCLVLAIATFLLCRSI[p.R631Q]QNHNTYLHLHLCVCLLLAKTLFLAGI	SIQNHNTYL,RSIQNHNTY,IQNHNTYLH,QNHNTYLHL,RSIQNHNTYL,IQNHNTYLHL,CRSIQNHNTY	UCEC
EMR2	c.224C>T	p.S75L	GFSSFSEIITTPMETCDDINECATL[p.S75L]LKVSCGKFSDCWNTEGSYDCVCSPGY	TLLKVSCGK,DINECATLL,LLKVSCGKF,NECATLLKV,ATLLKVSCGK,DINECATLLK,TLLKVSCGKF	CRC
ENAH	c.1541G>T	p.R514L	TPEPTRKPWERTNTMNGSKSPVISR[p.R514L]LDSPRKNQIVFDNRSYDSLHRPKSTP	VISRLDSPR,ISRLDSPRK,SKSPVISRL,VISRLDSPRK,GSKSPVISRL,PVISRLDSPR	LUAD
ENAM	c.1118G>A	p.R373H	PFYRNQQVQRGPRWNFFAWERKQVA[p.R373H]HPGNPVYHKAYPPTSRGNYPNYAGNP	QVAHPGNPV,VAHPGNPVY,KQVAHPGNPV,QVAHPGNPVY,FAWERKQVAH	CRC
ENOX2	c.1066C>T	p.R356W	QFEQIVAVYHSASKQKAWDHFTKAQ[p.R356W]WKNISVWCKQAEEIRNIHNDELMGIR	AQWKNISVW,KAQWKNISV,HFTKAQWKNI,QWKNISVWCK,KAQWKNISVW,AQWKNISVWC	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ENPEP	c.866T>G	p.F289C	EESVDDKWTRTTFEKSVPMSTYLVC[p.F289C]CAVHQFDSVKRISNSGKPLTIYVQPE	STYLVCCAV,MSTYLVCCA,CAVHQFDSV,LVCCAVHQF,YLVCCAVHQF,MSTYLVCCAV,CAVHQFDSVK	KIRC
ENPP1	c.2213G>A	p.G738E	YQDFRIPLSPVHKCSFYKNNTKVSY[p.G738E]EFLSPPQLNKNSSGIYSEALLTTNIV	NTKVSYEFL,YEFLSPPQL,SYEFLSPPQL,EFLSPPQLNK,KNNTKVSYEF,YEFLSPPQLN	LUAD
ENTPD2	c.611delG	p.G204fs	NFIKYGWVGRWFRPRKGTLGAMDLG[p.G204fs]VPLPRSLLRQPVQLRTEPARSSCISTASTTESTPTASSAMAVTRSSRGCWPAPSRPTASTPAGRGAFPPKCCSGMCTSHHAPWPSGPRTSTAVPGSACQGAVTPTSAEIWFLGSSASPPAPSPDALSMGSSSPQWLGTLWPSLPSSTLWTFCGLRWGCPWPPCSSWRQPQ*	TLGAMDLGV,SLLRQPVQL,WLGTLWPSL,TLWPSLPSS,STLWTFCGL,AVTPTSAEI,ASSAMAVTR,TLWTFCGLR,LWTFCGLRW,RSLLRQPVQ,LLRQPVQLR,AMAVTRSSR,RSSRGCWPA,SSRGCWPAP,RGCWPAPSR,AGRGAFPPK,HAPWPSGPR,STTESTPTA,ESTPTASSA,STPTASSAM,EIWFLGSSA,WPAPSRPTA,APSRPTAST,RPTASTPAG,FPPKCCSGM,WPSGPRTST,APSPDALSM,WPSLPSSTL,LPSSTLWTF,GAMDLGVPL,LGVPLPRSL,ARSSCISTA,MCTSHHAPW,SMGSSSPQW,CGLRWGCPW,TPTSAEIWF,SPQWLGTLW,CPWPPCSSW,AEIWFLGSS,GTLGAMDLGV,FLGSSASPPA,SMGSSSPQWL,TLWPSLPSST,AMDLGVPLPR,SAMAVTRSSR,STLWTFCGLR,QWLGTLWPSL,LWPSLPSSTL,SLPSSTLWTF,RSLLRQPVQL,RTEPARSSCI,RSSCISTAST,SSRGCWPAPS,RTSTAVPGSA,SLLRQPVQLR,TASSAMAVTR,HHAPWPSGPR,STPTASSAMA,TSAEIWFLGS,SSTLWTFCGL,WTFCGLRWGC,LPRSLLRQPV,QPVQLRTEPA,TPTASSAMAV,WPAPSRPTAS,WPSGPRTSTA,VPGSACQGAV,SPPAPSPDAL,ASTPAGRGAF,ESTPTASSAM,LSMGSSSPQW,LGAMDLGVPL,GMCTSHHAPW,CQGAVTPTSA,AEIWFLGSSA,SSSPQWLGTL,TPTSAEIWFL,WPSLPSSTLW,TESTPTASSA,LPSSTLWTFC	STAD
ENTPD7	c.979G>A	p.E327K	HTEHVYRVYVTTFLGFGGNFARQRY[p.E327K]KDLVLNETLNKNRLLGQKTGLSPDNP	GNFARQRYK,RQRYKDLVL,FARQRYKDL,KDLVLNETL,GGNFARQRYK,RQRYKDLVLN,FARQRYKDLV,YKDLVLNETL	CRC
EOMES	c.995delG	p.G332fs	LNPTAHYNVFVEVVLADPNHWRFQG[p.G332fs]ANG*	HWRFQGANG	STAD
EP300	c.3491G>A	p.C1164Y	YKYCSKLSEVFEQEIDPVMQSLGYC[p.C1164Y]YGRKLEFSPQTLCCYGKQLCTIPRDA	SLGYCYGRK,YCYGRKLEF,VMQSLGYCY,QSLGYCYGR,LGYCYGRKL,QSLGYCYGRK,GYCYGRKLEF,PVMQSLGYCY,MQSLGYCYGR	HNSC
EP300	c.4195G>A	p.D1399N	FGMHVQEYGSDCPPPNQRRVYISYL[p.D1399N]NSVHFFRPKCLRTAVYHEILIGYLEY	YLNSVHFFR,NSVHFFRPK,VYISYLNSV,ISYLNSVHF,SYLNSVHFF,RVYISYLNS,YISYLNSVH,RVYISYLNSV,SYLNSVHFFR,YISYLNSVHF,ISYLNSVHFF,LNSVHFFRPK	CESC,HNSC,LUSC
EPB41L3	c.2686G>T	p.A896S	SYSAGDSGDAAAQPAFTGIKGKEGS[p.A896S]SLTEGAKEEGGEEVAKAVLEQEETAA	GSSLTEGAK,IKGKEGSSL,KEGSSLTEGA	LUAD
EPG5	c.1105G>A	p.D369N	KVFSYHRYQRVEMNENALVELKKLF[p.D369N]NAKSEHLHQTLALHSYTSVLSRLQVE	KLFNAKSEH,ELKKLFNAK,VELKKLFNA,KLFNAKSEHL	CRC
EPG5	c.6866G>T	p.R2289L	MALSSLFMEVLMMMNNATIPTAEFL[p.R2289L]LGSIRTWIGQKMHGLVVLPLLTAACQ	LLGSIRTWI,TIPTAEFLL,FLLGSIRTW,FLLGSIRTWI,EFLLGSIRTW,ATIPTAEFLL,AEFLLGSIRT	LUAD
EPHA1	c.332G>T	p.G111V	IYRGEEASRVHVELQFTVRDCKSFP[p.G111V]VGAGPLGCKETFNLLYMESDQDVGIQ	FPVGAGPLG,TVRDCKSFPV,KSFPVGAGPL,FPVGAGPLGC	LUAD
EPHA1	c.550G>A	p.A184T	LVSGSVKLNVERCSLGRLTRRGLYL[p.A184T]TFHNPGACVALVSVRVFYQRCPETLN	YLTFHNPGA,LTRRGLYLT,TRRGLYLTF,LTFHNPGACV,LTRRGLYLTF	GBM
EPHA10	c.2604delC	p.P868fs	ERPYWDMSGQDVIKAVEDGFRLPPP[p.P868fs]GTVLTFCTD*	RLPPPGTVL,GFRLPPPGTV,LPPPGTVLTF,FRLPPPGTVL	STAD
EPHA2	c.1379delC	p.P460fs	NQTEPPKVRLEGRSTTSLSVSWSIP[p.P460fs]RRSRAECGSTRSLTARRETPTATMCAAPRVSP*	ATMCAAPRV,LSVSWSIPR,SVSWSIPRR,GSTRSLTAR,RSRAECGST,STRSLTARR,RSLTARRET,TARRETPTA,SWSIPRRSR,TATMCAAPR,ETPTATMCA,IPRRSRAEC,TPTATMCAA,AECGSTRSL,RRETPTATM,RETPTATMC,SLSVSWSIPR,LSVSWSIPRR,SWSIPRRSRA,RSRAECGSTR,VSWSIPRRSR,PTATMCAAPR,ETPTATMCAA,TATMCAAPRV,RAECGSTRSL,ARRETPTATM,RETPTATMCA,AECGSTRSLT	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
EPHA3	c.2405C>G	p.T802R	AAYTTRGGKIPIRWTSPEAIAYRKF[p.T802R]RSASDVWSYGIVLWEVMSYGERPYWE	RSASDVWSY,KFRSASDVW,IAYRKFRSA,AYRKFRSAS,EAIAYRKFR,RKFRSASDV,AIAYRKFRSA,KFRSASDVWS,IAYRKFRSAS,RKFRSASDVW,FRSASDVWSY	HNSC
EPHA6	c.2854G>C	p.D952H	TTGGKIPIRWTAPEAIAYRKFSSAS[p.D952H]HAWSYGIVMWEVMSYGERPYWEMSNQ	SSASHAWSY,KFSSASHAW,ASHAWSYGI,HAWSYGIVM,YRKFSSASH,RKFSSASHA,FSSASHAWSY,AYRKFSSASH,ASHAWSYGIV,SASHAWSYGI,RKFSSASHAW,SHAWSYGIVM,HAWSYGIVMW	HNSC
EPHB2	c.1175G>A	p.R392H	SGRGACTRCGDNVQYAPRQLGLTEP[p.R392H]HIYISDLLAHTQYTFEIQAVNGVTDQ	GLTEPHIYI,RQLGLTEPH,LGLTEPHIY,RQLGLTEPHI,QLGLTEPHIY,HIYISDLLAH,TEPHIYISDL	CRC
EPHB6	c.1010G>A	p.R337H	KACQACPRGLYKSSAGNAPCSPCPA[p.R337H]HSHAPNPAAPVCPCLEGFYRASSDPP	HSHAPNPAA	LUAD
EPHB6	c.160delG	p.G54fs	ALEEVLLDTTGETSEIGWLTYPPGG[p.G54fs]GTR*	LTYPPGGGTR	STAD
EPHX1	c.394delC	p.P132fs	ILNRYPHFKTKIEGLDIHFIHVKPP[p.P132fs]SCPQAIPRSPC*	KPPSCPQAI,HVKPPSCPQA,CPQAIPRSPC	STAD
EPHX4	c.845G>A	p.R282Q	TTEDLEAYIYVFSQPGALSGPINHY[p.R282Q]QNIFSCLPLKHHMVTTPTLLLWGEND	HYQNIFSCL,GPINHYQNI,YQNIFSCLP,QNIFSCLPL,YQNIFSCLPL,QNIFSCLPLK,GPINHYQNIF,NHYQNIFSCL	UCEC
EPPK1	c.6044delG	p.G2015fs	FQAMQKQLIEKAEALRLLEVQVATG[p.G2015fs]VSSTHSTTTGSHWKQPTDGAVCTRTSMRSFPTRST*	STTTGSHWK,AVCTRTSMR,TSMRSFPTR,CTRTSMRSF,RTSMRSFPT,SMRSFPTRS,LEVQVATGV,VQVATGVSS,HSTTTGSHW,WKQPTDGAV,GAVCTRTSM,LLEVQVATGV,RTSMRSFPTR,HSTTTGSHWK,STHSTTTGSH,CTRTSMRSFP,SMRSFPTRST,VQVATGVSST,VCTRTSMRSF	STAD
EPPK1	c.7132G>C	p.D2378H	HSHRVPVDVAYRRGYFDEEMNRVLA[p.D2378H]HPSDDTKGFFDPNTHENLTYLQLLQR	EEMNRVLAH,HPSDDTKGF,VLAHPSDDTK,HPSDDTKGFF,DEEMNRVLAH	ACC
EPRS	c.3451G>T	p.V1151L	MYPAYAKWVQSHRDLPIKLNQWCNV[p.V1151L]LRWEFKHPQPFLRTREFLWQEGHSAF	KLNQWCNVL,CNVLRWEFK,NQWCNVLRW,LNQWCNVLR,WCNVLRWEF,KLNQWCNVLR,QWCNVLRWEF,IKLNQWCNVL	LUAD
EPRS	c.4003C>A	p.L1335I	GITNALSEEDKEALIAKCNDYRRRL[p.L1335I]ISVNIRVRADLRDNYSPGWKFNHWEL	RLISVNIRV,RRRLISVNI,DYRRRLISV,RRRLISVNIR,RLISVNIRVR,NDYRRRLISV,YRRRLISVNI	TGCT
ERBB2	c.2264T>C	p.L755S	AFGTVYKGIWIPDGENVKIPVAIKV[p.L755S]SRENTSPKANKEILDEAYVMAGVGSP	VSRENTSPK,IPVAIKVSR,KVSRENTSPK,VSRENTSPKA	BRCA
ERBB2	c.2305G>T	p.D769Y	ENVKIPVAIKVLRENTSPKANKEIL[p.D769Y]YEAYVMAGVGSPYVSRLLGICLTSTV	ILYEAYVMA,YEAYVMAGV,NKEILYEAY,KEILYEAYV,EILYEAYVM,ILYEAYVMAG,ANKEILYEAY,EILYEAYVMA,KEILYEAYVM,SPKANKEILY,YEAYVMAGVG	BRCA
ERBB2	c.2310_2311insGCATACGTGATG	p.774_775insAYVM	AIKVLRENTSPKANKEILDEAYVMA[p.774_775insAYVM]YVMAGVGSPYVSRLLGICLTSTVQLVTQLMPYGCLLD	VMAYVMAGV,YVMAYVMAG,DEAYVMAYV,EAYVMAYVM,LDEAYVMAY,MAYVMAGVG,ILDEAYVMAY,YVMAYVMAGV,EAYVMAYVMA,DEAYVMAYVM	LUAD
ERBB2	c.2326_2327insTCT	p.776_776G>VC	AIKVLRENTSPKANKEILDEAYVMA[p.776_776G>VC]VCVGSPYVSRLLGICLTSTVQLVTQLMP	AVCVGSPYV,MAVCVGSPY,EAYVMAVCV,YVMAVCVGS,DEAYVMAVC,ILDEAYVMAV,MAVCVGSPYV,VMAVCVGSPY,DEAYVMAVCV	LUAD
ERBB2	c.2524G>A	p.V842I	LGSQDLLNWCMQIAKGMSYLEDVRL[p.V842I]IHRDLAARNVLVKSPNHVKITDFGLA	RLIHRDLAA,SYLEDVRLI,LIHRDLAAR,RLIHRDLAAR,YLEDVRLIHR,MSYLEDVRLI	CRC
ERBB2	c.2748G>A	p.M916I	LESILRRRFTHQSDVWSYGVTVWEL[p.M916I]ITFGAKPYDGIPAREIPDLLEKGERL	YGVTVWELI,VTVWELITF,LITFGAKPY,WELITFGAK,TVWELITFGA,SYGVTVWELI,ELITFGAKPY,GVTVWELITF,WELITFGAKP	HNSC
ERBB2	c.929C>A	p.S310Y	PEGRYTFGASCVTACPYNYLSTDVG[p.S310Y]YCTLVCPLHNQEVTAEDGTQRCEKCS	YLSTDVGYC,STDVGYCTLV,YLSTDVGYCT,YNYLSTDVGY,LSTDVGYCTL,VGYCTLVCPL	LUAD
ERBB2	c.929C>T	p.S310F	PEGRYTFGASCVTACPYNYLSTDVG[p.S310F]FCTLVCPLHNQEVTAEDGTQRCEKCS	STDVGFCTL,YLSTDVGFC,NYLSTDVGF,STDVGFCTLV,YLSTDVGFCT,YNYLSTDVGF,LSTDVGFCTL,VGFCTLVCPL	BLCA,BRCA,CESC,STAD
ERBB3	c.273G>A	p.M91I	VLTGHNADLSFLQWIREVTGYVLVA[p.M91I]INEFSTLPLPNLRVVRGTQVYDGKFA	YVLVAINEF,VAINEFSTL,INEFSTLPL,AINEFSTLPL,GYVLVAINEF,EVTGYVLVAI	BLCA

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ERBB3	c.310G>A	p.V104M	WIREVTGYVLVAMNEFSTLPLPNLR[p.V104M]MVRGTQVYDGKFAIFVMLNYNTNSSH	RMVRGTQVY,LPLPNLRMV,LRMVRGTQV,TLPLPNLRMV,NLRMVRGTQV,LRMVRGTQVY	CESC,CRC,STAD
ERBB3	c.310G>T	p.V104L	WIREVTGYVLVAMNEFSTLPLPNLR[p.V104L]LVRGTQVYDGKFAIFVMLNYNTNSSH	RLVRGTQVY,LPLPNLRLV,TLPLPNLRLV,NLRLVRGTQV,LRLVRGTQVY	BLCA
ERBB3	c.889G>T	p.D297Y	LEPNPHTKYQYGGVCVASCPHNFVV[p.D297Y]YQTSCVRACPPDKMEVDKNGLKMCEP	FVVYQTSCV,VVYQTSCVR,YQTSCVRAC,ASCPHNFVVY,FVVYQTSCVR	BLCA
ERC1	c.2075A>G	p.K692R	DLSEKEASLLDLKEHASSLASSGLK[p.K692R]RDSRLKTLEIALEQKKEECLKMESQL	GLKRDSRLK,SLASSGLKR,SSLASSGLKR,SGLKRDSRLK,LKRDSRLKTL	TGCT
ERCC2	c.41A>G	p.Y14C	MKLNVDGLLVYFP[p.Y14C]CDYIYPEQFSYMRELKRTLDAKGHGV	LVYFPCDYI,VYFPCDYIY,LLVYFPCDY,CDYIYPEQF,FPCDYIYPE,LLVYFPCDYI,LVYFPCDYIY,GLLVYFPCDY	BLCA
ERCC2	c.713A>G	p.N238S	LDPKIADLVSKELARKAVVVFDEAH[p.N238S]SIDNVCIDSMSVNLTRRTLDRCQGNL	VVFDEAHSI,EAHSIDNVCI	BLCA
ERCC2	c.934G>A	p.D312N	RLVEGLREASAARETDAHLANPVLP[p.D312N]NEVLQEAVPGSIRTAEHFLGFLRRLL	NPVLPNEVL,LPNEVLQEA,VLPNEVLQEA,LANPVLPNEV,LPNEVLQEAV	ACC
ERCC6	c.2338G>A	p.V780I	SLPDKNEQVLFCRLTDEQHKVYQNF[p.V780I]IDSKEVYRILNGEMQIFSGLIALRKI	FIDSKEVYR,NFIDSKEVY,YQNFIDSKEV,FIDSKEVYRI,KVYQNFIDSK,NFIDSKEVYR,QNFIDSKEVY	CRC
ERCC6L	c.1514G>A	p.R505Q	LVFSQSRQILNIIERLLKNRHFKTL[p.R505Q]QIDGTVTHLLEREKRINLFQQNKDYS	KTLQIDGTV,LQIDGTVTH,LQIDGTVTHL,KNRHFKTLQI	CRC
ERCC6L2	c.1333C>A	p.L445I	LGDTSILDDLFKSHGNSPTQLPKKV[p.L445I]ISGPMEKAKQRPKDFWDILNEQNDES	KVISGPMEK,VISGPMEKAK,SPTQLPKKVI,LPKKVISGPM	UCEC
ERN2	c.884C>A	p.T295K	TQDLGVPVMGVYTWHQDGLRQLPHL[p.T295K]KLARDTLHFLALRWGHIRLPASGPRD	GLRQLPHLK,KLARDTLHF,RQLPHLKLA,QLPHLKLAR,HLKLARDTL,KLARDTLHFL,RQLPHLKLAR,LKLARDTLHF	LUAD
ERRFI1	c.1261G>A	p.A421T	LLPERPPYLDKYEKFFREAEETNGG[p.A421T]TQIQPLPADCGISSATEKPDSKTKMD	AEETNGGTQI	CRC
ESCO1	c.899G>A	p.R300Q	TLPKSPQPSVPEQSDNELEQAGKSK[p.R300Q]QGSILQLCEEIAGEIESDNVEVKKES	KSKQGSILQ,GKSKQGSIL,SKQGSILQL,KSKQGSILQL	CRC
ESF1	c.295delA	p.T99fs	LSDSDSNLSGEDSKALSQKKIKKKK[p.T99fs]PRLKKKSIQKI*	RLKKKSIQK,KIKKKKPRL,KKKKPRLKK,KKKPRLKKK,KPRLKKKSI,LKKKSIQKI,RLKKKSIQKI,KIKKKKPRLK,KKKKPRLKKK	STAD
ESPN	c.1286_1348delCACCCCCACCACCCCCACCCAGCTTCCCCCCGCCACCCCCGCCCCCAGGCACCCAACTGCCCC	p.PPPPPPSFPPPPPPPGTQLPP430del	QSYMDMLNPELGLPRGTIGKPTPPP[p.PPPPPPSFPPPPPPPGTQLPP430del]GYPAPKPPVGPQAADIYMQTKNKLRHVETEALKKELSSCDGHDGLRRQDSSRKPRAFSKQPSTGDYYRQLGRCPGETLAARPGMAHSE	IGKPTPPPGY,KPTPPPGYPA	PAAD
ESPNP	c.1880G>A	p.R627Q	EEEQRWKEEEEARLASMPAWRWDLL[p.R627Q]QKKLEEE	AWRWDLLQK,AWRWDLLQKK,WRWDLLQKKL	GBM
ESPNP	c.191_198delACGCGCGC	p.H64fs	PLYLACQEGHLEVTQYLVQECGADP[p.H64fs]RPRRHDPTARRGADGPQPGHRVVGELHRREPVGAGQRRRHRHALRGEPRPQQGAQLAAAARRGDLG*	GQRRRHRHA,RRRHRHALR,RPRRHDPTA,GPQPGHRVV,QRRRHRHAL,RPQQGAQLA,AAAARRGDL,QQGAQLAAA,GELHRREPV,GQRRRHRHAL,LVQECGADPR,QPGHRVVGEL,EPRPQQGAQL,RPQQGAQLAA,LAAAARRGDL,QQGAQLAAAA	PAAD

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ESPNP	c.888_950delACCCCCACCCAGCTTCCCCCCGCCACCCCCGCCCCCAGGCACCCAACTGCCCCCACC	p.296_317PPPPSFPPPPPPPGTQLPPPPP	QSYMDMLNPELGLPWGTIGKPIPPP[p.296_317PPPPSFPPPPPPPGTQLPPPPP>P]SYPSPKPPVGPQAADIYMQTKNKLRHVETEALKKEPSSCDGHDGLRRQDSSRKPRAFSKQPSTGDYYRQLGRCPGETLVARPGMAHRE	IGKPIPPPSY	PAAD
ESRRA	c.655G>A	p.D219N	VNALVSHLLVVEPEKLYAMPDPAGP[p.D219N]NGHLPAVATLCDLFDREIVVTISWAK	GPNGHLPAV,MPDPAGPNGH	HNSC
ESYT1	c.2446C>T	p.R816W	LQVNSLIQTQKSAELAAALLSIYME[p.R816W]WAEDLPLRKGTKHLSPYATLTVGDSS	LLSIYMEWA,ALLSIYMEW,IYMEWAEDL,EWAEDLPLR,MEWAEDLPL,ALLSIYMEWA,YMEWAEDLPL,AALLSIYMEW	BRCA
ESYT3	c.1721C>T	p.S574F	QILPYADLTLEQRFQLDHSGLDSLI[p.S574F]FMRLVLRFLQVEERELGSPYTGPEAL	SLIFMRLVL,FMRLVLRFL,LIFMRLVLR,IFMRLVLRF,DSLIFMRLV,HSGLDSLIF,SGLDSLIFM,GLDSLIFMRL,SLIFMRLVLR,IFMRLVLRFL,SGLDSLIFMR,LIFMRLVLRF,HSGLDSLIFM	LUSC
ETFDH	c.841A>T	p.I281F	LYKKFDLRANCEPQTYGIGLKELWV[p.I281F]FDEKNWKPGRVDHTVGWPLDRHTYGG	WVFDEKNWK,IGLKELWVF	CLL
ETV6	c.1105C>T	p.R369W	YVYQLLSDSRYENFIRWEDKESKIF[p.R369W]WIVDPNGLARLWGNHKNRTNMTYEKM	WIVDPNGLA,KESKIFWIV,IFWIVDPNGL	CRC
EXOC1	c.1762C>T	p.R588C	QHNCGTPLPVSSEKDMIRQMMIKIF[p.R588C]CCIEPELNNLIALGDKIDSFNSLYML	MMIKIFCCI,RQMMIKIFC,QMMIKIFCCI,KIFCCIEPEL,RQMMIKIFCC	UCEC
EXOSC2	c.32G>C	p.R11P	MAMEMRLPVA[p.R11P]PKPLSERLGRDTKKHLVVPGDTITTD	EMRLPVAPK,APKPLSERL,MEMRLPVAP,MEMRLPVAPK,MRLPVAPKPL	KIRP
EXOSC8	c.480delA	p.L160fs	CDLICLDYDGNILDACTFALLAALK[p.L160fs]MYSCLKLL*	KMYSCLKLL,ALKMYSCLK,ALLAALKMY,FALLAALKM,AALKMYSCL,LKMYSCLKL,LLAALKMYSC,ALKMYSCLKL,AALKMYSCLK,LAALKMYSCL,FALLAALKMY,LKMYSCLKLL	STAD
EZH2	c.1529A>G	p.K510R	VDTPPRKKKRKHRLWAAHCRKIQLK[p.K510R]RDGSSNHVYNYQPCDHPRQPCDSSCP	RDGSSNHVY,LKRDGSSNH,KRDGSSNHVY	TGCT
EZH2	c.1922A>T	p.Y641F	LAPSDVAGWGIFIKDPVQKNEFISE[p.Y641F]FCGEIISQDEADRRGKVYDKYMCSFL	FISEFCGEI,QKNEFISEF,SEFCGEIIS,FISEFCGEII,VQKNEFISEF	DLBCL
F10	c.349G>A	p.E117K	TSPCQNQGKCKDGLGEYTCTCLEGF[p.E117K]KGKNCELFTRKLCSLDNGDCDQFCHE	KGKNCELFT,FKGKNCELF,YTCTCLEGFK,CTCLEGFKGK,GFKGKNCELF,KGKNCELFTR	UCEC
F5	c.1277A>T	p.Q426L	DESFTKHTVNPNMKEDGILGPIIRA[p.Q426L]LVRDTLKIVFKNMASRPYSIYPHGVT	ILGPIIRAL,ALVRDTLKI,LVRDTLKIV,RALVRDTLK,IRALVRDTL,ILGPIIRALV,ALVRDTLKIV,IIRALVRDTL,RALVRDTLKI,LVRDTLKIVF	LIHC
F5	c.3995T>C	p.L1332P	LSQTNLSPALGQMPISPDLSHTTLS[p.L1332P]PDFSQTNLSPELSQTNLSPALGQMPL	TLSPDFSQT,SPDFSQTNL,SHTTLSPDF,LSHTTLSPDF	CLL
F8	c.6806C>A	p.S2269Y	NPKEWLQVDFQKTMKVTGVTTQGVK[p.S2269Y]YLLTSMYVKEFLISSSQDGHQWTLFF	YLLTSMYVK,KYLLTSMYV,GVKYLLTSM,GVTTQGVKY,VKYLLTSMY,TTQGVKYLL,KYLLTSMYVK,GVKYLLTSMY,QGVKYLLTSM,VKYLLTSMYV	CRC
FAM104B	c.223G>C	p.D75H	SSSRINIPERASGPEGNLNQIVTEP[p.D75H]HANFPQFLHEGLSKPVYVINWFMSFG	HANFPQFLH,EPHANFPQF,IVTEPHANF,EPHANFPQFL,QIVTEPHANF,TEPHANFPQF	TGCT
FAM105A	c.376C>A	p.H126N	AREWKGETPRNKLMRKAYEELFWRH[p.H126N]NIKCVRQVRRDNYDALRSVLFQIFSQ	ELFWRHNIK,NIKCVRQVR,EELFWRHNI,FWRHNIKCVR,HNIKCVRQVR,NIKCVRQVRR,YEELFWRHNI	KIRC
FAM109A	c.466_474delGGGGGTGGC	p.GGG156del	LSRASFDYLRLVVRELEQQLAAVRG[p.GGG156del]MALPQPQPQSLPLPPSLPSALAPVPSLPSAPAPV	QLAAVRGMA,LAAVRGMAL,QQLAAVRGM,QLAAVRGMAL,EQQLAAVRGM,QQLAAVRGMA	ACC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
FAM111B	c.807delA	p.S269fs	KIYGKQSMVDEVSGKVLEMDISKKK[p.S269fs]HYNRKISIKKLNRMKVPLMKLITRV*	KLNRMKVPL,PLMKLITRV,RMKVPLMKL,ISKKKHYNR,SKKKHYNRK,KHYNRKISI,HYNRKISIK,YNRKISIKK,KISIKKLNR,SIKKLNRMK,LNRMKVPLM,ISIKKLNRM,MKVPLMKLI,KLNRMKVPLM,RMKVPLMKLI,ISIKKLNRMK,ISKKKHYNRK,KHYNRKISIK,HYNRKISIKK,KISIKKLNRM,SIKKLNRMKV,LNRMKVPLMK,KVPLMKLITR,DISKKKHYNR,KKHYNRKISI,KKLNRMKVPL,VPLMKLITRV	PRAD
FAM116A	c.1322delT	p.L441fs	IKQLQKGVQQKRPSEAQSVILRRYF[p.L441fs]WN*	SVILRRYFW	STAD
FAM120B	c.1400C>A	p.P467H	DSEPRQEVPMYTGSEPRQEVPMYTG[p.P467H]HESRQEVPMYTGPESRQEVLIRTDPE	HESRQEVPM,VPMYTGHES,RQEVPMYTGH,HESRQEVPMY	LUAD
FAM126B	c.1145G>A	p.R382H	LSSQPIGTKPSSSSQRGSLRKVATG[p.R382H]HSAKDKETASAIKSSESPRDSVVRKQ	KVATGHSAK,ATGHSAKDK,RKVATGHSA	GBM
FAM127C	c.156C>A	p.F52L	IPFPETFDGDTDRLPEFIVQTSSYM[p.F52L]LVDENTFSNDALKVTFLITRLTGPAL	VQTSSYMLV,MLVDENTFS,YMLVDENTF,FIVQTSSYML,IVQTSSYMLV,SYMLVDENTF	LUAD
FAM135B	c.1933A>C	p.S645R	KGIDQEGKMVLLSLKLTPSEPCDPL[p.S645R]RSTLREPLDIRSSLKDSHTEEQEELS	LRSTLREPL,EPCDPLRSTL	STAD
FAM135B	c.1942C>A	p.L648M	DQEGKMVLLSLKLTPSEPCDPLSST[p.L648M]MREPLDIRSSLKDSHTEEQEELSVLS	TMREPLDIR,LSSTMREPL,STMREPLDIR,EPCDPLSSTM	LUSC
FAM135B	c.2651G>A	p.R884H	GHCLPDGRTENTPGVETKGLNLKIP[p.R884H]HVIALENPRTRSLHRALEETPKGMPK	GLNLKIPHV,HVIALENPR,LKIPHVIAL,GLNLKIPHVI,NLKIPHVIAL,KGLNLKIPHV	CRC
FAM135B	c.720G>C	p.W240C	GYCKPTSSEGSFYITSENCMQHAHK[p.W240C]CHRDLCLLLLHAYRGLRLHFLVIMRD	MQHAHKCHR,CMQHAHKCHR	LUAD
FAM135B	c.855G>T	p.Q285H	LVIMRDIPELPHTELEALAVEETLS[p.Q285H]HLCSELQMLNNPEKIAEQISKDLAWL	TLSHLCSEL,HLCSELQML,SHLCSELQM,ETLSHLCSEL,LAVEETLSHL,LSHLCSELQM	LUSC
FAM151A	c.351delC	p.P117fs	LEADVNVEGLGTANETGVPIMAHPP[p.P117fs]LSTVTTHWSSGWTLCWALPKRASNWTSRTSRQWAPPWTSCGS*	IMAHPPLST,MAHPPLSTV,WTLCWALPK,TSRTSRQWA,RTSRQWAPP,TLCWALPKR,SNWTSRTSR,VPIMAHPPL,THWSSGWTL,SGWTLCWAL,TSRQWAPPW,RQWAPPWTS,WSSGWTLCW,IMAHPPLSTV,GWTLCWALPK,WTLCWALPKR,ASNWTSRTSR,HWSSGWTLCW,RTSRQWAPPW,TTHWSSGWTL,WSSGWTLCWA,MAHPPLSTVT,SSGWTLCWAL,WALPKRASNW,RQWAPPWTSC,PPLSTVTTHW	STAD
FAM155A	c.284A>G	p.Q95R	KEHQQQQRQQQQQQQQQRQRQQQQQ[p.Q95R]RRRQQEPSWPALLASMGESSPAAQAH	RQRQQQQQR,RRRQQEPSW,RQRQQQQQRR	TGCT
FAM155B	c.472G>A	p.E158K	VCGGVPEPTGLDAACTKLQSLQRLF[p.E158K]KPTTPAPPLRPPDSLSRAPAEFPSAK	RLFKPTTPA,LQSLQRLFK,KPTTPAPPL,LQRLFKPTT,KLQSLQRLFK,LQRLFKPTTP,RLFKPTTPAP,FKPTTPAPPL	UCEC
FAM169B	c.495G>T	p.K165N	NDRPRQPAPGDGSKERMCGEELEDT[p.K165N]NDDPECGVEEEDAGLAGQPPGKLTRS	DTNDDPECGV	CRC
FAM170A	c.166G>A	p.E56K	DALQPGSTRVAKGWSQGVGEVTSTS[p.E56K]KYCSCVSSSRKLIHSGIQRIHRDSPQ	STSKYCSCV,GEVTSTSKY,SKYCSCVSS,GVGEVTSTSK,VGEVTSTSKY,TSTSKYCSCV,SKYCSCVSSS	CRC
FAM171B	c.1375G>A	p.D459N	SYSPQKKEPSKAETEERVSMVKTRD[p.D459N]NFKIYNEDVSFLSVNQNNYSRNPTQS	MVKTRDNFK,KTRDNFKIY,SMVKTRDNF,SMVKTRDNFK,MVKTRDNFKI,KTRDNFKIYN,VSMVKTRDNF,VKTRDNFKIY	CRC
FAM179A	c.2491G>A	p.A831T	QVFDAFTPRLQDSNKKVNQWALESF[p.A831T]TKMIPLLRESLHPMLLSIIITVADNL	FTKMIPLLR,SFTKMIPLL,ESFTKMIPL,WALESFTKM,NQWALESFTK,SFTKMIPLLR,ESFTKMIPLL,WALESFTKMI,LESFTKMIPL	BRCA
FAM181A	c.326G>A	p.R109H	KAALDKSAPCRRSVDHRKYLQKQLK[p.R109H]HFSQKYSRLPRGLPGRAAEPYLKRGS	KQLKHFSQK,YLQKQLKHF,KHFSQKYSR,QLKHFSQKY,KYLQKQLKHF,KQLKHFSQKY,RKYLQKQLKH,KHFSQKYSRL	CRC

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FAM184B	c.2350C>T	p.R784W	RALGRQQASSQCPGDSKDHIIATEE[p.R784W]WGGPGQAGSPPGAAGQGSGEGCGLWE	EEWGGPGQA,EEWGGPGQAG,TEEWGGPGQA	ACC
FAM186A	c.4667_4702delTCCCTCCGCAGGCTCAGGAATTGGAGATCCCTCTCA	p.IPPQAQELEIPL1556del	LIPPQAQELGIPLTPQQVQALGIPL[p.IPPQAQELEIPL1556del]TPQQAQALGIPLTPQQAQELGIPLTPQQAQAQGIPLTPQQAQALGISLT	VQALGIPLT,VQALGIPLTP	KIRC
FAM18B2	c.152G>A	p.C51Y	PRKAKIRHPVASFFHLFFRVSAIIV[p.C51Y]YLLCELLSSSFITCMVTIILLLSCDF	IIVYLLCEL,YLLCELLSS,AIIVYLLCEL,IIVYLLCELL,YLLCELLSSS	ACC,KIRP,TGCT
FAM193A	c.1284_1285insC	p.D428fs	NYRRRCACDDCSLSHILTCGIMDPP[p.D428fs]RH*	LTCGIMDPPR	STAD
FAM193A	c.1284delC	p.D428fs	NYRRRCACDDCSLSHILTCGIMDPP[p.D428fs]SLMTSTFTSSHFKWILLLTILLRGARPVCHLQARGPAPALPSQFSSTPGSSSQTVARHQLFVVMMKMLHHCQPNLLIFIH*	SLMTSTFTS,WILLLTILL,ILLRGARPV,VMMKMLHHC,MLHHCQPNL,GIMDPPSLM,FTSSHFKWI,LLTILLRGA,LQARGPAPA,ALPSQFSST,TVARHQLFV,STFTSSHFK,HQLFVVMMK,MTSTFTSSH,GSSSQTVAR,TFTSSHFKW,SHFKWILLL,KWILLLTIL,QTVARHQLF,HCQPNLLIF,CQPNLLIFI,SSHFKWILL,VARHQLFVV,LTILLRGAR,QARGPAPAL,TSTFTSSHF,LMTSTFTSS,FKWILLLTI,RGARPVCHL,SQFSSTPGS,SQTVARHQL,ARHQLFVVM,RHQLFVVMM,QLFVVMMKM,MKMLHHCQP,KMLHHCQPN,TPGSSSQTV,PPSLMTSTF,LLLTILLRGA,TVARHQLFVV,KMLHHCQPNL,MLHHCQPNLL,SLMTSTFTSS,HLQARGPAPA,LQARGPAPAL,QLFVVMMKML,TSTFTSSHFK,TFTSSHFKWI,HFKWILLLTI,KWILLLTILL,SQTVARHQLF,SSHFKWILLL,GARPVCHLQA,VARHQLFVVM,RHQLFVVMMK,MTSTFTSSHF,WILLLTILLR,LLTILLRGAR,FTSSHFKWIL,STPGSSSQTV,QTVARHQLFV,GPAPALPSQF,LMTSTFTSSH,HQLFVVMMKM,CGIMDPPSLM,STFTSSHFKW,FKWILLLTIL,SQFSSTPGSS,ARHQLFVVMM,MKMLHHCQPN,HHCQPNLLIF,LPSQFSSTPG	STAD
FAM194B	c.404_421delAGGAGGAAGAGTATCTGG	p.EEEEYL135del	IEEEEYLGKEGYLEEEEYLGKEEHL[p.EEEEYL135del]GKEGYLEKEDYIEEVDYLGKKAYLEEEEYLGKKSYLEEEKALE	LGKEEHLGK,EEHLGKEGY,HLGKEGYLEK,KEEHLGKEGY,EEHLGKEGYL	KIRC
FAM194B	c.415T>C	p.Y139H	EYLGKEGYLEEEEYLGKEEHLEEEE[p.Y139H]HLGKEGYLEKEDYIEEVDYLGKKAYL	EEHLGKEGY,HLGKEGYLEK,EEEHLGKEGY,EEHLEEEEHL,EEHLGKEGYL	TGCT
FAM210B	c.336G>T	p.L112F	QQLKKIFQEYGTVGVSLHIGISLIS[p.L112F]FGIFYMVVSSGVDMPAILLKLGFKES	GISLISFGI,LISFGIFYM,ISFGIFYMV,SLISFGIFY,ISLISFGIF,SFGIFYMVV,HIGISLISF,ISLISFGIFY,SLISFGIFYM,LISFGIFYMV,ISFGIFYMVV,LHIGISLISF,GISLISFGIF	LUAD
FAM214B	c.124delG	p.A42fs	GPSQPPVRQGALQGGLLMGYSPAGG[p.A42fs]RHPPGSTRYPSFPLRLVPLSLIGP*	RYPSFPLRL,SFPLRLVPL,STRYPSFPL,RHPPGSTRY,MGYSPAGGR,YPSFPLRLV,SPAGGRHPP,RLVPLSLIG,FPLRLVPLS,STRYPSFPLR,RYPSFPLRLV,GGRHPPGSTR,LMGYSPAGGR,SPAGGRHPPG,FPLRLVPLSL,MGYSPAGGRH,GRHPPGSTRY,GSTRYPSFPL,TRYPSFPLRL	STAD
FAM216A	c.106C>T	p.P36S	RGLGAAEMPGQGPGSDWTERSSSAE[p.P36S]SPAVAGTEGGGGGSAGYSCYQN5KGS	RSSSAESPA,AESPAVAGT,RSSSAESPAV	KIRP
FAM21B	c.3691C>T	p.P1231S	DMDDIF5SGIQAKTTKPKSRSAQAA[p.P1231S]SEPRFEHKVSNIFDDPLNAFGGQ*	ASEPRFEHK,KSRSAQAAS,SAQAASEPR,AQAASEPRF,SEPRFEHKV,RSAQAASEPR,AASEPRFEHK,KSRSAQAASE,SAQAASEPRF	TGCT
FAM222F	c.2070_2071delTT	p.P690fs	PGGRGPQGALQSPSAQKRGLSPSPS[p.P690fs]CQQVQEATSLWKPIPC*	VQEATSLWK,EATSLWKPI,SPSPSCQQV,QQVQEATSL,QVQEATSLWK,CQQVQEATSL,QQVQEATSLW,QEATSLWKPI	KIRC
FAM222F	c.2071_2073delTCT	p.S691del	SPGGRGPQGALQSPSAQKRGLSPSP[p.S691del]PASKSKKRPLFGSPSPAEKTPHPGPGLR	LSPSPPASK,RGLSPSPPA,GLSPSPPASK	KIRC,PRAD
FAM32A	c.26A>G	p.K9R	MEAYEQVQ[p.K9R]RGPLKLKGVAELGVTKRKKKKKDKDK	VQRGPLKLK,YEQVQRGPL,QVQRGPLKLK,EQVQRGPLKL	TGCT

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FAM40B	c.2218C>T	p.R740C	LQTKYLGRQWRKSNMKTMSAIYQKV[p.R740C]CHRMNDDWAYGNDIDARPWDFQAEEC	AIYQKVCHR,IYQKVCHRM,AIYQKVCHRM,CHRMNDDWAY,SAIYQKVCHR	STAD
FAM46B	c.1247_1248AC>GT	p.H416R	RPPGTDGVVPATVNYYVTPVQPLLA[p.H416R]RAYPTWLPCN*	LLARAYPTW,LARAYPTWL,RAYPTWLPC,VQPLLARAY,LLARAYPTWL,PVQPLLARAY	TGCT
FAM47A	c.1114G>T	p.G372W	GSSLRSEPSETGVSRLRLAPPKTRR[p.G372W]WSSLHAEPSKTGVSHLSPEPPKTEVS	KTRRWSSLH,WSSLHAEPSK,KTRRWSSLHA,PPKTRRWSSL,RLAPPKTRRW	LUSC
FAM47A	c.2069G>T	p.R690L	EDKFFSQEKYWGRKFHTPSNSYTAQ[p.R690L]LVKMKYGAWYLKPKLWKKLRSDEPLI	NSYTAQLVK,YTAQLVKMK,SYTAQLVKM,YTAQLVKMKY,SNSYTAQLVK,LVKMKYGAWY,TPSNSYTAQL,NSYTAQLVKM,QLVKMKYGAW	LUAD
FAM47B	c.1701G>T	p.L567F	QRGRIRYGPWYFEPKLGKKLRSDEP[p.L567F]FIDPKPVLEKPDEPDILDGLYGPIAF	KLRSDEPFI,KKLRSDEPF,EPFIDPKPV,RSDEPFIDPK,FIDPKPVLEK,EPFIDPKPVL,GKKLRSDEPF,KKLRSDEPFI	LUAD
FAM47B	c.489G>T	p.W163C	GKDMPPDLLLQVLKQLDPERKLEDA[p.W163C]CARCEAREKTTEVPTESGKYPCGESC	CARCEAREK,DACARCEAR,LEDACARCEA	LUAD
FAM47C	c.1162C>T	p.P388S	VSPLRQLPPEAGVSHLCPEPPKTRV[p.P388S]SPLRPETPKNGVSPLFPEPPKTRISN	KTRVSPLRP,RVSPLRPET,PPKTRVSPL,KTRVSPLRPE,EPPKTRVSPL	KIRC
FAM48B1	c.1495A>G	p.I499V	ISSGNSFPPQQAGSPLKRPFSAAAA[p.I499V]VAAAAAAAAAAAAAAAAAAPAPALAA	FSAAAAVAA,SAAAAVAAA,RPFSAAAAV,FSAAAAVAAA,SAAAAVAAAA,RPFSAAAAVA	TGCT
FAM48B1	c.1546G>C	p.A516P	RPFSAAAAIAAAAAAAAAAAAAAAA[p.A516P]PAPAPALAAAAAPALAAAAAPALAAA	AAAPAPAPAL,APAPAPALAA	TGCT
FAM50A	c.950A>G	p.H317R	SDATVEKDESHAGKVVLRSWYEKNK[p.H317R]RIFPASRWEPYDPEKKWDKYTIR*	KNKRIFPAS,KRIFPASRW,SWYEKNKRIF,KNKRIFPASR,YEKNKRIFPA,NKRIFPASRW	CLL
FAM58BP	c.208G>A	p.A70T	LGMQSIPIATACTIYPKFFCETILD[p.A70T]TFDPYLIAMSSIYLAGKVEEQPLWAH	ILDTFDPYL,TILDTFDPY,DTFDPYLIA,ETILDTFDPY,TILDTFDPYL,ILDTFDPYLI,FFCETILDTF,DTFDPYLIAM	BRCA
FAM5B	c.1204C>T	p.R402C	AGLKVLFKKTHRILRRLFNLCKRCH[p.R402C]CQPRFRLPKERSLSYWWNRIQSLLYC	CQPRFRLPK,RCHCQPRFR,KRCHCQPRF,RCHCQPRFRL,HCQPRFRLPK,CKRCHCQPRF	CRC
FAM5C	c.1274C>G	p.S425W	WLTRIQSFLYCNENGLLGSFSEETH[p.S425W]WCTCPNDQVVCTAFLPCTVGDASACL	GSFSEETHW	TGCT
FAM5C	c.1369C>G	p.R457G	QVVCTAFLPCTVGDASACLTCAPDN[p.R457G]GTRCGTCNTGYMLSQGLCKPEVAEST	GTRCGTCNT,GTRCGTCNTG,LTCAPDNGTR	LUAD
FAM70B	c.56C>T	p.S19L	MQPPVPGPLGLLDPAEGL[p.S19L]LRRKKTSLWFVGSLLLVSVLIVTVGL	LLDPAEGLL,LLRRKKTSL,GLLDPAEGLL,GLLRRKKTSL,LLRRKKTSLW,LRRKKTSLWF	STAD
FAM70B	c.829C>A	p.P277T	GFRLTPEPVPTCSSYPLPLQPCSRF[p.P277T]TVAPSSALASSEDLQPPSPSSSGSGL	LQPCSRFTV,FTVAPSSAL,TVAPSSALA,CSRFTVAPS,RFTVAPSSA,QPCSRFTVA,FTVAPSSALA,CSRFTVAPSS,LQPCSRFTVA,SRFTVAPSSA,RFTVAPSSAL	LUAD
FAM71B	c.1333C>G	p.H445D	PSAEVWNENKERREKKDRHPSRKSS[p.H445D]DHRKAGESHRRRAGDKNQKASSHRSA	PSRKSSDHRK	CESC
FAM71B	c.1747C>A	p.L583M	VDIVAKMVEKQNIEAKVEKAQGGQE[p.L583M]MEMISGTMTSEKTEMIVFETKSI*	EKAQGGQEM,AQGGQEMEM,QEMEMISGT,EMEMISGTM,MEMISGTMT,QEMEMISGTM,VEKAQGGQEM,KAQGGQEMEM,MEMISGTMTS	LUAD
FAM73A	c.68G>T	p.G23V	MSDCCSAPGISWEAGVGRPAVP[p.G23V]VLELQIRRGAMSEETVSESQFSLKTA	RPAVPVLEL,VGRPAVPVL	CESC
FAM75A6	c.161C>T	p.P54L	FLTLVFALGFFFLLLPYLSYFHCDD[p.P54L]LPSPSPGKRKCPVGRRRRPRGRMKNH	LSYFHCDDL,YLSYFHCDDL	LUAD
FAM75A6	c.910C>A	p.R304S	ASSRWQETARTSCAFNSSVQQDPLS[p.R304S]SHPPETCQMEAGSLFLLSSDGQNVVG	VQQDPLSSH,SSHPPETCQM	LUAD

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FAM75D1	c.3793C>A	p.R1265S	NSQGISSGDMGTSQVVHVHLEDSGI[p.R1265S]SVAQKQEPRVPTCVLQKCQVTNFPPA	HLEDSGISV,SVAQKQEPR,LEDSGISVA,HLEDSGISVA,SVAQKQEPRV	LUAD
FAM75D5	c.665T>C	p.L222P	PPQPVSPLDSKFPIDHSLPQQLPSP[p.L222P]PFPPHHIQRAEPSLQPEASLSLNTVF	PQQLPSPPF,LPSPPFPPH,LPQQLPSPPF,QQLPSPPFPP	THCA
FAM78A	c.575G>T	p.W192L	TWAVPVSESNVAKLTNIYRDQSFTT[p.W192L]LLVATNTSTNDMIILQTLHWRMQLSI	LLVATNTST,YRDQSFTTL,RDQSFTTLL,QSFTTLLVA,IYRDQSFTTL,YRDQSFTTLL,DQSFTTLLVA	KIRC
FAM83B	c.617G>A	p.R206Q	DESNFNHFLNMTEKQGCSVQRLRNI[p.R206Q]QVRTVKGQDYLSKTGAKFHGKMEQKF	VQRLRNIQV,RLRNIQVRT,RNIQVRTVK,RLRNIQVRTV,VQRLRNIQVR,QVRTVKGQDY	UCEC
FAM86A	c.421G>A	p.A141T	SGGSVTLSESTAIISYGTTGLVTWD[p.A141T]TALYLAEWAIENPAVFTNRTVLELGS	LVTWDTALY,GLVTWDTAL,VTWDTALYL,VTWDTALYLA,GLVTWDTALY,LVTWDTALYL,DTALYLAEWA,TALYLAEWAI	TGCT
FAM86C2P	c.359G>A	p.C120Y	RASCSPLSYAGLGSDGKWNLVMTRN[p.C120Y]YFPTKSTWRWQC*	MTRNYFPTK,NYFPTKSTW,YFPTKSTWR,NLVMTRNYF,WNLVMTRNY,VMTRNYFPTK,YFPTKSTWRW,MTRNYFPTKS,KWNLVMTRNY,NYFPTKSTWR,LVMTRNYFPT,WNLVMTRNYF,RNYFPTKSTW	TGCT
FARP1	c.1148C>T	p.S383L	KVQFERKHSKIHSIRSLASQPTELN[p.S383L]LEVLEQSQQSTSLTFGEGAESPGGQS	QPTELNLEV,SQPTELNLEV,LASQPTELNL,QPTELNLEVL	UCEC
FARP1	c.896G>T	p.R299L	KRFLIKLRPDANSAYQDTLEFLMAS[p.R299L]LDFCKSFWKICVEHHAFFRLFEEPKP	FLMASLDFC,TLEFLMASL,LMASLDFCK,EFLMASLDF,ASLDFCKSF,FLMASLDFCK,SLDFCKSFWK,DTLEFLMASL,MASLDFCKSF,LEFLMASLDF,ASLDFCKSFW,LDFCKSFWKI	LUAD
FAS	c.781G>A	p.E261K	IAGVMTLSQVKGFVRKNGVNEAKID[p.E261K]KIKNDNVQDTAEQKVQLLRNWHQLHG	GVNEAKIDK	CESC
FASTKD1	c.9_10insA	p.K3fs	MKK[p.K3fs]NTCFPRVIGYKYASSKSYLSILLESVSISTHQL*	YLSILLESV,IGYKYASSK,KYASSKSYL,SYLSILLES,CFPRVIGYK,ASSKSYLSI,SSKSYLSIL,YKYASSKSY,SVSISTHQL,TCFPRVIGY,FPRVIGYKY,KKNTCFPRV,SKSYLSILL,LESVSISTH,ILLESVSIST,VIGYKYASSK,TCFPRVIGYK,CFPRVIGYKY,SYLSILLESV,SSKSYLSILL,NTCFPRVIGY,GYKYASSKSY,ESVSISTHQL,FPRVIGYKYA,YASSKSYLSI,MKKNTCFPRV,KKNTCFPRVI,YKYASSKSYL,ASSKSYLSIL,LSILLESVSI	STAD
FASTKD3	c.1873C>G	p.Q625E	RFCSNSKHLLGKEAIKQRHLQLLGY[p.Q625E]EVVQIPYHEIGMLKSRRELVEYLQRK	HLQLLGYEV,LQLLGYEVV,LLGYEVVQI,GYEVVQIPY,YEVVQIPYH,HLQLLGYEVV,QLLGYEVVQI,LGYEVVQIPY,EVVQIPYHEI,RHLQLLGYEV	BLCA
FAT1	c.13076G>T	p.R4359L	TKVVDLDPCLSKKPLEEKPSQPYSA[p.R4359L]LESLSEVQSLSSFQSESCDDNGYHWD	SALESLSEV,KPSQPYSAL,QPYSALESL,YSALESLSEV,SQPYSALESL,LESLSEVQSL	LUAD
FAT3	c.10720C>A	p.H3574N	PTAIPLEIFIVTMEDDFPGGVIGKI[p.H3574N]NATDQDMYDVLTFALKSEQKSLFKVN	KINATDQDM,KINATDQDMY,NATDQDMYDV,GKINATDQDM	LUAD
FAT3	c.12475G>A	p.A4159T	GLRPVVVPNIQAGHSYVGKEELIGI[p.A4159T]TVVLFVIFILVVLFIVFRKKVFRKNY	ELIGITVVL,ITVVLFVIF,TVVLFVIFI,KEELIGITV,LIGITVVLF,ELIGITVV,LIGITVVLFV,IGITVVLFVI,ITVVLFVIFI,TVVLFVIFIL,ELIGITVVLF,KEELIGITVV,GITVVLFVIF,EELIGITVVL	UCEC
FAT3	c.3797G>A	p.R1266H	VVQVLDENDNKPQFPEKVYQIKLPE[p.R1266H]HDRKKRGEPIYRAFAFDRDEGPNAEI	KVYQIKLPEH,QIKLPEHDRK	LUAD
FAT3	c.5696G>T	p.G1899V	TDVNDNPPVFTQAVFETILLLPTYV[p.G1899V]VVEVLKVSATDPDSEVPPELTYSLME	ILLLPTYVV,LLLPTYVVV,YVVVEVLKV,LPTYVVVEV,TILLLPTYVV,ILLLPTYVVV,LLPTYVVVEV,PTYVVVEVLK,TYVVVEVLKV,LPTYVVVEVL	LUAD
FBRSL1	c.2507C>T	p.A836V	GRSGAPAEREAEPRVKESRSPAKEE[p.A836V]VAKMPARASPPHSKAAPGDVKVKEER	EVAKMPARA,KEEVAKMPA,RSPAKEEVAK,SPAKEEVAKM,EEVAKMPARA	ACC
FBXL13	c.306T>A	p.S102R	RIQQIIYCHKLTIILTKWRNTARHK[p.S102R]RKKKEDELILKHELQLKKWKNRLILK	RNTARHKRK,TARHKRKKK,KWRNTARHKR,RNTARHKRKK,RKKKEDELIL	CLL

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FBXL14	c.143T>G	p.V48G	RDKGRAAQVCTAWRDAAYHKSVWRG[p.V48G]GEAKLHLRRANPSLFPSLQARGIRRV	SVWRGGEAK,KSVWRGGEA,KSVWRGGEAK,GEAKLHLRRA	TGCT
FBXO18	c.432G>T	p.M144I	KQPCTNDMAKSNSVGQDSCQDSEGD[p.M144I]IIFPAESSCALPQEGSAGPGSPGSAP	CQDSEGDII,SEGDIIFPA,IIFPAESSCA,CQDSEGDIIF	LUAD
FBXO21	c.432delT	p.F144fs	KRFFSEHVPCNGFSDIENLEGPEIF[p.F144fs]LRMNWCVS*	IFLRMNWCV,FLRMNWCVS,PEIFLRMNW,EIFLRMNWCV,LEGPEIFLRM,GPEIFLRMNW	STAD
FBXO24	c.1657A>G	p.M553V	HLPASRVVGTPEPSLGARAPQDPGG[p.M553V]VAQACEEYLSQIHSCQTLQDRTEKMK	GVAQACEEY,APQDPGGVA,GGVAQACEEY	HNSC
FBXO31	c.1329_1330insG	p.G443fs	TPGEDGGEPGDAVAAAEQPAQCGQG[p.G443fs]AAVRAARGRELQE*	AQCGQGAAV,AVRAARGRE,QGAAVRAAR,GQGAAVRAA,VRAARGREL,AVRAARGREL,QPAQCGQGAA	LUAD
FBXW7	c.1268G>T	p.G423V	SDDNTLKVWSAVTGKCLRTLVGHTG[p.G423V]VVWSSQMRDNIIISGSTDRTLKVWNA	TLVGHTGVV,GVVWSSQMR,RTLVGHTGV,LVGHTGVVW,TGVVWSSQM,RTLVGHTGVV,TLVGHTGVVW,HTGVVWSSQM	UCEC
FBXW7	c.1393C>T	p.R465C	DRTLKVWNAETGECIHTLYGHTSTV[p.R465C]CCMHLHEKRVVSGSRDATLRVWDIET	STVCCMHLH,GHTSTVCCM,TLYGHTSTVC,TVCCMHLHEK,HTSTVCCMHL,YGHTSTVCCM	CESC,CRC,STAD,UCEC,UCS
FBXW7	c.1394G>A	p.R465H	DRTLKVWNAETGECIHTLYGHTSTV[p.R465H]HCMHLHEKRVVSGSRDATLRVWDIET	STVHCMHLH,HCMHLHEKR,GHTSTVHCM,TVHCMHLHEK,HTSTVHCMHL,TLYGHTSTVH,YGHTSTVHCM	CLL,CRC,UCEC,UCS
FBXW7	c.1436G>A	p.R479Q	IHTLYGHTSTVRCMHLHEKRVVSGS[p.R479Q]QDATLRVWDIETGQCLHVLMGHVAAV	SQDATLRVW	STAD,UCS
FBXW7	c.1513C>G	p.R505G	DATLRVWDIETGQCLHVLMGHVAAV[p.R505G]GCVQYDGRRVVSGAYDFMVKVWDPET	VAAVGCVQY,HVAAVGCVQY	BLCA,CESC,HNSC,LUSC,UCS
FBXW7	c.1513C>T	p.R505C	DATLRVWDIETGQCLHVLMGHVAAV[p.R505C]CCVQYDGRRVVSGAYDFMVKVWDPET	VAAVCCVQY,VLMGHVAAVC,HVAAVCCVQY,AVCCVQYDGR	CRC,UCEC
FBXW7	c.1637C>T	p.S546L	FMVKVWDPETETCLHTLQGHTNRVY[p.S546L]LLQFDGIHVVSGSLDTSIRVWDVETG	LLQFDGIHV,VYLLQFDGI,TNRVYLLQF,YLLQFDGIH,YLLQFDGIHV,LLQFDGIHVV,RVYLLQFDGI,HTNRVYLLQF,LQGHTNRVYL	BLCA
FBXW7	c.1745C>T	p.S582L	GSLDTSIRVWDVETGNCIHTLTGHQ[p.S582L]LLTSGMELKDNILVSGNADSTVKIWD	QLLTSGMEL,LLTSGMELK,HTLTGHQLL,IHTLTGHQL,GHQLLTSGM,QLLTSGMELK,IHTLTGHQLL,TGHQLLTSGM,HQLLTSGMEL	CRC
FBXW7	c.2065C>T	p.R689W	ESGGSGGVVWRIRASNTKLVCAVGS[p.R689W]WNGTEETKLLVLDFDVDMK*	KLVCAVGSW,GSWNGTEETK,TKLVCAVGSW	CRC,UCEC,UCS
FBXW7	c.41G>A	p.R14Q	MNQELLSVGSKRR[p.R14Q]QTGGSLRGNPSSSQVDEEQMNRVVEE	KRRQTGGSL,RQTGGSLRG,KRRQTGGSLR,SKRRQTGGSL	CRC
FBXW9	c.893_894insG	p.G298fs	YDKKVTIYDPRDRMETRDALMGWGG[p.G298fs]AFEGL*	GWGGAFEGL,ALMGWGGAF,DALMGWGGAF,MGWGGAFEGL	STAD
FCAR	c.697G>A	p.V233M	SNALELVVTDSIHQDYTTQNLIRMA[p.V233M]MAGLVLVALLAILVENWHSHTALNKE	RMAMAGLVL,MAMAGLVLV,AMAGLVLVA,LIRMAMAGL,TQNLIRMAM,IRMAMAGLV,MAGLVLVAL,NLIRMAMAGL,RMAMAGLVLV,MAMAGLVLVA,AMAGLVLVAL,LIRMAMAGLV,IRMAMAGLVL	HNSC
FCGBP	c.12055G>A	p.V4019M	VYYEPEQTVLIDNCRQQCTCHVGKV[p.V4019M]MVCQEHSCKPGQVCQPSGGILSCVTK	VMVCQEHSCK	UCS
FCGBP	c.3064G>T	p.A1022S	EALCGLCGNFNGDPADDLALRGGGQ[p.A1022S]SANALAFGNSWQEETRPGCGATEPGD	ALRGGGQSA,GQSANALAF,LALRGGGQSA,GGQSANALAF	LUAD
FCGBP	c.7478C>T	p.A2493V	RFDFMGTCVYVLAQTCGTRPGLHRF[p.A2493V]VVLQENVAWGNGRVSVTRVITVQVAN	RPGLHRFVV,VVLQENVAW,GTRPGLHRFV,RPGLHRFVVL,FVVLQENVAW	PAAD
FCGR2A	c.665T>G	p.V222G	SSKPVTITVQVPSMGSSSPMGIIVA[p.V222G]GVIATAVAAIVAAVVALIYCRKKRIS	IVAGVIATA,PMGIIVAGV,SPMGIIVAG,IIVAGVIATA,IVAGVIATAV,GVIATAVAAI,SPMGIIVAGV	KIRP

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
FCGRT	c.118C>G	p.P40A	LFLLPGSLGAESHLSLLYHLTAVSS[p.P40A]AAPGTPAFWVSGWLGPQQYLSYNSLR	HLTAVSSAA,SSAAPGTPA,SAAPGTPAF,YHLTAVSSA,SSAAPGTPAF,YHLTAVSSAA,SAAPGTPAFW	THCA
FCRL2	c.1513G>T	p.V505L	MQQPESSANIRTLLENKDSQVIYSS[p.V505L]LKKS*	SQVIYSSLK,QVIYSSLKK,SQVIYSSLKK,DSQVIYSSLK,KDSQVIYSSL	LUAD
FEM1A	c.1858C>A	p.L620M	AIMNALIEAGAHMDATNAFKKTAYE[p.L620M]MLDEKLLARGTMQPFNYVTLQCLAAR	TAYEMLDEK,AFKKTAYEM,FKKTAYEML,YEMLDEKLL,KTAYEMLDEK,EMLDEKLLAR,NAFKKTAYEM,YEMLDEKLLA	PRAD
FER	c.1422delA	p.L474fs	SEKPLAEQDWYHGAIPRIEAQELLK[p.L474fs]NKETFWCERVMGNLVNMSFLYILMDRGDILSYNMLITCIDSRALGFQTFLNL*	CIDSRALGF,RVMGNLVNM,ILMDRGDIL,LVNMSFLYI,NMSFLYILM,LITCIDSRA,SYNMLITCI,RALGFQTFL,NLVNMSFLY,MDRGDILSY,SFLYILMDR,MLITCIDSR,ETFWCERVM,DILSYNMLI,MGNLVNMSF,CERVMGNLV,VNMSFLYIL,RGDILSYNM,SRALGFQTF,LGFQTFLNL,KETFWCERV,GDILSYNML,LMDRGDILSY,NLVNMSFLYI,MLITCIDSRA,ALGFQTFLNL,MSFLYILMDR,VMGNLVNMSF,LYILMDRGDI,KNKETFWCER,GNLVNMSFLY,NMLITCIDSR,DSRALGFQTF,QELLKNKETF,KETFWCERVM,LVNMSFLYIL,VNMSFLYILM,LSYNMLITCI,TCIDSRALGF,SRALGFQTFL,GDILSYNMLI	STAD
FERD3L	c.275C>A	p.P92H	CEVDQGDGEEEEEEERGRGVSLLGR[p.P92H]HKRKRVITYAQRQAANIRERKRMFNL	SLLGRHKRK,GVSLLGRHK,VSLLGRHKR,HKRKRVITY,VSLLGRHKRK,RGVSLLGRHK,SLLGRHKRKR,LGRHKRKRVI,RHKRKRVITY	LUAD
FEZ2	c.149C>T	p.P50L	NCNASPEPGAEAGAEAGGGADGFPA[p.P50L]LACSLEEKLSLCFRPSDPGAEPPRTA	ALACSLEEK,GGADGFPAL,ALACSLEEKL,FPALACSLEE	ACC
FEZF2	c.244G>A	p.E82K	GSQGKKLLNLCSPLPCMIPLQPLGY[p.E82K]KVPSKTLLSYSELWKSSLRAGGGGGG	YKVPSKTLL,MIPLQPLGYK,KVPSKTLLSY,LGYKVPSKTL,IPLQPLGYKV	CESC
FGB	c.1015G>C	p.E339Q	NYCGLPGEYWLGNDKISQLTRMGPT[p.E339Q]QLLIEMEDWKGDKVKAHYGGFTVQNE	RMGPTQLLI,LTRMGPTQL,GPTQLLIEM,TRMGPTQLL,QLTRMGPTQL,LTRMGPTQLL,SQLTRMGPTQ	LUAD
FGF14	c.686C>T	p.T229M	KPLEVAMYREPSLHDVGETVPKPGV[p.T229M]MPSKSTSASAIMNGGKPVNKSKTT*	VMPSKSTSA,MPSKSTSAS,GVMPSKSTSA,VPKPGVMPSK,MPSKSTSASA,GETVPKPGVM	GBM
FGF14	c.707C>T	p.A236V	YREPSLHDVGETVPKPGVTPSKSTS[p.A236V]VSAIMNGGKPVNKSKTT*	VTPSKSTSV,VSAIMNGGK,KSTSVSAIM,SKSTSVSAI,GVTPSKSTSV,SVSAIMNGGK,TPSKSTSVSA,SKSTSVSAIM	CRC
FGFR3	c.1138G>A	p.G380R	VVLPAEEELVEADEAGSVYAGILSY[p.G380R]RVGFFLFILVVAAVTLCRLRSPPKKG	YAGILSYRV,ILSYRVGFF,SYRVGFFLF,VYAGILSYR,GILSYRVGF,LSYRVGFFL,ILSYRVGFFL,RVGFFLFILV,SVYAGILSYR,VYAGILSYRV,LSYRVGFFLF,SYRVGFFLFI,AGILSYRVGF,GILSYRVGFF,YRVGFFLFIL	BLCA
FGFR3	c.1711_1712insG	p.R571fs	QGGPLYVLVEYAAKGNLREFLRARR[p.R571fs]APGPGLLLRHLQAARGAAHLQGPGVLCLPGGPGHGVLGLPEVHPQGPGCPQCAGDRGQRDEDRRLRAGPGRAQPRLLQEDDQRPAAREVDGA*	LLLRHLQAA,RARRAPGPG,LLRHLQAAR,RLRAGPGRA,GPGHGVLGL,FLRARRAPG,LQAARGAAH,REFLRARRA,ARRAPGPGL,RRAPGPGLL,RAPGPGLLL,RHLQAARGA,AHLQGPGVL,LQGPGVLCL,LQEDDQRPA,LPGGPGHGV,CLPGGPGHGV,GLLLRHLQAA,LQAARGAAHL,LLQEDDQRPA,RARRAPGPGL,RLRAGPGRAQ,RAGPGRAQPR,LLLRHLQAAR,LPGGPGHGVL,RPAAREVDGA,FLRARRAPGP,REFLRARRAP,RRAPGPGLLL,RHLQAARGAA,HLQAARGAAH,AAHLQGPGVL,HLQGPGVLCL,LQEDDQRPAA	KIRC
FGFR3	c.2147C>A	p.P716H	GGSPYPGIPVEELFKLLKEGHRMDK[p.P716H]HANCTHDLYMIMRECWHAAPSQRPTF	HANCTHDLY,KHANCTHDLY,RMDKHANCTH,HANCTHDLYM	KIRC
FGFR3	c.2420G>C	p.*807S	SSGDDSVFAHDLLPPAPPSSGGSRT[p.*807S]SRATGPQQCEGSLAAHPAAGAQPLPGMRLSADGETATQSFGLCVCVCVCVCVCVCAHPRVPVCVRILPPGAEVPWVSPLLCNGLLTGAAAPRGLCSGGTQCRM*	RILPPGAEV,RLSADGETA,CVCVCAHPR,GSRTSRATG,GSLAAHPAA,CVRILPPGA,LLTGAAAPR,LAAHPAAGA,ETATQSFGL,QSFGLCVCV,EVPWVSPLL,GPQQCEGSL,HPAAGAQPL,SPLLCNGLL,QQCEGSLAA,AGAQPLPGM,AQPLPGMRL,AEVPWVSPL,LPPGAEVPW,VPWVSPLLC,SLAAHPAAGA,TQSFGLCVCV,GLCVCVCVCV,LLCNGLLTGA,WVSPLLCNGL,ILPPGAEVPW,ETATQSFGLC,CVCAHPRVPV,QPLPGMRLSA,HPRVPVCVRI,QQCEGSLAAH,ADGETATQSF,GETATQSFGL,AEVPWVSPLL,CEGSLAAHPA,LPPGAEVPWV	MM

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
FGFR3	c.742C>T	p.R248C	RGNYTCVVENKFGSIRQTYTLDVLE[p.R248C]CSPHRPILQAGLPANQTAVLGSDVEF	DVLECSPHR,LECSPHRPI,LECSPHRPIL	BLCA
FGFR3	c.746C>G	p.S249C	GNYTCVVENKFGSIRQTYTLDVLER[p.S249C]CPHRPILQAGLPANQTAVLGSDVEFH	DVLERCPHR,LERCPHRPI,CPHRPILQA,LERCPHRPIL	BLCA,LUSC
FGFRL1	c.1435_1436delCA	p.H479fs	LGPGPVAGPKLYPKLYTDIHTHTHT[p.H479fs]LSHTLTRGGQGPPAHPLSVLDGTVSAVGTGGPARQADWEDGGRSCRRRQGTHGEEEWPAPQAVCV*	SVLDGTVSA,VLDGTVSAV,HTHTHTLSH,HTLSHTLTR,HTHTLSHTL,RSCRRRQGT,DIHTHTHTL,GPPAHPLSV,PPAHPLSVL,WPAPQAVCV,GQGPPAHPL,EEWPAPQAV,EEEWPAPQA,SVLDGTVSAV,HTHTHTLSHT,HTHTLSHTLT,LTRGGQGPPA,RSCRRRQGTH,GPPAHPLSVL,HPLSVLDGTV,TDIHTHTHTL,IHTHTHTLSH,RQGTHGEEEW,EEWPAPQAVC,EEEWPAPQAV,GEEEWPAPQA	BLCA
FGFRL1	c.728G>T	p.R243L	KYTCRVSNRAGAINATYKVDVIQRT[p.R243L]LSKPVLTGTHPVNTTVDFGGTTSFQC	RTLSKPVLT,IQRTLSKPV,VIQRTLSKPV,TLSKPVLTGT,RTLSKPVLTG,IQRTLSKPVL,YKVDVIQRTL	LUAD
FGFRL1	c.820G>T	p.V274L	TGTHPVNTTVDFGGTTSFQCKVRSD[p.V274L]LKPVIQWLKRVEYGAEGRHNSTIDVG	KVRSDLKPV,QCKVRSDLK,FQCKVRSDL,KVRSDLKPVI,DLKPVIQWLK,CKVRSDLKPV	LUAD
FGGY	c.412_413insG	p.G138fs	LDHRAVSQVNRINETKHSVLQYVGG[p.G138fs]GDVCGNAGPETSVAERELERDLLG*	SVAERELER,LQYVGGGDV,AERELERDL,VLQYVGGGDV,LQYVGGGDVC,AERELERDLL	STAD
FHDC1	c.298delT	p.F100fs	PGLPPTTHMNGYSHLGKKKRMRSFF[p.F100fs]GKLFRRSKFEAKPTSGPWQPGRNITTKLIQRPLRSSLGSRKTPPSLPFLGEEEL*	RMRSFFGKL,RSFFGKLFR,KRMRSFFGK,SFFGKLFRR,KTPPSLPFL,KKRMRSFFG,FGKLFRRSK,LFRRSKFEA,RSKFEAKPT,TTKLIQRPL,IQRPLRSSL,PLRSSLGSR,GSRKTPPSL,TSGPWQPGR,NITTKLIQR,GPWQPGRNI,LPFLGEEEL,MRSFFGKLF,GKLFRRSKF,RKTPPSLPF,KLFRRSKFEA,SLPFLGEEEL,RSFFGKLFRR,RMRSFFGKLF,KKRMRSFFGK,LFRRSKFEAK,RSKFEAKPTS,TTKLIQRPLR,IQRPLRSSLG,PLRSSLGSRK,GPWQPGRNIT,LIQRPLRSSL,KRMRSFFGKL,FGKLFRRSKF,SKFEAKPTSG,FEAKPTSGPW,SRKTPPSLPF,RKTPPSLPFL	STAD
FHDC1	c.760C>T	p.R254W	SGDVSKLSLADSFLYGLIQVPNYSL[p.R254W]WIEAMVLKKEFLPSCSSLYTDITVLR	YSLWIEAMV,SLWIEAMVL,LWIEAMVLK,WIEAMVLKK,IQVPNYSLW,NYSLWIEAM,IQVPNYSLWI,SLWIEAMVLK,NYSLWIEAMV,YSLWIEAMVL,VPNYSLWIEA	CRC
FHL1	c.552T>G	p.D184E	AKHCVKCNKAITSGGITYQDQPWHA[p.D184E]ECFVCVTCSKKLAGQRFTAVEDQYYC	AECFVCVTC,QPWHAECFV,AECFVCVTCS	CLL
FIGNL1	c.926delA	p.K309fs	NGPKEDSSLPTFKTAKEQLWVDQQK[p.K309fs]STTNLSVHQGLHMVV*	SVHQGLHMV,LSVHQGLHM,DQQKSTTNL,QKSTTNLSV,SVHQGLHMVV,QQKSTTNLSV,TTNLSVHQGL,QKSTTNLSVH,NLSVHQGLHM	STAD
FILIP1	c.1565T>A	p.I522K	LKDDLTKLKSFTVMLVDERKNMMEK[p.I522K]KKQEERKVDGLNKNFKVEQGKVMDVT	MMEKKKQEER	CLL
FKBPL	c.481G>C	p.E161Q	GPPEGWTELTMGVGPWREETWGELI[p.E161Q]QKCLESMCQGEEAELQLPGHSGPPVR	ETWGELIQK,LIQKCLESM,ELIQKCLESM	CESC
FKBPL	c.959G>T	p.R320L	AQAALGNLEKATADLKKVLAIDPKN[p.R320L]LAAQEELGKVVIQGKNQDAGLAQGLR	VLAIDPKNL,KNLAAQEEL,VLAIDPKNLA	LUAD
FLG	c.477delA	p.K159fs	KGNKGRSKSPRETGGKRHESSSEKK[p.K159fs]KEKDIHLLIEKKNMEKTIITQVKKRKTRLKILD*	KTIITQVKK,LIEKKNMEK,TIITQVKKR,QVKKRKTRL,KKKEKDIHL,KEKDIHLLI,KKNMEKTII,MEKTIITQV,KKRKTRLKI,NMEKTIITQV,LIIEKKNMEK,KTIITQVKKR,TIITQVKKRK,QVKKRKTRLK,ITQVKKRKTR,KKKEKDIHLL,TQVKKRKTRL,KKRKTRLKIL	STAD
FLG	c.8657G>A	p.R2886H	ASTHADISRHSQAVQGQSEGSRRSR[p.R2886H]HQGSSVSQDSDSEGHSEDSERWSGSA	GSRRSRHQG,RSRHQGSSV,RSRHQGSSVS,RRSRHQGSSV	GBM
FLG	c.9761C>A	p.P3254H	ERWSGSASRNHRGSVQEQSRHGSRH[p.P3254H]HRSHHEDRAGHGHSADRSRQSGTRHA	GSRHHRSHH,QSRHGSRHHR	LUAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
FLG2	c.1716G>T	p.L572F	GSGSSQSSGYGQYGSRETSGFGQHG[p.L572F]FGSGQSTGFGQYGSGSGQSSGFGQHG	FGSGQSTGF,GFGSGQSTGF	LUAD
FLG2	c.4634G>T	p.G1545V	HTHGQSGSQHGESESIIHDRHRITH[p.G1545V]VQTGDTTRHSYSGHEQTTQTGSRTTG	HVQTGDTTR	LUAD
FLG2	c.5703_5704delCA	p.H1901fs	RRSGHSESSDSEVHSGGSHTHSGHT[p.H1901fs]QPSQVSTWRVRIHSSQETPNYSWTDRRYH*	HSSQETPNY,TWRVRIHSS,RVRIHSSQE,QVSTWRVRI,TQPSQVSTW,SQETPNYSW,HTHSGHTQPS,RVRIHSSQET,IHSSQETPNY,ETPNYSWTDR,HTQPSQVSTW,SQVSTWRVRI,SSQETPNYSW,QPSQVSTWRV	GBM
FLJ43860	c.2549_2550insT	p.L850fs	SHTFQLWRALGAGQPTSHLVLTTLL[p.L850fs]GLSAGATPAHRCQRQQPLPQGEDLPAFAGCHEHAARAAVCPGVQAGRAGGLPQALPGPPHPDALCLGAEPAQRAPQAAGPGGGRAQPPKLQHVTGGTEEPAVHHGALA*	LVLTTLLGL,TLLGLSAGA,GLSAGATPA,ALCLGAEPA,AQPPKLQHV,ATPAHRCQR,AARAAVCPG,GGGRAQPPK,EPAVHHGAL,HRCQRQQPL,LSAGATPAH,PQGEDLPAF,HEHAARAAV,VQAGRAGGL,RAGGLPQAL,AQRAPQAAG,LQHVTGGTE,LPQGEDLPA,HLVLTTLLGL,VLTTLLGLSA,AVCPGVQAGR,AARAAVCPGV,AGRAGGLPQA,RAQPPKLQHV,LSAGATPAHR,FAGCHEHAAR,TTLLGLSAGA,HVTGGTEEPA,LPQGEDLPAF,LPGPPHPDAL,AHRCQRQQPL,GLSAGATPAH,GRAGGLPQAL,LQHVTGGTEE,EEPAVHHGAL,LPAFAGCHEH,LPQALPGPPH,HEHAARAAVC,AEPAQRAPQA,TEEPAVHHGA	PRAD
FLNA	c.3718G>A	p.V1240M	GTHTITYIPLCPGAYTVTIKYGGQP[p.V1240M]MPNFPSKLQVEPAVDTSGVQCYGPGI	TIKYGGQPM,YGGQPMPNF,KYGGQPMPNF,GQPMPNFPSK,QPMPNFPSKL,MPNFPSKLQV,VTIKYGGQPM	GBM
FLNB	c.1586_1587insG	p.W529fs	LDGVYAFEYYPSTPGRYSIAITWGG[p.W529fs]TPHSKEPL*	ITWGGTPHSK,YSIAITWGGT,IAITWGGTPH	STAD
FLNB	c.1586delG	p.W529fs	FLDGVYAFEYYPSTPGRYSIAITWG[p.W529fs]DTTFQRAPLKFKLALKRVCRKSVLGALGSMVGLSGGQRTSW*	VLGALGSMV,TTFQRAPLK,LALKRVCRK,TFQRAPLKF,FQRAPLKFK,RAPLKFKLA,PLKFKLALK,KFKLALKRV,KLALKRVCR,RVCRKSVLG,TWGDTTFQR,MVGLSGGQR,DTTFQRAPL,APLKFKLAL,AITWGDTTF,SVLGALGSM,KRVCRKSVL,LSGGQRTSW,SVLGALGSMV,ALKRVCRKSV,KLALKRVCRK,ITWGDTTFQR,TFQRAPLKFK,IAITWGDTTF,TTFQRAPLKF,RVCRKSVLGA,DTTFQRAPLK,RAPLKFKLAL,LKRVCRKSVL,KSVLGALGSM,FQRAPLKFKL,LKFKLALKRV,GLSGGQRTSW	STAD
FLT3	c.1800_1801insTTCAGAGAATATGAATATGAT	p.600_601insFREYEYD	LQMVQVTGSSDNEYFYVDFREYEYD[p.600_601insFREYEYD]FREYEYDLKWEFPRENLEFGKVLGSGAFGKVMNATAYGISKTGVSI	YEYDFREYE,REYEYDFRE,REYEYDFREY,YEYDFREYEY,DFREYEYDFR,VDFREYEYDF,YDFREYEYDL	LAML
FLT3	c.2503G>C	p.D835H	RDLAARNVLVTHGKVVKICDFGLAR[p.D835H]HIMSDSNYVVRGNARLPVKWMAPESL	HIMSDSNYV,RHIMSDSNY,CDFGLARHI,HIMSDSNYVV,CDFGLARHIM,ARHIMSDSNY,RHIMSDSNYV	LAML
FLT3	c.2503G>T	p.D835Y	RDLAARNVLVTHGKVVKICDFGLAR[p.D835Y]YIMSDSNYVVRGNARLPVKWMAPESL	ICDFGLARY,YIMSDSNYV,RYIMSDSNY,CDFGLARYI,YIMSDSNYVV,KICDFGLARY,RYIMSDSNYV,CDFGLARYIM,ARYIMSDSNY	LAML
FLT3	c.2505T>A	p.D835E	RDLAARNVLVTHGKVVKICDFGLAR[p.D835E]EIMSDSNYVVRGNARLPVKWMAPESL	EIMSDSNYV,REIMSDSNY,CDFGLAREI,EIMSDSNYVV,CDFGLAREIM,AREIMSDSNY,REIMSDSNYV	LAML
FMN2	c.2252C>T	p.S751F	CLEALRLEEKEVRHHRILEAKSIQT[p.S751F]FPTEEGGVLTLPPVDGLPGRPPCPPG	FPTEEGGVL,LEAKSIQTF,QTFPTEEGGV,ILEAKSIQTF,FPTEEGGVLT	BRCA
FMN2	c.2974C>A	p.P992T	GIPLPPPLPGAGIPPPPPLPGAGIP[p.P992T]TPPPLPGAGIPPPPPLPGAGIPPPPP	AGIPTPPPL	LUAD
FMNL1	c.2779G>C	p.E927Q	HFLDKAGSVSLDSVLADVRSLQRGL[p.E927Q]QLTQREFVRQDDCMVLKEFLRANSPT	SLQRGLQLT,RSLQRGLQL,QLTQREFVR,LQRGLQLTQ,GLQLTQREF,LQLTQREFV,GLQLTQREFV,RGLQLTQREF	CESC
FMO3	c.1530C>A	p.F510L	AILTQWDRSLKPMQTRVVGRLQKPC[p.F510L]LFFHWLKLFAIPILLIAVFLVLT*	CLFFHWLKL,RLQKPCLFF,LFFHWLKLF,LQKPCLFFH,RLQKPCLFFH,LQKPCLFFHW,CLFFHWLKLF,KPCLFFHWLK,GRLQKPCLFF	CRC
FMOD	c.993C>A	p.S331R	QKIPPVNTNLENLYLQGNRINEFSI[p.S331R]RSFCTVVDVVNFSKLQVLRLDGNEIK	FSIRSFCTV,SIRSFCTVV,RSFCTVVDV,INEFSIRSF,FSIRSFCTVV,RSFCTVVDVV,RINEFSIRSF,NEFSIRSFCT	KIRP

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
FN1	c.868C>T	p.R290C	RGEWKCERHTSVQTTSSGSGPFTDV[p.R290C]CAAVYQPQPHPQPPPYGHCVTDSGVV	FTDVCAAVY,GPFTDVCAAV	UCEC
FNBP4	c.172_177delACCACC	p.TT58del	PEPDTEPDSTAAVPSQPAPSAATTT[p.TT58del]AVTAAAASDDSPSEDEQEAVQEVPRVVQNPP	APSAATTTA,ATTTAVTAAA,APSAATTTAV	PRAD
FNDC1	c.1955G>A	p.R652H	QGTSHRPSLPASLNDNDLVDSDEDE[p.R652H]HAVGSLHPKGAFAQPRPALSPSRQSP	HAVGSLHPK,DEHAVGSLH,DEDEHAVGSL	CRC
FNDC1	c.3535_3537delGAC	p.D1180del	APGKSEPPSKRPLSSKSQQSVSAED[p.D1180del]EEEDAGFFKGGKEDLLSSSVPKWPSSST	AEDEEEDAGF	PAAD
FOLH1	c.1501delA	p.S501fs	NLTKELKSPDEGFEGKSLYESWTKK[p.S501fs]VLPQSSVACPG*	KVLPQSSVA,YESWTKKVL,KKVLPQSSV,SLYESWTKKV,LYESWTKKVL,KKVLPQSSVA	STAD
FOLH1	c.1927G>T	p.A643S	HPQEMKTYSVSFDSLFSAVKNFTEI[p.A643S]SSKFSERLQDFDKSNPIVLRMMNDQL	KNFTEISSK,NFTEISSKF,EISSKFSER,ISSKFSERL,EISSKFSERL,KNFTEISSKF	LUAD
FOXD4L4	c.1215delC	p.C405fs	GQFCSNSSSIRRTAPTAALPPRARC[p.C405fs]GRAPVGLVGAAEVSGSGGGL*	RARCGRAPV,CGRAPVGLV,EVSGSGGGL,APVGLVGAA,RARCGRAPVG,AEVSGSGGGL	KIRC
FOXK1	c.1060C>T	p.R354W	SGIYAHITKHYPYYRTADKGWQNSI[p.R354W]WHNLSLNRYFIKVPRSQEEPGKGSFW	WQNSIWHNL,NSIWHNLSL,WHNLSLNRY,SIWHNLSLNR,GWQNSIWHNL,IWHNLSLNRY,WHNLSLNRYF	CRC
FOXN3	c.287delC	p.P96fs	NLLKSFGESVLRSVSPVQDLDDDTP[p.P96fs]HPLPTLTCPTMPGRTPTANPPTPSAASYLWPSRTLQPSACQ*	TMPGRTPTA,LTCPTMPGR,AASYLWPSR,SYLWPSRTL,DTPHPLPTL,SAASYLWPS,LPTLTCPTM,PPTPSAASY,TPSAASYLW,SAASYLWPSR,ASYLWPSRTL,TLTCPTMPGR,HPLPTLTCPT,CPTMPGRTPT,WPSRTLQPSA,NPPTPSAASY	CRC,STAD
FOXQ1	c.404C>T	p.S135L	RSKPYTRRPKPPYSYIALIAMAIRD[p.S135L]LAGGRLTLAEINEYLMGKFPFFRGSY	AIRDLAGGR,IAMAIRDLA,ALIAMAIRDL,LIAMAIRDLA,AIRDLAGGRL,MAIRDLAGGR,RDLAGGRLTL	BLCA
FOXRED1	c.407G>T	p.R136L	SVGGICQQFSLPENIQLSLFSASFL[p.R136L]LNINEYLAVVDAPPLDLRFNPSGYLL	SLFSASFLL,FSASFLLNI,FLLNINEYL,LLNINEYLA,SFLLNINEY,LNINEYLAV,FLLNINEYLA,LLNINEYLAV,ASFLLNINEY,LFSASFLLNI,SFLLNINEYL,LSLFSASFLL,LNINEYLAVV	LUAD
FPGS	c.64A>G	p.I22V	MSRARSHLRAALFLAAASARG[p.I22V]VTTQVAARRGLSAWPVPQEPSMEYQD	SARGVTTQV,GVTTQVAAR,VTTQVAARR,LAAASARGV,FLAAASARGV,ASARGVTTQV,SARGVTTQVA	ACC
FPGT-TNNI3K	c.1364G>A	p.R455H	NVININHQGRDGHTGLHSACYHGHI[p.R455H]HLVQFLLDNGADMNLVACDPSRSSGE	CYHGHIHLV,HIHLVQFLL,ACYHGHIHL,HGHIHLVQF,GHIHLVQFL,YHGHIHLVQF,HSACYHGHIH,SACYHGHIHL,GHIHLVQFLL	CRC
FPR2	c.161G>A	p.R54Q	PLVVLGVTFVLGVLGNGLVIWVAGF[p.R54Q]QMTRTVTTICYLNLALADFSFTATLP	FQMTRTVTT,QMTRTVTTI,WVAGFQMTR,VIWVAGFQM,AGFQMTRTV,FQMTRTVTTI,IWVAGFQMTR,LVIWVAGFQM	GBM
FRAS1	c.1145G>T	p.C382F	FMSSNASEVKRIPEGEKWEDGPCKV[p.C382F]FECRGAQVTCYEPSCPPCPVGTLALE	WEDGPCKVF,FECRGAQVT,KVFECRGAQV,KWEDGPCKVF	LUAD
FRG1	c.254_256delAAG	p.E86del	AIEMDKGTYIHALDNGLFTLGAPHK[p.E86del]VDEGPSPPEQFTAVKLSDSRIALKSGYG	FTLGAPHKV	PRAD
FRG1B	c.101T>C	p.I34T	RIALKSGYGKYLGINSDELVGHSDA[p.I34T]TGPREQWEPVFQNGKMALLASNSCFI	DELVGHSDAT	PRAD
FRG1B	c.110G>A	p.R37K	LKSGYGKYLGINSDELVGHSDAIGP[p.R37K]KEQWEPVFQNGKMALLASNSCFIRCN	GPKEQWEPV,DAIGPKEQW,VGHSDAIGPK	UCS
FRG1B	c.115C>A	p.Q39K	SGYGKYLGINSDELVGHSDAIGPRE[p.Q39K]KWEPVFQNGKMALLASNSCFIRCNEA	GPREKWEPV,DAIGPREKW,HSDAIGPREK,KWEPVFQNGK,GPREKWEPVF	CLL
FRG1B	c.125C>A	p.P42Q	GKYLGINSDELVGHSDAIGPREQWE[p.P42Q]QVFQNGKMALLASNSCFIRCNEAGDI	GPREQWEQV,EQVFQNGKM,GPREQWEQVF,WEQVFQNGKM,QVFQNGKMAL,REQWEQVFQN	PRAD
FRG1B	c.145A>G	p.M49V	SDELVGHSDAIGPREQWEPVFQNGK[p.M49V]VALLASNSCFIRCNEAGDIEAKSKTA	FQNGKVALL,FQNGKVALLA,VFQNGKVALL,VALLASNSCF,WEPVFQNGKV	TGCT

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FRG1B	c.148G>C	p.A50P	DELVGHSDAIGPREQWEPVFQNGKM[p.A50P]PLLASNSCFIRCNEAGDIEAKSKTAG	FQNGKMPLL,VFQNGKMPL,MPLLASNSC,PLLASNSCF,FQNGKMPLLA,VFQNGKMPLL,MPLLASNSCF	KIRP,PRAD,SKCM
FRG1B	c.155T>C	p.L52S	LVGHSDAIGPREQWEPVFQNGKMAL[p.L52S]SASNSCFIRCNEAGDIEAKSKTAGEE	SASNSCFIR,LSASNSCFI,ALSASNSCF,FQNGKMALSA,ALSASNSCFI,KMALSASNSC,LSASNSCFIR,MALSASNSCF	PRAD,UCS
FRG1B	c.157G>A	p.A53T	VGHSDAIGPREQWEPVFQNGKMALL[p.A53T]TSNSCFIRCNEAGDIEAKSKTAGEEE	LLTSNSCFI,LTSNSCFIR,ALLTSNSCF,ALLTSNSCFI,FQNGKMALLT,KMALLTSNSC,LLTSNSCFIR,MALLTSNSCF	GBM,PRAD
FRG1B	c.163A>G	p.N55D	HSDAIGPREQWEPVFQNGKMALLAS[p.N55D]DSCFIRCNEAGDIEAKSKTAGEEEMI	LLASDSCFI,LASDSCFIR,ALLASDSCF,ALLASDSCFI,LLASDSCFIR,MALLASDSCF	PRAD
FRG1B	c.175A>G	p.I59V	IGPREQWEPVFQNGKMALLASNSCF[p.I59V]VRCNEAGDIEAKSKTAGEEEMIKSLS	LLASNSCFV,LASNSCFVR,ALLASNSCFV,LLASNSCFVR	PRAD,SKCM
FRG1B	c.194G>A	p.G65E	WEPVFQNGKMALLASNSCFIRCNEA[p.G65E]EDIEAKSKTAGEEEMIKSLSHSLPSS	FIRCNEAEDI	UCS
FRG1B	c.29T>C	p.I10T	MAVKLSDSR[p.I10T]TALKSGYGKYLGINSDELVGHSDAIG	LSDSRTALK,KLSDSRTAL,TALKSGYGK,RTALKSGYG,KLSDSRTALK,RTALKSGYGK,AVKLSDSRTA,TALKSGYGKY,VKLSDSRTAL	PRAD,UCS
FRG1B	c.31G>A	p.A11T	MAVKLSDSRI[p.A11T]TLKSGYGKYLGINSDELVGHSDAIGP	KLSDSRITL,ITLKSGYGK,LSDSRITLK,TLKSGYGKY,SRITLKSGY,TLKSGYGKYL,KLSDSRITLK,RITLKSGYGK,ITLKSGYGKY,VKLSDSRITL	PRAD
FRG1B	c.39A>T	p.K13N	MAVKLSDSRIAL[p.K13N]NSGYGKYLGINSDELVGHSDAIGPRE	IALNSGYGK,SRIALNSGY,ALNSGYGKY,ALNSGYGKYL,RIALNSGYGK,IALNSGYGKY,DSRIALNSGY	GBM,PRAD,UCS
FRG1B	c.59T>C	p.L20P	MAVKLSDSRIALKSGYGKY[p.L20P]PGINSDELVGHSDAIGPREQWEPVFQ	YPGINSDEL,KYPGINSDEL,KSGYGKYPGI,YPGINSDELV	KIRP
FRG1B	c.95A>T	p.D32V	DSRIALKSGYGKYLGINSDELVGHS[p.D32V]VAIGPREQWEPVFQNGKMALLASNSC	ELVGHSVAI,VAIGPREQW,DELVGHSVA,NSDELVGHSV,DELVGHSVAI	PRAD,UCS
FRG2B	c.424G>T	p.D142Y	ECSLSLNKKSRSSTPVHNSEIQETC[p.D142Y]YAHHRGRSRACTGRSKRHRSRALGVQ	NSEIQETCY,YAHHRGRSR,TCYAHHRGR,SEIQETCYA,IQETCYAHH,ETCYAHHRGR,CYAHHRGRSR,YAHHRGRSRA,SEIQETCYAH	LUAD
FRMD4A	c.3014delC	p.P1005fs	CKATSAALPQSQRSSTPSSEIGATP[p.P1005fs]QAAPTTS*	SEIGATPQA,SEIGATPQAA	STAD
FRMPD1	c.3277G>C	p.E1093Q	APKYTEPLLSPRDEPRSDECGINPG[p.E1093Q]QKIASIPTKEEPQGQLSLERDREVTN	NPGQKIASI,GQKIASIPT,GQKIASIPTK	LUAD
FRS2	c.140T>C	p.L47S	KVINVDDDGNELGSGIMELTDTELI[p.L47S]SYTRKRDSVKWHYLCLRRYGYDSNLF	LTDTELISY,DTELISYTR,ELISYTRKR,ISYTRKRDSV,SYTRKRDSVK,ELTDTELISY	TGCT
FSHB	c.128C>A	p.T43N	CNSCELTNITIAIEKEECRFCISIN[p.T43N]NTWCAGYCYTRDLVYKDPARPKIQKT	NTWCAGYCY,INNTWCAGY,FCISINNTW,RFCISINNTW,SINNTWCAGY,NTWCAGYCYT	LUAD
FUBP1	c.1288C>T	p.R430C	QSGARIELQRNPPPNADPNMKLFTI[p.R430C]CGTPQQIDYARQLIEEKIGGPVNPLG	CGTPQQIDY,FTICGTPQQI	UCEC

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FUT6	c.418_419insA	p.S140fs	NPSAQLPRSPRRQGQRWIWFSMESP[p.S140fs]KPLLAAESHGRILQSHHVLPQRLRHLHALRLAGAVVRPACPPTAQPLGQDRAGGLGSVQLGAKLRQGALLPEPAGPSQGGRVRTLPQAPAPGNHDGDAVPVQVLSGLRELLAPRLHHREAVEERPGGLGRARGAGPQQKQLREVPATRRLHPRGRLPEPQGPGPVPAGAGQGPRPLPELLSLAGDAAASLLQLGTRFLQGLLETAGGIQVPDTRHSGLVHLRGWCGAWAARNLIFLGPHLSGGLIYLRTRLPEASPA*	VLSGLRELL,FLQGLLETA,GLLETAGGI,NLIFLGPHL,HLSGGLIYL,FSMESPKPL,VLPQRLRHL,ALRLAGAVV,GLGSVQLGA,PLPELLSLA,LLSLAGDAA,LLQLGTRFL,FLGPHLSGG,IWFSMESPK,RLRHLHALR,ASLLQLGTR,LSGGLIYLR,AWAARNLIF,RILQSHHVL,VVRPACPPT,KLRQGALLP,RVRTLPQAP,GLRELLAPR,RARGAGPQQ,ATRRLHPRG,RLHPRGRLP,GTRFLQGLL,AARNLIFLG,QSHHVLPQR,LLAPRLHHR,QLREVPATR,PATRRLHPR,GWCGAWAAR,ESPKPLLAA,DAAASLLQL,WAARNLIFL,RPACPPTAQ,VPVQVLSGL,APRLHHREA,HPRGRLPEP,GPRPLPELL,RPLPELLSL,VPDTRHSGL,GPHLSGGLI,QRLRHLHAL,GAKLRQGAL,SLLQLGTRF,HLRGWCGAW,SMESPKPLL,MESPKPLLA,LQSHHVLPQ,LRHLHALRL,RHLHALRLA,HLHALRLAG,AKLRQGALL,RQGALLPEP,SQGGRVRTL,KQLREVPAT,REVPATRRL,LSLAGDAAA,LAGDAAASL,LETAGGIQV,TRHSGLVHL,RGWCGAWAA,GAWAARNLI,FSMESPKPLL,LLAAESHGRI,RLAGAVVRPA,GLRELLAPRL,SLAGDAAASL,SLLQLGTRFL,FLGPHLSGGL,RLRHLHALRL,HLHALRLAGA,VLSGLRELLA,LLSLAGDAAA,QLGTRFLQGL,LLETAGGIQV,HLRGWCGAWA,WIWFSMESPK,GLGSVQLGAK,HLSGGLIYLR,GAWAARNLIF,AWAARNLIFL,HGRILQSHHV,HVLPQRLRHL,ALRLAGAVVR,VVRPACPPTA,KLRQGALLPE,GGRVRTLPQA,RVRTLPQAPA,RTLPQAPAPG,RARGAGPQQK,ATRRLHPRGR,RLHPRGRLPE,RGWCGAWAAR,ELLAPRLHHR,QLREVPATRR,VPATRRLHPR,EAVEERPGGL,QVPDTRHSGL,LPQRLRHLHA,APGNHDGDAV,APRLHHREAV,GPQQKQLREV,LPEPQGPGPV,PQRLRHLHAL,GPHLSGGLIY,MESPKPLLAA,LAAESHGRIL,GRILQSHHVL,HALRLAGAVV,RAGGLGSVQL,RQGALLPEPA,VQVLSGLREL,RELLAPRLHH,QQKQLREVPA,REVPATRRLH,GQGPRPLPEL,GDAAASLLQL,ASLLQLGTRF,LQLGTRFLQG,RFLQGLLETA,IQVPDTRHSG,VHLRGWCGAW,RNLIFLGPHL,AESHGRILQS,PELLSLAGDA,VPDTRHSGLV	KIRC
FYB	c.972delG	p.G324fs	NQEELASGTPPARFPKAPSKLTVGG[p.G324fs]HGAKVRKRKRETRIQPPRNRSHCLPCLPWVHLHQNPTDHQMLT*	LTVGGHGAK,GGHGAKVRK,HGAKVRKRK,KVRKRKRET,RIQPPRNRS,RNRSHCLPC,TVGGHGAKV,PPRNRSHCL,HQNPTDHQM,IQPPRNRSH,SHCLPCLPW,LPCLPWVHL,LPWVHLHQN,CLPCLPWVHL,KLTVGGHGAK,KVRKRKRETR,RIQPPRNRSH,RNRSHCLPCL,ETRIQPPRNR,LTVGGHGAKV,QPPRNRSHCL,RSHCLPCLPW,LHQNPTDHQM,HQNPTDHQML,LPWVHLHQNP	STAD
FZD3	c.1099G>A	p.D367N	LTIILLAMNKIEGDNISGVCFVGLY[p.D367N]NVDALRYFVLAPLCLYVVVGVSLLLA	NVDALRYFV,GLYNVDALR,LYNVDALRY,YNVDALRYF,GVCFVGLYNV,GLYNVDALRY,LYNVDALRYF,YNVDALRYFV	CRC
FZD6	c.1247G>A	p.R416Q	ISLNHVRQVIQHDGRNQEKLKKFMI[p.R416Q]QIGVFSGLYLVPLVTLLGCYVYEQVN	KLKKFMIQI,IQIGVFSGL,KFMIQIGVF,QIGVFSGLY,KKFMIQIGV,FMIQIGVFSG,MIQIGVFSGL,KLKKFMIQIG,IQIGVFSGLY,KKFMIQIGVF	UCEC
GABRA3	c.218G>A	p.R73H	LSPKHAPDIPDDSTDNITIFTRILD[p.R73H]HLLDGYDNRLRPGLGDAVTEVKTDIY	ILDHLLDGY,IFTRILDHL,HLLDGYDNR,FTRILDHLL,HLLDGYDNRL,TIFTRILDHL,IFTRILDHLL,RILDHLLDGY	UCEC
GABRA4	c.1379G>A	p.R460Q	PFSRANAAETISAARALPSASPTSI[p.R460Q]QTGYMPRKASVGSASTRHVFGSRLQR	SIQTGYMPR,IQTGYMPRK,SPTSIQTGY,SIQTGYMPRK,TSIQTGYMPR,ASPTSIQTGY,SPTSIQTGYM,IQTGYMPRKA	CRC,UCEC
GABRA5	c.377G>A	p.S126N	RQSWKDERLRFKGPMQRLPLNNLLA[p.S126N]NKIWTPDTFFHNGKKSIAHNMTTPNK	NKIWTPDTF,ANKIWTPDTF,NKIWTPDTFF	CRC
GABRA5	c.670C>A	p.Q224K	SEVVYVWTNGSTKSVVVAEDGSRLN[p.Q224K]KYHLMGQTVGTENISTSTGEYTIMTA	KYHLMGQTV,GSRLNKYHL,SRLNKYHLM,GSRLNKYHLM,AEDGSRLNKY,NKYHLMGQTV	LUAD
GABRA6	c.940G>A	p.V314I	SARHSLPKVSYATAMDWFIAVCFAF[p.V314I]IFSALIEFAAVNYFTNLQTQKAKRKA	FIAVCFAFI,FAFIFSALI,FIFSALIEF,IAVCFAFIF,CFAFIFSAL,FIFSALIEFA,WFIAVCFAFI,CFAFIFSALI,AFIFSALIEF,FIAVCFAFIF,VCFAFIFSAL	GBM
GABRB1	c.1246C>T	p.R416C	KATMYSYDSASIQYRKPLSSREAYG[p.R416C]CALDRHGVPSKGRIRRRASQLKVKIP	SSREAYGCA,EAYGCALDR,SREAYGCAL,SSREAYGCAL	PRAD

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GABRB3	c.1498G>A	p.D500N	RSLPHKKTHLRRRSSQLKIKIPDLT[p.D500N]NVNAIDRWSRIVFPFTFSLFNLVYWL	LTNVNAIDR,IKIPDLTNV,KIKIPDLTNV,KIPDLTNVNA,DLTNVNAIDR,NVNAIDRWSR,IPDLTNVNAI	CRC
GABRD	c.1236delG	p.Q412fs	GSYRSVGVETGETKKEGAARSGGQG[p.Q412fs]ASVPGSGPSTQTPLTFTPALCSLRRLRPSMSSTGRHTPCEHRTQATLACPGARRQLPRNFLGERALGLPSPLRVSKWDDSRPRKTRGSLGLPEL*	FLGERALGL,RLRPSMSST,ATLACPGAR,ALGLPSPLR,RVSKWDDSR,TFTPALCSL,AARSGGQGA,RSGGQGASV,SLRRLRPSM,RQLPRNFLG,RALGLPSPL,KWDDSRPRK,KTRGSLGLP,FTPALCSLR,ALCSLRRLR,TLACPGARR,QTPLTFTPA,TPLTFTPAL,RPRKTRGSL,PSTQTPLTF,CEHRTQATL,TQATLACPG,ARRQLPRNF,RRQLPRNFL,RNFLGERAL,GERALGLPS,RKTRGSLGL,RGSLGLPEL,ALGLPSPLRV,ATLACPGARR,RALGLPSPLR,CSLRRLRPSM,SLRRLRPSMS,RLRPSMSSTG,RTQATLACPG,KTRGSLGLPE,TFTPALCSLR,QTPLTFTPAL,LTFTPALCSL,TPALCSLRRL,LPRNFLGERA,RPRKTRGSLG,GSGPSTQTPL,GPSTQTPLTF,TQTPLTFTPA,TQATLACPGA,LACPGARRQL,GARRQLPRNF,RQLPRNFLGE,ERALGLPSPL,TRGSLGLPEL,LPSPLRVSKW,CEHRTQATLA,GERALGLPSP	STAD
GABRG1	c.613G>A	p.E205K	LRLTINAECYLQLHNFPMDEHSCPL[p.E205K]KFSSYGYPKNEIEYKWKKPSVEVADP	KFSSYGYPK,PLKFSSYGY,DEHSCPLKF,HSCPLKFSSY,CPLKFSSYGY,MDEHSCPLKF	SKCM
GABRR2	c.1103C>T	p.A368V	VSYVKAVDIYLWVSFVFVFLSVLEY[p.A368V]VAVNYLTTVQERKERKLREKFPCMCG	VFLSVLEYV,FLSVLEYVA,VAVNYLTTV,VLEYVAVNY,LEYVAVNYL,FVFLSVLEYV,FLSVLEYVAV,VLEYVAVNYL,YVAVNYLTTV,SVLEYVAVNY,LEYVAVNYLT	PRAD
GADL1	c.1054C>A	p.L352I	VAWNPHKMLMAGIQCCALLVKDKSD[p.L352I]ILKKCYSAKASYLFQQDKFYDVSYDT	KSDILKKCY,ILKKCYSAK,ILKKCYSAKA,LVKDKSDILK,DILKKCYSAK	LUAD
GAL3ST3	c.811G>T	p.A271S	ESLVLLRRLLAWDLDDVLYAKLNAR[p.A271S]SASSRLAAIPAALARAARTWNALDAG	SASSRLAAI,KLNARSASS,RSASSRLAA,NARSASSRL,YAKLNARSA,VLYAKLNARS,KLNARSASSR,NARSASSRLA,RSASSRLAAI,LNARSASSRL,ARSASSRLAA	LUAD
GALNT13	c.1072G>T	p.G358C	LEIVTCSHVGHVFRKATPYTFPGGT[p.G358C]CHVINKNNRRLAEVWMDEFKDFFYII	GGTCHVINK,YTFPGGTCH,FPGGTCHVI,YTFPGGTCHV,TFPGGTCHVI	LUSC
GALNT14	c.702T>A	p.D234E	VNRDWLQPLLHRVKEDYTRVVCPVI[p.D234E]EIINLDTFTYIESASELRGGFDWSLH	RVVCPVIEI,IEIINLDTF,CPVIEIINL,EIINLDTFTY,RVVCPVIEII	LUAD
GALNTL1	c.950_951insG	p.W317fs	GIFVIDKSWFNHLGKYDAQMDIWGG[p.W317fs]REF*	AQMDIWGGR,MDIWGGREF,DAQMDIWGGR,QMDIWGGREF	STAD
GALNTL2	c.1183G>A	p.E395K	AMDRHYFQNTGAYDSLMSLRGGENL[p.E395K]KLSFKAWLCGGSVEILPCSRVGHIYQ	SLRGGENLK,GGENLKLSF,NLKLSFKAW,LKLSFKAWL,SLRGGENLKL,MSLRGGENLK,NLKLSFKAWL,RGGENLKLSF,GENLKLSFKA	UCEC
GALNTL5	c.133G>A	p.A45T	TALLFIYLHHNHVSSWQKKSQEPLS[p.A45T]TWSPGKKVHQQIIYGSEQIPKPHVIV	LSTWSPGKK,KSQEPLSTW,KKSQEPLSTW	LIHC
GALNTL5	c.785G>T	p.R262I	LEPLLHAIAKDPKMVVCPLIDVIDD[p.R262I]ITLEYKPSPLVRGTFDWNLQFKWDNV	VIDDITLEY,PLIDVIDDI,VIDDITLEYK,DVIDDITLEY,ITLEYKPSPL,CPLIDVIDDI	CRC
GALNTL6	c.1694_1696delAGA	p.K567del	WGYRKDRTLFHPVSNSCMDCNPAEK[p.K567del]IFMARCDPLSETQQWIFEHINMTVLEKF	NPAEKIFMA,CMDCNPAEKI,NPAEKIFMAR,MDCNPAEKIF	BRCA
GARS	c.124C>G	p.P42A	LLLLPPRLLARPSLLLRRSLSAASC[p.P42A]APISLPAAASRSSMDGAGAEEVLAPL	RSLSAASCA,LSAASCAPI,APISLPAAA,AASCAPISL,SLSAASCAPI,SAASCAPISL	ACC
GART	c.2420delA	p.K807fs	IESMQINGSVLKNGSLTNHFSFEKK[p.K807fs]RPEWLS*	FEKKRPEWL,FSFEKKRPEW	OV
GAS2L2	c.566A>C	p.D189A	AAPTLVQLEEEIEEEVRRELALPPP[p.D189A]APSPPAPPRRQPCHFRNLDQMVQSLV	RELALPPPA,LPPPAPSPPA,RELALPPPAP	TGCT

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
GAS6	c.449delG	p.G150fs	CDRKGTQACQDLMGNFFCLCKAGWG[p.G150fs]AGSATKMSTNAARRTGAASRSATTSRVASTVPATAASSSPLMAGPAKT*	TTSRVASTV,ATAASSSPL,KMSTNAARR,GWGAGSATK,ATKMSTNAA,ARRTGAASR,RTGAASRSA,ASRSATTSR,RSATTSRVA,STVPATAAS,NAARRTGAA,WGAGSATKM,SRVASTVPA,TAASSSPLM,ATTSRVASTV,RVASTVPATA,ATKMSTNAAR,AASRSATTSR,SSPLMAGPAK,AGWGAGSATK,STNAARRTGA,AARRTGAASR,RTGAASRSAT,ASRSATTSRV,TSRVASTVPA,ATAASSSPLM,SRVASTVPAT	STAD
GAS8	c.937C>A	p.R313S	EEMSEMQKQLANYERDKQILLCTKA[p.R313S]SLKVREKELKDLQWEHEVLEQRFTKV	ILLCTKASL,LLCTKASLK,KASLKVREK,CTKASLKVR,SLKVREKEL,LLCTKASLKV,ILLCTKASLK,SLKVREKELK,KQILLCTKAS	LUAD
GATA3	c.1002_1003insG	p.N334fs	ARRAGTSCANCQTTTTTTLWRRNANG[p.N334fs]GPCLQCLWALLQASQY*	CLQCLWALL,WALLQASQY,RNANGGPCL,LWALLQASQY,RRNANGGPCL,LQCLWALLQA	BRCA
GATA3	c.1200_1201insA	p.H400fs	CKKVHDSLEDFPKNSSFNPAALSRH[p.H400fs]NVLPEPHLALQPLQPHADHAHADAPAIQPVLWTTPPLQHGHRHGLEPCSMLTGPPARVPAVPFDLHFCRSSIMKPKRDGYMFLKAESKIMFATLQRSSLWCLCSNH*	VLPEPHLAL,ALQPLQPHA,AIQPVLWTT,MLTGPPARV,FLKAESKIM,IMFATLQRS,YMFLKAESK,KIMFATLQR,SMLTGPPAR,HFCRSSIMK,MFLKAESKI,CSMLTGPPA,RSSIMKPKR,IMKPKRDGY,KAESKIMFA,VPFDLHFCR,AALSRHNVL,EPHLALQPL,GPPARVPAV,KPKRDGYMF,FATLQRSSL,DLHFCRSSI,LHFCRSSIM,ESKIMFATL,LALQPLQPH,LQPHADHAH,HAHADAPAI,LQHGHRHGL,RHGLEPCSM,PARVPAVPF,PAVPFDLHF,LKAESKIMF,ATLQRSSLW,LQRSSLWCL,AESKIMFAT,ADAPAIQPV,APAIQPVLW,SMLTGPPARV,YMFLKAESKI,TLQRSSLWCL,CSMLTGPPAR,LHFCRSSIMK,FCRSSIMKPK,IMKPKRDGYM,GYMFLKAESK,SIMKPKRDGY,TTPPLQHGHR,AVPFDLHFCR,HADAPAIQPV,NPAALSRHNV,QPVLWTTPPL,KPKRDGYMFL,DLHFCRSSIM,MFATLQRSSL,FLKAESKIMF,RHNVLPEPHL,HLALQPLQPH,ADAPAIQPVL,HRHGLEPCSM,ARVPAVPFDL,VPAVPFDLHF,FDLHFCRSSI,MKPKRDGYMF,MFLKAESKIM,AESKIMFATL,IMFATLQRSS,FATLQRSSLW,LQRSSLWCLC,PPARVPAVPF,PEPHLALQPL	BRCA
GATA3	c.1222_1223insC	p.S408fs	EDFPKNSSFNPAALSRHMSSLSHIS[p.S408fs]ALQPLQPHADHAHADAPAIQPVLWTTPPLQHGHRHGLEPCSMLTGPPARVPAVPFDLHFCRSSIMKPKRDGYMFLKAESKIMFATLQRSSLWCLCSNH*	ALQPLQPHA,AIQPVLWTT,MLTGPPARV,FLKAESKIM,IMFATLQRS,YMFLKAESK,KIMFATLQR,SMLTGPPAR,HFCRSSIMK,MFLKAESKI,MSSLSHISA,SSLSHISAL,CSMLTGPPA,RSSIMKPKR,IMKPKRDGY,KAESKIMFA,VPFDLHFCR,GPPARVPAV,KPKRDGYMF,FATLQRSSL,DLHFCRSSI,LHFCRSSIM,ESKIMFATL,SHISALQPL,SALQPLQPH,LQPHADHAH,HAHADAPAI,LQHGHRHGL,RHGLEPCSM,PARVPAVPF,PAVPFDLHF,LKAESKIMF,ATLQRSSLW,LQRSSLWCL,AESKIMFAT,ADAPAIQPV,APAIQPVLW,SMLTGPPARV,YMFLKAESKI,TLQRSSLWCL,HMSSLSHISA,CSMLTGPPAR,LHFCRSSIMK,FCRSSIMKPK,IMKPKRDGYM,GYMFLKAESK,SIMKPKRDGY,TTPPLQHGHR,AVPFDLHFCR,MSSLSHISAL,HADAPAIQPV,QPVLWTTPPL,KPKRDGYMFL,DLHFCRSSIM,MFATLQRSSL,FLKAESKIMF,LSHISALQPL,ADAPAIQPVL,HRHGLEPCSM,ARVPAVPFDL,VPAVPFDLHF,FDLHFCRSSI,MKPKRDGYMF,MFLKAESKIM,AESKIMFATL,IMFATLQRSS,FATLQRSSLW,LQRSSLWCLC,PPARVPAVPF	BRCA

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
GATA3	c.1223_1224insT	p.S408fs	EDFPKNSSFNPAALSRHMSSLSHIS[p.S408fs]ALQPLQPHADHAHADAPAIQPVLWTTPPLQHGHRHGLEPCSMLTGPPARVPAVPFDLHFCRSSIMKPKRDGYMFLKAESKIMFATLQRSSLWCLCSNH*	ALQPLQPHA,AIQPVLWTT,MLTGPPARV,FLKAESKIM,IMFATLQRS,YMFLKAESK,KIMFATLQR,SMLTGPPAR,HFCRSSIMK,MFLKAESKI,MSSLSHISA,SSLSHISAL,CSMLTGPPA,RSSIMKPKR,IMKPKRDGY,KAESKIMFA,VPFDLHFCR,GPPARVPAV,KPKRDGYMF,FATLQRSSL,DLHFCRSSI,LHFCRSSIM,ESKIMFATL,SHISALQPL,SALQPLQPH,LQPHADHAH,HADAPAI,LQHGHRHGL,RHGLEPCSM,PARVPAVPF,PAVPFDLHF,LKAESKIMF,ATLQRSSLW,LQRSSLWCL,AESKIMFAT,ADAPAIQPV,APAIQPVLW,SMLTGPPARV,YMFLKAESKI,TLQRSSLWCL,HMSSLSHISA,CSMLTGPPAR,LHFCRSSIMK,FCRSSIMKPK,IMKPKRDGYM,GYMFLKAESK,SIMKPKRDGY,TTPPLQHGHR,AVPFDLHFCR,MSSLSHISAL,HADAPAIQPV,QPVLWTTPPL,KPKRDGYMFL,DLHFCRSSIM,MFATLQRSSL,FLKAESKIMF,LSHISALQPL,ADAPAIQPVL,HRHGLEPCSM,ARVPAVPFDL,VPAVPFDLHF,FDLHFCRSSI,MKPKRDGYMF,MFLKAESKIM,AESKIMFATL,IMFATLQRSS,FATLQRSSLW,LQRSSLWCLC,PPARVPAVPF	BRCA
GATA3	c.1290_1291insT	p.S430fs	ISPFSHSSHMLTTPTPMHPPSSLSF[p.S430fs]WTTPPLQHGHRHGLEPCSMLTGPPARVPAVPFDLHFCRSSIMKPKRDGYMFLKAESKIMFATLQRSSLWCLCSNH*	MLTGPPARV,FLKAESKIM,IMFATLQRS,YMFLKAESK,KIMFATLQR,SMLTGPPAR,HFCRSSIMK,MFLKAESKI,LSFWTTPPL,CSMLTGPPA,RSSIMKPKR,IMKPKRDGY,KAESKIMFA,VPFDLHFCR,GPPARVPAV,KPKRDGYMF,FATLQRSSL,DLHFCRSSI,LHFCRSSIM,ESKIMFATL,LQHGHRHGL,RHGLEPCSM,PARVPAVPF,PAVPFDLHF,LKAESKIMF,ATLQRSSLW,LQRSSLWCL,AESKIMFAT,HPPSSLSFW,SLSFWTTPPL,SMLTGPPARV,YMFLKAESKI,TLQRSSLWCL,CSMLTGPPAR,MHPPSSLSFW,LHFCRSSIMK,FCRSSIMKPK,IMKPKRDGYM,GYMFLKAESK,SIMKPKRDGY,TTPPLQHGHR,AVPFDLHFCR,KPKRDGYMFL,DLHFCRSSIM,MFATLQRSSL,FLKAESKIMF,HRHGLEPCSM,ARVPAVPFDL,VPAVPFDLHF,FDLHFCRSSI,MKPKRDGYMF,MFLKAESKIM,AESKIMFATL,IMFATLQRSS,FATLQRSSLW,LQRSSLWCLC,PPARVPAVPF	BRCA
GATA3	c.1301_1302insC	p.H434fs	FSHSSHMLTTPTPMHPPSSLSFGPH[p.H434fs]PPLQHGHRHGLEPCSMLTGPPARVPAVPFDLHFCRSSIMKPKRDGYMFLKAESKIMFATLQRSSLWCLCSNH*	MLTGPPARV,FLKAESKIM,IMFATLQRS,YMFLKAESK,KIMFATLQR,SMLTGPPAR,HFCRSSIMK,MFLKAESKI,CSMLTGPPA,RSSIMKPKR,IMKPKRDGY,KAESKIMFA,VPFDLHFCR,GPPARVPAV,KPKRDGYMF,FATLQRSSL,DLHFCRSSI,LHFCRSSIM,ESKIMFATL,LSFGPHPPL,LQHGHRHGL,RHGLEPCSM,PARVPAVPF,PAVPFDLHF,LKAESKIMF,ATLQRSSLW,LQRSSLWCL,AESKIMFAT,SLSFGPHPPL,SMLTGPPARV,YMFLKAESKI,TLQRSSLWCL,CSMLTGPPAR,LHFCRSSIMK,FCRSSIMKPK,IMKPKRDGYM,GYMFLKAESK,SIMKPKRDGY,AVPFDLHFCR,KPKRDGYMFL,DLHFCRSSIM,MFATLQRSSL,FLKAESKIMF,HRHGLEPCSM,ARVPAVPFDL,VPAVPFDLHF,FDLHFCRSSI,MKPKRDGYMF,MFLKAESKIM,AESKIMFATL,IMFATLQRSS,FATLQRSSLW,LQRSSLWCLC,PPARVPAVPF	BRCA
GATA3	c.1304_1305insC	p.H435fs	HSSHMLTTPTPMHPPSSLSFGPHHP[p.H435fs]LQHGHRHGLEPCSMLTGPPARVPAVPFDLHFCRSSIMKPKRDGYMFLKAESKIMFATLQRSSLWCLCSNH*	MLTGPPARV,FLKAESKIM,IMFATLQRS,YMFLKAESK,KIMFATLQR,SMLTGPPAR,HFCRSSIMK,MFLKAESKI,CSMLTGPPA,RSSIMKPKR,IMKPKRDGY,KAESKIMFA,VPFDLHFCR,LSFGPHHPL,GPPARVPAV,KPKRDGYMF,FATLQRSSL,DLHFCRSSI,LHFCRSSIM,ESKIMFATL,LQHGHRHGL,RHGLEPCSM,PARVPAVPF,PAVPFDLHF,LKAESKIMF,ATLQRSSLW,LQRSSLWCL,HPLQHGHRH,AESKIMFAT,SLSFGPHHPL,SMLTGPPARV,YMFLKAESKI,TLQRSSLWCL,CSMLTGPPAR,LHFCRSSIMK,FCRSSIMKPK,IMKPKRDGYM,GYMFLKAESK,SIMKPKRDGY,AVPFDLHFCR,KPKRDGYMFL,DLHFCRSSIM,MFATLQRSSL,FLKAESKIMF,HRHGLEPCSM,ARVPAVPFDL,VPAVPFDLHF,FDLHFCRSSI,MKPKRDGYMF,MFLKAESKIM,AESKIMFATL,IMFATLQRSS,FATLQRSSLW,LQRSSLWCLC,PPARVPAVPF	BRCA
GATA3	c.1329G>T	p.M443I	TTPTPMHPPSSLSFGPHHPSSMVTA[p.M443I]IG*	HPSSMVTAI	LUAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
GATA3	c.983_984insCTGGAGG	p.L328fs	RRLSAARRAGTSCANCQTTTTTLWR[p.L328fs]LEEECQWGPCLQCLWALLQASQY*	CLQCLWALL,QWGPCLQCL,TTTTTLWRL,WALLQASQY,EECQWGPCL,QWGPCLQCLW,LWALLQASQY,QTTTTTLWRL,CQWGPCLQCL,LQCLWALLQA	BRCA
GBP7	c.1292_1293insG	p.G431fs	QAELKRLSELLTESISRGTFFVPGG[p.G431fs]AQYLLRSKKED*	FVPGGAQYL,AQYLLRSKK,GAQYLLRSK,FFVPGGAQY,VPGGAQYLL,FVPGGAQYLL,GAQYLLRSKK,FFVPGGAQYL,TFFVPGGAQY	STAD
GCDH	c.1167delG	p.L389fs	VSLLKRNNCGKALDIARQARDMLGG[p.L389fs]MGFLTSIT*	MLGGMGFLT,RDMLGGMGF,GGMGFLTSI,RQARDMLGGM,RDMLGGMGFL	STAD
GCDH	c.244C>T	p.R82C	EEQLTTDEILIRDTFRTYCQERLMP[p.R82C]CILLANRNEVFHREIISEMGELGVLG	RLMPCILLA,MPCILLANR,QERLMPCIL,LMPCILLANR,CQERLMPCIL,QERLMPCILL	LUAD
GDAP1	c.919A>G	p.T307A	RVLKRKTFNKVLGHVNNILISAVLP[p.T307A]AAFRVAKKRAPKVLGTTLVVGLLAGV	ILISAVLPA,LISAVLPAA,AVLPAAFRV,VLPAAFRVA,SAVLPAAFR,LPAAFRVAK,ISAVLPAAF,ILISAVLPAA,VLPAAFRVAK,ISAVLPAAFR,AVLPAAFRVA,SAVLPAAFRV,LISAVLPAAF	BRCA
GDF5	c.315_316insA	p.E105fs	GQTGGLTQPKKDEPKKLPPRPGGPE[p.E105fs]TQARTPSPNKAGYSPDCDPKRTASRRQGTPKSRICPQLLPAEEGQGARAPTRAQGAVSPTPHHTPRVHALAVQDAVRC*	RICPQLLPA,ASRRQGTPK,QARTPSPNK,RTASRRQGT,KSRICPQLL,HTPRVHALA,SPTPHHTPR,HALAVQDAV,APTRAQGAV,TPRVHALAV,RQGTPKSRI,RAQGAVSPT,AQGAVSPTP,HHTPRVHAL,TPSPNKAGY,AEEGQGARA,LLPAEEGQGA,TQARTPSPNK,TASRRQGTPK,QARTPSPNKA,AGYSPDCDPK,ASRRQGTPKS,KSRICPQLLP,RVHALAVQDA,RTPSPNKAGY,HALAVQDAVR,HTPRVHALAV,TPKSRICPQL,SPTPHHTPRV,SRICPQLLPA,AQGAVSPTPH	TGCT
GDPD5	c.1779_1780insC	p.G593fs	SVCSDNSYDTYANSTATPVGPRGGG[p.G593fs]QPHQDPHRAEWALAEDMSVPPVPDTEAGEPRRAGGSVSELGVLWERAPQPPCGLQPLVSRSLS*	GPRGGGQPH,EPRRAGGSV,QPPCGLQPL,HQDPHRAEW,AEWALAEDM,WALAEDMSV,AEDMSVPPV,RAGGSVSEL,WERAPQPPC,LQPLVSRSL,SELGVLWER,DPHRAEWAL,ALAEDMSVPP,GLQPLVSRSL,RAEWALAEDM,RRAGGSVSEL,AEWALAEDMS,SELGVLWERA,QPPCGLQPLV	KIRP
GEM	c.803G>T	p.R268L	RDSKEKNERRLAYQKRKESMPRKAR[p.R268L]LFWGKIVAKNNKNMAFKLKSKSCHDL	RLFWGKIVA,SMPRKARLF,RKARLFWGK,KARLFWGKI,LFWGKIVAK,MPRKARLFW,ESMPRKARL,RLFWGKIVAK,SMPRKARLFW,KARLFWGKIV,MPRKARLFWG,KESMPRKARL,RKARLFWGKI	LUAD
GEN1	c.1526C>T	p.S509L	VMSFQSHMTLKPTCEIFHKQNSKLN[p.S509L]LGISPDPTLPQESISASLNSLLLPKN	HKQNSKLNL,SKLNLGISP,LGISPDPTL,KQNSKLNLGI,FHKQNSKLNL	UCEC
GFM1	c.49_50insC	p.A17fs	MRLLGAAAVAALGRGRAP[p.A17fs]RLPRLAEEAG*	RLPRLAEEA,ALGRGRAPR,RGRAPRLPR,APRLPRLAE,AALGRGRAPR,RGRAPRLPRL	KICH
GFRAL	c.922C>A	p.Q308K	LGTVLQVQCTCRTITQSEESLCKIF[p.Q308K]KHMLHRKSCFNYPTLSNVKGMALYTR	KIFKHMLHR,IFKHMLHRK,SLCKIFKHM,SLCKIFKHML,KIFKHMLHRK,KHMLHRKSCF	LUAD
GGA2	c.188C>T	p.A63V	MSEQDWSAIQNFCEQVNTDPNGPTH[p.A63V]VPWLLAHKIQSPQEKEALYALTVLEM	HVPWLLAHK,THVPWLLAH,VPWLLAHKI,GPTHVPWLL,NTDPNGPTHV,HVPWLLAHKI,DPNGPTHVPW	UCEC
GIGYF2	c.680G>A	p.R227H	PNFEEGGPTSVGRKHEFIRSESENW[p.R227H]HIFREEQNGEDEDGGWRLAGSRRDGE	ESENWHIFR,SESENWHIF,RSESENWHIF	UCEC
GIMAP7	c.827delT	p.V276fs	LLKLKYDEKIKNIREEAERNIFKDV[p.V276fs]LIGFGRCFQKYGIGFCRNVSFILPNLL*	NVSFILPNL,IGFGRCFQK,IFKDVLIGF,CFQKYGIGF,IGFCRNVSF,GFGRCFQKY,VLIGFGRCF,VSFILPNLL,LIGFGRCFQK,KYGIGFCRNV,IGFGRCFQKY,FQKYGIGFCR,NVSFILPNLL,NIFKDVLIGF,AERNIFKDVL,RCFQKYGIGF,GIGFCRNVSF,IGFCRNVSFI,RNVSFILPNL	STAD
GIMAP8	c.1630G>T	p.A544S	SCCEKGDTFFVLVFQLGRFTEEDKT[p.A544S]SVAKLEAIFGADFTKYAIMLFTRKED	KTSVAKLEA,FTEEDKTSV,SVAKLEAIF,KTSVAKLEAI,TSVAKLEAIF,EEDKTSVAKL	KIRP

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
GIPC3	c.679delG	p.G227fs	SRSSKCPVEAKVTSGRETLRLRSGG[p.G227fs]LPQWRKRPVSLRRRHLGRLMTCWKATWAFGTPSWRPPWWRRPRRQRAPRSLHAV*	RLMTCWKAT,RAPRSLHAV,SLRRRHLGR,TCWKATWAF,TWAFGTPSW,RLRSGGLPQ,QWRKRPVSL,RKRPVSLRR,RRRHLGRLM,LGRLMTCWK,CWKATWAFG,SWRPPWWRR,RPRRQRAPR,RQRAPRSLH,WAFGTPSWR,RPPWWRRPR,MTCWKATWA,LPQWRKRPV,TLRLRSGGL,LRSGGLPQW,LMTCWKATW,RRQRAPRSL,TPSWRPPWW,LMTCWKATWA,GLPQWRKRPV,SLRRRHLGRL,HLGRLMTCWK,RSGGLPQWRK,VSLRRRHLGR,RLMTCWKATW,MTCWKATWAF,RLRSGGLPQW,QWRKRPVSLR,RKRPVSLRRR,SWRPPWWRRP,WWRRPRRQRA,RQRAPRSLHA,TWAFGTPSWR,TPSWRPPWWR,RPPWWRRPRR,ETLRLRSGGL,LPQWRKRPVS,RPVSLRRRHL,RPRRQRAPRS,PQWRKRPVSL,LRRRHLGRLM,RHLGRLMTCW,ATWAFGTPSW,FGTPSWRPPW	STAD
GIT2	c.368G>T	p.R123L	KVHPNKAEFIRAKYQMLAFVHRLPC[p.R123L]LDDDSVTAKDLSKQLHSSVRTGNLET	CLDDDSVTA,LPCLDDDSV,RLPCLDDDSV,LAFVHRLPCL	LUAD
GJA1	c.932delC	p.A311fs	YKLVTGDRNNSSCRNYNKQASEQNW[p.A311fs]VITVQNKIEWGRREAPSLTPMHSLLISPMITRILKN*	SLTPMHSLL,LISPMITRI,KQASEQNWV,LLISPMITR,SPMITRILK,QASEQNWVI,WVITVQNKI,REAPSLTPM,SEQNWVITV,WGRREAPSL,MHSLLISPM,IEWGRREAP,KQASEQNWVI,SLTPMHSLLI,LLISPMITRI,LISPMITRIL,SLLISPMITR,ISPMITRILK,NWVITVQNKI,TVQNKIEWGR,APSLTPMHSL,RREAPSLTPM,REAPSLTPMH,PMHSLLISPM,MHSLLISPMI,IEWGRREAPS	KIRC
GJB3	c.479G>A	p.R160H	LIFKLIIEFLFLYLLHTLWHGFNMP[p.R160H]HLVQCANVAPCPNIVDCYIARPTEKK	NMPHLVQCA,HLVQCANVA,MPHLVQCAN,LWHGFNMPHL,MPHLVQCANV	GBM
GJB4	c.64C>A	p.R22S	MNWAFLQGLLSGVNKYSTVLS[p.R22S]SIWLSVVFIFRVLVYVVAAEEVWDDE	VLSSIWLSV,SIWLSVVFI,LSSIWLSVV,KYSTVLSSI,SSIWLSVVF,STVLSSIWL,NKYSTVLSS,YSTVLSSIW,TVLSSIWLSV,VLSSIWLSVV,KYSTVLSSIW,SIWLSVVFIF,SSIWLSVVFI,LSSIWLSVVF,NKYSTVLSSI,YSTVLSSIWL	LUAD
GLB1L2	c.1221C>G	p.I407M	KMPYEPLTPVLYLSLWDALKYLGEP[p.I407M]MKSEKPINMENLPVNGGNGQSFGYIL	ALKYLGEPM,EPMKSEKPI,MKSEKPINM,ALKYLGEPMK,DALKYLGEPM	LUAD
GLI1	c.815delG	p.W272fs	QEQLVHHINSEHIHGERKEFVCHWG[p.W272fs]AAPGS*	KEFVCHWGA,KEFVCHWGAA	STAD
GLI3	c.2993C>T	p.P998L	VHAPRRCSDGGAHGYGRRHLQPHDA[p.P998L]LGHGVRRASDPVRTGSEGLALPRVPR	ALGHGVRRA,DALGHGVRR,RHLQPHDAL,RRHLQPHDAL	ACC
GLI3	c.3098delC	p.P1033fs	PVRTGSEGLALPRVPRFSSLSSCNP[p.P1033fs]RRWPRPRRSAVSCFRITRGPRAASPETSTRPPVLPASPRTSPWSP*	AVSCFRITR,SSLSSCNPR,SLSSCNPRR,SCNPRRWPR,RWPRPRRSA,RRSAVSCFR,RSAVSCFRI,CFRITRGPR,ITRGPRAAS,STRPPVLPA,NPRRWPRPR,WPRPRRSAV,RPRRSAVSC,GPRAASPET,LPASPRTSP,FSSLSSCNPR,SSLSSCNPRR,SSCNPRRWPR,SAVSCFRITR,RWPRPRRSAV,CFRITRGPRA,ITRGPRAASP,RAASPETSTR,STRPPVLPAS,CNPRRWPRPR,SCFRITRGPR,WPRPRRSAVS,RPRRSAVSCF,SPETSTRPPV,LPASPRTSPW,RRWPRPRRSA,RRSAVSCFRI,FRITRGPRAA	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
GLIPR1L2	c.276delA	p.G92fs	IPRGSNLRFMTWDVALSRTARAWGK[p.G92fs]NVCLRIIFIYKMYKWSILNFMVLVKICGSALKMNLLQVLLSEVGMQRRKCTILKMAVALETVLIIFSLFGTTLTKLVVLLLHVQKLDILYMQQFSYATMRQEEH*	HVQKLDILY,SILNFMVLV,ALKMNLLQV,KMNLLQVLL,LLQVLLSEV,KMAVALETV,LIIFSLFGT,TLTKLVVLL,KLVVLLLHV,VLLLHVQKL,YMQQFSYAT,VLVKICGSA,CLRIIFIYK,IIFIYKMYK,KMYKWSILN,ILNFMVLVK,SLFGTTLTK,VVLLLHVQK,ILYMQQFSY,QQFSYATMR,IFIYKMYKW,IYKMYKWSI,MYKWSILNF,KWSILNFMV,TVLIIFSLF,IFSLFGTTL,LYMQQFSYA,TARAWGKNV,MQRRKCTIL,QRRKCTILK,RIIFIYKMY,LLSEVGMQR,CTILKMAVA,ETVLIIFSL,LVKICGSAL,YKMYKWSIL,GMQRRKCTI,VQKLDILYM,MQQFSYATM,RAWGKNVCL,KNVCLRIIF,LRIIFIYKM,YKWSILNFM,WSILNFMVL,KICGSALKM,LKMNLLQVL,LQVLLSEVG,RRKCTILKM,LKMAVALET,MAVALETVL,VALETVLII,ALETVLIIF,LHVQKLDIL,LDILYMQQF,FIYKMYKWSI,YKWSILNFMV,WSILNFMVLV,ILNFMVLVKI,NLLQVLLSEV,KMAVALETVL,VLIIFSLFGT,IIFSLFGTTL,SLFGTTLTKL,TLTKLVVLLL,ILYMQQFSYA,YMQQFSYATM,VLVKICGSAL,ALKMNLLQVL,RIIFIYKMYK,KMYKWSILNF,SILNFMVLVK,LVKICGSALK,MQRRKCTILK,FSLFGTTLTK,RAWGKNVCLR,LVVLLLHVQK,MQQFSYATMR,AWGKNVCLRI,IYKMYKWSIL,MYKWSILNFM,KWSILNFMVL,VALETVLIIF,ETVLIIFSLF,LYMQQFSYAT,RTARAWGKNV,CLRIIFIYKM,DILYMQQFSY,CTILKMAVAL,MAVALETVLI,VGMQRRKCTI,GMQRRKCTIL,LQVLLSEVGM,ARAWGKNVCL,GKNVCLRIIF,LRIIFIYKMY,IIFIYKMYKW,VKICGSALKM,LKMNLLQVLL,QRRKCTILKM,LKMAVALETV,LETVLIIFSL,LHVQKLDILY,HVQKLDILYM,KLDILYMQQF,QQFSYATMRQ	STAD
GLOD4	c.667_668insC	p.Q223fs	KLELQGVKGGVDHAAAFGRIAFSCP[p.Q223fs]PERVARLRRLDEKGEPEDSDSPGEPGHPRESNSTGGHSGRP*	IAFSCPPER,NSTGGHSGR,HPRESNSTG,RESNSTGGH,CPPERVARL,RIAFSCPPER,VARLRRLDEK,FSCPPERVAR,IAFSCPPERV	LUAD
GLRA3	c.1360C>A	p.L454I	DTISRACFPLAFLIFNIFYWVIYKI[p.L454I]IRHEDIHQQQD*	FYWVIYKII,IFYWVIYKII,IYKIIRHEDI,FYWVIYKIIR	CRC
GLRA3	c.396C>A	p.F132L	AYSEYPDDSLDLDPSMLDSIWKPDL[p.F132L]LFANEKGANFHEVTTDNKLLRIFKNG	LLFANEKGA,SIWKPDLLF,IWKPDLLFA,DSIWKPDLL,SIWKPDLLFA,LFANEKGANF	CRC
GLT8D2	c.533C>T	p.A178V	IYLDDDVIVQGDIQELYDTTLALGH[p.A178V]VAAFSDDCDLPSAQDINRLVGLQNTY	TLALGHVAA,DTTLALGHV,TTLALGHVA,LALGHVAAF,DTTLALGHVA,TTLALGHVAA,TLALGHVAAF	GBM
GLTSCR2	c.1166A>G	p.Q389R	RHQELFRLRGIKAQVALRLAELARR[p.Q389R]RRRRQARREAEADKPRRLGRLKYQAP	RRRRRQARR,ELARRRRRR,RLAELARRR,LARRRRRRQA,RRRRRRQARR,RLAELARRRR	ACC
GLYR1	c.1139_1140insG	p.G380fs	CYVDMSTVDADTVTELAQVIVSRGG[p.G380fs]ALSGSPRLRESAAV*	SPRLRESAA,GALSGSPRL,RGGALSGSPR,QVIVSRGGAL,SPRLRESAAV	STAD
GNA13	c.598A>G	p.R200G	KYFLDNLDKLGEPDYIPSQQDILLA[p.R200G]GRPTKGIHEYDFEIKNVPFKMVDVGG	ILLAGRPTK,SQQDILLAG,LLAGRPTKGI	BLCA
GNAO1	c.848C>A	p.P283Q	KWFTDTSIILFLNKKDIFEEKIKKS[p.P283Q]QLTICFPEYTGPSAFTEAVAYIQAQY	KIKKSQLTI,QLTICFPEY,KKSQLTICF,KIKKSQLTIC,SQLTICFPEY,IKKSQLTICF,FEEKIKKSQL	LUAD
GNAS	c.2530C>T	p.R844C	QYFLDKIDVIKQADYVPSDQDLLRC[p.R844C]CVLTSGIFETKFQVDKVNFHMFDVGG	CCVLTSGIF,RCCVLTSGIF	LIHC
GNAS	c.2531G>A	p.R844H	QYFLDKIDVIKQADYVPSDQDLLRC[p.R844H]HVLTSGIFETKFQVDKVNFHMFDVGG	LLRCHVLTS,CHVLTSGIF,RCHVLTSGIF	PAAD
GNB1	c.239T>C	p.I80T	LAKIYAMHWGTDSRLLVSASQDGKL[p.I80T]TIWDSYTTNKVHAIPLRSSWVMTCAY	LTIWDSYTT,SQDGKLTIW,GKLTIWDSY,TIWDSYTTNK,ASQDGKLTIW	CLL
GNG12	c.202delA	p.T68fs	CEEHARSDPLLIGIPTSENPFKDKK[p.T68fs]LASSYSGIEKQLLASSQQRKL*	KLASSYSGI,ASSYSGIEK,LLASSQQRK,KDKKLASSY,KKLASSYSG,KQLLASSQQ,IEKQLLASS,LLASSQQRKL,QLLASSQQRK,LASSYSGIEK,SYSGIEKQLL,FKDKKLASSY,KKLASSYSGI,SSYSGIEKQL,SENPFKDKKL	STAD
GNPNAT1	c.162delT	p.F54fs	AISPTHPGEGLVLRPLCTADLNRGF[p.F54fs]LRYWVS*	RGFLRYWVS,DLNRGFLRY,TADLNRGFLR,CTADLNRGFL,ADLNRGFLRY	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
GNPTAB	c.3566G>A	p.R1189Q	VKAVLRDFYESMFPIPSQFELPREY[p.R1189Q]QNRFLHMHELQEWRAYRDKLKFWTHC	EYQNRFLHM,LPREYQNRF,REYQNRFLH,YQNRFLHMH,LPREYQNRFL,REYQNRFLHM,SQFELPREYQ	UCEC
GOLGA4	c.4608G>T	p.Q1536H	KKESNLETELKSQTARIMELEDHIT[p.Q1536H]HKTIEIESLNEVLKNYNQQKDIEHKE	MELEDHITH,HKTIEIESL,LEDHITHKTI	CRC
GOLGA5	c.1474C>A	p.L492I	ELEELRHEKEMQREEIQKLMGQIHQ[p.L492I]IRSELQDMEAQQVNEAESAREQLQDL	KLMGQIHQI,KLMGQIHQIR,HQIRSELQDM,QKLMGQIHQI,GQIHQIRSEL	KIRC
GOT2	c.1063C>T	p.R355W	ILNTPDLRKQWLQEVKVMADRIIGM[p.R355W]WTQLVSNLKKEGSTHNWQHITDQIGM	RIIGMWTQL,IIGMWTQLV,WTQLVSNLK,MWTQLVSNL,MADRIIGMW,RIIGMWTQLV,GMWTQLVSNL,MWTQLVSNLK,WTQLVSNLKK,VMADRIIGMW	PRAD
GP2	c.122C>T	p.S41L	LALVSCILTQASAVQRGYGNPIEAS[p.S41L]LYGLDLDCGAPGTPEAHVCFDPCQNY	NPIEASLYG,YGNPIEASLY,NPIEASLYGL,IEASLYGLDL	CRC
GPATCH4	c.629_630insA	p.K210fs	FLARLKGQDPGAPQLQSESKPPKKK[p.K210fs]EKEKEAERGGRSYSI*	EAERGGRSY,KEAERGGRSY,AERGGRSYSI	PRAD
GPATCH4	c.629delA	p.K210fs	AFLARLKGQDPGAPQLQSESKPPKK[p.K210fs]RKRKGGRKRRKKLQHLKGMMQMRSTQNMLSRTSEKARRRKGDIKKERSQMKERVQLKGMRRRTLQEQVGLGN*	MQMRSTQNM,QMRSTQNML,MLSRTSEKA,NMLSRTSEK,QMKERVQLK,RSTQNMLSR,RVQLKGMRR,KRKRKGGRK,KGGRKRRKK,RRKKLQHLK,LSRTSEKAR,RTSEKARRR,KARRRKGDI,RRRKGDIKK,KGMRRRTLQ,GMRRRTLQE,HLKGMMQMR,LKGMRRRTL,KKLQHLKGM,QHLKGMMQM,GMMQMRSTQ,SQMKERVQL,KERVQLKGM,RTLQEQVGL,MQMRSTQNML,MMQMRSTQNM,SQMKERVQLK,RTSEKARRRK,KKRKRKGGRK,KRKGGRKRRK,KRRKKLQHLK,QMRSTQNMLS,QNMLSRTSEK,LSRTSEKARR,KARRRKGDIK,RSQMKERVQL,RVQLKGMRRR,MLSRTSEKAR,QLKGMRRRTL,LQHLKGMMQM,RKRRKKLQHL,RKKLQHLKGM,KKLQHLKGMM,MKERVQLKGM,KERSQMKERV	STAD
GPC5	c.1040G>T	p.R347L	LVNDAVLQAHLNGQKLLEQVNRICG[p.R347L]LPVRTPTQSPRCSFDQSKEKHGMKTT	EQVNRICGL,QVNRICGLPV,VNRICGLPVR,LEQVNRICGL	LUSC
GPC6	c.640G>A	p.A214T	CVSKYTDQLKPFGDVPRKLKIQVTR[p.A214T]TFIAARTFVQGLTVGREVANRVSKVS	VTRTFIAAR,RTFIAARTF,KIQVTRTFI,QVTRTFIAA,TFIAARTFV,LKIQVTRTF,IQVTRTFIA,RTFIAARTFV,KLKIQVTRTF,KIQVTRTFIA,VTRTFIAART,QVTRTFIAAR,LKIQVTRTFI,IQVTRTFIAA,TRTFIAARTF	CRC
GPLD1	c.2150G>A	p.R717Q	TRMYALTSDAQPLLLSTFSGDRRFS[p.R717Q]QFGGVLHLSDLDDDGLDEIIMAAPLR	SQFGGVLHL,SGDRRFSQF,RRFSQFGGV,RFSQFGGVL,FSGDRRFSQF,RRFSQFGGVL,FSQFGGVLHL,SQFGGVLHLS	CRC
GPM6A	c.149C>T	p.A50V	IPYASLIATILLYAGVALFCGCGHE[p.A50V]VLSGTVNILQTYFEMARTAGDTLDVF	VLSGTVNIL,EVLSGTVNI,ALFCGCGHEV,EVLSGTVNIL,HEVLSGTVNI	KIRC
GPNMB	c.522C>G	p.I174M	GQSHHNVFPDGKPFPHHPGWRRWNF[p.I174M]MYVFHTLGQYFQKLGRCSVRVSVNTA	FMYVFHTLG,RRWNFMYVF,NFMYVFHTL,GWRRWNFMY,RWNFMYVFH,MYVFHTLGQY,GWRRWNFMYV,RWNFMYVFHT,HPGWRRWNFM,WNFMYVFHTL,WRRWNFMYVF,FMYVFHTLGQ	LUAD
GPNMB	c.9_10delTC	p.C3fs	MECL[p.C3fs]LFPGISAPGCKIAT*	LLFPGISAP,MECLLFPGI,LLFPGISAPG,MECLLFPGIS	TGCT
GPR110	c.1327A>G	p.R443G	TALPLNFSRKFIDWKGIPVNKSQLK[p.R443G]GGYSYQIKMCPQNTSIPIRGRVLIGS	KGGYSYQIK,SQLKGGYSY,LKGGYSYQI,GGYSYQIKM,QLKGGYSYQI,VNKSQLKGGY,KSQLKGGYSY,SQLKGGYSYQ,KGGYSYQIKM	CLL
GPR112	c.3848C>A	p.S1283Y	KDQMTISLGKTPRTMEVTEMSPSKN[p.S1283Y]YFISYSRGTPSLEMTDTGFPETTKIS	KNYFISYSR,MSPSKNYFI,PSKNYFISY,EMSPSKNYF,TEMSPSKNY,VTEMSPSKNY,EMSPSKNYFI,SPSKNYFISY,TEMSPSKNYF	UCEC
GPR123	c.1889T>C	p.L630P	PRTPHCVGKKVPQPVGAADLAPDTS[p.L630P]PCRKEGSSASRSCRPGPGHLTRREED	DLAPDTSPCR	CLL
GPR125	c.338G>A	p.R113Q	LSNNKISELKNGSFSGLSLLERLDL[p.R113Q]QNNLISSIDPGAFWGLSSLKRLDLTN	LQNNLISSI,LERLDLQNNL	CRC

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GPR137B	c.718G>T	p.G240C	KISKMSLANIYLESKGSSVCQVTAI[p.G240C]CVTVILLYTSRACYNLFILSFSQNKS	QVTAICVTV,ICVTVILLY,TAICVTVIL,CQVTAICVT,CQVTAICVTV,AICVTVILLY,SVCQVTAICV,QVTAICVTVI,TAICVTVILL	LUAD
GPR156	c.2262C>A	p.F754L	PVPSGCASLSSQHSYFDTESSSSDE[p.F754L]LFCRCHRPYCEICFQSSSDSSDSGTS	SSSDELFCR,LFCRCHRPY,TESSSSDEL,SSSSDELFCR,ELFCRCHRPY,TESSSSDELF	CRC
GPR158	c.1696G>A	p.D566N	LIGWTSSVCQNLEKQISLIGQGKTS[p.D566N]NHLIFNMCLIDRWDYMTAVAEFLFLL	KTSNHLIFN,TSNHLIFNM,GQGKTSNHL,GKTSNHLIF,KTSNHLIFNM,GQGKTSNHLI,QGKTSNHLIF	CRC
GPR158	c.2284C>A	p.P762T	NPHLQKKRCSKKGLGRSIMRRITEI[p.P762T]TETVSRQCSKEDKEGADHGTAKGTAL	RITEITETV,RRITEITETV	LUAD
GPR161	c.1550delG	p.G517fs	AEAKINLFGEEALPGVLVTARTVPG[p.G517fs]AASGAAEAAELL*	TARTVPGAA,VTARTVPGA,TVPGAASGA,VPGAASGAA,LVTARTVPGA,RTVPGAASGA,VTARTVPGAA,TVPGAASGAA	STAD
GPR21	c.647G>A	p.R216H	FTLFIVMMLYAPAALIVCFTYFNIF[p.R216H]HICQQHTKDISERQARFSSQSGETGE	FTYFNIFHI,TYFNIFHIC,CFTYFNIFHI,IFHICQQHTK,FTYFNIFHIC	CRC
GPR6	c.106_165delGCGGCGGCGGCGGCCACAGCAGCAGGGGGGCCGGACACGGGCGAATGGGGACCCCCTGCT	p.AAAAATAAGGPDTGEWGPPA36del	AAMNASAASLNDSQVVVVAAEGAAA[p.AAAAATAAGGPDTGEWGPPA36del]LGAGGGANGSLELSSQLSAGPPGLLLPAVNPWDVLLCVSGTVIAGENALVVALIASTPALRTPMFVLVGSLATADLLAGCGLILH	VAAEGAAAL,AEGAAALGA,VVAAEGAAAL,AEGAAALGAG	PAAD
GPR98	c.12424C>T	p.R4142W	RFTIQLISIDEVEISPVKGSASIII[p.R4142W]WGDKRASGEVGIAPSSRHILIGEPSA	ASIIIWGDK,SIIIWGDKR,KGSASIIIW,SASIIIWGDK,VKGSASIIIW	CRC,UCEC
GPR98	c.12919G>T	p.G4307W	QRVNITIIRSSGDFGHVRLWYKTMS[p.G4307W]WTAEAGLDFVPAAGELLFEAGEMRKS	WTAEAGLDF,KTMSWTAEA,RLWYKTMSW,WYKTMSWTA,MSWTAEAGL,TMSWTAEAGL,WTAEAGLDFV,RLWYKTMSWT,SWTAEAGLDF,VRLWYKTMSW,LWYKTMSWTA,YKTMSWTAEA	LUAD
GPR98	c.18455A>T	p.Y6152F	AYRHFWMLVLFVIFNSLQGLYVFMV[p.Y6152F]FFILHNQMCCPMKASYTVEMNGHPGP	YVFMVFFIL,QGLYVFMVF,LYVFMVFFI,VFFILHNQM,GLYVFMVFF,GLYVFMVFFI,LQGLYVFMVF,QGLYVFMVFF,LYVFMVFFIL,MVFFILHNQM	CLL
GPRASP1	c.2117C>T	p.S706L	KEPCMYPAGGGSWKSRPEEEEDIVN[p.S706L]LWFWSRKYTKPEAIIGSWLWATEESN	IVNLWFWSR,VNLWFWSRK,NLWFWSRKY,EEEDIVNLW,EEDIVNLWF,EEEEDIVNL,IVNLWFWSRK,LWFWSRKYTK,VNLWFWSRKY,DIVNLWFWSR,EEEDIVNLWF,EEDIVNLWFW	HNSC
GPRC5A	c.88G>A	p.V30I	VPDGCRNGLKSKYYRLCDKAEAWGI[p.V30I]ILETVATAGVVTSVAFMLTLPILVCK	IILETVATA,AWGIILETV,EAWGIILET,KAEAWGIIL,AEAWGIILE,ILETVATAGV,GIILETVATA,EAWGIILETV,AEAWGIILET	CRC
GPRIN1	c.693_716delGAAGGAGGATCCTGGGTCTTTGAG	p.231_239RKEDPGSLR>R	KEDLGSLGKVDPLCSSKTYTVSPRK[p.231_239RKEDPGSLR>R]VDPVSSDKVDPVFPRKEEPRYSGKEHPVSSEKVAPTSAEKVDLVLSGKR	TVSPRKVDPV,KTYTVSPRKV	KIRC
GPRIN2	c.1337G>A	p.R446H	APASEDSLSVEGRRGPLRAVMQSLR[p.R446H]HPSCCGCSGAAPE*	MQSLRHPSC	ACC
GPRIN2	c.298A>C	p.T100P	ARASGPKARPSAGGHWWSSTVGNVS[p.T100P]PMGGSDLCRLRAPSAAAMQRSHSDLV	STVGNVSPM,SSTVGNVSPM	CESC
GPRIN2	c.721G>A	p.V241M	KAAEQLATTTCHALPPAALLCGMRE[p.V241M]MRAGGCCHALPATGILAFPKLVASVS	ALLCGMREM,LLCGMREMR,REMRAGGCC,AALLCGMREM,REMRAGGCCH,MRAGGCCHAL	ACC
GPRIN3	c.1898delG	p.R633fs	PSDPMGDSSPGSGKKTPSRSVKASP[p.R633fs]PGPAASASSSRSKS*	ASASSSRSK,RSVKASPPG,KASPPGPAA,SPPGPAASA,AASASSSRSK,SVKASPPGPA,VKASPPGPAA	HNSC
GPT2	c.29G>C	p.R10P	MQRAAALVR[p.R10P]PGCGPRTPSSWGRSQSSAAAEASAVL	LVRPGCGPR,RPGCGPRTPS,MQRAAALVRP	TGCT
GRAMD2	c.369C>G	p.I123M	DFLLQGRLYISPNWLCFHASLFGKD[p.I123M]MKVVIPVVSVQMIKKHKMARLLPNGL	SLFGKDMKV,ASLFGKDMK,HASLFGKDM,KDMKVVIPV,SLFGKDMKVV,HASLFGKDMK,FHASLFGKDM,KDMKVVIPVV,MKVVIPVVSV	CESC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
GRAP2	c.207G>T	p.E69D	GYVPKNFIDIQFPKWFHEGLSRHQA[p.E69D]DNLLMGKEVGFFIIRASQSSPGDFSI	QADNLLMGK,SRHQADNLL,RHQADNLLM,HQADNLLMG,GLSRHQADNL,HQADNLLMGK,SRHQADNLLM	CRC
GRB14	c.898G>A	p.A300T	RHLQFFSEFGNSDIYVSLAGKKKHG[p.A300T]TPTNYGFCFKPNKAGGPRDLKMLCAE	KKHGTPTNY,HGTPTNYGF,TPTNYGFCF,GTPTNYGFCF,KKKHGTPTNY,KHGTPTNYGF	BRCA
GRB7	c.716G>T	p.R239L	ISHEDLIQNFLNAGSFPEIQGFLQL[p.R239L]LGSGRKLWKRFFCFLRRSGLYYSTKG	LGSGRKLWK,EIQGFLQLL,LLGSGRKLW,LLGSGRKLWK,LQLLGSGRKL,QLLGSGRKLW,PEIQGFLQLL	LUAD
GREB1	c.1031C>A	p.S344Y	ESPSAPDGGCPQGGGNRAKYESAGM[p.S344Y]YCVPQVGLVGPASVTFPVVASGEPVS	AGMYCVPQV,MYCVPQVGL,AKYESAGMY,YESAGMYCV,GMYCVPQVG,GMYCVPQVGL,KYESAGMYCV,MYCVPQVGLV,RAKYESAGMY,YESAGMYCVP	KIRC
GRHL1	c.1822G>T	p.G608W	LVNMDDNIVKHYSNEDTFQLQIEEA[p.G608W]WGSYKLTLTE!*	AWGSYKLTL,QIEEAWGSY,FQLQIEEAW,EEAWGSYKL,QIEEAWGSYK,TFQLQIEEAW,LQIEEAWGSY,IEEAWGSYKL,EEAWGSYKLT	LUAD
GRIA1	c.652C>T	p.R218C	EGYRMLFQDLEKKKERLVVVDCESE[p.R218C]CLNAILGQIIKLEKNGIGYHYILANL	CLNAILGQI,CESECLNAI,CLNAILGQII,CESECLNAIL	CRC
GRIA2	c.2534G>A	p.R845Q	LVGGLGLAMLVALIEFCYKSRAEAK[p.R845Q]QMKVAKNAQNINPSSSQNSQNFATYK	KSRAEAKQM,AEAKQMKVA,KQMKVAKNA,KSRAEAKQMK,YKSRAEAKQM,KQMKVAKNAQ	CRC
GRID1	c.1864G>A	p.E622K	PRPSASATLHSAIWIVYGAFVQQGG[p.E622K]KSSVNSMAMRIVMGSWWLFTLIVCSS	GAFVQQGGK,KSSVNSMAM,VQQGGKSSV,GGKSSVNSM,FVQQGGKSSV,KSSVNSMAMR,GKSSVNSMAM	DLBCL
GRID1	c.2048G>T	p.R683L	VSRMDNPIRTFQDLSKQVEMSYGTV[p.R683L]LDSAVYEYFRAKGTNPLEQDSTFAEL	VLDSAVYEY,VEMSYGTVL,LDSAVYEYF,VLDSAVYEYF,TVLDSAVYEY,MSYGTVLDSA	LUAD
GRID2	c.1947delG	p.T649fs	YTTLATRMMMGAWWLFALIVISSYT[p.T649fs]QTSLLSSLLHALKVPSSLSRTFPSKQKSLMAQS*	SLLSSLLHA,LLSSLLHAL,TQTSLLSSL,LSSLLHALK,SLSRTFPSK,SSYTQTSLL,SSLSRTFPS,KQKSLMAQS,QTSLLSSLL,HALKVPSSL,VPSSLSRTF,FPSKQKSLM,ISSYTQTSL,SLLSSLLHAL,VISSYTQTSL,YTQTSLLSSL,TQTSLLSSLL,LLSSLLHALK,ALKVPSSLSR,SSLSRTFPSK,KVPSSLSRTF,LSRTFPSKQK,RTFPSKQKSL,FPSKQKSLMA,ISSYTQTSLL,LHALKVPSSL	HNSC
GRIK1	c.1103G>A	p.R368Q	VSSLQCHRHKPWRLGPRFMNLIKEA[p.R368Q]QWDGLTGHITFNKTNGLRKDFDLDII	AQWDGLTGH,KEAQWDGLT,AQWDGLTGHI,LIKEAQWDGL,FMNLIKEAQW,KEAQWDGLTG	LUAD
GRIN2B	c.1556G>A	p.R519Q	WNGMIGEVVMKRAYMAVGSLTINEE[p.R519Q]QSEVVDFSVPFIETGISVMVSRSNGT	TINEEQSEV,EEQSEVVDF,LTINEEQSEV,TINEEQSEVV,EQSEVVDFSV,NEEQSEVVDF	OV
GRK4	c.64_65insA	p.K22fs	MELENIVANSLLLKARQGGYGKK[p.K22fs]KWS*	RQGGYGKKKW	STAD
GRM3	c.2046C>A	p.F682L	SALLTKTNCIARIFDGVKNGAQRPK[p.F682L]LISPSSQVFICLGLILVQIVMVSVWL	KLISPSSQV,LISPSSQVF,LISPSSQVFI,KLISPSSQVF,AQRPKLISPS,VKNGAQRPKL	HNSC
GRM3	c.547C>T	p.R183C	ANLLRLFQIPQISYASTSAKLSDKS[p.R183C]CYDYFARTVPPDFYQAKAMAEILRFF	LSDKSCYDY,KSCYDYFAR,AKLSDKSCY,LSDKSCYDYF,KLSDKSCYDY,SAKLSDKSCY	GBM
GRM5	c.2685_2686insC	p.P895fs	SSGETLRYKDRRLAQHKSEIECFTP[p.P895fs]QREYGEWWESNNEQFQWKIRHVGPE*	WWESNNEQF,EIECFTPQR,SEIECFTPQ,REYGEWWES,EQFQWKIRH,FQWKIRHVG,TPQREYGEW,ESNNEQFQW,EWWESNNEQF,EQFQWKIRHV,IECFTPQREY,WESNNEQFQW,FQWKIRHVGP,REYGEWWESN,GEWWESNNEQ,TPQREYGEWW	LUAD
GRM6	c.1089G>T	p.E363D	GFDQYFMTRSLENNRRNIWFAEFWE[p.E363D]DNFNCKLTSSGTQSDDSTRKCTGEER	WEDNFNCKL,EFWEDNFNCK,AEFWEDNFNC	UCEC
GRM6	c.2152_2153insG	p.A718fs	SPTSQLVITFSLTSLQVVGMIAWLG[p.A718fs]GPAPTQRD*	MIAWLGGPA,GMIAWLGGPA	KIRC
GRM7	c.2036G>A	p.R679Q	VCSFRRVFLGLGMCISYAALLTKTN[p.R679Q]QIYRIFEQGKKSVTAPRLISPTSQLA	ALLTKTNQI,LTKTNQIYR,KTNQIYRIF,LLTKTNQIY,QIYRIFEQGK,LTKTNQIYRI,KTNQIYRIFE,ALLTKTNQIY,LLTKTNQIYR,TKTNQIYRIF	CRC

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GRM8	c.2554C>T	p.R852C	SVSLGMLYMPKVYIIIFHPEQNVQK[p.R852C]CKRSFKAVVTAATMQSKLIQKGNDRP	VQKCKRSFK,KCKRSFKAV,CKRSFKAVV,NVQKCKRSFK,VQKCKRSFKA,KCKRSFKAVV	LIHC
GTF2E1	c.575G>T	p.R192L	AMPKKDARTLLARFNEQIEPIYALL[p.R192L]LETEDVNLAYEILEPEPTEIPALKQS	ALLLETEDV,IEPIYALLL,LETEDVNLA,LLLETEDVNL,LETEDVNLAY,EPIYALLLET	LUAD
GTF3A	c.918G>T	p.K306N	HAGCGKTFAMKQSLTRHAVVHDPDK[p.K306N]NKMKLKVKKSREKRSLASHLSGYIPP	VVHDPDKNK,KNKMKLKVK,AVVHDPDKNK,KNKMKLKVKK	CRC
GTF3C1	c.2299delA	p.S767fs	KEGPSGSGDSQLSASSRSESGRMKK[p.S767fs]VIIKWA*	RMKKVIIKW,SGRMKKVII,RMKKVIIKWA,SGRMKKVIIK	STAD
GTF3C4	c.1685delA	p.E562fs	LIDLVRWKILKDKHIPQFLQEALEK[p.E562fs]RLKAVESPIFGVLSFSS*	AVESPIFGV,ALEKRLKAV,RLKAVESPI,SPIFGVLSF,LKAVESPIF,VESPIFGVL,FLQEALEKRL,KAVESPIFGV,RLKAVESPIF,EALEKRLKAV,KRLKAVESPI,VESPIFGVLS,QEALEKRLKA	STAD
GUCY2C	c.1645G>T	p.G549C	NFTEKQKIELNKLLQIDYYNLTKFY[p.G549C]CTVKLDTMIFGVIEYCERGSLREVLN	NLTKFYCTV,LTKFYCTVK,TKFYCTVKL,FYCTVKLDTM,LTKFYCTVKL,YNLTKFYCTV,CTVKLDTMIF	BRCA
GUSB	c.1498T>C	p.C500R	PSRPVTFVSNSNYAADKGAPYVDVI[p.C500R]RLNSYYSWYHDYGHLELIQLQLATQF	RLNSYYSWY,IRLNSYYSW,VIRLNSYYS,DVIRLNSYY,APYVDVIRL,VDVIRLNSY,YVDVIRLNSY,RLNSYYSWYH,DVIRLNSYYS,VDVIRLNSYY,VIRLNSYYSW,IRLNSYYSWY	KIRC
GUSB	c.1501T>G	p.L501V	SRPVTFVSNSNYAADKGAPYVDVIC[p.L501V]VNSYYSWYHDYGHLELIQLQLATQFE	CVNSYYSWY,DVICVNSYY,VDVICVNSY,ICVNSYYSW,APYVDVICV,YVDVICVNSY,CVNSYYSWYH,DVICVNSYYS,VDVICVNSYY,ICVNSYYSWY	KIRC
GXYLT1	c.667_668insT	p.L223fs	SQRLFLPLILKEVDSLLYVDTDILF[p.L223fs]FTTS*	YVDTDILFF,YVDTDILFFT,LYVDTDILFF	STAD
H1FOO	c.642_643insA	p.A214fs	PGAATEKARKQGGAAKDTRAQSGEA[p.A214fs]KEGAPQARQGHAGTFQCWWAQQEGKGQRQQEQPRRC*	APQARQGHA,ARQGHAGTF,GHAGTFQCW,HAGTFQCWW,EAKEGAPQAR,QARQGHAGTF,GEAKEGAPQA,RQGHAGTFQC	BLCA
H2AFV	c.374A>G	p.Q125R	LIKATIAGGGVIPHIHKSLIGKKGQ[p.Q125R]RKTA*	SLIGKKGQR,KSLIGKKGQR	TGCT
H2AFY2	c.432delG	p.K144fs	GKSETILSPPPEKRGRKATSGKKGG[p.K144fs]RNPRLPNHGRPKSPNQRTAIKKELQIPPLKMGQGMDSPFCLLRALFWDRSCP*	GMDSPFCLL,RLPNHGRPK,LLRALFWDR,SPFCLLRAL,MGQGMDSPF,KKELQIPPL,KSPNQRTAIK,GMDSPFCLLR,KMGQGMDSPF,SGKKGGRNPR,GGRNPRLPNH,HGRPKSPNQR,RTAIKKELQI,CLLRALFWDR,RPKSPNQRTA,IPPLKMGQGM,SPFCLLRALF,NQRTAIKKEL,IKKELQIPPL,KELQIPPLKM,GQGMDSPFCL	STAD
H3F3C	c.392G>T	p.R131L	DTNLCAIHAKRVTIMPKDIQLARRI[p.R131L]LGERA*	LARRILGER,QLARRILGER,KDIQLARRIL	LUAD
HAO1	c.514C>T	p.R172C	AEKMGYKAIFVTVDTPYLGNRLDDV[p.R172C]CNRFKLPPQLRMKNFETSTLSFSPEE	RLDDVCNRF,RLDDVCNRFK	CRC
HAO2	c.34C>A	p.H12N	MSLVCLTDFQA[p.H12N]NAREQLSKSTRDFIEGGADDSITRDD	CLTDFQANA,FQANAREQL,QANAREQLSK,CLTDFQANAR	LUAD
HARS2	c.503G>A	p.R168H	NKVKKMKRYHVGKVWRRESPTIVQG[p.R168H]HYREFCQCDFDIAGQFDPMIPDAECL	IVQGHYREF,PTIVQGHYR,SPTIVQGHY,HYREFCQCDF,TIVQGHYREF,RESPTIVQGH	CRC
HAUS6	c.1588delA	p.S530fs	ENSPLSDVAKNTESSAFGGSLPAKK[p.S530fs]VIHFKKSKIIW*	KVIHFKKSK,PAKKVIHFK,AKKVIHFKK,LPAKKVIHF,IHFKKSKII,SLPAKKVIHF,PAKKVIHFKK,KVIHFKKSKI,IHFKKSKIIW	STAD
HBB	c.126C>A	p.F42L	GKVNVDEVGGEALGRLLVVYPWTQR[p.F42L]LFESFGDLSTPDAVMGNPKVKAHGKK	VVYPWTQRL,RLFESFGDL,VYPWTQRLF,WTQRLFESF,RLFESFGDLS,VVYPWTQRLF,PWTQRLFESF,LVVYPWTQRL,YPWTQRLFES	CRC
HBB	c.257T>G	p.F86C	VKAHGKKVLGAFSDGLAHLDNLKGT[p.F86C]CATLSELHCDKLHVDPENFRLLGNVL	NLKGTCATL,KGTCATLSEL	KIRC
HCN1	c.1496G>T	p.G499V	PLFANADPNFVTAMLSKLRFEVFQP[p.G499V]VDYIIREGAVGKKMYFIQHGVAGVIT	VFQPVDYII,EVFQPVDYI,LRFEVFQPV,FEVFQPVDY,KLRFEVFQPV,RFEVFQPVDY,VFQPVDYIIR,EVFQPVDYII,FEVFQPVDYI	LUSC
HCN1	c.1976G>T	p.R659L	QAIAPINYPQMTTLNSTSSTTTPTS[p.R659L]LMRTQSPPVYTATSLSHSNLHSPSPS	LMRTQSPPV,TTTPTSLMR,STTTPTSLM,SSTTTPTSL,SLMRTQSPPV,STTTPTSLMR,LMRTQSPPVY,SSTTTPTSLM	LUSC

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HCN1	c.2140G>T	p.A714S	QPSAILSPCSYTTAVCSPPVQSPLA[p.A714S]SRTFHYASPTASQLSLMQQQPQQQVQ	ASRTFHYAS,PLASRTFHY,LASRTFHYA,VQSPLASRT,PLASRTFHYA,ASRTFHYASP,VQSPLASRTF,SPLASRTFHY	LUSC
HCN1	c.692C>A	p.P231Q	IILDPKVIKMNYLKSWFVVDFISSI[p.P231Q]QVDYIFLIVEKGMDSEVYKTARALRI	FISSIQVDY,QVDYIFLIV,IQVDYIFLI,SSIQVDYIF,VVDFISSIQV,FISSIQVDYI,SIQVDYIFLI,IQVDYIFLIV,SSIQVDYIFL,ISSIQVDYIF	LUAD
HCN1	c.976C>A	p.P326T	LIGMMLLLCHWDGCLQFLVPLLQDF[p.P326T]TPDCWVSLNEMVNDSWGKQYSYALFK	FTPDCWVSL,FLVPLLQDFT	LUSC
HCN4	c.1574G>A	p.R525H	IVGATCYAMFIGHATALIQSLDSSR[p.R525H]HQYQEKYKQVEQYMSFHKLPPDTRQR	SLDSSRHQY,SSRHQYQEK,RHQYQEKYK,IQSLDSSRH,SRHQYQEKY,QSLDSSRHQY,SSRHQYQEKY,HQYQEKYKQV	CRC
HCRTR2	c.26_27insC	p.S9fs*	MSGTKLEDSPP[p.S9fs]LSQLVICFGAE*	DSPPLSQLV,SPPLSQLVI,TKLEDSPPL,LEDSPPLSQL	STAD
HCRTR2	c.26delC	p.S9fs	MSGTKLEDSP[p.S9fs]LVATGHLLRS*	LVATGHLLR,SPLVATGHL,LEDSPLVAT,GTKLEDSPLV,SPLVATGHLL	STAD
HCRTR2	c.298G>T	p.D100Y	VCVAVWKNHHMRTVTNYFIVNLSLA[p.D100Y]YVLVTITCLPATLVVDITETWFFGQS	FIVNLSLAY,IVNLSLAYV,NLSLAYVLV,SLAYVLVTI,YVLVTITCL,VNLSLAYVL,FIVNLSLAYV,SLAYVLVTIT,YFIVNLSLAY,AYVLVTITCL,IVNLSLAYVL,LSLAYVLVTI	HNSC
HDAC4	c.2703delC	p.P901fs	PDEVGTGPGVGFNVNMAFTGGLDPP[p.P901fs]WETLSTWRPSERWSCRSPASLPRMWCWCHQASMPWRATPPLLGATTSPPDASGT*	GLDPPWETL,RMWCWCHQA,HQASMPWRA,ASLPRMWCW,RWSCRSPAS,RSPASLPRM,PWRATPPLL,LSTWRPSER,RPSERWSCR,MPWRATPPL,WSCRSPASL,WCWCHQASM,WCHQASMPW,FTGGLDPPW,PPWETLSTW,SPASLPRMW,RMWCWCHQAS,SMPWRATPPL,RWSCRSPASL,MWCWCHQASM,CWCHQASMPW,SCRSPASLPR,TLSTWRPSER,MPWRATPPLL,SERWSCRSPA,CRSPASLPRM,HQASMPWRAT,WETLSTWRPS,DPPWETLSTW	STAD
HDAC5	c.3130G>A	p.A1044T	CVSALLSVELQPLDEAVLQQKPNIN[p.A1044T]TVATLEKVIEIQSKHWSCVQKFAAGL	QQKPNINTV,NTVATLEKV,KPNINTVAT,LQQKPNINTV,NINTVATLEK,NTVATLEKVI,KPNINTVATL,QQKPNINTVA	CRC
HDLBP	c.1507C>T	p.R503C	SNLIRIEGDPQGVQQAKRELLELAS[p.R503C]CMENERTKDLIIEQRFHRTIIGQKGE	LASCMENER,RELLELASC,LELASCMEN,ELASCMENER,RELLELASCM	TGCT
HDLBP	c.2240delG	p.G747fs	EKQTKSFTVDIRAKPEYHKFLIGKG[p.G747fs]AAKFARCATALEHVSSSLRLRTRTRT*	ALEHVSSSL,HVSSSLRLR,SSSLRLRTR,SLRLRTRTR,LIGKGAAKF,AKFARCATA,KFARCATAL,FLIGKGAAKF,KFLIGKGAAK,KGAAKFARCA,AAKFARCATA,SSLRLRTRTR,VSSSLRLRTR,TALEHVSSSL,SLRLRTRTRT,FARCATALEH,HKFLIGKGAA,AKFARCATAL,LEHVSSSLRL	STAD
HEATR7B2	c.3325G>A	p.E1109K	TVVVNLLQKPLPFDRDTKTLWKALA[p.E1109K]KKPASSGKLLQALIDKLETELEDDIA	KTLWKALAK,TLWKALAKK,WKALAKKPA,KTLWKALAKK,LAKKPASSGK,AKKPASSGKL	BLCA
HECA	c.998_999insG	p.R333fs	MAGGHVFRNAHFDYSPAGLAVHRGG[p.R333fs]TLRHPRAVPSAAGPLRTPHSHPQA*	AVHRGGTLR,RGGTLRHPR,GTLRHPRAV,RTPHSHPQA,HPRAVPSAA,LAVHRGGTL,GLAVHRGGTL,RGGTLRHPRA,LAVHRGGTLR,HPRAVPSAAG,RAVPSAAGPL,LRHPRAVPSA,SAAGPLRTPH	STAD
HECTD2	c.55C>G	p.P19A	MSEAVRVPSPATPLVVAA[p.P19A]AAPEERKGKESEREKLPPIVSAGAGA	ATPLVVAAA,AAAAPEERK,TPLVVAAAA,VAAAAPEERK,ATPLVVAAAA	ACC
HECW1	c.547G>T	p.A183S	ICFKYYHGVSGALRATTPSVTVKNS[p.A183S]SAPIFKSIGADETVQGQGSRRLISFS	KNSSAPIFK,TVKNSSAPI,SSAPIFKSI,VKNSSAPIF,VTVKNSSAPI,NSSAPIFKSI,TVKNSSAPIF	LUAD
HERC1	c.6989G>A	p.R2330H	PVLAVIGGVDAGLRVGGRCVHKQTG[p.R2330H]HHATLLGVVKEGSTSAKVQWDEAEIT	HKQTGHHAT,KQTGHHATL,HKQTGHHATL,KQTGHHATLL	GBM
HERC2	c.986C>T	p.S329F	SQMLSAILLLLQLWDSGAQETDNER[p.S329F]FAQGTSAPLLPLLQRFQSIICRKDAP	FAQGTSAPL,AQETDNERF,ERFAQGTSA,RFAQGTSAPL,GAQETDNERF,NERFAQGTSA,FAQGTSAPLL	CESC
HES3	c.286C>A	p.P96T	SCLPGVSQLLRRGDEVGSGLRCPLV[p.P96T]TESAAGSTMDSAGLGQEAPALFRPCT	TESAAGSTM,CPLVTESAA,VTESAAGSTM	ACC

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HEXDC	c.1444A>C	p.T482P	CRSWRLPCSWLSTRMPWRSGWRKTC[p.T482P]PPACSGCKLCCRTSARCLPPRCHPPA	GWRKTCPPA	KIRC,LUSC
HGF	c.1400C>A	p.S467Y	NPDDDAHGPWCYTGNPLIPWDYCPI[p.S467Y]YRCEGDTTPTIVNLDHPVISCAKTKQ	IPWDYCPIY,LIPWDYCPIY,IPWDYCPIYR	CRC
HGF	c.2057T>C	p.M686T	AEKIGSGPCEGDYGGPLVCEQHKMR[p.M686T]TVLGVIVPGRGCAIPNRPGIFVRVAY	KMRTVLGVI,EQHKMRTVL,HKMRTVLGV,CEQHKMRTV,KMRTVLGVIV,TVLGVIVPGR,CEQHKMRTVL,HKMRTVLGVI	LUAD
HGF	c.686G>C	p.G229A	PQCSEVECMTCNGESYRGLMDHTES[p.G229A]AKICQRWDHQTPHRHKFLPERYPDKG	GLMDHTESA,LMDHTESAK,LMDHTESAKI,GLMDHTESAK,HTESAKICQR,TESAKICQRW	CESC
HHIPL1	c.2075T>C	p.V692A	AFRDGEVRLVRPAGLSSGSGRVEVF[p.V692A]AGGRWGTVCDDSWNISGAAVVCRQLG	VEVFAGGRW,EVFAGGRWGT	ACC
HIF3A	c.214G>A	p.A72T	VSAHLDKASIMRLTISYLRMHRLCA[p.A72T]TGEWNQVGAGGEPLDACYLKALEGFV	RMHRLCATG,LRMHRLCAT,HRLCATGEW,YLRMHRLCAT,MHRLCATGEW	CESC
HIP1	c.2819G>T	p.R940L	AQLVAASKVKADKDSPNLAQLQQAS[p.R940L]LGVNQATAGVVASTISGKSQIEETDN	QLQQASLGV,LAQLQQASL,LQQASLGVN,AQLQQASLGV,NLAQLQQASL,QQASLGVNQA	LUAD
HIPK4	c.839G>A	p.R280H	PDAANPWQLKSSADYLAETKVRPLE[p.R280H]HRKYMLKSLDQIETVNGGSVASRLTF	KVRPLEHRK,LEHRKYMLK,RPLEHRKYM,HRKYMLKSL,KVRPLEHRKY,ETKVRPLEHR,RPLEHRKYML,EHRKYMLKSL	CRC
HIST1H1B	c.564G>C	p.K188N	AAAGVKKVAKSPKKAKAAAKPKKAT[p.K188N]NSPAKPKAVKPKAAKPKAAKPKAAKP	ATNSPAKPK,KKATNSPAK,KATNSPAKPK,ATNSPAKPKA,KPKKATNSPA	CESC
HIST1H1C	c.194C>T	p.A65V	VSELITKAVAASKERSGVSLAALKK[p.A65V]VLAAAGYDVEKNNSRIKLGLKSLVSK	ALKKVLAAA,VLAAAGYDV,AALKKVLAA,KKVLAAAGY,KVLAAAGYDV,SLAALKKVLA,LAALKKVLAA,LKKVLAAAGY	DLBCL
HIST1H1D	c.243C>G	p.I81M	SGVSLAALKKALAAAGYDVEKNNSR[p.I81M]MKLGLKSLVSKGTLVQTKGTGASGSF	RMKLGLKSL,NSRMKLGLK,MKLGLKSLV,RMKLGLKSLV,YDVEKNNSRM,SRMKLGLKSL	BLCA
HIST1H1E	c.398G>C	p.G133A	NKKAASGEAKPKAKKAGAAKAKKPA[p.G133A]AAAKKPKKATGAATPKKSAKKTPKKA	AAAAKKPKK,AAKAKKPAA,AKKPAAAAK,KAKKPAAAAK,AAKAKKPAAA,AKAKKPAAAA	DLBCL
HIST1H1E	c.74G>C	p.R25P	MSETAPAAPAAPAPAEKTPVKKKA[p.R25P]PKSAGAAKRKASGPPVSELITKAVAA	KTPVKKKAPK,KAPKSAGAAK,KKAPKSAGAA	LUAD
HIST1H2AL	c.89G>C	p.R30P	GKQGGKARAKAKTRSSRAGLQFPVG[p.R30P]PVHRLLRKGNYAERVGAGAPVYLAAV	GLQFPVGPV,FPVGPVHRL,LQFPVGPVH,QFPVGPVHRL,FPVGPVHRLL	CESC
HIST1H2BF	c.229G>A	p.E77K	DTGISSKAMGIMNSFVNDIFERIAG[p.E77K]KASRLAHYNKRSTITSREIQTAVRLL	RIAGKASRL,GKASRLAHY,DIFERIAGK,RIAGKASRLA,KASRLAHYNK,AGKASRLAHY,DIFERIAGKA	HNSC
HIST1H2BJ	c.38A>G	p.K13R	MPEPAKSAPAPK[p.K13R]RGSKKAVTKAQKKDGKKRKRSRKESY	RGSKKAVTK,APAPKRGSK,SAPAPKRGSK,APKRGSKKAV	TGCT
HIST1H3B	c.142G>T	p.A48S	TKAARKSAPATGGVKKPHRYRPGTV[p.A48S]SLREIRRYQKSTELLIRKLPFQRLVR	RYRPGTVSL,SLREIRRYQ,VSLREIRRY,TVSLREIRR,HRYRPGTVS,SLREIRRYQK,GTVSLREIRR,RYRPGTVSLR,TVSLREIRRY,RPGTVSLREI,HRYRPGTVSL	DLBCL
HIST1H3B	c.220G>A	p.E74K	LREIRRYQKSTELLIRKLPFQRLVR[p.E74K]KIAQDFKTDLRFQSSAVMALQEACEA	LVRKIAQDF,FQRLVRKIA,KLPFQRLVRK,LVRKIAQDFK,LPFQRLVRKI,RLVRKIAQDF	LUSC
HIST1H3C	c.110A>T	p.K37M	TGGKAPRKQLATKAARKSAPATGGV[p.K37M]MKPHRYRPGTVALREIRRYQKSTELL	GVMKPHRYR,VMKPHRYRP,KSAPATGGVM,VMKPHRYRPG	HNSC
HIST1H4C	c.203G>C	p.R68P	GVKRISGLIYEETRGVLKVFLENVI[p.R68P]PDAVTYTEHAKRKTVTAMDVVYALKR	FLENVIPDA,VIPDAVTYT,NVIPDAVTY,LENVIPDAV,FLENVIPDAV,NVIPDAVTYT,IPDAVTYTEH,LENVIPDAVT	HNSC
HIST2H2AC	c.89G>C	p.R30P	GKQGGKARAKAKSRSSRAGLQFPVG[p.R30P]PVHRLLRKGNYAERVGAGAPVYMAAV	GLQFPVGPV,FPVGPVHRL,LQFPVGPVH,QFPVGPVHRL,FPVGPVHRLL	CESC

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HIST2H2BE	c.161G>A	p.G54D	KRKRSRKESYSIYVYKVLKQVHPDT[p.G54D]DISSKAMGIMNSFVNDIFERIAGEAS	KQVHPDTDI	LUSC
HIVEP3	c.1601delC	p.P534fs	LSSHSEKTKPEQSLLSLQHPPSTAP[p.P534fs]LCLS*	LQHPPSTAPL,HPPSTAPLCL	STAD
HIVEP3	c.1660delC	p.H554fs	PSTAPPVPLLRSHSMPSAACTISTP[p.H554fs]TTPSEVATPSMTISPTPKP*	SMTISPTPK,STPTTPSEV,EVATPSMTI,TPSMTISPT,TPSEVATPS,SEVATPSMT,PSMTISPTPK,TPSEVATPSM,SEVATPSMTI	STAD
HLA-A	c.233A>G	p.Q78R	DDTQFVRFDSDAASQRMEPRAPWIE[p.Q78R]REGPEYWDQETRNVKAQSQTDRVDLG	WIEREGPEY,IEREGPEYW,PWIEREGPEY	BLCA,PRAD
HLA-C	c.312C>A	p.N104K	EGPEYWDRNTQIYKAQAQTDRESLR[p.N104K]KLRGYYNQSEAGSHTLQSMYGCDVGP	QTDRESLRK,SLRKLRGYY,KLRGYYNQS,SLRKLRGYYN,KLRGYYNQSE,RESLRKLRGY,ESLRKLRGYY	CESC
HLA-DMA	c.250G>A	p.E84K	LSEAYDEDQLFFFDFSQNTRVPRLP[p.E84K]KFADWAQEQGDAPAILFDKEFCEWMI	RLPKFADWA,NTRVPRLPK,RVPRLPKFA,TRVPRLPKF	CRC
HLA-DMA	c.706_707insG	p.A236fs	YTAIAYWVPRNALPSDLLENVLCGV[p.A236fs]GLWPGCAGHHRGHCSHHLLPEALLR*	HLLPEALLR,RGHCSHHLL,SHHLLPEAL,LENVLCGVGL,HHRGHCSHHL,CSHHLLPEAL	LUAD
HLA-DPB1	c.340_341insA	p.G114fs	NSQKDILEEKRAVPDRMCRHNYELG[p.G114fs]EAHDPAAPSPA*	ELGEAHDPA,HNYELGEAH,RHNYELGEAH,YELGEAHDPA	CESC
HLA-DQB2	c.740G>A	p.R247H	AQSKMLSGIGGFVLGLIFLGLGLII[p.R247H]HHRGQKGPRGPPPAGNISAMIQSGER	LIIHHRGQK,GLIIHHRGQK	PRAD
HLA-DQB2	c.748G>A	p.G250S	KMLSGIGGFVLGLIFLGLGLIIRHR[p.G250S]SQKGPRGPPPAGNISAMIQSGERAQA	LIIRHRSQK,RHRSQKGPR,GLIIRHRSQK	PRAD
HLCS	c.1084G>A	p.E362K	LPPSSNIVQTPEDFNLLKSSNFRRY[p.E362K]KVLREILTTLGLSCDMKQVPALTPLY	KSSNFRRYK,RYKVLREIL,SSNFRRYKV,NFRRYKVLR,SNFRRYKVL,RRYKVLREI,KVLREILTTL,KSSNFRRYKV,SSNFRRYKVL,SNFRRYKVLR,RYKVLREILT,FRRYKVLREI,RRYKVLREIL	CRC
HLX	c.34T>A	p.S12T	MFAAGLAPFYA[p.S12T]TNFSLWSAAYCSSAGPGGCSFPLDPA	ATNFSLWSA,PFYATNFSL,FYATNFSLW,LAPFYATNF,TNFSLWSAA,GLAPFYATNF,PFYATNFSLW,ATNFSLWSAA,TNFSLWSAAY,YATNFSLWSA,APFYATNFSL	HNSC
HLX	c.693C>G	p.N231K	GRPAGVHLSGLQPSAGQFFASLDPI[p.N231K]KEASAILSPLNSNPRNSVQHQFQDTF	KEASAILSP,DPIKEASAI,QFFASLDPIK,KEASAILSPL,DPIKEASAIL	TGCT
HMCN1	c.398C>A	p.S133Y	RELYVQGGGDCPEMSIGAIKIALEI[p.S133Y]YLPGSFIYVFTDARSKDYRLTHEVLQ	YLPGSFIYV,IYLPGSFIY,AIKIALEIY,EIYLPGSFI,LEIYLPGSF,IKIALEIYL,YLPGSFIYVF,IYLPGSFIYV,AIKIALEIYL,GAIKIALEIY,EIYLPGSFIY,ALEIYLPGSF,LEIYLPGSFI	UCEC
HMG20A	c.744G>C	p.E248D	EEFLNHSKAREAELRQLRKSNMEFE[p.E248D]DRNAALQKHVESMRTAVEKLEVDVIQ	MEFEDRNAA,MEFEDRNAAL	CRC
HNF1B	c.1250C>T	p.T417M	GHNLLSPDGKMISVSGGGLPPVSTL[p.T417M]MNIHSLSHHNPQQSQNLIMTPLSGVM	GLPPVSTLM,STLMNIHSL,LMNIHSLSH,MNIHSLSHH,PPVSTLMNI,TLMNIHSLSH,LMNIHSLSHH,GGLPPVSTLM,LPPVSTLMNI	GBM
HNF1B	c.906C>G	p.N302K	GVSPSKAHGLGSNLVTEVRVYNWFA[p.N302K]KRRKEEAFRQKLAMDAYSSNQTHSLN	RVYNWFAKR,VYNWFAKRR,FAKRRKEEA,AKRRKEEAF,RVYNWFAKRR,EVRVYNWFAK,WFAKRRKEEA,FAKRRKEEAF	KIRC
HOOK1	c.1083delA	p.L361fs	QVKTLQETNMMYMHNTVSLEEELKK[p.L361fs]QMQHVHN*	LEEELKKQM,LKKQMQHVH,EELKKQMQHV	STAD
HOXA5	c.31G>T	p.G11C	MSSYFVNSFC[p.G11C]CRYPNGPDYQLHNYGDHSSVSEQFRD	FVNSFCCRY,CRYPNGPDY,YFVNSFCCR,YFVNSFCCRY,CCRYPNGPDY,SYFVNSFCCR	LUAD
HOXD10	c.452A>G	p.Y151C	AEVPSYQRLVPESCPVENPEVPVPG[p.Y151C]CFRLSQTYATGKTQEYNNSPEGSSTV	CFRLSQTYA,EVPVPGCFR,VPVPGCFRL,GCFRLSQTY,EVPVPGCFRL,NPEVPVPGCF	HNSC
HOXD8	c.201G>C	p.Q67H	GRHAAAAAALQLYGNSAAGFPHAPP[p.Q67H]HAHAHPHPSPPPSGTGCGGREGRGQE	FPHAPPHAH,AGFPHAPPH,AGFPHAPPHA,FPHAPPHAHA	KIRP

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HOXD8	c.364delC	p.P122fs	GSPAAAYQAAPPPPPHPPPPPPPPP[p.P122fs]AAGLPVTGSPRSFTDTITYRDSRFLRPSKRPSWYNILTVNRPVVILARTQTT*	FTDTITYRD,RSFTDTITY,KRPSWYNIL,ITYRDSRFL,TYRDSRFLR,DSRFLRPSK,SFTDTITYR,DTITYRDSR,WYNILTVNR,NILTVNRPV,TVNRPVVIL,SPRSFTDTI,RPSKRPSWY,SKRPSWYNI,RSFTDTITYR,ITYRDSRFLR,RDSRFLRPSK,RFLRPSKRPS,VNRPVVILAR,DSRFLRPSKR,SWYNILTVNR,TVNRPVVILA,LPVTGSPRSF,SPRSFTDTIT,RPSWYNILTV,FLRPSKRPSW,SKRPSWYNIL,YNILTVNRPV	STAD
HPD	c.852_853delAG	p.R284fs	GGAGVQHIALKTEDIITAIRHLRER[p.R284fs]PGVLICSLHVLQTTAGEAEDGQDQGEGEH*	GVLICSLHV,VLICSLHVL,SLHVLQTTA,VLQTTAGEA,HLRERPGVL,RPGVLICSL,RERPGVLIC,HLRERPGVLI,RHLRERPGVL,RERPGVLICS	UCEC
HPS3	c.1403C>T	p.S468L	NHIILLTKAEPEAIPERRQSPKRLL[p.S468L]LRKDTSVKIKIPPVAEAGWNLYIVNT	LLLRKDTSV,LLRKDTSVK,RQSPKRLLL,RLLLRKDTSV,LLRKDTSVKI,LLLRKDTSVK,RQSPKRLLLR,QSPKRLLLRK,RRQSPKRLLL	CRC
HPS3	c.2436G>C	p.K812N	VACLPDVVLQELFFKLTSQYIWRLS[p.K812N]NRQPPDTTPLRTSEDLINACSHYGLI	QYIWRLSNR,SQYIWRLSN,SQYIWRLSNR,NRQPPDTTPL	HNSC
HPSE2	c.174G>T	p.K58N	LHLSLSSQAGDRRPLPVDRAAGLKE[p.K58N]NTLILLDVSTKNPVRTVNENFLSLQL	GLKENTLIL,LKENTLILL,GLKENTLILL,RAAGLKENTL,KENTLILLDV	CRC
HRAS	c.181C>A	p.Q61K	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61K]KEEYSAMRDQYMRTGEGFLCVFAINN	LDTAGKEEY,AGKEEYSAM,ILDTAGKEEY,DTAGKEEYSA	THCA
HRAS	c.182A>G	p.Q61R	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61R]REEYSAMRDQYMRTGEGFLCVFAINN	LDTAGREEY,AGREEYSAM,ILDTAGREEY,AGREEYSAMR,DTAGREEYSA	THCA
HRAS	c.34G>A	p.G12S	MTEYKLVVVGA[p.G12S]SGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGASGV,KLVVVGASGV,YKLVVVGASG	HNSC
HRAS	c.35G>A	p.G12D	MTEYKLVVVGA[p.G12D]DGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGADGV,VVGADGVGK,KLVVVGADGV,VVVGADGVGK	BLCA,HNSC
HRAS	c.35G>C	p.G12A	MTEYKLVVVGA[p.G12A]AGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGAAGV,VVGAAGVGK,YKLVVVGAA,KLVVVGAAGV,VVVGAAGVGK,YKLVVVGAAG,GAAGVGKSAL	HNSC
HRAS	c.38G>T	p.G13V	MTEYKLVVVGAG[p.G13V]VVGKSALTIQLIQNHFVDEYDPTIED	KLVVVGAGV,VVGAGVVGK,KLVVVGAGVV,VVVGAGVVGK,YKLVVVGAGV	HNSC
HRC	c.1317_1318insC	p.P439fs	PHHHHHRVPREEDEEVSAELGHQAP[p.P439fs]QPQAKPPR*	HQAPQPQAK,AELGHQAPQ	KIRC
HRCT1	c.275A>C	p.H92P	LGIFHHHRHPGHVSHVPNVGLHHHHH[p.H92P]PPRHTPHHLHHHHHPHRHHPRHAR*	GLHHHHPPR,PPRHTPHHL,VGLHHHHPPR,HPPRHTPHHL,HHHPPRHTPH	BLCA
HRNR	c.1delA	p.M1fs	[p.M1fs]CLNSYKASSLSSMFSTNMPPSMGSMIR*	NMPPSMGSM,SYKASSLSS,KASSLSSMF,MPPSMGSMI,LNSYKASSL,YKASSLSSM,LSSMFSTNM,FSTNMPPSM,SMFSTNMPP,SLSSMFSTNM,CLNSYKASSL,SMFSTNMPPS,NMPPSMGSMI,SYKASSLSSM,KASSLSSMFS,YKASSLSSMF,MFSTNMPPSM,TNMPPSMGSM	OV
HRNR	c.7615G>A	p.G2539S	QHGSGSSQSSGYGRQGSGSGQSPGH[p.G2539S]SQRGSGSRQSPSYGRHGSGSGRSSSS	HSQRGSGSR	CESC
HRSP12	c.359G>A	p.R120Q	IYKQYFKSNFPARAAYQVAALPKGS[p.R120Q]QIEIEAVAIQGPLTTASL*	SQIEIEAVA,LPKGSQIEI,AALPKGSQI,SQIEIEAVAI,ALPKGSQIEI	CRC
HS3ST1	c.859G>A	p.E287K	RDRCLHESKGRAHPQVDPKLLNKLH[p.E287K]KYFHEPNKKFFELVGRTFDWH*	KLLNKLHKY,HKYFHEPNK,LLNKLHKYF,KLLNKLHKYF,KYFHEPNKKF,LHKYFHEPNK	CRC
HS3ST3A1	c.1195G>T	p.G399W	EIDREVVRRLREFYRPFNLKFYQMT[p.G399W]WHDFGWDG*	FYQMTWHDF,NLKFYQMTW,LKFYQMTWH,YQMTWHDFG,QMTWHDFGW,FNLKFYQMTW,KFYQMTWHDF,YQMTWHDFGW	LUAD
HSD17B1	c.937G>A	p.G313S	VPAKAEAGAEAGGGAGPGAEDEAGR[p.G313S]SAVGDPELGDPPAAPQ*	AEDEAGRSA,RSAVGDPEL,AEDEAGRSAV,GRSAVGDPEL	ACC
HSD17B6	c.627C>G	p.F209L	EAFSDILRREIQHFGVKISIVEPGY[p.F209L]LRTGMTNMTQSLERMKQSWKEAPKHI	YLRTGMTNM,SIVEPGYLR,YLRTGMTNMT,ISIVEPGYLR,GYLRTGMTNM,VEPGYLRTGM	LUAD
HSF4	c.505C>T	p.R169W	QALRGVQESTEARLRELRQQNEILW[p.R169W]WEVVTLRQSHGQQHRVIGKLIQCLFG	ILWWEVVTL,RQQNEILWW,LWWEVVTLR,NEILWWEVV,WEVVTLRQS,QQNEILWWEV,ILWWEVVTLR,EILWWEVVTL,WEVVTLRQSH,NEILWWEVVT	TGCT

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
HSPA13	c.253G>T	p.V85L	DENGHISIPSMVSFTDNDVYVGYES[p.V85L]LELADSNPQNTIYDAKRFIGKIFTAE	DVYVGYESL,YVGYESLELA,VYVGYESLEL	LUAD
HSPA4L	c.1447C>T	p.R483C	RIGSFTIQNVFPQSDGDSSKVKVKV[p.R483C]CVNIHGIFSVASASVIEKQNLEGDHS	KVKVKVCVN,KVKVCVNIH,VCVNIHGIF,CVNIHGIFSV,SSKVKVKVCV,KVKVKVCVNI,KVKVCVNIHG,VKVCVNIHGI,KVCVNIHGIF	UCEC
HSPBAP1	c.845G>T	p.R282L	HYVESIDPVTVSINSWIELEEDHLA[p.R282L]LVEEAITRMLVCALKTAENPQNTRAW	HLALVEEAI,LEEDHLALV,ALVEEAITRM,IELEEDHLAL	LUAD
HTR2A	c.656C>T	p.S219L	LKIIAVWTISVGISMPIPVFGLQDD[p.S219L]LKVFKEGSCLLADDNFVLIGSFVSFF	LQDDLKVFK,GLQDDLKVF,PVFGLQDDLK,GLQDDLKVFK,IPVFGLQDDL,FGLQDDLKVF,LKVFKEGSCL	UCEC
HTR3B	c.706C>T	p.R236C	SVSSTYSILQSSAGGFAQIQFNVVM[p.R236C]CRHPLVYVVSLLIPSIFLMLVDLGSF	VVMCRHPLV,IQFNVVMCR,VMCRHPLVY,MCRHPLVYV,NVVMCRHPL,VMCRHPLVYV,VVMCRHPLVY,QIQFNVVMCR,NVVMCRHPLV,AQIQFNVVMC,IQFNVVMCRH,FNVVMCRHPL	CRC
HTR5A	c.454C>T	p.R152C	ASIWNVTAIALDRYWSITRHMEYTL[p.R152C]CTRKCVSNVMIALTWALSAVISLAPL	CTRKCVSNV,HMEYTLCTR,YTLCTRKCV,RHMEYTLCT,HMEYTLCTRK,CTRKCVSNVM,MEYTLCTRKC	CRC
HTR5A	c.894G>T	p.W298C	DTWREQKEQRAALMVGILIGVFVLC[p.W298C]CIPFFLTELISPLCSCDIPAIWKSIF	VLCCIPFFL,CIPFFLTEL,VFVLCCIPF,FVLCCIPFF,FVLCCIPFFL,CIPFFLTELI,VFVLCCIPFF,GVFVLCCIPF	LUAD
HTRA3	c.1208A>G	p.Q403R	DFPEVSSGIYVQEVAPNSPSQRGGI[p.Q403R]RDGDIIVKVNGRPLVDSSELQEAVLT	GIRDGDIIVK	GBM
HYAL4	c.664G>A	p.D222N	AFMKETIKLGIKSRPKGLWGYYLYP[p.D222N]NCHNYNVYAPNYSGSCPEDEVLRNNE	YLYPNCHNY,YPNCHNYNV,GLWGYYLYPN,YLYPNCHNYN,YYLYPNCHNY,LYPNCHNYNV,YPNCHNYNVY	TGCT
HYDIN	c.1352G>A	p.R451Q	NPLEAKLYQQTIYCDILGREIRLPL[p.R451Q]QIKGEGMGPKIHFNFELLDIGKVFTG	EIRLPLQIK,REIRLPLQI,QIKGEGMGPK,LPLQIKGEGM	CRC
HYDIN	c.2816G>A	p.R939Q	PELNLGAHFSLDTHYYHFKLINKGR[p.R939Q]QIQQLFWMNDSFRPQAKLSKKGRVKK	RQIQQLFWM,KLINKGRQI,KGRQIQQLF,KGRQIQQLFW,FKLINKGRQI,NKGRQIQQLF,RQIQQLFWMN	CRC
HYDIN	c.3559C>T	p.R1187C	VHYPNLSFETKELDFGCILNDTELI[p.R1187C]CYVTITNCSPLVVKFRWFFLVNDEEN	LNDTELICY,TELICYVTI,ILNDTELICY,DTELICYVTI,TELICYVTIT	CRC
HYOU1	c.472C>T	p.R158C	TVHFQISSQLQFSPEEVLGMVLNYS[p.R158C]CSLAEDFAEQPIKDAVITVPVFFNQA	MVLNYSCSL,VLNYSCSLA,YSCSLAEDF,GMVLNYSCSL,MVLNYSCSLA,NYSCSLAEDF	CRC
IARS2	c.2494C>T	p.R832C	YCEKENDPKRRSCQTALVEILDVIV[p.R832C]CSFAPILPHLAEEVFQHIPYIKEPKS	VIVCSFAPI,CSFAPILPH,ILDVIVCSF,ILDVIVCSFA,VIVCSFAPIL,DVIVCSFAPI,EILDVIVCSF,CSFAPILPHL	SKCM
IBA57	c.390C>A	p.S130R	RTLYDVILYGLQEHSEVSGFLLECD[p.S130R]RSVQGALQKHLALYRIRRKVTVEPHP	FLLECDRSV,RSVQGALQK,LECDRSVQGA	ACC
IBTK	c.3638delA	p.K1213fs	PVNAWASSLHSVSSKSFRDFLLEEK[p.K1213fs]SLLLAIVQAIMSKKFLLKELKILRHQKLSDALPMVPQDQKATIFQIYHF*	FLLEEKSLL,LLEEKSLLL,SLLLAIVQA,LLLAIVQAI,AIMSKKFLL,FLLKELKIL,KLSDALPMV,LLAIVQAIM,AIVQAIMSK,IVQAIMSKK,IMSKKFLLK,KFLLKELKI,ATIFQIYHF,ELKILRHQK,LLKELKILR,VPQDQKATI,VQAIMSKKF,SKKFLLKEL,LKILRHQKL,RHQKLSDAL,QKLSDALPM,QKATIFQIY,EEKSLLLAI,LEEKSLLLA,FLLEEKSLLL,SLLLAIVQAI,LLLAIVQAIM,LLEEKSLLLA,AIVQAIMSKK,AIMSKKFLLK,LAIVQAIMSK,IVQAIMSKKF,KATIFQIYHF,KSLLLAIVQA,MSKKFLLKEL,DQKATIFQIY,VPQDQKATIF,ELKILRHQKL,HQKLSDALPM,RDFLLEEKSL,LEEKSLLLAI,VQAIMSKKFL,KKFLLKELKI,LRHQKLSDAL,EEKSLLLAIV,LPMVPQDQKA	STAD
IDE	c.110delA	p.K37fs	ALPSTFRSVLGARLPPPERLCGFQK[p.K37fs]RLTAK*	GFQKRLTAK,CGFQKRLTAK	STAD
IDH1	c.394C>G	p.R132G	VFREAIICKNIPRLVSGWVKPIIIG[p.R132G]GHAYGDQYRATDFVVPGPGKVEITYT	PIIIGGHAY,GGHAYGDQY,KPIIIGGHAY,IGGHAYGDQY	GBM

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
IDH1	c.394C>T	p.R132C	VFREAIICKNIPRLVSGWVKPIIIG[p.R132C]CHAYGDQYRATDFVVPGPGKVEITYT	PIIIGCHAY,GCHAYGDQY,KPIIIGCHAY,IGCHAYGDQY	LAML,LIHC,MM,SKCM
IDH1	c.395G>A	p.R132H	VFREAIICKNIPRLVSGWVKPIIIG[p.R132H]HHAYGDQYRATDFVVPGPGKVEITYT	PIIIGHHAY,GHHAYGDQY,KPIIIGHHAY,IGHHAYGDQY	GBM,LAML,PRAD
IDH2	c.419G>A	p.R140Q	TITPDEARVEEFKLKKMWKSPNGTI[p.R140Q]QNILGGTVFREPIICKNIPRLVPGWT	IQNILGGTV,QNILGGTVF,SPNGTIQNI,TIQNILGGTV,SPNGTIQNIL,IQNILGGTVF	LAML
IDH2	c.515G>A	p.R172K	VFREPIICKNIPRLVPGWTKPITIG[p.R172K]KHAHGDQYKATDFVADRAGTFKMVFT	WTKPITIGK,KHAHGDQYK,GKHAHGDQY,IGKHAHGDQY	LAML
IDUA	c.1120A>C	p.T374P	DNAFLSYHPHPFAQRTLTARFQVNN[p.T374P]PRPPHVQLLRKPVLTAMGLLALLDEE	NPRPPHVQL,FQVNNPRPP,TARFQVNNPR,QVNNPRPPHV,NPRPPHVQLL,FQVNNPRPPH	ACC
IDUA	c.99T>G	p.H33Q	AALLALLASLLAAPPVAPAEAPHLV[p.H33Q]QVDAARALWPLRRFWRSTGFCPPLPH	HLVQVDAAR,VQVDAARAL,AEAPHLVQV,HLVQVDAARA,APHLVQVDAA,VQVDAARALW	KIRP
IERS	c.580C>G	p.R194G	SRAARRPCGCPLGGEDPPGTPAATP[p.R194G]GAACCCAPQPAEDEPPAPPAVCPRKR	TPAATPGAA,TPAATPGAAC	KIRP
IFNA10	c.236T>C	p.V79A	KDRHDFRIPQEEFDGNQFQKAQAIS[p.V79A]ALHEMIQQTFNLFSTEDSSAAWEQSL	ALHEMIQQT,AISALHEMI,KAQAISALH,QAISALHEM,QKAQAISAL,FQKAQAISAL,QAISALHEMI,AQAISALHEM,ALHEMIQQTF	GBM,LUSC
IFNA10	c.238C>T	p.L80F	DRHDFRIPQEEFDGNQFQKAQAISV[p.L80F]FHEMIQQTFNLFSTEDSSAAWEQSLL	KAQAISVFH,QAISVFHEM,QKAQAISVF,AQAISVFHEM,VFHEMIQQTF,QAISVFHEMI,FQKAQAISVF	GBM
IFT140	c.1990G>A	p.E664K	VDEGLKNYVPVNHFWDQSEPRLFVC[p.E664K]KAVQETPRSQPQSANGQPQDGRAGPA	QSEPRLFVCK,EPRLFVCKAV,SEPRLFVCKA	HNSC
IFT172	c.2509G>A	p.A837T	YERAGDLFEKIHNPQKALECYRKGN[p.A837T]TFMKAVELARLAFPVEVVKLEEAWGD	CYRKGNTFM,KGNTFMKAV,NTFMKAVEL,CYRKGNTFMK,TFMKAVELAR,NTFMKAVELA,LECYRKGNTF,RKGNTFMKAV	STAD
IFT172	c.2831C>T	p.A944V	AQHYASLQEYEIAEELYTKGDRTKD[p.A944V]VIDMYTQAGRWEQAHKLAMKCMRPED	RTKDVIDMY,DVIDMYTQA,RTKDVIDMYT	CRC
IGF2BP2	c.556A>T	p.T186S	SSPSPPQRAQRGDHSSREQGHAPGG[p.T186S]SSQARQIDFPLRILVPTQFVGAIIGK	SSQARQIDF,GSSQARQIDF	CLL
IGF2R	c.3942_3943insG	p.T1314fs	HKVAGLLTQKLTYENGLLKMNFTGG[p.T1314fs]GHLP*	KMNFTGGGH,MNFTGGGHL,KMNFTGGGHL,LKMNFTGGGH	STAD
IGHMBP2	c.1843C>A	p.R615S	FLAEDRRINVAVTRARRHVAVICDS[p.R615S]STVNNHAFLKTLVEYFTQHGEVRTAF	AVICDSSTV,STVNNHAFL,SSTVNNHAF,STVNNHAFLK,DSSTVNNHAF	LUAD
IGJ	c.230G>A	p.R77Q	KCARITSRIIRSSEDPNEDIVERNI[p.R77Q]QIIVPLNNRENISDPTSPLRTRFVYH	QIIVPLNNR,DIVERNIQI,VERNIQIIV,RNIQIIVPL	CRC
IK	c.268_269delGA	p.E90fs	DPAARRRKKKSYYAKLRQQEIERER[p.E90fs]ASREVPGSCQGTERWSEQRL*	EIERERASR,REVPGSCQG,TERWSEQRL,RQQEIERERA,IERERASREV,REVPGSCQGT	UCEC
IKZF3	c.485T>G	p.L162R	KRSHTGERPFQCNQCGASFTQKGNL[p.L162R]RRHIKLHTGEKPFKCHLCNYACQRRD	KGNLRRHIK,SFTQKGNLR,FTQKGNLRR,ASFTQKGNLR,KGNLRRHIKL,SFTQKGNLRR,NLRRHIKLHT,TQKGNLRRHI	CLL
IL17B	c.100C>T	p.R34W	FLLTISIFLGLGQPRSPKSKRKGQG[p.R34W]WPGPLAPGPHQVPLDLVSRMKPYARM	GQGWPGPLA,RKGQGWPGPL,WPGPLAPGPH	BRCA
IL17RA	c.2409_2410insC	p.Q803fs	PYEEEQRQSVQSDQGYISRSSPQPP[p.Q803fs]RGTHGNGGRGGRGAGPREAGPATLSRGPGEPEEPPAAAAFPPAAEELGLGHDGVRVRGAQCMRAAPQGPPRSQL*	GLGHDGVRV,RAAPQGPPR,RGGRGAGPR,RVRGAQCMR,GPREAGPAT,VRVRGAQCM,EEPPAAAAF,REAGPATLS,ISRSSPQPPR,GVRVRGAQCM,RVRGAQCMRA,GPREAGPATL,APQGPPRSQL,AAFPPAAEEL,EELGLGHDGV	CRC

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IL1R2	c.1091_1092insG	p.L364fs	KEASSTFSWGIVLAPLSLAFLVLGG[p.L364fs]NMDAQTVQTQNWKSRWSDCAMASSSRLSILSQVK*	RLSILSQVK,QTVQTQNWK,KSRWSDCAM,MASSSRLSI,AQTVQTQNW,CAMASSSRL,ASSSRLSIL,SRLSILSQV,FLVLGGNMDA,AMASSSRLSI,KSRWSDCAMA,SSRLSILSQV,TVQTQNWKSR,MASSSRLSIL,LAFLVLGGNM,VQTQNWKSRW,WKSRWSDCAM,DAQTVQTQNW	CLL
IL1RAP	c.149T>G	p.F50C	DDWGLDTMRQIQVFEDEPARIKCPL[p.F50C]CEHFLKFNYSTAHSAGLTLIWYWTRQ	RIKCPLCEH,IKCPLCEHF,CEHFLKFNY,RIKCPLCEHF,CPLCEHFLKF,CEHFLKFNYS	KIRC
IL1RAPL2	c.1940C>T	p.T647M	KHEIPATTLPVPSLGNHHTYCNLPL[p.T647M]MLLNGQLPLNNTLKDTQEFHRNSSLL	MLLNGQLPL,TYCNLPLML,HTYCNLPLM,LMLLNGQLPL,HTYCNLPLML,TYCNLPLMLL,LPLMLLNGQL,HHTYCNLPLM	CRC
IL2	c.308G>T	p.R103M	CLEEELKPLEEVLNLAQSKNFHLRP[p.R103M]MDLISNINVIVLELKGSETTFMCEYA	RPMDLISNI,NFHLRPMDL,SKNFHLRPM,QSKNFHLRPM,KNFHLRPMDL,MDLISNINVI	LUAD
IL25	c.502_503delTG	p.C168fs	HGEKGTHKGYCLERRLYRVSLACVC[p.C168fs]AAPCDGLAGPAGGWSLFGKPGARCTTTCHEGPGCPDAWPL*	AGGWSLFGK,SLFGKPGAR,GPAGGWSLF,HEGPGCPDA,SLACVCAAPC,RVSLACVCAA,WSLFGKPGAR,GPGCPDAWPL,LAGPAGGWSL,HEGPGCPDAW	KIRP
IL3	c.268G>A	p.A90T	DILMENNLRRPNLEAFNRAVKSLQN[p.A90T]TSAIESILKNLLPCLPLATAAPTRHP	TSAIESILK,KSLQNTSAI,NTSAIESIL,LQNTSAIESI,NTSAIESILK,AVKSLQNTSA,VKSLQNTSAI	CRC
IL32	c.643C>A	p.P215T	LWKQFQSFCCSLSELFMSSFQSYGA[p.P215T]TRGDKEELTPQKCSEPQSSK*	SYGATRGDK,SFQSYGATR,SSFQSYGAT,FQSYGATRG,SSFQSYGATR,QSYGATRGDK	LUAD
IL32	c.653_654insG	p.D218fs	QFQSFCCSLSELFMSSFQSYGAPRG[p.D218fs]EQGGADTPEVL*	APRGEQGGA	SKCM
IL5RA	c.139C>A	p.L47I	LLPDEKISLLPPVNFTIKVTGLAQV[p.L47I]ILQWKPNPDQEQRNVNLEYQVKINAP	GLAQVILQW,GLAQVILQWK,IKVTGLAQVI,TGLAQVILQW	CRC
IL6ST	c.647C>A	p.P216H	FVNIEVWVEAENALGKVTSDHINFD[p.P216H]HVYKVKPNPPHNLSVINSEELSSILK	TSDHINFDH,HINFDHVYK,DHINFDHVY,TSDHINFDHV,HINFDHVYKV,SDHINFDHVY	MM
IL7R	c.161C>T	p.S54L	DLEDAELDDYSFSCYSQLEVNGSQH[p.S54L]LLTCAFEDPDVNITNLEFEICGALVE	EVNGSQHLL,SQHLLTCAF,LEVNGSQHL,GSQHLLTCAF,LEVNGSQHLL	LUSC
ILF3	c.1450G>A	p.E484K	VKVLQDMGLPTGAEGRDSSKGEDSA[p.E484K]KETEAKPAVVAPAPVVEAVSTPSAAF	SSKGEDSAK,KETEAKPAV,KETEAKPAVV,GEDSAKETEA	BLCA
INADL	c.4018C>G	p.P1340A	KLVFIRNEDAVNQMAVTPFPVPSSS[p.P1340A]ASSIEDQSGTEPISSEEDGSVEVGIK	FPVPSSSAS,VPSSSASSI,TPFPVPSSSA,FPVPSSSASS	LUSC
INF2	c.1581delC	p.S527fs	PLLPGMGWGPPPPPPPLLPCTCSPP[p.S527fs]WREAWRRSSWPRWTMAWAQHGSPAIGG*	SWPRWTMAW,AWRRSSWPR,RSSWPRWTM,SSWPRWTMA,WPRWTMAWA,WAQHGSPAI,REAWRRSSW,WRRSSWPRW,AWAQHGSPA,AQHGSPAIG,LPCTCSPPW,AWRRSSWPRW,SSWPRWTMAW,RSSWPRWTMA,MAWAQHGSPA,CSPPWREAWR,EAWRRSSWPR,WTMAWAQHGS,WPRWTMAWAQ,LLPCTCSPPW,WREAWRRSSW,RRSSWPRWTM,AWAQHGSPAI	STAD
ING1	c.658G>T	p.A220S	DECYERFSRETDGAQKRRMLHCVQR[p.A220S]SLIRSQELGDEKIQIVSQMVELVENR	MLHCVQRSL,RSLIRSQEL,RMLHCVQRS,RMLHCVQRSL,MLHCVQRSLI,RSLIRSQELG	LUAD
INMT	c.167G>T	p.G56V	PSPEAEMLKFNLECLHKTFGPGGLQ[p.G56V]VDTLIDIGSGPTIYQVLAACDSFQDI	LQVDTLIDI,GLQVDTLIDI,KTFGPGGLQV	LUAD
INMT	c.635C>T	p.S212F	LKPGGHLVTTVTLRLPSYMVGKREF[p.S212F]FCVALEKEEVEQAVLDAGFDIEQLLH	EFFCVALEK,YMVGKREFF,GKREFFCVA,KREFFCVAL,REFFCVALE,MVGKREFFCV,YMVGKREFFC,SYMVGKREFF,GKREFFCVAL,REFFCVALEK	SKCM
INPP5D	c.1568G>A	p.R523Q	SFMFNGTSLGFVNSHLTSGSEKKLR[p.R523Q]QNQNYMNILRFLALGDKKLSPFNITH	RQNQNYMNI,KLRQNQNYM,KKLRQNQNY,KLRQNQNYMN,RQNQNYMNIL,KKLRQNQNYM	CRC
INPP5K	c.787C>T	p.R263C	EGRLLFPPTYKFDRNSNDYDTSEKK[p.R263C]CKPAWTDRILWRLKRQPCAGPDTPIP	KCKPAWTDR,SEKKCKPAW	CRC

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INPPL1	c.1478C>T	p.T493M	VFGTQENSVGDREWLDLLRGGLKEL[p.T493M]MDLDYRPIAMQSLWNIKVAVLVKPEH	LMDLDYRPI,LKELMDLDY,ELMDLDYRPI,GLKELMDLDY,LLRGGLKELM,MDLDYRPIAM	HNSC
INPPL1	c.2921delC	p.A974fs	APREEPLTPRLKPEGAPEPEGVAAP[p.A974fs]HPRTASITLPTTSLKGSRTSCCPRSHPRLPGPLSHLPPRTKWPLQCLLHSLGTTGTLVWERGVLQMRSLEAHCPLQTFHLHHCRTQPSSCPPAWILYQGQWSGAVVGLRPVAHHLPRPIQGLHCPQAPHQPALSWGKWPVGMTGPARCCRWPRR*	RLPGPLSHL,SLGTTGTLV,YQGQWSGAV,ALSWGKWPV,VLQMRSLEA,GLRPVAHHL,HLPRPIQGL,ITLPTTSLK,LSHLPPRTK,TTGTLVWER,QTFHLHHCR,HQPALSWGK,MTGPARCCR,AWILYQGQW,SWGKWPVGM,RTASITLPT,GSRTSCCPR,RTSCCPRSH,RSHPRLPGP,RTKWPLQCL,RSLEAHCPL,RPVAHHLPR,PARCCRWPR,SCPPAWILY,EGVAAPHPR,SCCPRSHPR,WSGAVVGLR,APHPRTASI,HPRTASITL,HPRLPGPLS,LPPRTKWPL,CPQAPHQPA,APHQPALSW,WPVGMTGPA,LQMRSLEAH,EAHCPLQTF,SHLPPRTKW,TKWPLQCLL,LLHSLGTTG,HSLGTTGTL,LGTTGTLVW,RGVLQMRSL,TQPSSCPPA,SSCPPAWIL,ILYQGQWSG,GQWSGAVVG,VAHHLPRPI,GLHCPQAPH,PQAPHQPAL,EPEGVAAPH,CPLQTFHLH,QPSSCPPAW,QPALSWGKW,LEAHCPLQT,SSCPPAWILY,HLPPRTKWPL,ILYQGQWSGA,YQGQWSGAVV,GQWSGAVVGL,LLHSLGTTGT,SITLPTTSLK,TSCCPRSHPR,GTTGTLVWER,RTASITLPTT,KGSRTSCCPR,RSHPRLPGPL,RTKWPLQCLL,RTQPSSCPPA,PARCCRWPRR,LQTFHLHHCR,QWSGAVVGLR,HSLGTTGTLV,APHPRTASIT,CPRSHPRLPG,HPRLPGPLSH,WPLQCLLHSL,CPQAPHQPAL,LEAHCPLQTF,LVWERGVLQM,ASITLPTTSL,LSHLPPRTKW,LHSLGTTGTL,SLGTTGTLVW,LQMRSLEAHC,MRSLEAHCPL,TQPSSCPPAW,HQPALSWGKW,LSWGKWPVGM,WERGVLQMRS,QPSSCPPAWI	STAD
INPPL1	c.3460delC	p.P1154fs	SEVDYAPAGPARSALLPGPLELQPP[p.P1154fs]GDCPRTMAGPSASLHPASGRASRKTWQRRLRACRAGGPAGWARQA*	TMAGPSASL,SLHPASGRA,ASLHPASGR,RASRKTWQR,RTMAGPSAS,ASRKTWQRR,KTWQRRLRA,WQRRLRACR,RLRACRAGG,RACRAGGPA,HPASGRASR,CPRTMAGPS,GPSASLHPA,SGRASRKTW,RTMAGPSASL,RASRKTWQRR,ASRKTWQRRL,KTWQRRLRAC,RLRACRAGGP,ELQPPGDCPR,SASLHPASGR,TWQRRLRACR,CPRTMAGPSA,WQRRLRACRA,TMAGPSASLH,ASGRASRKTW	STAD
INTS12	c.1A>G	p.M1V	[p.M1V]VAATVNLELDPIFLKALGFLHSKSKD	VAATVNLEL	MM
INTS4	c.1378T>G	p.S460A	MRKISNNITLREDQLDTVLAVLEDS[p.S460A]ARDIREALHELLCCTNVSTKEGIHLA	VLAVLEDSA,SARDIREAL,SARDIREALH,DSARDIREAL	TGCT
INTS7	c.2818C>T	p.R940C	GIVWKTGPRTTIFVKSLEDPYSQQI[p.R940C]CLQQQQAQQPLQQQQQRNAYTRF*	DPYSQQICL,QQICLQQQQA	UCEC
INTS7	c.317G>T	p.R106I	LCVLKVTQQSEKHLEKILNVDEFVK[p.R106I]IIFSVIHSNDPVARAITLRMLGSLAS	FVKIIFSVI,EFVKIIFSV,DEFVKIIFS,ILNVDEFVKI,EFVKIIFSVI,DEFVKIIFSV	UCEC
INVS	c.2396G>A	p.R799K	WKPSRRHDTEPKAKCAPQKRRTQEL[p.R799K]KGGRCSPAGSSRPGSARGEAVHAGQN	PQKRRTQELK,ELKGGRCSPA	CESC
INVS	c.2444delG	p.R815fs	KRRTQELRGGRCSPAGSSRPGSARG[p.R815fs]RRSMLGRILPTIVHQETK*	SMLGRILPT,MLGRILPTI,SARGRRSML,RGRRSMLGR,RSMLGRILP,GSARGRRSM,RRSMLGRIL,SMLGRILPTI,MLGRILPTIV,ILPTIVHQET,SSRPGSARGR,SARGRRSMLG,RGRRSMLGRI,RSMLGRILPT	STAD
IPO11	c.2532delT	p.S844fs	ERYPVVMSTYLGVMGRVLLQNTSFF[p.S844fs]LHYLMRWPINLIRRWTSFWEI*	LLQNTSFFL,YLMRWPINL,LMRWPINLI,TSFFLHYLM,SFFLHYLMR,FFLHYLMRW,RRWTSFWEI,LQNTSFFLH,QNTSFFLHY,NTSFFLHYL,LHYLMRWPI,NLIRRWTSF,LIRRWTSFW,WPINLIRRW,NTSFFLHYLM,VLLQNTSFFL,FLHYLMRWPI,YLMRWPINLI,TSFFLHYLMR,SFFLHYLMRW,HYLMRWPINL,RWPINLIRRW,LMRWPINLIR,LQNTSFFLHY,INLIRRWTSF,NLIRRWTSFW,IRRWTSFWEI	STAD
IRAK3	c.800G>A	p.R267Q	PYMRNGTLFDRLQCVGDTAPLPWHI[p.R267Q]QIGILIGISKAIHYLHNVQPCSVICG	IQIGILIGI,APLPWHIQI,WHIQIGILI,LPWHIQIGI,QIGILIGISK,TAPLPWHIQI,LPWHIQIGIL	CRC

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IREB2	c.1256G>A	p.R419Q	HLEHTGFSKAKLESMETYLKAVKLF[p.R419Q]QNDQNSSGEPEYSQVIQINLNSIVPS	FQNDQNSSG	CRC
IRF4	c.368A>G	p.K123R	RCALNKSNDFEELVERSQLDISDPY[p.K123R]RVYRIVPEGAKKGAKQLTLEDPQMSM	ISDPYRVYR,RVYRIVPEG,DISDPYRVY,DPYRVYRIV,QLDISDPYRV,RVYRIVPEGA,SQLDISDPYR,DISDPYRVYR,LDISDPYRVY	MM
IRS4	c.1771_1772insG	p.G591fs	GHGSGGGQGPGDGHGSGGGKNSGGG[p.G591fs]QRLRKWERIRW*	GQRLRKWER,RLRKWERIR,RLRKWERIRW,GKNSGGGQRL	STAD
IRS4	c.63_65delGGC	p.21_22AA>A	MASCSFTRDQATRRLRGAAAAAAA[p.21_22AA>A]LAAVVTTPLLSSGTPTALIGTGSSCPGA	RGAAAAAAAL	PAAD
IRX3	c.1265T>C	p.L422P	LVSAPLGKFPAWTNRPFPGPPPGPR[p.L422P]PHPLSLLGSAPPHLLGLPGAAGHPAA	PPGPRPHPL,GPRPHPLSL,GPRPHPLSLL	ACC
IRX6	c.1274C>T	p.A425V	CDESSCIPKAFGNPKFALQGLPLNC[p.A425V]VPCPRRSEPVVQCQYPSGAEAG*	PLNCVPCPR,ALQGLPLNCV,VPCPRRSEPV	STAD
ISX	c.256C>T	p.R86C	AASGSGLEKPPKDQPQEGRKSKRRV[p.R86C]CTTFTTEQLHELEKIFHFTHYPDVHI	KSKRRVCTT,CTTFTTEQL,SKRRVCTTF,RRVCTTFTT,KSKRRVCTTF	SKCM
ISX	c.5G>T	p.C2F	M[p.C2F]FAEVGPALCRGMERNSLGCCEAPKKL	MFAEVGPAL	LUSC
ITGA10	c.2006G>A	p.R669Q	PIVHLTPSLEVTPQAISVVQRDCRR[p.R669Q]QGQEAVCLTAALCFQVTSRTPGRWDH	CRRQGQEAV,RQGQEAVCL,RRQGQEAVCL,RQGQEAVCLT	HNSC
ITGA4	c.2018C>T	p.T673M	YLAVGSMKTLMLNVSLFNAGDDAYE[p.T673M]MTLHVKLPVGLYFIKILELEEKQINC	MTLHVKLPV,DAYEMTLHV,YEMTLHVKL,NAGDDAYEM,AYEMTLHVKL,DAYEMTLHVK,EMTLHVKLPV,FNAGDDAYEM,YEMTLHVKLP	CRC
ITGA4	c.2700C>A	p.F900L	GIVRFLSKTDKRLLYCIKADPHCLN[p.F900L]LLCNFGKMESGKEASVHIQLEGRPSI	HCLNLLCNF,CLNLLCNFGK,IKADPHCLNL	CRC
ITGA5	c.143C>A	p.A48D	PPLLPLLLLLLPPPPRVGGFNLDAE[p.A48D]DPAVLSGPPGSFFGFSVEFYRPGTDG	NLDAEDPAV	KICH
ITGA8	c.1846G>T	p.G616C	TEFRDKLSPINISLNYSLDESTFKE[p.G616C]CLEVKPILNYYRENIVSEQAHILVDC	STFKECLEV,TFKECLEVK,KECLEVKPI,DESTFKECL,CLEVKPILNY,STFKECLEVK,ESTFKECLEV,KECLEVKPIL	LUAD
ITGAX	c.2054G>A	p.R685H	KRSKNLLGSRDLQSSVTLDLALDPG[p.R685H]HLSPRATFQETKNRSLSRVRVLGLKA	GHLSPRATF	LUSC
ITGAX	c.848G>A	p.R283H	TDGKKEGDSLDYKDVIPMADAAGII[p.R283H]HYAIGVGLAFQNRNSWKELNDIASKP	GIIHYAIGV,DAAGIIHYA,ADAAGIIHY,IHYAIGVGL,MADAAGIIHY,IIHYAIGVGL,HYAIGVGLAF,DAAGIIHYAI,IHYAIGVGLA	LUAD
ITGB1	c.1132C>A	p.L378I	PKSAVGTLSANSSNVIQLIIDAYNS[p.L378I]ISSEVILENGKLSEGVTISYKSYCKN	LIIDAYNSI,QLIIDAYNSI,AYNSISSEVI,DAYNSISSEV	STAD
ITGB1	c.472G>A	p.D158N	LKFKRAEDYPIDLYYLMDLSYSMKD[p.D158N]NLENVKSLGTDLMNEMRRITSDFRIG	SMKDNLENV,LSYSMKDNL,YSMKDNLENV,SMKDNLENVK	HNSC
ITGB8	c.21_22insT	p.A7fs	MCGSALAFF[p.A7fs]YRCICLPAKRPARSRLVPLGSLGVFTCSWTGPR*	CGSALAFFY,ALAFFYRCI,LVPLGSLGV,GSALAFFYR,FTCSWTGPR,FYRCICLPA,RSRLVPLGS,CLPAKRPAR,RPARSRLVP,VPLGSLGVF,PARSRLVPL,AKRPARSRL,SRLVPLGSL,SLGVFTCSW,RLVPLGSLGV,FFYRCICLPA,CGSALAFFYR,FYRCICLPAK,RSRLVPLGSL,MCGSALAFFY,VFTCSWTGPR,RPARSRLVPL,LAFFYRCICL,GSLGVFTCSW,SALAFFYRCI	STAD
ITIH1	c.760G>T	p.G254W	KGHVLFRPTVSQQQSCPTCSTSLLN[p.G254W]WHFKVTYDVSRDKICDLLVANNHFAH	SLLNWHFKV,TSLLNWHFK,STSLLNWHF,LNWHFKVTY,STSLLNWHFK,CSTSLLNWHF,LLNWHFKVTY,TSLLNWHFKV	LUAD
ITIH2	c.2524C>G	p.L842V	TLDKEMSFSVLLHRVWKKHPVNVDF[p.L842V]VGIYIPPTNKFSPKAHGLIGQFMQEP	VNVDFVGIY,NVDFVGIYI,HPVNVDFVG,VGIYIPPTNK,PVNVDFVGIY,HPVNVDFVGI	LUAD
ITK	c.586G>A	p.E196K	PEETVVIALYDYQTNDPQELALRRN[p.E196K]KEYCLLDSSEIHWWRVQDRNGHEGYV	LALRRNKEY,RRNKEYCLL,KEYCLLDSS,ALRRNKEYCL,ELALRRNKEY	CRC

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ITK	c.86G>T	p.R29L	FILLEEQLIKKSQQKRRTSPSNFKV[p.R29L]LFFVLTKASLAYFEDRHGKKRTLKGS	SNFKVLFFV,VLFFVLTKA,KVLFFVLTK,NFKVLFFVL,SPSNFKVLF,KVLFFVLTKA,TSPSNFKVLF,RTSPSNFKVL,SPSNFKVLFF,SNFKVLFFVL,LFFVLTKASL	LUAD
ITM2C	c.499G>A	p.E167K	ADIIHDFQRGLTAYHDISLDKCYVI[p.E167K]KLNTTIVLPPRNFWELLMNVKRGTYL	YVIKLNTTI,VIKLNTTIV,SLDKCYVIK,IKLNTTIVL,SLDKCYVIKL,YVIKLNTTIV,ISLDKCYVIK,CYVIKLNTTI	UCEC
ITPR1	c.4707G>T	p.M1569I	CGLERDKFDNKTVTFEEHIKEEHNM[p.M1569I]CHYLCFIVLVKVKDSTEYTGPESYVA	NMCHYLCFI,HNMCHYLCF,KEEHNMCHY,CHYLCFIVL,EEHNMCHYL,NMCHYLCFIV,HNMCHYLCFI,IKEEHNMCHY,KEEHNMCHYL,MCHYLCFIVL	TGCT
ITPR2	c.1073C>A	p.P358Q	RDGVPPTSKKKRQAGEKIMYTLVSV[p.P358Q]QHGNDIASLFELDATTLQRADCLVPR	IMYTLVSVQ,VQHGNDIAS,IMYTLVSVQH,VQHGNDIASL,QHGNDIASLF	LUAD
IWS1	c.2404delA	p.S802fs	FQATSKKGISRLDKQMRKFTDIRKK[p.S802fs]ADLHTQ*	RKFTDIRKKA	STAD
JAG1	c.1384G>A	p.A462T	DCLPGWMGQNCDININDCLGQCQND[p.A462T]TSCRDLVNGYRCICPPGYAGDHCERD	TSCRDLVNGY,CQNDTSCRDL	CRC
JAK1	c.928G>A	p.V310I	IFETSMLLISSENEMNWFHSNDGGN[p.V310I]ILYYEVMVTGNLGIQWRHKPNVVSVE	SNDGGNILY,NILYYEVMV,ILYYEVMVT,HSNDGGNIL,GNILYYEVM,HSNDGGNILY,SNDGGNILYY,FHSNDGGNIL	CRC
JAKMIP2	c.848G>T	p.R283I	MSSPKREIPGRAGDGSEHCSSPDLR[p.R283I]INQKRIAELNATIRKLEDRNTLLGDE	INQKRIAEL,RINQKRIAEL,SSPDLRINQK	UCEC
JARID2	c.1180_1181insG	p.G394fs	VNHTISGKTESSNAKTRKQVLSLGG[p.G394fs]GVQVHWARRQWPQGQWQVEPKVMH*	GQWQVEPKV,QWPQGQWQV,GVQVHWARR,RQWPQGQWQ,WQVEPKVMH,VLSLGGGVQV,RQWPQGQWQV,KQVLSLGGGV,LSLGGGVQVH,SLGGGVQVHW,VQVHWARRQW,ARRQWPQGQW,GQWQVEPKVM	STAD
JARID2	c.1266delG	p.V422fs	TGPAVNGLKVSGRLNPKSCTKEVGG[p.V422fs]GSCGRACSCGRGCGTPRGDWKRHTRRRSRSRPPRR*	CGRACSCGR,KRHTRRRSR,HTRRRSRSR,RRSRSRPPR,RSRSRPPRR,EVGGGSCGR,HTRRRSRSRP,RRRSRSRPPR	STAD
JHDM1D	c.289delA	p.R97fs	HHAVDIDLYHCPNCAVLHGSSLMKK[p.R97fs]GGTGTDMTTQKLMMVPNQCKLELELSLRNYALESSQVPMK*	MMVPNQCKL,MTTQKLMMV,LMMVPNQCK,VPNQCKLEL,ELSLRNYAL,KKGGTGTDM,TDMTTQKLM,NQCKLELEL,CKLELELSL,ALESSQVPM,LELSLRNYA,GTDMTTQKLM,LMMVPNQCKL,SLMKKGGTGT,KLMMVPNQCK,ALESSQVPMK,GTGTDMTTQK,YALESSQVPM,MKKGGTGTDM,TDMTTQKLMM,LELELSLRNY,LELSLRNYAL,RNYALESSQV	STAD
JHDM1D	c.938G>A	p.R313H	TSVWYHVLWGEKIFYLIKPTDENLA[p.R313H]HYESWSSSVTQSEVFFGDKVDKCYKC	PTDENLAHY,AHYESWSSS,DENLAHYES,KPTDENLAHY,AHYESWSSSV,DENLAHYESW	GBM
JMJD1C	c.3592C>A	p.R1198S	SHSVTTFRNDCRSPTHLTVSSTNTL[p.R1198S]SSMPALHRAPVFHPPIHHSLERKEGS	LSSMPALHR,SSMPALHRA,NTLSSMPAL,SSTNTLSSM,TLSSMPALHR,STNTLSSMPA,VSSTNTLSSM	LUAD
JMJD4	c.32C>T	p.A11V	MRAGPEPQAL[p.A11V]VGQKRGALRLLVPRLVLTVSAPAEVR	LVGQKRGAL,LVGQKRGALR	ACC
JMY	c.2429_2464delCACCACCACCTCCCCCACCTCCTCCCCCTCCCCCAC	p.PPPPPPPPPPPPP811del	LNNNLEPCSVTINPLPSPLPPTPPP[p.PPPPPPPPPPPP811del]LPVAKDSGPETLEKDLPRKEGNEKRIPKSASAPSAHLFDSSQLVSARKKLRKTAEGLQRRR	SPLPPTPPPL,LPPTPPPLPV	PAAD
JPH1	c.1183G>A	p.A395T	ARTKVEIANSRTAHARAKADAADQA[p.A395T]TLAARQECDIARAVARELSPDFYQPG	DAADQATLA,TLAARQECDI,DAADQATLAA,KADAADQATL	GBM
JPH3	c.1299G>C	p.Q433H	EARIARITAKEFSPSFQHRENGLEY[p.Q433H]HRPKRQTSCDDIEVLSTGTPLQQESP	NGLEYHRPKR,YHRPKRQTSC	CESC
JSRP1	c.275T>C	p.V92A	EKEPAARGTPGTGKERLKAGASPRS[p.V92A]APARKKAQTAPPLQPPPPPPALSEEL	KAGASPRSA,SPRSAPARK,RSAPARKKA,ASPRSAPARK,GASPRSAPAR,APARKKAQTA,LKAGASPRSA	KIRP

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JUP	c.1880C>T	p.S627L	RVAAGVLCELAQDKEAADAIDAEGA[p.S627L]LAPLMELLHSRNEGTATYAAAVLFRI	ALAPLMELL,AEGALAPLM,GALAPLMEL,DAIDAEGAL,DAIDAEGALA,IDAEGALAPL	CESC
KAL1	c.907G>A	p.V303I	SKHFRSSKDPSAPPAPANLRLANST[p.V303I]INSDGSVTVTIVWDLPEEPDIPVHHY	STINSDGSV,NLRLANSTI,TINSDGSVTV,NSTINSDGSV,ANLRLANSTI	CRC
KANK3	c.1076G>A	p.R359H	VEADAWVTEALLGLPAAAERELELL[p.R359H]HASLEHQRGVSELLRGRLRELEEARE	AERELELLH,RELELLHAS,LLHASLEHQR,AERELELLHA,RELELLHASL,LELLHASLEH	ACC
KANK4	c.757T>C	p.S253P	VQEGAEPPEGVVKVPNHLPLPGPPF[p.S253P]PFQNVLVVLEDKEDEHNAREAEVLFT	PLPGPPFPF,PFQNVLVVL,FPFQNVLVV,GPPFPFQNV,LPLPGPPFPF,GPPFPFQNVL,FPFQNVLVVL,PPFPFQNVLV	KIRC
KANSL3	c.1127G>A	p.G376E	IGWNTGALVACHVSVMEYVTAVVCL[p.G376E]EFPLLTVDGPRGDVDDPLLDMKTPVL	AVVCLEFPL,CLEFPLLTV,VTAVVCLEF,LEFPLLTVD,YVTAVVCLEF,TAVVCLEFPL	TGCT
KBTBD13	c.242C>T	p.A81V	GGFRATLQVLRGDRPALAAEDELLQ[p.A81V]VVECAAFLQAPALARFLEHNLTSDNC	QVVECAAFL,LQVVECAAF,AEDELLQVV,LLQVVECAAF,LQVVECAAFL,DELLQVVECA	ACC
KBTBD6	c.1325_1326insG	p.G442fs	LADRLLCREGMDVAYLNGYIYILGG[p.G442fs]ARPYYWS*	YILGGARPY,ILGGARPYY,YIYILGGAR,ILGGARPYYW,IYILGGARPY,YILGGARPYY,GYIYILGGAR	STAD
KBTBD8	c.1645G>A	p.V549I	YLKLVLFQNKLHLFVRATQVTVEEH[p.V549I]IFRTSRKNSLYQYDDIADQWMKVYET	VTVEEHIFR,TQVTVEEHI,IFRTSRKNSL,QVTVEEHIFR,TQVTVEEHIF	CRC
KCNA1	c.1126G>T	p.G376C	EAESHFSSIPDAFWWAVVSMTTVGY[p.G376C]CDMYPVTIGGKIVGSLCAIAGVLTIA	TTVGYCDMY,VGYCDMYPV,MTTVGYCDMY,TVGYCDMYPV,GYCDMYPVTI,SMTTVGYCDM	LUAD
KCNA3	c.1244C>T	p.A415V	TLKASMRELGLLIFFLFIGVILFSS[p.A415V]VVYFAEADDPTSGFSSIPDAFWWAVV	ILFSSVVYF,GVILFSSVV,VILFSSVVY,SSVVYFAEA,FIGVILFSSV,ILFSSVVYFA,FSSVVYFAEA,VILFSSVVYF,GVILFSSVVY	CRC
KCNB2	c.692G>A	p.R231H	STIALSLNTLPELQETDEFGQLNDN[p.R231H]HQLAHVEAVCIAWFTMEYLLRFLSSP	HQLAHVEAV,QLNDNHQLA,GQLNDNHQL,GQLNDNHQLA,HQLAHVEAVC,DEFGQLNDNH	BRCA
KCNC1	c.1363delA	p.K455fs	VPVIVNNFGMYYSLAMAKQKLPKKK[p.K455fs]RSIFRGHRSWDLPIIVNLS*	KQKLPKKKR,RSWDLPIIV,LPKKKRSIF,SIFRGHRSW,GHRSWDLPI,WDLPIIVNL,IFRGHRSWDL,KKRSIFRGHR,RGHRSWDLPI,LPKKKRSIFR,RSIFRGHRSW,GHRSWDLPII	STAD
KCND3	c.1313C>T	p.S438L	NQRADKRRAQKKARLARIRVAKTGS[p.S438L]LNAYLHSKRNGLLNEALELTGTPEEE	SLNAYLHSK,KTGSLNAYL,LNAYLHSKR,IRVAKTGSL,AKTGSLNAY,GSLNAYLHSK,KTGSLNAYLH,SLNAYLHSKR,RIRVAKTGSL,RVAKTGSLNA,VAKTGSLNAY,AKTGSLNAYL	CRC,UCEC
KCNH2	c.446G>C	p.G149A	MFILNFEVVMEKDMVGSPAHDTNHR[p.G149A]APPTSWLAPGRAKTFRLKLPALLALT	RAPPTSWLA,NHRAPPTSW,HRAPPTSWL	STAD
KCNH8	c.1365G>A	p.M455I	SSLTSVGFGNVSANTDAEKIFSICT[p.M455I]ILIGALMHALVFGNVTAIIQRMYSRW	KIFSICTIL,ILIGALMHA,SICTILIGA,IFSICTILI,CTILIGALM,EKIFSICTI,KIFSICTILI,FSICTILIGA,ILIGALMHAL,SICTILIGAL,AEKIFSICTI,EKIFSICTIL	LUAD
KCNJ10	c.305delC	p.P102fs	GTWFLFGVVWYLVAVAHGDLLELDP[p.P102fs]RPTTPPVWYRCTHSLEPSSSPLNPKPPLAMASATSVRNVHWPLCFLLPSWCSPPSWKSSSQVPSWRRLPGPRSGLRPFVSASMQLWPPTMASPAS*	LAMASATSV,SMQLWPPTM,MQLWPPTMA,SLEPSSSPL,NVHWPLCFL,RLPGPRSGL,AMASATSVR,SSSQVPSWR,SSQVPSWRR,VWYRCTHSL,RNVHWPLCF,VHWPLCFLL,SVRNVHWPL,SWCSPPSWK,SWRRLPGPR,SGLRPFVSA,PTTPPVWYR,DPRPTTPPV,SPLNPKPPL,KPPLAMASA,VPSWRRLPG,GPRSGLRPF,WPPTMASPA,FLLPSWCSP,KSSSQVPSW,SQVPSWRRL,LRPFVSASM,FVSASMQLW,ASMQLWPPT,WPLCFLLPS,LPSWCSPPS,LELDPRPTT,FLLPSWCSPP,SMQLWPPTMA,PLAMASATSV,LLPSWCSPPS,GLRPFVSASM,LAMASATSVR,PSWCSPPSWK,KSSSQVPSWR,SSSQVPSWRR,PFVSASMQLW,HSLEPSSSPL,SVRNVHWPLC,SWKSSSQVPS,SWRRLPGPRS,RSGLRPFVSA,ASMQLWPPTM,RPTTPPVWYR,MASATSVRNV,TSVRNVHWPL,NVHWPLCFLL,GPRSGLRPFV,RPFVSASMQL,SATSVRNVHW,VRNVHWPLCF,RNVHWPLCFL,WKSSSQVPSW,SQVPSWRRLP,RRLPGPRSGL,MQLWPPTMAS,WPLCFLLPSW,LPSWCSPPSW,DPRPTTPPVW	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
KCNJ3	c.1290G>T	p.L430F	KITGREDFPKKLLRMSSTTSEKAYS[p.L430F]FGDLPMKLQRISSVPGNSEEKLVSKT	YSFGDLPMK,AYSFGDLPM,SFGDLPMKL,TTSEKAYSF,KAYSFGDLPM,AYSFGDLPMK,YSFGDLPMKL,STTSEKAYSF,SEKAYSFGDL	LUAD
KCNK17	c.61A>G	p.S21G	MYRPRARAAPEGRVRGCAVP[p.S21G]GTVLLLLAYLAYLALGTGVFWTLEGR	GTVLLLLAY,RVRGCAVPG,CAVPGTVLL,VPGTVLLLL,RVRGCAVPGT,PGTVLLLLAY,RGCAVPGTVL,CAVPGTVLL,VPGTVLLLLA	ACC
KCNK18	c.68G>T	p.G23V	MEVSGHPQARRCCPEALGKLFP[p.G23V]VLCFLCFLVTYALVGAVVFSAIEDGQ	ALGKLFPVL,KLFPVLCFL,VLCFLCFLV,EALGKLFPV,GKLFPVLCF,FPVLCFLCF,KLFPVLCFLC,LFPVLCFLCF,FPVLCFLCFL,LGKLFPVLCF,GKLFPVLCFL,PEALGKLFPV	LUAD
KCNK2	c.17C>G	p.S6W	MLPSA[p.S6W]WRERPGYRAGVAAPDLLDPKSAAQNS	AWRERPGYR,SAWRERPGY,MLPSAWRER,SAWRERPGYR,AWRERPGYRA,PSAWRERPGY	BLCA
KCNK2	c.497G>T	p.R166L	HWDLGSSFFFAGTVITTIGFGNISP[p.R166L]LTEGGKIFCIIYALLGIPLFGFLLAG	IGFGNISPL,SPLTEGGKIF	LUAD
KCNMB2	c.453T>G	p.N151K	KLLLYHTEETIKINQKCSYIPKCGK[p.N151K]KFEESMSLVNVVMENFRKYQHFSCYS	CGKKFEESM,KKFEESMSL,CSYIPKCGKK,SYIPKCGKKF,KKFEESMSLV	STAD
KCNS2	c.631G>A	p.D211N	SRVFSILSILVVMGSIITMCLNSLP[p.D211N]NFQIPDSQGNPGEDPRFEIVEHFGIA	MCLNSLPNF,CLNSLPNFQI,TMCLNSLPNF	UCEC
KCTD20	c.942delA	p.L314fs	KLYRFFKYIENRDVAKTVLKERGLK[p.L314fs]TFALELKVTLPVKKKLREGLAAGLKSSIIMYNAPSSRCHGKRKKGRVAMWISSVFEANPSRIW*	KTFALELKV,RVAMWISSV,GLKTFALEL,KLREGLAAG,KVTLPVKKK,IMYNAPSSR,SVFEANPSR,VAMWISSVF,ELKVTLPVK,KSSIIMYNA,SSRCHGKRK,KRKKGRVAM,KGRVAMWIS,GLKSSIIMY,LKERGLKTF,FALELKVTL,LELKVTLPV,KKLREGLAA,LAAGLKSSI,AGLKSSIIM,RKKGRVAMW,MWISSVFEA,FEANPSRIW,KERGLKTFA,ALELKVTLPV,KLREGLAAGL,GLAAGLKSSI,AMWISSVFEA,IMYNAPSSRC,SVFEANPSRI,GLKTFALELK,IIMYNAPSSR,TFALELKVTL,RVAMWISSVF,VFEANPSRIW,RGLKTFALEL,SSRCHGKRKK,KGRVAMWISS,AGLKSSIIMY,VTLPVKKKLR,VLKERGLKTF,KERGLKTFAL,LAAGLKSSII,AAGLKSSIIM,GKRKKGRVAM,RKKGRVAMWI,GRVAMWISSV,REGLAAGLKS	CRC
KCTD21	c.17C>T	p.T6M	MSDPI[p.T6M]MLNVGGKLYTTSLATLTSFPDSMLGA	MSDPIMLNV,MLNVGGKLY,IMLNVGGKL,IMLNVGGKLY	STAD
KDELC1	c.1339C>A	p.L447I	LKWAKDHDEEAKKIAKAGQEFARNN[p.L447I]IMGDDIFCYYFKLFQEYANLQVSEPQ	IMGDDIFCY,GQEFARNNI,QEFARNNIM,IMGDDIFCYY,NIMGDDIFCY,GQEFARNNIM,RNNIMGDDIF	CRC
KDM1B	c.1083C>A	p.F361L	HLSNLEYACGSNLHQVSARSWDHNE[p.F361L]LFAQFAGDHTLLTPGYSVIIEKLAEG	RSWDHNELF,ARSWDHNEL,DHNELFAQF,NELFAQFAG,SARSWDHNEL,RSWDHNELFA,ARSWDHNELF,WDHNELFAQF	UCEC
KDM3B	c.3946delC	p.P1316fs	SLRDLLHSGPGKLPQTPLDTGIPFP[p.P1316fs]RSSLHPQQE*	FPRSSLHPQ,IPFPRSSLH,TGIPFPRSSL	STAD
KDM5A	c.1267C>T	p.P423S	VSSIEEDVIVEYGADISSKDFGSGF[p.P423S]SVKDGRRKILPEEEEYALSGWNLNNM	SVKDGRRKI,DFGSGFSVK,KDFGSGFSV,SSKDFGSGFS,KDFGSGFSVK,SVKDGRRKIL	TGCT
KEAP1	c.1408C>T	p.R470C	PERDEWHLVAPMLTRRIGVGVAVLN[p.R470C]CLLYAVGGFDGTNRLNSAECYYPERN	VAVLNCLLY,AVLNCLLYA,VLNCLLYAV,CLLYAVGGF,GVAVLNCLLY,AVLNCLLYAV	LUSC
KEAP1	c.1438G>T	p.G480W	PMLTRRIGVGVAVLNRLLYAVGGFD[p.G480W]WTNRLNSAECYYPERNEWRMITAMNT	LYAVGGFDW,AVGGFDWTNR,LLYAVGGFDW,FDWTNRLNSA	LUSC
KEAP1	c.1807G>T	p.G603W	LDSVECYDPDTDTWSEVTRMTSGRS[p.G603W]WVGVAVTMEPCRKQIDQQNCTC*	RMTSGRSWV,SWVGVAVTM,SGRSWVGVA,TRMTSGRSW,GRSWVGVAV,RSWVGVAVT,MTSGRSWVGV,SGRSWVGVAV,RSWVGVAVTM,VTRMTSGRSW,RMTSGRSWVG	LUAD
KEAP1	c.431C>T	p.S144F	GMEVVSIEGIHPKVMERLIEFAYTA[p.S144F]FISMGEKCVLHVMNGAVMYQIDSVVR	FISMGEKCV,TAFISMGEK,FAYTAFISM,YTAFISMGE,LIEFAYTAF,IEFAYTAFI,RLIEFAYTAF,LIEFAYTAFI,FISMGEKCVL,YTAFISMGEK,IEFAYTAFIS,EFAYTAFISM	LUAD
KEAP1	c.463G>T	p.V155F	PKVMERLIEFAYTASISMGEKCVLH[p.V155F]FMNGAVMYQIDSVVRACSDFLVQQLD	VLHFMNGAV,FMNGAVMYQ,HFMNGAVMY,CVLHFMNGA,MGEKCVLHF,GEKCVLHFM,LHFMNGAVM,CVLHFMNGAV,FMNGAVMYQI,SMGEKCVLHF,LHFMNGAVMY,VLHFMNGAVM	LUSC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
KEAP1	c.779G>T	p.R260L	DDLNVRCESEVFHACINWVKYDCEQ[p.R260L]LRFYVQALLRAVRCHSLTPNFLQMQL	QLRFYVQAL,KYDCEQLRF,LRFYVQALL,QLRFYVQALL,KYDCEQLRFY,WVKYDCEQLR,EQLRFYVQAL,VKYDCEQLRF,CEQLRFYVQA	LUAD
KEL	c.1231G>A	p.V411M	RKLSQKLRELTEQPPMPARPRWMKC[p.V411M]MEETGTFFEPTLAALFVREAFGPSTR	CMEETGTFF,KCMEETGTF,MKCMEETGTF,KCMEETGTFF	GBM
KHDRBS2	c.608C>T	p.S203L	LNGSEDSGRGRGIRGRGIRIAPTAP[p.S203L]LRGRGGAIPPPPPPGRGVLTPRGSTV	RIAPTAPLR,APLRGRGGA,PLRGRGGAI,IRIAPTAPL,GIRIAPTAPL,APLRGRGGAI	LUAD
KIAA0020	c.188A>G	p.K63R	RKVAKEGGPKVTSRNFEKSITKLGK[p.K63R]RGVKQFKNKQQGDKSPKNKFQPANKF	KSITKLGKR,ITKLGKRGV,RGVKQFKNK,LGKRGVKQF,ITKLGKRGVK,LGKRGVKQFK,KLGKRGVKQF	TGCT
KIAA0182	c.359_360insC	p.T120Fs	STPKRVPMGPIIVPPGGHSVPSTPP[p.T120fs]RGDHRSNQNREWCLEE*	HSVPSTPPR,RSNQNREWCL	STAD
KIAA0195	c.2706delC	p.I902Fs	GLETGWNCHISLTPNGDMPGSEIPP[p.I902fs]PAPATQAPCMMT*	APATQAPCM,SEIPPPAPA,APATQAPCMM,SEIPPPAPAT,MPGSEIPPPA	STAD
KIAA0240	c.2683delA	p.K895Fs	PMNHDQFHLVPNHIVVSAEGNISKK[p.K895fs]QNALAEH*	ISKKQNALA,NISKKQNAL,KKQNALAEH	STAD
KIAA0528	c.542G>A	p.R181Q	YRAVIIHGFVEELVVNEDPEYQWID[p.R181Q]QIRTPRASNEARQRLISLMSGELQRK	EYQWIDQIR,WIDQIRTPR,PEYQWIDQI,QWIDQIRTPR,YQWIDQIRTP,DPEYQWIDQI	CRC
KIAA0556	c.3244C>T	p.R1082W	SHSITIDFTHPCHVALIRIWNYNKS[p.R1082W]WIHSFRGVKDITMLLDTQCIFEGEIA	WIHSFRGVK,YNKSWIHSF,KSWIHSFRG,NKSWIHSFR,RIWNYNKSW,WNYNKSWIH,NYNKSWIHSF,RIWNYNKSWI,KSWIHSFRGV,SWIHSFRGVK,YNKSWIHSFR,IRIWNYNKSW	CRC
KIAA0556	c.988C>A	p.L330I	FPDQERMCSRPGSRRERPLSATRKT[p.L330I]ICEAEYPEEDASAVLQAIQVENAALQ	ATRKTICEA,RKTICEAEY,RPLSATRKTI,TRKTICEAEY	UCEC
KIAA0586	c.4775delC	p.A1592fs	PRWESSATLRFTDAPCQDVSDAAVS[p.A1592fs]DLEDCSQSLSLSTMQEDMESSGADTF*	DVSDAAVSDL,SDLEDCSQSL	STAD
KIAA0907	c.1337A>C	p.Q446P	GQSPMGGPFIPAAPVKTALPAGPQP[p.Q446P]PPQPQPPLPSQPQAQKRRFTEELPDE	QPPPQPQPPL	BLCA
KIAA0907	c.1546_1547delAG	p.R516Fs	TGFSSQNEIEGAGSKPASSSGKERE[p.R516fs]GQAVDASTSLSSDWNKNRVR*	TSLSSDWNK,LSSDWNKNR,QAVDASTSL,STSLSSDWNK,SLSSDWNKNR,KEREGQAVDA,REGQAVDAST,GQAVDASTSL,DASTSLSSDW	GBM
KIAA1109	c.14039T>C	p.L4680P	SMSLHGNHMTLACFHGPNFRSKSWA[p.L4680P]PFHLEEPNIAFWTEAQKIWEDGSSDH	RSKSWAPFH,KSWAPFHLE,FRSKSWAPF,SKSWAPFHL,NFRSKSWAPF,RSKSWAPFHL,APFHLEEPNI	CLL
KIAA1109	c.14810C>A	p.S4937Y	ITYTTVDWRDFMCNTWHLEPTLRLI[p.S4937Y]YWTGRKIDPVGVDYILQKLGFHHART	RLIYWTGRK,LEPTLRLIY,LIYWTGRKI,EPTLRLIYW,HLEPTLRLIY,RLIYWTGRKI,TLRLIYWTGR	CRC
KIAA1109	c.4763delA	p.E1588fs	ANSLLDRGMQLSGSTSNTPYTPLEK[p.E1588fs]NSLITQMMKH*	NSLITQMMK,EKNSLITQM,KNSLITQMM,TPLEKNSLI,KNSLITQMMK,LEKNSLITQM,EKNSLITQMM	STAD
KIAA1147	c.446C>T	p.A149V	YFRKGPFFGLACFANMPVESELERG[p.A149V]VRMKSVGILSPSYTLLYRYMHFLENQ	GVRMKSVGI,SELERGVRM,VRMKSVGIL,VESELERGV,GVRMKSVGIL,LERGVRMKSV	UCEC
KIAA1211	c.3608C>A	p.P1203Q	SVTVEISDSAPPAPLVKEVTKRFST[p.P1203Q]QDAAPVSTEPAWLALAKRKAKAWSDC	FSTQDAAPV,KRFSTQDAA,VTKRFSTQDA	LUAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
KIAA1211	c.924delT	p.R308fs	ERAPREEQQRSLEAPGWEDAERRER[p.R308fs]RSASAWRRRRSEGVCRPRPKRRRGGGWRRTPGWRSGGGRRRRKEDARRSSKGRRRRRLRDGKSWNSRRRRCRGRPRRWRRLGRAGGARRRRIWGKRRRRARRTWRTGGGSSVSF*	RSASAWRRR,SASAWRRRR,KRRRGGGWR,GWRRTPGWR,GWRSGGGRR,RSGGGRRRR,SGGGRRRRK,RSSKGRRRR,SSKGRRRRR,KGRRRRRLR,RRRRLRDGK,KSWNSRRRR,RRRCRGRPR,RGRPRRWRR,RWRRLGRAG,LGRAGGARR,RAGGARRRR,GARRRRIWG,ARRRRIWGK,RRRRIWGKR,RIWGKRRRR,RRRARRTWR,RARRTWRTG,DGKSWNSRR,RPRRWRRLG,RERRSASAW,RRLRDGKSW,RRRRARRTW,WRTGGGSSV,TGGGSSVSF,AERRERRSA,RTGGGSSVSF,RERRSASAWR,RSASAWRRRR,AWRRRRSEGV,KRRRGGGWRR,RSGGGRRRRK,RSSKGRRRRR,SSKGRRRRRL,KGRRRRRLRD,RRRRRLRDGK,RLRDGKSWNS,KSWNSRRRRC,NSRRRRCRGR,RRRRCRGRPR,RRRCRGRPRR,RCRGRPRRWR,RGRPRRWRRL,RPRRWRRLGR,RWRRLGRAGG,LGRAGGARRR,RAGGARRRRI,GARRRRIWGK,RIWGKRRRRA,RRRRARRTWR,RARRTWRTGG,TWRTGGGSSV,DARRSSKGRR,DGKSWNSRRR,SWNSRRRRCR,RPRPKRRRGG,RPKRRRGGGW,ERRERRSASA,RRERRSASAW,RRRLRDGKSW	CESC
KIAA1211	c.926_927insG	p.E309fs	RAPREEQQRSLEAPGWEDAERRERE[p.E309fs]GARAPGGGGGAKASAGPGSGGEAAAGGGRQAGGAEAAGGGGRKMRGGAQKAGGGGG*	RKMRGGAQK,KMRGGAQKA,REREGARAP,RQAGGAEAA,AERREREGA,RAPGGGGGAK,KMRGGAQKAG,REREGARAPG,RQAGGAEAAG,RKMRGGAQKA	CESC
KIAA1429	c.413C>T	p.S138F	LRGWYNCLTLAIYGSVDRVISHDRD[p.S138F]FPPPPPPPPPPPQPQPSLKRNPKHAD	RVISHDRDF	HNSC
KIAA1429	c.4576G>A	p.D1526N	VLSAPESLQNLFNNRTAYVLADVMD[p.D1526N]NQLKSMWFTPFQAEEIDTDLDLVKVD	VMDNQLKSM,MDNQLKSMW,VLADVMDNQL,DVMDNQLKSM,VMDNQLKSMW,MDNQLKSMWF	HNSC
KIAA1549	c.3816G>T	p.L1272F	DGERLSAVKSSDLINKMDLQRAAIIf[p.L1272F]FGYRiQGVIAQPVDRVKRPSPESQSN	RAAIIFGYR,LQRAAIIFG,QRAAIIFGY,AAIIFGYRI,FGYRIQGVI,IIFGYRIQGV,RAAIIFGYRI,IFGYRIQGVI,LQRAAIIFGY,MDLQRAAIIF	LUAD
KIAA1751	c.189G>C	p.L63F	LQEAEDDVDPGHSSSVKELDTDADK[p.L63F]FKKKTAEDRTQAFHLRQNLSALDKMH	KFKKKTAEDR,KELDTDADKF	LUSC
KIAA1751	c.291G>C	p.K97N	TQAFHLRQNLSALDKMHEEQELFTE[p.K97N]NMRGELRACRQRRDLIDKQQEAVAAE	EQELFTENM,EEQELFTEN,FTENMRGELR,NMRGELRACR,EEQELFTENM,TENMRGELRA	KIRC
KIAA1755	c.324A>C	p.Q108H	CLRDEVVVHLAPLNPLLLRQGDFYL[p.Q108H]HVEPQEEQSVCIMIKCLSLDLCTVDK	RQGDFYLHV,LLRQGDFYLH,RQGDFYLHVE	LUAD
KIAA1804	c.1420G>A	p.V474M	AALQQKSQEELLKRREQQLAEREID[p.V474M]MLERELNILIFQLNQEKPKVKKRKGK	MLERELNIL,REIDMLERE,QLAEREIDML,MLERELNILI,QQLAEREIDM,REIDMLEREL,IDMLERELNI	CRC
KIAA1804	c.1429C>T	p.R477W	QQKSQEELLKRREQQLAEREIDVLE[p.R477W]WELNILIFQLNQEKPKVKKRKGKFKR	EWELNILIF,EIDVLEWEL,DVLEWELNI,LEWELNILI,WELNILIFQ,VLEWELNILI,AEREIDVLEW,REIDVLEWEL,LEWELNILIF,WELNILIFQL	CRC
KIAA1967	c.1243delC	p.P415fs	TGIDLSGCTKWWRFAEFQYLQPGPP[p.P415fs]GGFRQWWCTCRMSGPSCLLWRSGRPCASRKLQRQLPQPRRHKGKRSLLNRHLMPWSKQQTLLDGTQKLQRPPHSRKRTLISQRPLHPP*	RQWWCTCRM,RMSGPSCLL,TLLDGTQKL,QTLLDGTQK,MSGPSCLLW,LWRSGRPCA,RSGRPCASR,SGRPCASRK,ASRKLQRQL,KGKRSLLNR,RSLLNRHLM,KLQRPPHSR,LQRPPHSRK,HSRKRTLIS,RTLISQRPL,SCLLWRSGR,MPWSKQQTL,PPHSRKRTL,LQPGPPGGF,CRMSGPSCL,RQLPQPRRH,RRHKGKRSL,KRSLLNRHL,LLNRHLMPW,LLNRHLMPWS,HLMPWSKQQT,LMPWSKQQTL,RSGRPCASRK,KLQRPPHSRK,MSGPSCLLWR,YLQPGPPGGF,RMSGPSCLLW,SLLNRHLMPW,SGRPCASRKL,LQRQLPQPRR,RQLPQPRRHK,KGKRSLLNRH,LNRHLMPWSK,LQRPPHSRKR,HSRKRTLISQ,RTLISQRPLH,GFRQWWCTCR,KLQRQLPQPR,MPWSKQQTLL,RPPHSRKRTL,FQYLQPGPPG,FRQWWCTCRM,RQWWCTCRMS,CRMSGPSCLL,RRHKGKRSLL,GKRSLLNRHL,KRSLLNRHLM,KRTLISQRPL	STAD
KIAA2022	c.1034G>T	p.C345F	NVRDKTTLLMQEDAQFNFFPSVFTT[p.C345F]FPKRESKSGALKQSSDFSQFKVPDVS	SVFTTFPKR,TTFPKRESK,PSVFTTFPK,FFPSVFTTF,FTTFPKRESK,NFFPSVFTTF,FPSVFTTFPK	LUSC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
KIAA2026	c.1720C>T	p.R574C	PAKMILDNHDISVEMGVKSNYEIRI[p.R574C]CRPCEIKKTDCCKENLEKPRSPGEVT	RICRPCEIK,ICRPCEIKK,SNYEIRICR,YEIRICRPC,RICRPCEIKK,KSNYEIRICR,EIRICRPCEI	UCEC
KIAA2026	c.2069delA	p.K690fs	LEQSLQSHKKLKLTKMRAKKKKKKK[p.K690fs]RN*	RAKKKKKKKR	STAD
KIDINS220	c.2552A>G	p.N851S	SNINGHDYMRNIVHLPVFLNSRGLS[p.N851S]SARKFLVTSATNGDVPCSDTTGIQED	FLNSRGLSS,GLSSARKFL,SARKFLVTS,NSRGLSSAR,LSSARKFLV,RGLSSARKF,FLNSRGLSSA,GLSSARKFLV,NSRGLSSARK,RGLSSARKFL,SARKFLVTSA,SRGLSSARKF	TGCT
KIF13A	c.3345delA	p.K1115fs	LNCVRERWSDALIKRREYLDEQIKK[p.K1115fs]SAIKQRKQRTMWSGKPSLWSSG*	TMWSGKPSL,KQRTMWSGK,MWSGKPSLW,KQRKQRTMW,RTMWSGKPS,SAIKQRKQR,IKQRKQRTM,YLDEQIKKSA,TMWSGKPSLW,KSAIKQRKQR,AIKQRKQRTM,KQRKQRTMWS,RKQRTMWSGK,KQRTMWSGKP,RTMWSGKPSL,QIKKSAIKQR,IKQRKQRTMW	STAD
KIF14	c.1793G>A	p.R598Q	VFTLVMTQTKTEFVEGEEHDHRITS[p.R598Q]QINLIDLAGSERCSTAHTNGDRLKEG	RITSQINLI,SQINLIDLA,HRITSQINL,HRITSQINLI,SQINLIDLAG	CRC
KIF15	c.754G>C	p.E252Q	TSMNRESSRSHAVFTITIESMEKSN[p.E252Q]QIVNIRTSLLNLVDLAGSERQKDTHA	SMEKSNQIV,KSNQIVNIR,ESMEKSNQI,QIVNIRTSLL,ESMEKSNQIV,IESMEKSNQI,MEKSNQIVNI,NQIVNIRTSL	LUAD
KIF16B	c.434G>A	p.R145Q	GLIPRICEGLFSRINETTRWDEASF[p.R145Q]QTEVSYLEIYNERVRDLLRRKSSKTF	SFQTEVSYL,ASFQTEVSY,DEASFQTEV,QTEVSYLEIY,FQTEVSYLEI,EASFQTEVSY,ASFQTEVSYL,DEASFQTEVS	CRC
KIF18A	c.49C>T	p.R17C	MSVTEEDLCHHMKVVV[p.R17C]CVRPENTKEKAAGFHKVVHVVDKHIL	HMKVVVCVR,VVCVRPENTK,CVRPENTKEK,HHMKVVVCVR	CRC
KIF1B	c.3958C>T	p.R1320W	TVTIIHEKGSELHWKDVRELVVGRI[p.R1320W]WNKPEVDEAAVDAILSLNIISAKYLK	LVVGRIWNK,RELVVGRIW	BRCA
KIF20B	c.160G>A	p.E54K	NFDGIKLDLSHEFSLVAPNTEANSF[p.E54K]KSKDYLQVCLRIRPFTQSEKELESEG	KSKDYLQVC,FKSKDYLQV,NTEANSFKSK,SFKSKDYLQV,KSKDYLQVCL,EANSFKSKDY	UCEC
KIF20B	c.2971G>A	p.E991K	NEIETATRSITNNVSQIKLMHTKID[p.E991K]KLRTLDSVSQISNIDLLNLRDLSNGS	LMHTKIDKL,KLMHTKIDK,KLRTLDSVS,TKIDKLRTL,KLMHTKIDKL,HTKIDKLRTL,LMHTKIDKLR	CRC
KIF23	c.1048G>A	p.E350K	KEQITISQLSLVDLAGSERTNRTRA[p.E350K]KGNRLREAGNINQSLMTLRTCMDVLR	RTNRTRAKG,RTRAKGNRL,RTRAKGNRLR,RAKGNRLREA	BLCA
KIF23	c.449G>A	p.R150Q	SPGEGGLLPRCLDMIFNSIGSFQAK[p.R150Q]QYVFKSNDRNSMDIQCEVDALLERQK	FQAKQYVFK,SFQAKQYVF,IGSFQAKQY,SFQAKQYVFK,KQYVFKSNDR,SIGSFQAKQY,GSFQAKQYVF	UCEC
KIF25	c.7T>A	p.W3R	MT[p.W3R]RTSGQLQREKQARPGSGAVLAFPDDK	MTRTSGQLQ,RTSGQLQREK,MTRTSGQLQR	PRAD
KIF26B	c.3194delC	p.S1065fs	SLQSSRESLNSCGFVEGKPRPMGSP[p.S1065fs]GWASPACPRPRSTSHPALLPRDAKSTPRRGSCRLPPHCLPRARIPAWRLGSPCCSPRCVRPRLE*	RLPPHCLPR,TSHPALLPR,RSTSHPALL,RGSCRLPPH,RARIPAWRL,STPRRGSCR,KPRPMGSPG,RPMGSPGWA,CPRPRSTSH,RPRSTSHPA,HPALLPRDA,TPRRGSCRL,LPRARIPAW,IPAWRLGSP,SPRCVRPRL,LPPHCLPRA,RLPPHCLPRA,STSHPALLPR,RPRSTSHPAL,KSTPRRGSCR,RARIPAWRLG,WASPACPRPR,LPRARIPAWR,RLGSPCCSPR,KPRPMGSPGW,RPMGSPGWAS,SPACPRPRST,IPAWRLGSPC,MGSPGWASPA	STAD
KIF26B	c.3337G>A	p.V1113M	RCKVYTQKGVLPSPAPLPPSSKDSG[p.V1113M]MASRESLLQPEVRTPPVGMSPQVLKK	GMASRESLL,SGMASRESL,SSKDSGMASR,LPPSSKDSGM,SGMASRESLL	BRCA
KIF26B	c.3341C>T	p.A1114V	CKVYTQKGVLPSPAPLPPSSKDSGV[p.A1114V]VSRESLLQPEVRTPPVGMSPQVLKKS	SSKDSGVVSR	CRC
KIF26B	c.6097G>A	p.A2033T	SKEAMCFNAKLKILEHRQQRIAEVR[p.A2033T]TKYEWLMKELEATKQYLMLDPNKWLS	RTKYEWLMK,RIAEVRTKY,EVRTKYEWL,AEVRTKYEW,QQRIAEVRTK,RTKYEWLMKE,RQQRIAEVRT,QRIAEVRTKY,AEVRTKYEWL,TKYEWLMKEL,IAEVRTKYEW	LIHC
KIF27	c.2775G>T	p.K925N	LDACNLKRRKGSFGSIDHLQKLDEQ[p.K925N]NKWLDEEVEKVLNQRQELEELEADLK	KLDEQNKWL,EQNKWLDEEV,LQKLDEQNKW	UCEC

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KIF9	c.1438G>A	p.G480R	ISAIQKAGLVDVDGHLVGEPEGQNF[p.G480R]RLGVAPFSTKPGKKAKSKKTFKEPLS	NFRLGVAPF,GQNFRLGVA,RLGVAPFSTK,QNFRLGVAPF,GEPEGQNFRL	LUAD
KIF9	c.1781G>A	p.R594Q	IRPDTPPSKPVAFEEFKNEQGSEIN[p.R594Q]QIFKENKSILNERRKRASETTQHINA	GSEINQIFK,QGSEINQIFK,EQGSEINQIF,NQIFKENKSI,NEQGSEINQI	UCEC
KIRREL	c.1003delC	p.P335fs	VDPKPTTTDIGSDVTLTCVWVGNPP[p.P335fs]SLSPGPKRTQIWS*	VWVGNPPSL,SPGPKRTQI,CVWVGNPPSL,SPGPKRTQIW	STAD
KIRREL	c.1810G>T	p.G604C	VDLKQDLRCDTIDTREEYEMKDPTN[p.G604C]CYYNVRAHEDRPSSRAVLYADYRAPG	EMKDPTNCY,PTNCYYNVR,MKDPTNCYY,YEMKDPTNC,DPTNCYYNV,EMKDPTNCYY,YEMKDPTNCY	LUAD
KIRREL2	c.1947delC	p.V649fs	PPSPLGPPGTPTFYDFNPHLGMVPP[p.V649fs]ADFTEPGQAISPHPTLELSPATSNPHPLGPQIWPPGLPPSHMLPSPHLATRVSRLTCDIFPMEESWDLQLAIMDCSDF*	HMLPSPHLA,RLTCDIFPM,HLATRVSRL,ATRVSRLTC,LPSPHLATR,ESWDLQLAI,HPTLELSPA,NPHPLGPQI,SPHLATRVS,FPMEESWDL,LAIMDCSDF,LGMVPPADF,GQAISPHPT,QAISPHPTL,SHMLPSPHL,VSRLTCDIF,MEESWDLQL,EPGQAISPH,EESWDLQLA,DIFPMEESW,AISPHPTLEL,HLATRVSRLT,IFPMEESWDL,MLPSPHLATR,ESWDLQLAIM,NPHLGMVPPA,SPATSNPHPL,WPPGLPPSHM,LPSPHLATRV,QLAIMDCSDF,HLGMVPPADF,ADFTEPGQAI,GQAISPHPTL,HMLPSPHLAT,RVSRLTCDIF,SRLTCDIFPM,EESWDLQLAI,HPTLELSPAT,NPHPLGPQIW,FPMEESWDLQ,MEESWDLQLA	STAD
KIT	c.1669T>G	p.W557G	VAGMMCIIVMILTYKYLQKPMYEVQ[p.W557G]GKVVEEINGNNYVYIDPTQLPYDHKW	PMYEVQGKV,VQGKVVEEI,EVQGKVVEEI,KPMYEVQGKV	TGCT
KIT	c.2446G>C	p.D816H	RDLAARNILLTHGRITKICDFGLAR[p.D816H]HIKNDSNYVVKGNARLPVKWMAPESI	HIKNDSNYV,RHIKNDSNY,CDFGLARHI,HIKNDSNYVV,ARHIKNDSNY,RHIKNDSNYV	TGCT
KIT	c.2446G>T	p.D816Y	RDLAARNILLTHGRITKICDFGLAR[p.D816Y]YIKNDSNYVVKGNARLPVKWMAPESI	ICDFGLARY,YIKNDSNYV,RYIKNDSNY,DFGLARYIK,CDFGLARYI,YIKNDSNYVV,KICDFGLARY,RYIKNDSNYV,ARYIKNDSNY	TGCT
KIT	c.2447A>T	p.D816V	RDLAARNILLTHGRITKICDFGLAR[p.D816V]VIKNDSNYVVKGNARLPVKWMAPESI	VIKNDSNYV,RVIKNDSNY,CDFGLARVI,RVIKNDSNYV,VIKNDSNYVV,ARVIKNDSNY	LAML,TGCT
KIT	c.2464A>T	p.N822Y	NILLTHGRITKICDFGLARDIKNDS[p.N822Y]YYVVKGNARLPVKWMAPESIFNCVYT	KNDSYYVVK,SYYVVKGNA,RDIKNDSYY,YYVVKGNAR,DIKNDSYYV,IKNDSYYVV,YYVVKGNARL,LARDIKNDSY,SYYVVKGNAR,DIKNDSYYVV,DSYYVVKGNA	TGCT
KIT	c.2466T>G	p.N822K	NILLTHGRITKICDFGLARDIKNDS[p.N822K]KYVVKGNARLPVKWMAPESIFNCVYT	KNDSKYVVK,RDIKNDSKY,IKNDSKYVV,KYVVKGNARL,LARDIKNDSK	TGCT
KLC2	c.1703delC	p.T568fs	SFGKLRDALRRSSEMLVKKLQGGTP[p.T568fs]RSPLTPG*	TPRSPLTPG,LQGGTPRSPL	STAD
KLF3	c.312delA	p.I104fs	SLKFPSSHRRASPGLSMPSSSPPIK[p.I104fs]NTHPLLQACSPSACRCPCHQ*	LLQACSPSA,QACSPSACR,PPIKNTHPL,SPSACRCPC,LQACSPSAC,SPPIKNTHPL	STAD
KLF3	c.671_672insC	p.S224fs	GIEPQRTDYYPEEMSPPLMNSVSPP[p.S224fs]ASIVARESPFGHRAAWEETFTCGIPGYSKEAEDTQM*	LMNSVSPPA,SVSPPASIV,TFTCGIPGY,NSVSPPASI,FTCGIPGYS,SPFGHRAAW,SIVARESPF,RESPFGHRA,HRAAWEETF,SKEAEDTQM,WEETFTCGI,PLMNSVSPPA,FTCGIPGYSK,VARESPFGHR,ETFTCGIPGY,NSVSPPASIV,ASIVARESPF,LMNSVSPPAS,MNSVSPPASI,RESPFGHRAA,GHRAAWEETF,YSKEAEDTQM	STAD
KLF4	c.1300A>C	p.K434Q	GRRSWPRKRTATHTCDYAGCGKTYT[p.K434Q]QSSHLKAHLRTHTGEKPYHCDWDGCG	KTYTQSSHL,TQSSHLKAH,KTYTQSSHLK,QSSHLKAHLR,GKTYTQSSHL,TQSSHLKAHL	BRCA
KLF5	c.1255G>C	p.E419Q	LRTHTGEKPYKCTWEGCDWRFARSD[p.E419Q]QLTRHYRKHTGAKPFQCGVCNRSFSR	RSDQLTRHY,FARSDQLTR,DQLTRHYRK,WRFARSDQL,RSDQLTRHYR,ARSDQLTRHY	LUAD,LUSC
KLF5	c.353C>T	p.S118L	EKYLTPQLPPVPIIPEHKKYRRDSA[p.S118L]LVVDQFFTDTEGLPYSINMNVFLPDI	KYRRDSALV,SALVVDQFF,KKYRRDSAL,YRRDSALVV,KYRRDSALVV,HKKYRRDSAL,KKYRRDSALV,RDSALVVDQF	BLCA
KLHDC2	c.962G>C	p.W321S	DAWTYCISKNEWIQFNHPYTEKPRL[p.W321S]SHTACASDEGEVIVFGGCANNLLVHH	KPRLSHTAC,KPRLSHTACA,TEKPRLSHTA	TGCT

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KLHDC7A	c.1903G>A	p.E635K	DRWDFAPPLPSDTFALAHTATVRAK[p.E635K]KIFVTGGSLRFLLFRFSAQEQRWWAG	HTATVRAKK,TVRAKKIFV,RAKKIFVTG,KIFVTGGSL,KIFVTGGSLR,TVRAKKIFVT,RAKKIFVTGG,HTATVRAKKI,KKIFVTGGSL	SKCM
KLHL13	c.637G>A	p.E213K	FLISGVTLDNCVEVGRIANTYNLTE[p.E213K]MDKYVNSFVLKNFPALLSTGEFLKLP	NLTEMDKYV,EMDKYVNSF,ANTYNLTEM,TEMDKYVNS,EMDKYVNSFV,NTYNLTEMDK,TEMDKYVNSF,IANTYNLTEM,MDKYVNSFVL	UCEC
KLHL14	c.693delC	p.P231fs	KYLVEDVLLLNFEEMRALLDSLPPP[p.P231fs]WSRSWRSSRCPCCGWSTTARPACSMRLTS*	WSRSWRSSR,SWRSSRCPC,TARPACSMR,DSLPPPWSR,TTARPACSM,RPACSMRLT,LLDSLPPPW,LPPPWSRSW,TTARPACSMR,RSWRSSRCPC,SWRSSRCPCC,SSRCPCCGWS,STTARPACSM,TARPACSMRL,RPACSMRLTS,ALLDSLPPPW,SLPPPWSRSW,RSSRCPCCGW	STAD
KLHL15	c.554A>G	p.D185G	DNFVPLMSRPDFLSYLSFEKLMSYL[p.D185G]GNDHLSRFPEIELYEAVQSWLRHDRR	MSYLGNDHL,LMSYLGNDH,LGNDHLSRF,FEKLMSYLG,LMSYLGNDHL,YLGNDHLSRF,SYLGNDHLSR	BLCA
KLHL28	c.97G>A	p.E33K	YMLANLTHLHSEQLLQGLNLLRQHH[p.E33K]KLCDIILRVGDVKIHAHKVVLASVSP	KLCDIILRV,LNLLRQHHK,NLLRQHHKL,RQHHKLCDI,GLNLLRQHHK,RQHHKLCDII	UCEC
KLHL5	c.976C>T	p.R326C	QLSQVVEACCKFLMKQLHPSNCLGI[p.R326C]CSFADAQGCTDLHKVAHNYTMEHFME	SNCLGICSF	CRC
KLK2	c.169C>A	p.P57T	EKHSQPWQVAVYSHGWAHCGGVLVH[p.P57T]TQWVLTAAHCLKKNSQVWLGRHNLFE	VLVHTQWVL,GVLVHTQWV,HTQWVLTAA,TQWVLTAAH,VHTQWVLTAA	CRC
KLK2	c.481G>A	p.E161K	VKVLGLPTQEPALGTTCYASGWGSI[p.E161K]KPEEFLRPRSLQCVSLHLLSNDMCAR	YASGWGSIK,SIKPEEFLR,GSIKPEEFLR,GWGSIKPEEF	CESC
KLK6	c.359G>A	p.R120H	QSSVVRAVIHPDYDAASHDQDIMLL[p.R120H]HLARPAKLSELIQPLPLERDCSANTT	MLLHLARPA,LLHLARPAK,DIMLLHLAR,IMLLHLARPA,LLHLARPAKL,MLLHLARPAK,HDQDIMLLHL	GBM
KPNA4	c.86G>A	p.R29Q	NEKLDNQRLKNFKNKGRDLETMRRQ[p.R29Q]QNEVVVELRKNKRDEHLLKRRNVPHE	QQNEVVVEL,TMRRQQNEV,RRQQNEVVV,RQQNEVVVE,TMRRQQNEVV,ETMRRQQNEV,MRRQQNEVVV,RQQNEVVVEL	CRC
KPRP	c.1659_1660insC	p.E553fs	YCGPSSYNQGQESGAGCGPGDVFPE[p.E553fs]PEGSGWPWRPRQCLCWSERGSKECLFLKER*	GSKECLFLK,WPWRPRQCL,RPRQCLCWS,SERGSKECL,FPEPEGSGW,EPEGSGWPW,CLCWSERGSK,RGSKECLFLK,EGSGWPWRPR,SERGSKECLF	HNSC
KRAS	c.176C>G	p.A59G	PTIEDSYRKQVVIDGETCLLDILDT[p.A59G]GGQEEYSAMRDQYMRTGEGFLCVFAI	LDTGGQEEY,GGQEEYSAM,ILDTGGQEEY	MM
KRAS	c.180_181TC>AA	p.Q61K	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61K]KEEYSAMRDQYMRTGEGFLCVFAINNT	LDTAGKEEY,AGKEEYSAM,ILDTAGKEEY,DTAGKEEYSA	CRC,THCA
KRAS	c.182A>G	p.Q61R	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61R]REEYSAMRDQYMRTGEGFLCVFAINN	LDTAGREEY,AGREEYSAM,ILDTAGREEY,AGREEYSAMR,DTAGREEYSA	MM,TGCT
KRAS	c.182A>T	p.Q61L	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61L]LEEYSAMRDQYMRTGEGFLCVFAINN	LDTAGLEEY,AGLEEYSAM,ILDTAGLEEY,LLDILDTAGL,DTAGLEEYSA	CRC,LUAD,TGCT
KRAS	c.183A>C	p.Q61H	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61H]HEEYSAMRDQYMRTGEGFLCVFAINN	LDTAGHEEY,AGHEEYSAM,ILDTAGHEEY,DTAGHEEYSA	LUAD,PAAD,STAD
KRAS	c.183A>T	p.Q61H	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61H]HEEYSAMRDQYMRTGEGFLCVFAINN	LDTAGHEEY,AGHEEYSAM,ILDTAGHEEY,DTAGHEEYSA	MM,TGCT
KRAS	c.34G>A	p.G12S	MTEYKLVVVGA[p.G12S]SGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGASGV,KLVVVGASGV,YKLVVVGASG	CRC,STAD
KRAS	c.34G>C	p.G12R	MTEYKLVVVGA[p.G12R]RGVGKSALTIQLIQNHFVDEYDPTIE	ARGVGKSAL,KLVVVGARGV,VVVGARGVGK,EYKLVVVGAR,GARGVGKSAL,RGVGKSALTI	MM,PAAD,TGCT
KRAS	c.34G>T	p.G12C	MTEYKLVVVGA[p.G12C]CGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGACGV,VVGACGVGK,KLVVVGACGV,VVVGACGVGK	CRC,LUAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
KRAS	c.35G>A	p.G12D	MTEYKLVVVGA[p.G12D]DGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGADGV,VVGADGVGK,KLVVVGADGV,VVVGADGVGK	CESC,CRC,GBM,KIRP,LAML,LUAD,MM,PAAD,STAD,UCEC,UCS
KRAS	c.35G>C	p.G12A	MTEYKLVVVGA[p.G12A]AGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGAAGV,VVGAAGVGK,YKLVVVGAA,KLVVVGAAGV,VVVGAAGVGK,YKLVVVGAAG,GAAGVGKSAL	CRC,LUAD,MM,TGCT,UCEC
KRAS	c.35G>T	p.G12V	MTEYKLVVVGA[p.G12V]VGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGAVGV,VVGAVGVGK,YKLVVVGAV,KLVVVGAVGV,VVVGAVGVGK,GAVGVGKSAL	BRCA,CESC,CRC,LUAD,OV,PAAD,TGCT,UCEC,UCS
KRAS	c.37G>T	p.G13C	MTEYKLVVVGAG[p.G13C]CVGKSALTIQLIQNHFVDEYDPTIED	VVGAGCVGK,KLVVVGAGCV,VVVGAGCVGK	LUAD
KRAS	c.38G>A	p.G13D	MTEYKLVVVGAG[p.G13D]DVGKSALTIQLIQNHFVDEYDPTIED	VVGAGDVGK,KLVVVGAGDV,VVVGAGDVGK	CESC,CLL,CRC,DLBCL,LUAD,MM,STAD,UCEC
KRAS	c.436G>A	p.A146T	PSRTVDTKQAQDLARSYGIPFIETS[p.A146T]TKTRQRVEDAFYTLVREIRQYRLKKI	ETSTKTRQR,GIPFIETSTK,ETSTKTRQRV	CRC,MM,TGCT
KRBA1	c.2515A>G	p.R839G	DRLATALAGLAQEVATMRTQVNRLG[p.R839G]GRPQGPGPMGQASWMWTLPRGPRWAH	RTQVNRLGG,TQVNRLGGR,RTQVNRLGGR	TGCT
KRT2	c.896T>G	p.L299W	KRTAAENDFVTLKKDVDNAYMIKVE[p.L299W]WQSKVDLLNQEIEFLKVLYDAEISQI	YMIKVEWQS,MIKVEWQSK,IKVEWQSKV,VEWQSKVDL,NAYMIKVEW,MIKVEWQSKV,YMIKVEWQSK,VEWQSKVDLL	KIRC
KRT4	c.462_463insC	p.F154fs	RGNKSISMSVAGSRQGACFGGAGGF[p.F154fs]RHWWLWWWIWGLLQW*	WLWWWIWGL,GGFRHWWLW,GFRHWWLWW,FRHWWLWWW,RHWWLWWWI,HWWLWWWIW,LWWWIWGLL,WWIWGLLQW,CFGGAGGFR,GGAGGFRHW,WLWWWIWGLL,AGGFRHWWLW,GFRHWWLWWW,RHWWLWWWIW,WWLWWWIWGL,WWWIWGLLQW,FGGAGGFRHW	KIRC
KRT6B	c.590T>C	p.L197P	NKFASFIDKVRFLEQQNKVLDTKWT[p.L197P]PLQEQGTKTVRQNLEPLFEQYINNLR	VLDTKWTPL,KVLDTKWTPL	CRC
KRT8	c.175T>G	p.S59A	TQKSYKVSTSGPRAFSSRSYTSGPG[p.S59A]ARISSSSFSRVGSSNFRGGLGGGYGG	RSYTSGPGA,GARISSSSF,SYTSGPGAR,YTSGPGARI,RSYTSGPGAR,SYTSGPGARI,GARISSSSFS	ACC,KIRP,LIHC
KRTAP1-1	c.346A>G	p.I116V	CGTGCGIGGGIGYGQEGSSGAVSTR[p.I116V]VRWCRPDCRVEGTCLPPCCVVSCTPP	VSTRVRWCR,STRVRWCRP,RVRWCRPDC,GAVSTRVRW,AVSTRVRWCR,STRVRWCRPD,RVRWCRPDCR,SGAVSTRVRW	TGCT
KRTAP27-1	c.372G>T	p.M124I	ACQSESSSAGLACVSQPCQSESTQQ[p.M124I]IGFVAQSCQPASLKGNSCPPKTSKSK	CQSESTQQI,ESTQQIGFV,SESTQQIGF,QSESTQQIGF,QQIGFVAQSC,SESTQQIGFV	LUAD
KRTAP4-11	c.144C>G	p.S48R	TCCRPSCCETTCCRTTYCRPSCCVS[p.S48R]RCCRPQCCQSVCCQPTCCRPRCCISS	VSRCCRPQC	GBM,PRAD
KRTAP4-5	c.220A>T	p.S74C	VCYQPTCCHPSCCISSCCRPYCCES[p.S74C]CCCRPCCCQTTCCRTTCCRTTCCCPS	CESCCCRPC	KIRP
KRTAP4-5	c.272G>T	p.C91F	CRPYCCESSCCRPCCCQTTCCRTTC[p.C91F]FRTTCCCPSCCVSSCCRPQCCQSVCC	TCCRTTCFR,TTCCRTTCFR	LUAD

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KRTAP 4-8	c.188C>G	p.T63S	TCYRPSYSVSCCCRPQCCQSVCCQP[p.T63S]SCCRPSCCVSSCCKPQCCQSVCCQPT	SVCCQPSCCR	TGCT
KRTAP 4-9	c.53A>T	p.D18V	MVSSCCGSVCSDQGCGQ[p.D18V]VLCQETCCRPSCCETTCCRTTCCRPS	CSDQGCGQV,SDQGCGQVL,QVLCQETCCR	PRAD
KRTAP 5-1	c.578C>A	p.S193Y	GSCGGSKGGCGSCGGCKGGCGSCGG[p.S193Y]YKGGCGSGCGGCGSGCGVPVCCCSCS	GGCGSCGGY,KGGCGSCGGY	LUAD
KSR2	c.1664C>T	p.T555M	FNLPASHYYKYKQQFIFPDVVPVPE[p.T555M]MPTRAPQVILHPVTSNPILEGNPLLQ	MPTRAPQVI,FPDVVPVPEM,MPTRAPQVIL,PEMPTRAPQV	HNSC
L1CAM	c.1894C>A	p.R632S	LVVGSPGPVPRLVLSDLHLLTQSQV[p.R632S]SVSWSPAEDHNAPIEKYDIEFEDKEM	LLTQSQVSV,QVSVSWSPA,TQSQVSVSW,SQVSVSWSP,HLLTQSQVSV,SQVSVSWSPA,LTQSQVSVSW	LUAD
L1CAM	c.557C>T	p.T186M	PPSAEPLRIYWMNSKILHIKQDERV[p.T186M]MMGQNGNLYFANVLTSDNHSDYICHA	MMGQNGNLY,VMMGQNGNL,HIKQDERVM,IKQDERVMM,VMMGQNGNLY,MMGQNGNLYF,RVMMGQNGNL,LHIKQDERVM	CRC
L2HGDH	c.1321_1323delCCT	p.P441del	VEDFVFDAGVGDIGNRILHVRNAPS[p.P441del]AATSSIAISGMIADEVQQRFEL*	HVRNAPSAA,SAATSSIAI,APSAATSSI,LHVRNAPSA,ILHVRNAPSA,HVRNAPSAAT,NAPSAATSSI,APSAATSSIA,LHVRNAPSAA	TGCT
L3MBTL4	c.485G>T	p.W162L	HPVGWCEKTKHELHIPKGYRKDKFV[p.W162L]LMDYLKACKLQNAPKKLFRNRSPNGP	VLMDYLKAC,LMDYLKACK,KFVLMDYLK,KDKFVLMDY,YRKDKFVLM,LMDYLKACKL,VLMDYLKACK,KGYRKDKFVL,RKDKFVLMDY	LUAD
LACTB	c.13A>C	p.M5L	MYRL[p.M5L]LSAVTARAAAPGGLASSCGRRGVHQR	LLSAVTARA,RLLSAVTAR,YRLLSAVTA,RLLSAVTARA,LLSAVTARAA,MYRLLSAVTA,LSAVTARAAA	ACC
LALBA	c.121G>A	p.A41T	AILAKQFTKCELSQLLKDIDGYGGI[p.A41T]TLPELICTMFHTSGYDTQAIVENNES	TLPELICTM,IDGYGGITL,GYGGITLPEL,TLPELICTMF,ITLPELICTM	CRC
LAMA1	c.3088G>T	p.D1030Y	NTCDPETGECVCPPHTQGVKCEECE[p.D1030Y]YGHWGYDAEVGCQACNCSLVGSTHHR	GVKCEECEY,CEYGHWGYDA,EECEYGHWGY	LUAD
LAMA4	c.1673C>T	p.A558V	SLSTSADSLTTPRLTLSELDDIIKN[p.A558V]VSGIYAEIDGAKSELQVKLSNLSNLS	ELDDIIKNV,NVSGIYAEI,IIKNVSGIY,DIIKNVSGI,IKNVSGIYA,IIKNVSGIYA,DIIKNVSGIY,KNVSGIYAEI,SELDDIIKNV	CRC
LAMA4	c.1915G>A	p.E639K	NGLVQKALDASNVYENIVNYVSEAN[p.E639K]KTAEFALNTTDRIYDAVSGIDTQIIY	VNYVSEANK,YVSEANKTA,EANKTAEFA,SEANKTAEF,IVNYVSEANK,EANKTAEFAL,VSEANKTAEF,SEANKTAEFA	BLCA
LAMA4	c.3879G>A	p.M1293I	PNGLLFYYASGSDVFSISLDNGTVI[p.M1293I]IDVKGIKVQSVDKQYNDGLSHFVISS	SLDNGTVII,VIIDVKGIK,TVIIDVKGI,VIIDVKGIKV,TVIIDVKGIK,ISLDNGTVII	LUSC
LAMA5	c.6668T>G	p.L2223R	SSMAWARLHRLNASIADLQSQLRSP[p.L2223R]RGPRHETAQQLEVLEQQSTSLGQDAR	QLRSPRGPR,LQSQLRSPR,SPRGPRHET,SQLRSPRGPR,QLRSPRGPRH,DLQSQLRSPR,SPRGPRHETA	KIRP
LAMB4	c.1762G>T	p.G588W	GLAPLGSETFGQSPAVHVVLGEPVP[p.G588W]WNPVTWTGPGFARVLPGAGLRFAVNN	GEPVPWNPV,VVLGEPVPW,HVVLGEPVPW,EPVPWNPVTW	LUAD
LAMB4	c.3715G>T	p.G1239W	EADFKDLRGNVSEIERILKHPVFPS[p.G1239W]WKFLKVKDYHDSVRRQIMQLNEQLKA	VFPSWKFLK,KHPVFPSWK,FPSWKFLKV,HPVFPSWKF,LKHPVFPSW,WKFLKVKDY,PVFPSWKFLK,KHPVFPSWKF,VFPSWKFLKV,SWKFLKVKDY,HPVFPSWKFL,ILKHPVFPSW	LUAD
LAMC3	c.521_522CC>AG	p.P174Q	KRSRADGPWEPYQFYSASCQKTYGR[p.P174Q]QEGQYLRPGEDERVAFCTSEFSDISPL	TYGRQEGQY,YGRQEGQYL,KTYGRQEGQY,TYGRQEGQYL,RQEGQYLRPG	TGCT
LARP1	c.668_669insC	p.A223fs	PRHIPANRGEIKGSESATYVPVAPP[p.A223fs]HPSLATRDQTGACLARPG*	APPHPSLAT,SLATRDQTGA,ATYVPVAPPH,ATRDQTGACL,VPVAPPHPSL	STAD

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LARP4B	c.487delA	p.T163fs	PENSETGGNESQPDSQEDPREVLKK[p.T163fs]HWNSAYLGRTLLVTCILYHRWIVTSMCQSQRWLTSTTSRSSALMWT*	CILYHRWIV,VLKKHWNSA,YLGRTLLVT,ILYHRWIVT,VTSMCQSQR,AYLGRTLLV,RTLLVTCIL,LYHRWIVTS,SAYLGRTLL,RWLTSTTSR,STTSRSSAL,TTSRSSALM,LKKHWNSAY,TLLVTCILY,HWNSAYLGR,LVTCILYHR,YHRWIVTSM,KKHWNSAYL,NSAYLGRTL,SMCQSQRWL,CQSQRWLTS,SQRWLTSTT,TSRSSALMW,TSMCQSQRW,SAYLGRTLV,RTLLVTCILY,LYHRWIVTSM,STTSRSSALM,VLKKHWNSAY,LLVTCILYHR,IVTSMCQSQR,EVLKKHWNSA,NSAYLGRTLL,LKKHWNSAYL,WNSAYLGRTL,CQSQRWLTST,SQRWLTSTTS,REVLKKHWNS,TTSRSSALMW	STAD
LARS	c.554_555insC	p.P185fs	MKSLGLSDEEIVKFSEAEHWLDYFP[p.P185fs]ATGYSGFKKNGFEGRLASFLHHH*	ATGYSGFKK,RLASFLHHH,GFEGRLASF,FPATGYSGF,LDYFPATGY,FEGRLASFL,WLDYFPATGY,YFPATGYSGF,NGFEGRLASF,AEHWLDYFPA,FKKNGFEGRL	KIRC
LAT2	c.53T>G	p.L18W	MSSGTELLWPGAALLVL[p.L18W]WGVAASLCVRCSRPGAKRSEKIYQQR	AALLVLWGV,VLWGVAASL,LLVLWGVAA,GAALLVLWGV,ALLVLWGVAA,LVLWGVAASL,WPGAALLVLW	GBM
LBX1	c.526C>T	p.R176W	SPADRDQIAQQLGLTNAQVITWFQN[p.R176W]WRAKLKRDLEEMKADVESAKKLGPSG	VITWFQNWR,QVITWFQNW,WFQNWRAKL,TWFQNWRAK,ITWFQNWRA,ITWFQNWRAK,QVITWFQNWR,TWFQNWRAKL,WFQNWRAKLK,NWRAKLKRDL,AQVITWFQNW	CRC
LCP1	c.1334_1335insC	p.P445fs	SDALVIFQLYEKIKVPVDWNRVNKP[p.P445fs]AIPQTGRQYEEA*	RVNKPAIPQT	KIRC
LHCGR	c.47T>A	p.L16Q	MKQRFSALQLLKLLL[p.L16Q]QLQPPLPRALREALCPEPCNCVPDGA	QLLKLLLQL,LLLQLQPPL,QLQPPLPRA,KLLLQLQPPL,QLQPPLPRAL,LQLLKLLLQL,LQLQPPLPRA	TGCT
LILRA1	c.1228C>T	p.H410Y	SPVTSAHSGTYRCYGSLSSNPYLLS[p.H410Y]YPSDSLELMVSGAAETLSPPQNKSDS	SSNPYLLSY,LLSYPSDSL,SYPSDSLEL,YPSDSLELM,NPYLLSYPS,LSSNPYLLSY,YLLSYPSDSL,SYPSDSLELM,LSYPSDSLEL,YPSDSLELMV	BLCA
LILRB1	c.1417_1419delCTC	p.L479del	GLGRHLGVVIGILVAVILLLLLLLL[p.L479del]FLILRHRRQGKHWTSTQRKADFQHPAGA	ILLLLLLLF	BLCA
LILRB5	c.1792T>C	p.S598P	TKDRQAEEDRQMDTERVLSSPGPQA[p.S598P]PPPPPRSLPLTLPRCRLLHLKPPRM*	APPPPPRSL,PPPPPRSLPL	PRAD
LIM2	c.448T>A	p.S150T	IMAFAHQPTFSRISRPFSAGIMFFS[p.S150T]TTLFVVLALAIYTGVTVSFLGRRFGD	GIMFFSTTL,MFFSTTLFV,FFSTTLFVV,IMFFSTTLF,FSTTLFVVL,STTLFVVLA,TTLFVVLAL,IMFFSTTLFV,MFFSTTLFVV,GIMFFSTTLF,FFSTTLFVVL,FSAGIMFFST,FSTTLFVVLA,STTLFVVLAL,TTLFVVLALA,AGIMFFSTTL	LUAD
LIMK2	c.608G>A	p.R203H	TTVQVKEVNRMHISPNNRNAIHPGD[p.R203H]HILEINGTPVRTLRVEEVEDAISQTS	NAIHPGDHI,HPGDHILEI,AIHPGDHIL,HILEINGTPV	GBM
LIN9	c.547C>T	p.R183W	FCVCLKESFPNLKTRKLTRVEWGKI[p.R183W]WRLMGKPRRCSSAFFEEERSALKQKR	RVEWGKIWR,IWRLMGKPR,VEWGKIWRL,WGKIWRLMGK,KIWRLMGKPR,IWRLMGKPRR,VEWGKIWRLM	UCEC
LIN9	c.691G>A	p.E231K	QKRQKIRLLQQRKVADVSQFKDLPD[p.E231K]KIPLPLVIGTKVTARLRGVHDGLFTG	SQFKDLPDK,LPDKIPLPL,KDLPDKIPL,VSQFKDLPDK,SQFKDLPDKI,FKDLPDKIPL,LPDKIPLPLV	CESC
LINGO2	c.1228C>A	p.P410T	PDTIRERSFKDFHSTALSFYFTCKK[p.P410T]TKIREKKLQHLLVDEGQTVQLECSAD	KTKIREKKL,FTCKKTKIR,FYFTCKKTKI,SFYFTCKKTK,TCKKTKIREK,YFTCKKTKIR	HNSC
LIPJ	c.707C>A	p.P236Q	GSKLCPLQIFDKICLNILFMMFGYD[p.P236Q]QKNLNMSRLDVYFSHNPAGTSVQNML	FMMFGYDQK,DQKNLNMSR,MMFGYDQKN,MMFGYDQKNL,LFMMFGYDQK,FGYDQKNLNM	LUAD
LLGL2	c.2864_2865insG	p.P955fs	PRCLVDSAETKNHRPGNGAGPKKAP[p.P955fs]EPSQELRDSE*	KKAPEPSQEL	BLCA
LMLN	c.595G>T	p.G199C	PVIVPEEHLQQCRVYRGGKWPHGAV[p.G199C]CVPDQEGISDADFVLYVGALATERCS	GKWPHGAVC,GKWPHGAVCV	LUSC
LMX1B	c.844_846delCAG	p.Q285del	RHQQQQEQQNSQRLGQGEPGPGQGL[p.Q285del]QEVLSSRMEGMMASYTPLAPPQQQIVAM	LQEVLSSRM,GLQEVLSSRM	THCA

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LOC100132247	c.1594A>C	p.T532P	ADDNLKTPSERQLTALPPSADDNIK[p.T532P]PPAERLRGPLPPSADDNLKTPSERQL	DNIKPPAER,NIKPPAERLR,PPAERLRGPL	LIHC
LOC151174	c.268C>T	p.P90S	AEGIAMLLGTAGPSRLPAAPDASQA[p.P90S]SLRSPWALSVAAALCSPVSCHPCGRH	SLRSPWALS,APDASQASL,SQASLRSPW,ASLRSPWAL,SLRSPWALSV,SQASLRSPWA,ASQASLRSPW	CESC
LOC401296	c.430C>A	p.L144M	CVLAPGSGSRPTPHIVYSVPAARTC[p.L144M]MGAPGSLSPCHLCVHICAHTYSGTPV	AARTCMGAPG,RTCMGAPGSL,VPAARTCMGA,YSVPAARTCM	TGCT
LOC554223	c.438_458delGCGGGCGCCGTGGATGGAGCA	p.RAPWMEQ147del	LSVGDVDDTQCVRLDSDATSPRMEP[p.RAPWMEQ147del]EGPEYWEEETGTAKAKAQFYRVNLRTLSGYYNQSEA*	RMEPEGPEY,RMEPEGPEYW	PRAD
LOC649330	c.278G>A	p.G93E	AGEDGRMIASQVVDINLAAEPKVNR[p.G93E]ENAGVKRSAAEMYGSSFDLDYGFQRD	KVNRENAGV,VNRENAGVK,KVNRENAGVK,RENAGVKRSA	SKCM
LPHN2	c.2716T>A	p.F906I	EFIFLIGIDKTKYAIACPIFAGLLH[p.F906I]IFFLAAFAWMCLEGVQLYLMLVEVFE	GLLHIFFLA,LLHIFFLAA,HIFFLAAFA,IFAGLLHIF,IFFLAAFAW,LHIFFLAAF,FAGLLHIFF,GLLHIFFLAA,IFAGLLHIFF,IFFLAAFAWM,CPIFAGLLHI,LLHIFFLAAF,PIFAGLLHIF,HIFFLAAFAW	TGCT
LPHN3	c.2220G>T	p.E740D	FPENMGHGSTIQLSANTLKQNGRNG[p.E740D]DIRVAFVLYNNLGPYLSTENASMKLG	DIRVAFVLY,KQNGRNGDI,RNGDIRVAF,GDIRVAFVL,GRNGDIRVAF,GDIRVAFVLY	LUAD
LPHN3	c.2477G>A	p.R826H	VFTVKHIKQSEENFNPNCSFWSYSK[p.R826H]HTMTGYWSTQGCRLLTTNKTHTTCSC	YSKHTMTGY,CSFWSYSKH,HTMTGYWST,FWSYSKHTM,SKHTMTGYW,SFWSYSKHTM,SYSKHTMTGY,WSYSKHTMTG,YSKHTMTGYW	PRAD
LPHN3	c.3548G>A	p.R1183Q	SGSRTPGRYSTGSQSRIRRMWNDTV[p.R1183Q]QKQSESSFITGDINSSASLNREGLLN	RMWNDTVQK,VQKQSESSF,TVQKQSESSF,RMWNDTVQKQ,VQKQSESSFI	CRC
LPIN1	c.2921C>T	p.S974L	SDTFSNFTFWREPLPPFENQDIHSA[p.S974L]LA*	FENQDIHSAL	BLCA
LPPR2	c.556G>T	p.A186S	TDQGACAGSPSLVAAARRAFPCKDA[p.A186S]SLCAYAVTYTAMYVTLVFRVKGSRLV	SLCAYAVTY,DASLCAYAV,CKDASLCAY,SLCAYAVTYT,RAFPCKDASL,ASLCAYAVTY,FPCKDASLCA,KDASLCAYAV	ACC
LPPR4	c.1579C>A	p.R527S	LKIQPGAVPGCNNSMPGGPRVSIQS[p.R527S]SPGSSQLVHIPEETQENISTSPKSSS	RVSIQSSPG,IQSSPGSSQ,QSSPGSSQLV,IQSSPGSSQL,SPGSSQLVHI	LUAD
LRBA	c.6307G>A	p.E2103K	VSLSTPAQLVAPSVVVKGTLSVTSS[p.E2103K]KLYFEVDEEDPNFKKIDPKILAYTEG	LSVTSSKLY,TLSVTSSKL,GTLSVTSSK,TSSKLYFEV,SVTSSKLYF,VTSSKLYFEV,KGTLSVTSSK,TLSVTSSKLY,LSVTSSKLYF	UCEC
LRCH2	c.2150A>G	p.D717G	SIHVPSPAVPKLSMAKCRRNVENFL[p.D717G]GACKKLGVSQERLCLPHHILEERGLV	FLGACKKLGV	KIRC
LRFN5	c.396C>A	p.N132K	NSNRLTKITNDMFSGLSNLHHLILN[p.N132K]KNQLTLISSTAFDDVFALEELDLSYN	ILNKNQLTL,NLHHLILNK,ILNKNQLTLI,SNLHHLILNK,LILNKNQLTL	LUAD
LRIG1	c.70C>G	p.L24V	MARPVRGGLGAPRRSPCLLLLWL[p.L24V]VLLRLEPVTAAAGPRAPCAAACTCAG	LLLLWLVLL,LLWLVLLRL,LVLLRLEPV,LLLWLVLLR,LLLWLVLLRL,WLVLLRLEPV,SPCLLLLWLV	ACC
LRIG1	c.76C>G	p.L26V	MARPVRGGLGAPRRSPCLLLLWLLL[p.L26V]VRLEPVTAAAGPRAPCAAACTCAGDS	LLLLWLLLV,LLWLLLVRL,LLLVRLEPV,VRLEPVTAA,CLLLLWLLLV,LLLWLLLVRL,WLLLVRLEPV	ACC
LRP1	c.3172C>A	p.P1058T	TCDGDNDCGDYSDETHANCTNQATR[p.P1058T]TPGGCHTDEFQCRLDGLCIPLRWRCD	ATRTPGGCH,ATRTPGGCHT,TPGGCHTDEF	KIRP,PRAD
LRP1	c.4462_4463insG	p.G1488fs	GSGHMEVLRGHEFLSHPFAVTLYGG[p.G1488fs]GGLLD*	TLYGGGGLL	STAD

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LRP1	c.4462delG	p.G1488fs	GSGHMEVLRGHEFLSHPFAVTLYGG[p.G1488fs]RSTGLTGEQTHWLRPTSGPATMSPWYRGPTPSPLTCRCTTPPASPWLPIPVRPMGARAPAPTCVSSTTTGPCPAPAPTS*	WLRPTSGPA,PVRPMGARA,FAVTLYGGR,PATMSPWYR,TTPPASPWL,TTGPCPAPA,RPTSGPATM,PPASPWLPI,RPMGARAPA,YRGPTPSPL,CTTPPASPW,WLPIPVRPM,GPATMSPWY,TLYGGRSTGL,GLTGEQTHWL,TMSPWYRGPT,WYRGPTPSPL,HWLRPTSGPA,GARAPAPTCV,SGPATMSPWY,PFAVTLYGGR,LTGEQTHWLR,CTTPPASPWL,TTTGPCPAPA,SPWYRGPTPS,TPPASPWLPI,LPIPVRPMGA,IPVRPMGARA,RPMGARAPAP,APAPTCVSST,WLRPTSGPAT,LRPTSGPATM,TSGPATMSPW,RCTTPPASPW,GEQTHWLRPT	STAD
LRP10	c.15_17delCCT	p.L11del	MLLATLLLLL[p.L11del]GGALAHPDRIIFPNHACEDPPAVLLEVQ	TLLLLLGGA	PRAD
LRP11	c.275C>G	p.P92R	QQERPQEELELELRAGGGPQEDCPG[p.P92R]RGSGGYSAMPDAIIRTKDSLAAGASF	RGSGGYSAM,CPGRGSGGY,GRGSGGYSAM	ACC
LRP12	c.928G>T	p.G310C	CTWLIDTGDHRKVILRFTDFKLDGT[p.G310C]CYGDYVKIYDGLEENPHKLLRVLTAF	GTCYGDYVK,KLDGTCYGDY,TDFKLDGTCY,TCYGDYVKIY	TGCT
LRP1B	c.10687G>T	p.G3563C	FDCADGSDERNCETSCSKDQFRCSN[p.G3563C]CQCIPAKWKCDGHEDCKYGEDEKSCE	CSNCQCIPAK	LUAD
LRP1B	c.4174C>T	p.L1392F	SLRTTLIAGAMEHPRAIALDPRYGI[p.L1392F]FFWTDWDANFPRIESASMSGAGRKTI	RYGIFFWTD,ALDPRYGIF,YGIFFWTDW,DPRYGIFFW,GIFFWTDWDA,IALDPRYGIF,RYGIFFWTDW,FFWTDWDANF,ALDPRYGIFF	UCS
LRP2	c.12117G>C	p.M4039I	FGTCPQHCRNTKGSYECVCADGFTS[p.M4039I]ISDRPGKRCAAEGSSPLLLLPDNVRI	TSISDRPGK,DGFTSISDR,SISDRPGKR,FTSISDRPGK,TSISDRPGKR	LUAD
LRP2	c.1547C>T	p.A516V	IDMVNLDGSYRVTLITENLGHPRGI[p.A516V]VVDPTVGYLFFSDWESLSGEPKLERA	IVVDPTVGY,LGHPRGIVV,VVDPTVGYLF,IVVDPTVGYL,GIVVDPTVGY,HPRGIVVDPT	LUSC
LRP2	c.2210C>T	p.S737L	IFSSQVAIRGIPFTLSTQEDVMVPV[p.S737L]LGNPSFFVGIDFDAQDSTIFFSDMSK	VLGNPSFFV,VPVLGNPSF,QEDVMVPVL,VPVLGNPSFF,MVPVLGNPSF,TQEDVMVPVL	CRC
LRP2	c.7295G>T	p.R2432I	NHSPPFQTINVERTVMSLDYDSVSD[p.R2432I]IIYFTQNLASGVGQISYATLSSGIHT	SVSDIIYFT,IIYFTQNLA,DIIYFTQNL,LDYDSVSDI,YDSVSDIIY,DSVSDIIYFT,DIIYFTQNLA,LDYDSVSDII,YDSVSDIIYF,SDIIYFTQNL	UCEC
LRP2	c.9127C>T	p.R3043C	CGDYSDERGCLYQTCQQNQFTCQNG[p.R3043C]CCISKTFVCDEDNDCGDGSDELMHLC	CQNGCCISK	CRC
LRP5	c.4825T>C	p.S1609P	LSAEDSCPPSPATERSYFHLFPPPP[p.S1609P]PPCTDSS*	HLFPPPPPPC	PRAD
LRP6	c.2024G>A	p.R675Q	NNNNVAIPLTGVKEASALDFDVTDN[p.R675Q]QIYWTDISLKTISRAFMNGSALEHVV	FDVTDNQIY,QIYWTDISL,NQIYWTDISL,QIYWTDISLK	CRC
LRRC16A	c.679G>A	p.D227N	LDHRDLIPIIAALEYNQWFTKLSSK[p.D227N]NLKLSTDVCEQILRVVSRSNRLEELV	KLSSKNLKL,FTKLSSKNLK,TKLSSKNLKL	BLCA
LRRC16B	c.2359C>T	p.R787W	AVDKELQVILESMVSLTQELCPVAM[p.R787W]WVAEGHNKMLSNVAERVTVPRNFIRG	ELCPVAMWV,WVAEGHNKM,QELCPVAMW,AMWVAEGHNK,MWVAEGHNKM,ELCPVAMWVA,WVAEGHNKML,QELCPVAMWV	PRAD
LRRC18	c.652C>T	p.R218W	RRLENLYVVEEKDLCAACLRKCQNA[p.R218W]WDNLNRIKNMATTTPRKTIFPNLISP	NAWDNLNRI,CLRKCQNAW,RKCQNAWDNL	CRC
LRRC31	c.68A>C	p.K23T	RKKTSSEGETKPQTSTVNKFLR[p.K23T]ASNAESRKEDNDLKTSDSQPSDWIQK	FLRASNAES,RASNAESRK,STVNKFLRA,FLRASNAESR	CRC
LRRC37A2	c.305C>G	p.T102S	ELEQPHTQQGPEKLAGNAIYTKPSF[p.T102S]SQEHKAAVSVLTPFSKGAPSTSSPAK	FSQEHKAAV,SQEHKAAVSV	PRAD
LRRC37A3	c.1217C>A	p.A406D	ETPGQPPEHHEVTVSPPGHHQTHHL[p.A406D]DSPSVSVKPPDVQLTIAAEPSAEVGT	HLDSPSVSV,HLDSPSVSVK,QTHHLDSPSV,HQTHHLDSPS	CESC

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LRRC43	c.1674delC	p.D558fs	KEPAKEWKVLKKKKEPPKELRQDPP[p.D558fs]SSRCWAGAW*	SSRCWAGAW,ELRQDPPSSR,RQDPPSSRCW	STAD
LRRC7	c.4166G>A	p.R1389H	VPPDTITKKAGSHIQTLMGSQSLQH[p.R1389H]HSREQQPYEGNINKVTIQQFQSPLPI	HSREQQPYE,SQSLQHHSR,HHSREQQPY,LMGSQSLQHH,QHHSREQQPY	CRC
LRRCC1	c.17C>T	p.A6V	MEAAA[p.A6V]VVVAAEAEVENEDGDSSCGDVCFMDK	VVVAAEAEV,EAAAVVVAA,MEAAAVVVA,AVVVAAEAEV,MEAAAVVVAA	TGCT
LRRIQ1	c.2375G>T	p.W792L	RKRPVKCPANMTPALDKLEILRCGP[p.W792L]LDTLQQVTTVTFQDLPGCVLSTLAEC	LEILRCGPL,GPLDTLQQV,ILRCGPLDTL	LUAD
LRRIQ3	c.732_733insA	p.K244fs	LIVQRWIRGFLVRKNLSPVFFHKKK[p.K244fs]TAGKNY*	KKKTAGKNY,FFHKKKTAGK,HKKKTAGKNY	PRAD
LRRTM4	c.728C>A	p.S243Y	SKINFAHFPRLFNLRSIYLQWNRIR[p.S243Y]YISQGLTWTWSSLHNLDLSGNDIQGI	LQWNRIRYI,RIRYISQGL,YISQGLTWT,RYISQGLTW,YLQWNRIRY,YLQWNRIRYI,IYLQWNRIRY,YISQGLTWTW,RIRYISQGLT,LQWNRIRYIS,NRIRYISQGL,IRYISQGLTW	LUAD
LRTM2	c.416C>T	p.S139L	DLTNLTELQLRNNSIRTLDRDLLRH[p.S139L]LPLLRHLDLSINGLAQLPPGLFDGLL	LLRHLPLLR,LPLLRHLDL,DLLRHLPLL,RDLLRHLPL,RHLPLLRHL,DLLRHLPLLR,RDLLRHLPLL,LRHLPLLRHL	BLCA
LRTM2	c.526C>G	p.L176V	GLAQLPPGLFDGLLALRSLSLRSNR[p.L176V]VQNLDRLTFEPLANLQLLQVGDNPWE	SLSLRSNRV,VQNLDRLTF,LRSNRVQNL,SLRSNRVQNL,RSNRVQNLDR,RVQNLDRLTF,RSLSLRSNRV	CESC
LSG1	c.1550G>T	p.R517L	ITPREDEDPHRPPTSEELLTAYGYM[p.R517L]LGFMTAHGQPDQPRSARYILKDYVSG	LLTAYGYML,TAYGYMLGF,AYGYMLGFM,GYMLGFMTA,YMLGFMTAH,LTAYGYMLGF,YMLGFMTAHG,TAYGYMLGFM,YGYMLGFMTA	LUSC
LTA4H	c.319T>C	p.F107L	YKGSPMEISLPIALSKNQEIVIEIS[p.F107L]LETSPKSSALQWLTPEQTSGKEHPYL	EISLETSPK,QEIVIEISL,LETSPKSSA,NQEIVIEISL,LETSPKSSAL	KIRC
LTB4R	c.217T>C	p.F73L	QKRSVTALMVLNLALADLAVLLTAP[p.F73L]LFLHFLAQGTWSFGLAGCRLCHYVCG	VLLTAPLFL,LTAPLFLHF,LAVLLTAPL,TAPLFLHFL,AVLLTAPLF,LTAPLFLHFL,DLAVLLTAPL,LLTAPLFLHF,TAPLFLHFLA,LAVLLTAPLF	TGCT
LUC7L3	c.442T>A	p.S148T	GKNEEKIQVLTDKIDVLLQQIEELG[p.S148T]TEGKVEEAQGMMKLVEQLKEERELLR	IEELGTEGKV	TGCT
LUM	c.929G>T	p.R310L	QLEKFDIKSFCKILGPLSYSKIKHL[p.R310L]LLDGNRISETSLPPDMYECLRVANEV	SYSKIKHLL,YSKIKHLLL,SYSKIKHLLL,LSYSKIKHLL	LUSC
LUM	c.988C>T	p.R330C	KIKHLRLDGNRISETSLPPDMYECL[p.R330C]CVANEVTLN*	DMYECLCVA,YECLCVANEV	GBM
LY9	c.205A>C	p.I69L	RASGKDSAPTVVSGILGGSVTLPLN[p.I69L]LSVDTEIENVIWIGPKNALAFARPKE	VTLPLNLSV,SVTLPLNLSV	BRCA
LYPD4	c.191C>A	p.T64K	AVAFHNWKWLLMRNMVCKLQEGCEE[p.T64K]KLVFIETGTARGVVGFKGCSSSSSYP	EEKLVFIET,KLQEGCEEKL,KLVFIETGTA,QEGCEEKLVF,CEEKLVFIET	TGCT
LYST	c.2130G>T	p.Q710H	DLLWKWDALKAYQNFVFEEDRLHSI[p.Q710H]HIANHICNLIQKGNIVVQWKLYNYIF	HIANHICNL,HSIHIANHI,EEDRLHSIH,HIANHICNLI,RLHSIHIANH,FEEDRLHSIH,IHIANHICNL,EEDRLHSIHI	KIRC
LZTS1	c.1294_1341delAGGACCCAGGACCTGGAGGGCGCCCTGCGCACCAAGGGCCTGGAGCTG	p.RTQDLEGALRTKGLEL432del	AKASEILGLKAQLKDTRGKLEGLEL[p.RTQDLEGALRTKGLEL432del]EVCENELQRKKNEAELLREKVNLLEQELQELRAQAALARDMGPPTFPEDVPALQRELERLRAELREERQGHDQ	KLEGLELEV,GKLEGLELEV	PAAD
LZTS2	c.298delC	p.P100fs	VPPRKAVPVTSFTYINEDFRTESPP[p.P100fs]AQAVMLRMPESSGHTMPTSAAHHQSSSLSLESWRRTWRRS*	SSLSLESWR,HTMPTSAAH,SWRRTWRRS,ESWRRTWRR,ESSGHTMPT,SPPAQAVML,MPESSGHTM,AAHHQSSSL,TESPPAQAV,HHQSSSLSL,SSSLSLESW,SLESWRRTW,RMPESSGHTM,SSSLSLESWR,SSLSLESWRR,MLRMPESSGH,HTMPTSAAHH,SLESWRRTWR,SAAHHQSSSL,TESPPAQAVM,AHHQSSSLSL,HQSSSLSLES,QSSSLSLESW,LSLESWRRTW,MPTSAAHHQS	CRC
MAEL	c.1033C>T	p.R345C	EAHVPLQDYEASNSVTPKMVVLDAG[p.R345C]CYQKLRVGSSGFSHFNSSNEEQRSNT	VLDAGCYQK,MVVLDAGCY,DAGCYQKLR,VLDAGCYQKL,VVLDAGCYQK,KMVVLDAGCY	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
MAF	c.158delG	p.G53fs	MKFEVKKEPVETDRIISQCGRLIAG[p.G53fs]ARCPPPP*	CGRLIAGAR,SQCGRLIAGA,RLIAGARCPP	CLL
MAGEC1	c.1826T>A	p.L609H	PQGEDSLSPHYFPQSPPQGEDSMSP[p.L609H]HYFPQSPLQGEEFQSSLQSPVSICSS	GEDSMSPHY,SMSPHYFPQ,SMSPHYFPQS,QGEDSMSPHY,SPHYFPQSPL,GEDSMSPHYF	CLL
MAGEC1	c.714_716delCCC	p.P239del	FQSSPERTQSTFEGFAQSPLQIPVS[p.P239del]SSSSTLLSLFQSFSERTQSTFEGFAQSS	IPVSSSSST,VSSSSSTLL,IPVSSSSSTL	KIRC
MAGEE1	c.1138G>A	p.V380M	SVLPIPGEGLSTSVPPTASDGSDTS[p.V380M]MPPTPGEGASTLVQPTAPDGPGSSVL	ASDGSDTSM,SMPPTPGEGA,TASDGSDTSM	CRC
MAGEE2	c.133delC	p.Q45fs	GDGRGEIQATNASGSPTSMLVVDAP[p.Q45fs]SALRRQSTLSVSTLPRPFRTRMTWRS*	MLVVDAPSA,LVVDAPSAL,TLSVSTLPR,VVDAPSALR,VSTLPRPFR,TLPRPFRTR,PFRTRMTWR,SALRRQSTL,LPRPFRTRM,RPFRTRMTW,LRRQSTLSV,RQSTLSVST,QSTLSVSTL,SVSTLPRPF,SMLVVDAPSA,MLVVDAPSAL,ALRRQSTLSV,RQSTLSVSTL,STLSVSTLPR,LVVDAPSALR,VVDAPSALRR,SVSTLPRPFR,STLPRPFRTR,RPFRTRMTWR,APSALRRQST,LPRPFRTRMT,LSVSTLPRPF,RRQSTLSVST	STAD
MAGI1	c.3467G>T	p.G1156V	KGFGFSLRGGREYNMDLYVLRLAED[p.G1156V]VPAERCGKMRIGDEILEINGETTKNM	YVLRLAEDV,VPAERCGKM,RLAEDVPAER	LUAD
MAGI1	c.3592C>T	p.R1198C	INGETTKNMKHSRAIELIKNGGRRV[p.R1198C]CLFLKRGDGSVPEYDPSSDRHGPATG	GGRRVCLFL,GRRVCLFLK,GGRRVCLFLK,IKNGGRRVCL,KNGGRRVCLF	CRC
MAGI2	c.1348C>A	p.L450M	LSTTLKKSNMGFGFTIIGGDEPDEF[p.L450M]MQVKSVIPDGPAAQDGKMETGDVIVY	EFMQVKSVI,MQVKSVIPD,DEFMQVKSV,MQVKSVIPDG,DEFMQVKSVI	UCEC
MAGI2	c.3130C>A	p.P1044T	PSSEKQSPMAQQSPLAQQSPLAQPS[p.P1044T]TATPNSPIAQPAPPQPLQLQGHENSY	STATPNSPI,STATPNSPIA,SPLAQPSTAT,QQSPLAQPST	LUAD
MAML2	c.1771C>A	p.Q591K	QANQQMPSVLPSQNKPSLLHYTQQQ[p.Q591K]KQQQQQQQQQQQQQQQQQQQQQQQQQ	LLHYTQQQK,SLLHYTQQQK	KIRP
MAMLD1	c.1715A>T	p.Q572L	YLQQPTPTQASSATASSTATATLQL[p.Q572L]LQQQQQQQQQPDHSSFLLQQMMQQPQ	STATATLQLL	TGCT,UCS
MAMSTR	c.484_485insC	p.P162fs	QPHPRMKPSPLTPCPPGVPSPSPPP[p.P162fs]TQVGTSDP*	SPSPPPTQV	STAD
MAN1C1	c.1291_1292insG	p.G431fs	MEAKNMYYEALEAIETYLLNVSPGG[p.G431fs]ADLHCRVARGDSGPQDGAPGLFLRGHDRPWRRGCQGRKEGPLPRARSPDHQDVSRVIRPLRHQTWA*	LLNVSPGGA,RGHDRPWRR,VSRVIRPLR,DGAPGLFLR,DVSRVIRPL,GPQDGAPGL,RPWRRGCQG,RPLRHQTWA,FLRGHDRPW,YLLNVSPGGA,LFLRGHDRPW,QGRKEGPLPR,RARSPDHQDV,VSRVIRPLRH,FLRGHDRPWR,DVSRVIRPLR,VIRPLRHQTW	STAD
MAP1A	c.6187delC	p.P2063fs	GPTVPPRPEPGPSMEPSLTPPAVPP[p.P2063fs]VLLS*	LTPPAVPPV,SLTPPAVPPV	STAD
MAP1B	c.6138G>T	p.E2046D	EGYSYETSTKTTRTPDTSTYCYETA[p.E2046D]DKITRTPQASTYSYETSDLCYTAEKK	ETADKITRT,STYCYETADK,TYCYETADKI	CRC
MAP1S	c.1232C>G	p.S411C	EKMGVGRLDMYVLHPPSAGAERTLA[p.S411C]CVCALLVWHPAGPGEKVVRVLFPGCT	RTLACVCAL,TLACVCALL,AERTLACVC,RTLACVCALL,TLACVCALLV,LACVCALLVW,AERTLACVCA	ACC
MAP2	c.1590G>T	p.K530N	QAVTDSAMTSKTLEKAMTEPSALIE[p.K530N]NSSIQELFEMRVDDKDKIEGVGAATS	SALIENSSI,IENSSIQEL,IENSSIQELF	CRC
MAP2	c.4414_4415insA	p.K1472fs	EPSTVSRDEVRRKKAVYKKAELAKK[p.K1472fs]NRSSGPLSLQEIHFKTCYQIY*	SLQEIHFKT,LSLQEIHFK,KNRSSGPLS,HFKTCYQIY,KKNRSSGPL,NRSSGPLSL,QEIHFKTCY,IHFKTCYQI,KNRSSGPLSL,IHFKTCYQIY,EIHFKTCYQI,AKKNRSSGPL,LQEIHFKTCY	STAD
MAP2K1	c.171G>C	p.K57N	ALQKKLEELELDEQQRKRLEAFLTQ[p.K57N]NQKVGELKDDDFEKISELGAGNGGVV	TQNQKVGEL,TQNQKVGELK,EAFLTQNQKV	CLL

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MAP2K1	c.171G>T	p.K57N	ALQKKLEELELDEQQRKRLEAFLTQ[p.K57N]NQKVGELKDDDFEKISELGAGNGGVV	TQNQKVGEL,TQNQKVGELK,EAFLTQNQKV	LUAD
MAP2K1	c.370C>T	p.P124S	IHLEIKPAIRNQIIRELQVLHECNS[p.P124S]SYIVGFYGAFYSDGEISICMEHMDGG	NSSYIVGFY,SYIVGFYGA,VLHECNSSY,HECNSSYIV,CNSSYIVGF,CNSSYIVGFY,VLHECNSSYI,SYIVGFYGAF,SSYIVGFYGA,QVLHECNSSY	SKCM
MAP2K4	c.551C>T	p.S184L	PYIVQFYGALFREGDCWICMELMST[p.S184L]LFDKFYKYVYSVLDDVIPEEILGKIT	MSTLFDKFY,STLFDKFYK,TLFDKFYKY,ELMSTLFDK,LMSTLFDKF,ICMELMSTL,CMELMSTLF,LMSTLFDKFY,STLFDKFYKY,LFDKFYKYV,TLFDKFYKYV,WICMELMSTL,MSTLFDKFYK,ICMELMSTLF,ELMSTLFDKF	BRCA
MAP2K4	c.752G>T	p.S251I	IHRDIKPSNILLDRSGNIKLCDFGI[p.S251I]IGQLVDSIAKTRDAGCRPYMAPERID	IIGQLVDSI,IKLCDFGII,GIIGQLVDSI	BRCA
MAP2K4	c.783_784delAA	p.T261fs	DRSGNIKLCDFGISGQLVDSIAKTR[p.T261fs]CWL*	SIAKTRCWL	BRCA
MAP2K4	c.860G>A	p.R287H	RDAGCRPYMAPERIDPSASRQGYDV[p.R287H]HSDVWSLGITLYELATGRFPYPKWNS	DVHSDVWSL,RQGYDVHSDV,QGYDVHSDVW,YDVHSDVWSL	CRC
MAP2K5	c.1334A>G	p.Q445R	VQFNDGNAAVVSMWVCRALEERRSQ[p.Q445R]RGPP*	RALEERRSQR	KIRC
MAP3K1	c.2281_2284delATAG	p.I761fs	LNCILGNQTESNNWQELLGRLCLID[p.I761fs]CCWNFLLNFILILSVLMFHKLSLLKSGIRSCCPS*	LIDCCWNFL,FLLNFILIL,FILILSVLM,VLMFHKLSL,LMFHKLSLL,KLSLLKSGI,ILSVLMFHK,MFHKLSLLK,CLIDCCWNF,CWNFLLNFI,NFLLNFILI,ILILSVLMF,CCWNFLLNF,WNFLLNFIL,LSVLMFHKL,CLIDCCWNFL,LIDCCWNFLL,FLLNFILILS,LLNFILILSV,ILSVLMFHKL,VLMFHKLSLL,LILSVLMFHK,LMFHKLSLLK,CWNFLLNFIL,NFLLNFILIL,NFILILSVLM,SVLMFHKLSL,LNFILILSVL,FILILSVLMF,HKLSLLKSGI	BRCA
MAP3K1	c.4036_4038delGTT	p.V1346del	LFIEWMAGGSVAHLLSKYGAFKESV[p.V1346del]INYTEQLLRGLSYLHENQIIHRDVKGAN	SVINYTEQL,AFKESVINY,SVINYTEQLL,KYGAFKESVI,GAFKESVINY,ESVINYTEQL	BRCA
MAP3K1	c.4150_4151insT	p.L1384fs	LHENQIIHRDVKGANLLIDSTGQRL[p.L1384fs]KNCRFWSCSQVGIKRNWCRRVSGTITGDNCIYGT*	WSCSQVGIK,RLKNCRFWS,GIKRNWCRR,VGIKRNWCR,GQRLKNCRF,CRFWSCSQV,SQVGIKRNW,LIDSTGQRLK,RFWSCSQVGI,RLKNCRFWSC,GIKRNWCRRV,GTITGDNCIY,STGQRLKNCR,QVGIKRNWCR,VGIKRNWCRR,GQRLKNCRFW	BRCA
MAP3K1	c.953_954insA	p.L318fs	DGFSPYSPEETNRRVNKVMRARLYL[p.L318fs]TAADRA*	VMRARLYLT,RLYLTAADR,RARLYLTAA,MRARLYLTA,VMRARLYLTA,RLYLTAADRA,KVMRARLYLT,RARLYLTAAD,MRARLYLTAA	BRCA
MAP3K1	c.971C>T	p.P324L	YSPEETNRRVNKVMRARLYLLQQIG[p.P324L]LNSFLIGGDSPDNKYRVFIGPQNCSC	QQIGLNSFL,LYLLQQIGL,LQQIGLNSF,RLYLLQQIGL,QQIGLNSFLI,LLQQIGLNSF,LQQIGLNSFL	GBM
MAP3K12	c.1345_1347delAGG	p.R449del	KLHFEKIKSEGTCLHRLEEELVMRR[p.R449del]EELRHALDIREHYERKLERANNLYMELN	LVMRREELR,ELVMRREEL,ELVMRREELR,MRREELRHAL,EELVMRREEL	STAD
MAP3K4	c.824G>A	p.R275Q	ENTSGFWLNRSNELIWLELQAWHAG[p.R275Q]QTINDQDFFLYTARQAIPDIINEILT	LQAWHAGQT,QAWHAGQTI,GQTINDQDF,LQAWHAGQTI,QTINDQDFFL,GQTINDQDFF,LELQAWHAGQ	CRC
MAP3K7	c.1570G>C	p.E524Q	AYLTLDHQLQPLAPCPNSKESMAVF[p.E524Q]QQHCKMAQEYMKVQTEIALLLQRKQE	MAVFQQHCK,AVFQQHCKM,SMAVFQQHCK,QQHCKMAQEY,MAVFQQHCKM,KESMAVFQQH	HNSC
MAP4K2	c.1021C>G	p.R341G	SRGQHGPAERTPSEIQFHQVKFGAP[p.R341G]GRKETDPLNEPWEEEWTLLGKEELSG	QVKFGAPGR,HQVKFGAPG,QVKFGAPGRK,HQVKFGAPGR,APGRKETDPL	TGCT
MAP4K3	c.1970delC	p.P657fs	LFDYARQMQKLPVAIPAHKLPDRIL[p.P657fs]QGNFLYQQKSLKPNGARSVVL*	RILQGNFLY,FLYQQKSLK,KSLKPNGAR,KPNGARSVV,YQQKSLKPN,SLKPNGARSV,NFLYQQKSLK,KPNGARSVVL,GNFLYQQKSL,YQQKSLKPNG,LPDRILQGNF	HNSC
MAP7D1	c.239_240insC	p.A80fs	ATSSKQLPLEPESPSGQVGPRPAPP[p.A80fs]AGRVPFL*	RPAPPAGRV,APPAGRVPF,PPAGRVPFL,RPAPPAGRVP,APPAGRVPFL	STAD
MAP7D2	c.1459C>T	p.R487C	ERLEKEEQDRLEREELKRKAEEERL[p.R487C]CLEEEARKQEEERKRQEEEKKKQEGE	RKAEEERLCL,EERLCLEEEA	CRC

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MAP7D3	c.922delC	p.Q308fs	PQTKVEESPLEKVETPPKASVDAPP[p.Q308fs]R*	KASVDAPPR	STAD
MAP9	c.1455G>T	p.K485N	QKKAAKREEALASFEAWKAMKEKEA[p.K485N]NKIAAKKRLEEKNKKKTEEENAARKG	AMKEKEANK,KEANKIAAK,KEKEANKIA,AMKEKEANKI,KAMKEKEANK,EANKIAAKKR,KEKEANKIAA	HNSC
MAPK1	c.964G>A	p.E322K	NPHKRIEVEQALAHPYLEQYYDPSD[p.E322K]KPIAEAPFKFDMELDDLPKEKLKELI	YYDPSDKPI,KPIAEAPFK,QYYDPSDKPI,SDKPIAEAPF,KPIAEAPFKF	CESC,HNSC
MAPK13	c.943G>A	p.E315K	ELDVDKRLTAAQALTHPFFEPFRDP[p.E315K]KEETEAQQPFDDSLEHEKLTVDEWKQ	KEETEAQQPF	BRCA
MAPK15	c.1533delG	p.Q511fs	PPRLPPEARPGRRMFSTSALQGAQG[p.Q511fs]VPGLCLEATPKPTGLSATRHWATCPCWRGTMCEPPYSLHLALCSCPSPFPRPLSSLLHPLALPALPGPLKFQGACPGLLGGADEGPAPAPLTSSNKVMSAPN	TMCEPPYSL,PLSSLLHPL,LLHPLALPA,GLSATRHWA,SLHLALCSC,ALPALPGPL,GLCLEATPK,CSCPSPFPR,KFQGACPGL,RGTMCEPPY,HWATCPCWR,EPPYSLHLA,TPKPTGLSA,PPYSLHLAL,CPSPFPRPL,SPFPRPLSS,FPRPLSSLL,APLTSSNKV,SSLLHPLAL,ALCSCPSPF,LQGAQGVPG,AQGVPGLCL,RHWATCPCW,LKFQGACPG,FQGACPGLL,DEGPAPAPL,CEPPYSLHL,GTMCEPPYSL,SLLHPLALPA,LLHPLALPAL,GLSATRHWAT,ALPALPGPLK,PFPRPLSSLL,KFQGACPGLL,ATRHWATCPC,TSALQGAQGV,TPKPTGLSAT,EPPYSLHLAL,SPFPRPLSSL,FPRPLSSLLH,RPLSSLLHPL,LPALPGPLKF,APLTSSNKVM,LALCSCPSPF,LQGAQGVPGL,LEATPKPTGL,WRGTMCEPPY,LSSLLHPLAL,LALPALPGPL,LKFQGACPGL,CEPPYSLHLA	STAD
MAPK4	c.298G>A	p.V100M	DNIVKVYEVLGPKGTDLQGELFKFS[p.V100M]MAYIVQEYMETDLARLLEQGTLAEEH	LFKFSMAYI,ELFKFSMAY,SMAYIVQEY,MAYIVQEYM,FKFSMAYIV,GELFKFSMA,FSMAYIVQEY,ELFKFSMAYI,SMAYIVQEYM,LQGELFKFSM,GELFKFSMAY,FKFSMAYIVQ	BRCA
MAPK7	c.1502C>A	p.A501D	KAALKAALLKSLRSRLRDGPSAPLE[p.A501D]DPEPRKPVTAQERQREREEKRRRRQE	LEDPEPRKPV	KIRP,TGCT
MAPK8IP1	c.651_652insCC	p.L217fs	SSSPLKTGEQTPPHEHICLSDELPP[p.L217fs]PRAAPPPPQIEAPPPTALAAAAQPPRWHLRVVPLLPRLGVGATRIETESTTRPMCD*	RVVPLLPRL,LLPRLGVGA,RLGVGATRI,RWHLRVVPL,RAAPPPPQI,AQPPRWHLR,LAAAAQPPR,EAPPPTALA,APPPTALAA,PPRWHLRVV,VPLLPRLGV,LPRLGVGAT,IEAPPPTAL,AAQPPRWHL,WHLRVVPLL,DELPPPRAA,ETESTTRPM,QPPRWHLRV,ALAAAAQPPR,HLRVVPLLPR,AAQPPRWHLR,RWHLRVVPLL,CLSDELPPPR,EAPPPTALAA,APPPTALAAA,IEAPPPTALA,LAAAAQPPRW,AAAQPPRWHL,LRVVPLLPRL,IETESTTRPM,DELPPPRAAP,QPPRWHLRVV	CRC
MAPKAPK2	c.640_641insC	p.T214fs	ENLLYTSKRPNAILKLTDFGFAKET[p.T214fs]HQPQLFDHSLLYTVLCGSRSAGSREV*	QLFDHSLLY,LLYTVLCGS,QPQLFDHSL,AKETHQPQL,KETHQPQLF,FDHSLLYTV,QLFDHSLLYT,GSRSAGSREV,PQLFDHSLLY,LLYTVLCGSR,YTVLCGSRSA,QPQLFDHSLL,FAKETHQPQL,AKETHQPQLF,HQPQLFDHSL,FDHSLLYTVL	KIRC
11-Mar	c.578G>T	p.R193L	PICKICFQGAEQGELLNPCRCDGSV[p.R193L]LYTHQLCLLKWISERGSWTCELCCYR	VLYTHQLCL,LYTHQLCLL,GSVLYTHQL,VLYTHQLCLL,NPCRCDGSVL	LUAD
5-Mar	c.508C>T	p.R170C	GLPTIPVMLILGKMIRWEDYVLRLW[p.R170C]CKYSNKLQILNSIFPGIGCPVPRIPA	RLWCKYSNK,LWCKYSNKL,YVLRLWCKY,DYVLRLWCK,CKYSNKLQI,RLWCKYSNKL,CKYSNKLQIL	BRCA
MARCKS	c.454delA	p.K152fs	ASSTSSPKAEDGATPSPSNETPKKK[p.K152fs]RSAFPSRSLSS*	KKRSAFPSR,RSAFPSRSL,SAFPSRSLS,TPKKKRSAF,KKKRSAFPSR,RSAFPSRSLS,KRSAFPSRSL,SAFPSRSLSS	KIRC
MARS2	c.1442G>A	p.R481Q	LPKQVADHYDNFRIYKALEAVSSCV[p.R481Q]QQTNGFVQRHAPWKLNWESPVDAPWL	SCVQQTNGF,VQQTNGFVQ,SSCVQQTNGF,QQTNGFVQRH	HNSC
MAS1L	c.970A>G	p.R324G	ISLFLIINSSANPIIYFFVGSLRKK[p.R324G]GLKESLRVILQRALADKPEVGRNKKA	GLKESLRVI,GSLRKKGLK,RKKGLKESL,GLKESLRVIL,VGSLRKKGLK	PRAD,THCA
MAT2A	c.497A>G	p.E166G	YATDETEECMPLTIVLAHKLNAKLA[p.E166G]GLRRNGTLPWLRPDSKTQVTVQYMQD	KLNAKLAGL,KLNAKLAGLR,LAGLRRNGTL,GLRRNGTLPW,HKLNAKLAGL	TGCT
MAX	c.106A>T	p.R36W	SDEEQPRFQSAADKRAHHNALERKR[p.R36W]WDHIKDSFHSLRDSVPSLQGEKASRA	RWDHIKDSF,KRWDHIKDSF	MM

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MAX	c.83A>G	p.H28R	DNDDIEVESDEEQPRFQSAADKRAH[p.H28R]RNALERKRRDHIKDSFHSLRDSVPSL	RAHRNALER,SAADKRAHR,AHRNALERK,DKRAHRNAL,RAHRNALERK,QSAADKRAHR	UCEC
MB21D2	c.931C>G	p.Q311E	EWRLSFARSEVQLKKCISSSLMQAY[p.Q311E]EACKAIIIKLLSRPKAISPYHLRSMM	SLMQAYEAC,MQAYEACKA,LMQAYEACK,QAYEACKAI,YEACKAIII,LMQAYEACKA,MQAYEACKAI,SLMQAYEACK,EACKAIIIKL,QAYEACKAII	HNSC,LUSC
MBD6	c.2194delC	p.P732fs	SVTTATTDPGASSLGKAPSNSGRPP[p.P732fs]NSLALCWVPACWVTCLH*	SLALCWVPA,SGRPPNSLA,VPACWVTCL,PPNSLALCW,SLALCWVPAC,ALCWVPACWV,SGRPPNSLAL,NSLALCWVPA,WVPACWVTCL,RPPNSLALCW,LALCWVPACW	STAD
MBD6	c.2338_2339insG	p.G780fs	LPSLLQPPGPLLSGQLGLQLLPGGG[p.G780fs]SSSTPLRGF*	SSSTPLRGF,LLPGGGSSST,LQLLPGGGSS,GSSSTPLRGF	STAD
MBOAT2	c.128G>A	p.R43Q	AVQLPIDQVNFVVCQLFALLAAIWF[p.R43Q]QTYLHSSKTSSFIRHVVATLLGLYLA	LAAIWFQTY,LLAAIWFQT,AIWFQTYLH,AAIWFQTYL,FQTYLHSSK,LLAAIWFQTY,ALLAAIWFQT,WFQTYLHSSK,LAAIWFQTYL,FQTYLHSSKT	CRC,UCEC
MBOAT7	c.1270C>T	p.R424W	HWFLKMRAYDYMCMGFVLLSLADTL[p.R424W]WYWASIYFCIHFLALAALGLGLALGG	LSLADTLWY,SLADTLWYW,TLWYWASIY,LWYWASIYF,WYWASIYFC,DTLWYWASI,LLSLADTLW,LLSLADTLWY,SLADTLWYWA,LSLADTLWYW,TLWYWASIYF,WYWASIYFCI,DTLWYWASIY,VLLSLADTLW,ADTLWYWASI	HNSC
MC5R	c.325G>A	p.A109T	LVSMSSAWETITIYLLNNKHLVIAD[p.A109T]TFVRHIDNVFDSMICISVVASMCSLL	HLVIADTFV,LVIADTFVR,KHLVIADTF,TFVRHIDNV,VIADTFVRHI,TFVRHIDNVF,HLVIADTFVR,DTFVRHIDNV,NKHLVIADTF	UCEC
MCF2L2	c.2777G>A	p.R926Q	KTMKLMTLSIRQLGRGSHRKFEIAS[p.R926Q]QNGLEKYILQAASKEIRDCWFSEISK	ASQNGLEKY,IASQNGLEK,FEIASQNGL,SQNGLEKYI,IASQNGLEKY,RKFEIASQNG,SQNGLEKYIL	CRC
MCHR1	c.917C>T	p.S306F	QFFLAFALPFVVITAAYVRILQRMT[p.S306F]FSVAPASQRSIRLRTKRVTRTAIAIC	ILQRMTFSV,RMTFSVAPA,RILQRMTFS,LQRMTFSVA,MTFSVAPAS,VRILQRMTF,RILQRMTFSV,ILQRMTFSVA,TFSVAPASQR,YVRILQRMTF,LQRMTFSVAP,QRMTFSVAPA,RMTFSVAPAS	LUSC
MCOLN3	c.421G>A	p.V141I	VYTQSDVYDQLIFAVNQYLQLYNVS[p.V141I]IGNHAYENKGTKQSAMAICQHFYKRG	YLQLYNVSI,NVSIGNHAY,LQLYNVSIG,SIGNHAYENK,QYLQLYNVSI,YNVSIGNHAY	GBM
MECOM	c.2744G>A	p.R915Q	SELLQSVPSMFNFRAPPNALPENLL[p.R915Q]QKGKERYTCRYCGKIFPRSANLTRHL	LLQKGKERY,NALPENLLQK	PRAD
MECOM	c.2905C>T	p.R969C	TGEQPYRCKYCDRSFSISSNLQRHV[p.R969C]CNIHNKEKPFKCHLCDRCFGQQTNLD	NLQRHVCNI,RHVCNIHNK,LQRHVCNIH,HVCNIHNKEK,CNIHNKEKPF	CRC
MED12	c.107T>G	p.L36R	HRPLKRPRLGPPDVYPQDPKQKEDE[p.L36R]RTALNVKQGFNNQPAVSGDEHGSAKN	QKEDERTAL,KQKEDERTAL,RTALNVKQGF,KEDERTALNV	CLL
MED12	c.130G>A	p.G44S	LGPPDVYPQDPKQKEDELTALNVKQ[p.G44S]SFNNQPAVSGDEHGSAKNVSFNPAKI	KQSFNNQPA,TALNVKQSF,QSFNNQPAV,KQSFNNQPAV,LTALNVKQSF,VKQSFNNQPA	CLL
MED12	c.3670C>T	p.L1224F	IRSSCDRHLLAASQNRIVDGAVFAV[p.L1224F]FKAVFVLGDAELKGSGFTVTGGTEEL	AVFAVFKAV,FAVFKAVFV,AVFKAVFVL,VFAVFKAVF,VDGAVFAVF,FAVFKAVFVL,AVFAVFKAVF,IVDGAVFAVF	PRAD
MED12L	c.3875G>A	p.C1292Y	LCTDKELILDPVLSNMQAQKLLQLI[p.C1292Y]YYPHGIKECTEGDNLQRQHIKRILQN	QLIYYPHGI,LIYYPHGIK,AQKLLQLIY,QKLLQLIYY,QAQKLLQLIY,LQLIYYPHGI,QLIYYPHGIK,AQKLLQLIYY	TGCT
MED12L	c.6211C>T	p.P2071S	QDPMRPRQPQVRQQQRLLQMQQPQQ[p.P2071S]SQPQQPPQPQQSSQSQSQTLGLQAMQ	LQMQQPQQS,MQQPQQSQP,LQMQQPQQSQ,MQQPQQSQPQ	KIRC
MED12L	c.6331_6333delCAG	p.Q2115del	LGLQAMQPQQPLFPRQGLQQTQQQQ[p.Q2115del]TAALVRQLQKQLSSNQPQQGVTPYGHPS	QQTQQQQTA,TQQQQTAAL,TQQQQTAALV,LQQTQQQQTA,QQTQQQQTAA	PRAD
MED15	c.104G>T	p.S35I	WRSTAFRQKLVSQIEDAMRKAGVAH[p.S35I]IKSSKDMESHVFLKAKTRDEYLSLVA	GVAHIKSSK,MRKAGVAHI,AHIKSSKDM,AMRKAGVAHI,MRKAGVAHIK,AGVAHIKSSK	THCA
MED16	c.1347C>G	p.H449Q	TAGPAVHLKAMQLSWTSLALVGIDS[p.H449Q]QGKLSVLRLSPSMGHPLEVGLALRHL	DSQGKLSVLR,IDSQGKLSVL,SQGKLSVLRL	KIRP

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
MEF2A	c.295C>T	p.P99S	EPHESRTNSDIVEALNKKEHRGCDS[p.P99S]SDPDTSYVLTPHTEEKYKKINEEFDN	SSDPDTSYV,DSSDPDTSY,DSSDPDTSYV,CDSSDPDTSY	KIRP
MEF2A	c.380G>A	p.R127Q	DTSYVLTPHTEEKYKKINEEFDNMM[p.R127Q]QNHKIAPGLPPQNFSMSVTVPVTSPN	NMMQNHKIA,MMQNHKIAP,MQNHKIAPG,MQNHKIAPGL,MMQNHKIAPG,EEFDNMMQNH	TGCT
MEFV	c.1130G>A	p.R377H	CPRCQDSHERKSPGSLSPQPLPQCK[p.R377H]HHLKQVQLLFCEDHDEPICLICSLSQ	KHHLKQVQL,HHLKQVQLL,HHLKQVQLLF,QPLPQCKHHL,CKHHLKQVQL,KHHLKQVQLL	BRCA
MEGF10	c.3158C>T	p.S1053L	NPYATIKDPPVLIPKSSECGYVEMK[p.S1053L]LPARRDSPYAEINNSTSANRNVYEVE	YVEMKLPAR,LPARRDSPY,KLPARRDSPY,YVEMKLPARR,LPARRDSPYA,SECGYVEMKL	UCEC
MEGF6	c.1178A>G	p.Y393C	RTCIDVDDCADSPCCQQVCTNNPGG[p.Y393C]CECGCYAGYRLSADGCGCEDVDECAS	CECGCYAGY,NPGGCECGCY	THCA
MEGF6	c.1746_1747insC	p.A582fs	DTFGKNCSFSCSCQNGGTCDSVTGA[p.A582fs]LPLPPGCQWN*	LPLPPGCQW,CDSVTGALPL	KIRC
MET	c.3280C>T	p.H1094Y	VVIGPSSLIVHFNEVIGRGHFGCVY[p.H1094Y]YGTLLDNDGKKIHCAVKSLNRITDIG	RGHFGCVYY,HFGCVYYGTL	KIRP
MET	c.3749T>C	p.M1250T	LARDMYDKEYYSVHNKTGAKLPVKW[p.M1250T]TALESLQTQKFTTKSDVWSFGVLLWE	KLPVKWTAL,VKWTALESL,TALESLQTQK,AKLPVKWTAL,LPVKWTALES	KIRP
METTL15	c.157C>G	p.Q53E	VWPNRIHTTAEKYREYEAREQTDQT[p.Q53E]EAQELHRSQDRDFETMAKLHIPVMVD	REQTDQTEA	BRCA
METTL16	c.599G>A	p.R200Q	EIIYDFCMCNPPFFANQLEAKGVNS[p.R200Q]QNPRRPPPSSVNTGGITEIMAEGGEL	SQNPRRPPP,SQNPRRPPPS	CRC
METTL21A	c.521G>A	p.R174Q	EETFTDLLQTLEHLCSNHSVILLAC[p.R174Q]QIRYERDNNFLAMLERQFTVRKVHYD	ILLACQIRY,LACQIRYER,VILLACQIRY,SVILLACQIR,LLACQIRYER	CRC
METTL6	c.168C>A	p.F56L	DFKQQKLEQEAQKNWDLFYKRNSTN[p.F56L]LFKDRHWTTREFEELRSCREFEDQKL	FYKRNSTNL,KRNSTNLFK,YKRNSTNLF,LFYKRNSTNL,FYKRNSTNLF,YKRNSTNLFK,LFKDRHWTTR	CRC
METTL9	c.170A>T	p.Y57F	LYVNMTSGPGGPAAAAGGRKENHQW[p.Y57F]FVCNREKLCESLQAVFVQSYLDQGTQ	QWFVCNREK,NHQWFVCNR,GRKENHQWF,KENHQWFVC,HQWFVCNREK,ENHQWFVCNR	CLL
MEX3C	c.1600C>A	p.R534S	IWTPFEPVNPLSGFGSDPSGNMKTQ[p.R534S]SRGSQPSTPRLSPTFPESIEHPLAARR	TQSRGSQPS,KTQSRGSQPS,TQSRGSQPST	TGCT
MEX3C	c.537_545delCGCGGCGGC	p.179_182AAAA>A	IPGGSLGSVLLPAARFDAREAAAAA[p.179_182AAAA>A]GVLYGGDDAQGMMAAMLSHAYGPGGCGAAAAALN	EAAAAAGVL,REAAAAAGV,EAAAAAGVLY,REAAAAAGVL	ACC
MFF	c.19_20AG>TT	p.S7F	MSKGTS[p.S7F]FDTSLGRVSRAAFPSPTAAEMAEISRI	TSFDTSLGR,KGTSFDTSL,GTSFDTSLGR,TSFDTSLGRV,SKGTSFDTSL	TGCT
MFF	c.484C>T	p.R162C	TTPQNEEIRAVGRLKRERSMSENAV[p.R162C]CQNGQLVRNDSLWHRSDSAPRNKISR	RSMSENAVC,SENAVCQNG,NAVCQNGQLV	CRC
MFGE8	c.508G>A	p.D170N	GASRLASHEYLKAFKVAYSLNGHEF[p.D170N]NFIHDVNKKHKEFVGNWNKNAVHVNL	SLNGHEFNF,HEFNFIHDV,SLNGHEFNFI,YSLNGHEFNF,EFNFIHDVNK,HEFNFIHDVN	UCEC
MFSD5	c.839G>A	p.R280Q	FEAWYIHEHVERHDFPAEWIPATFA[p.R280Q]QAAFWNHVLAVVAGVAAEAVASWIGL	WIPATFAQA,AQAAFWNHV,QAAFWNHVL,IPATFAQAA,ATFAQAAFW,FAQAAFWNHV,AQAAFWNHVL,WIPATFAQAA,QAAFWNHVLA,IPATFAQAAF,AEWIPATFAQ	CRC
MGA	c.7304G>A	p.R2435Q	WSDKLQKEAEAFAYYRRTHTANERR[p.R2435Q]QRGEMRDLFEKLKITLGLLHSSKVSK	HTANERRQR,NERRQRGEM,RQRGEMRDL,RQRGEMRDLF	OV
MGAT4B	c.1330A>C	p.T444P	STSLKTYQHFTLEKAYLREDFFWAF[p.T444P]PPAAGDFIRFRFFQPLRLERFFFRSG	FFWAFPPAA,AFPPAAGDF,DFFWAFPPA,FPPAAGDFI,AFPPAAGDFI,WAFPPAAGDF,PPAAGDFIRF,REDFFWAFPP,EDFFWAFPPA	GBM

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
MGAT4C	c.1034C>T	p.T345M	LAQKNVIRFKPSLFQHMGYYSSYKG[p.T345M]MENKLKDDDFEEESFDIPDNPPASLY	SSYKGMENK,SYKGMENKL,GYYSSYKGM,YSSYKGMENK,SYKGMENKLK,MGYYSSYKGM,SSYKGMENKL,MENKLKDDDF	PRAD
MGST2	c.304delA	p.K102fs	FATCLGLVYIYGRHLYFWGYSEAAK[p.K102fs]NGSPVSD*	EAAKNGSPV,SEAAKNGSPV	STAD
MGST3	c.429_430insT	p.G143fs	SIALLGLVGTTVCSAFQHLGWVKSG[p.G143fs]FGQWTQMLPLKNYRGLKTLIHFK*	GQWTQMLPL,GLKTLIHFK,QMLPLKNYR,GFGQWTQML,RGLKTLIHF,QWTQMLPLK,PLKNYRGLK,TQMLPLKNY,LPLKNYRGL,HLGWVKSGF,WVKSGFGQW,SGFGQWTQM,KNYRGLKTL,WTQMLPLKNY,MLPLKNYRGL,GQWTQMLPLK,RGLKTLIHFK,TQMLPLKNYR,GWVKSGFGQW,QHLGWVKSGF,KSGFGQWTQM,SGFGQWTQML,FGQWTQMLPL,LKNYRGLKTL,KNYRGLKTLI,YRGLKTLIHF	KIRC
MICA	c.952delG	p.G318fs	HPVPSGKVLVLQSHWQTFHVSAVAA[p.G318fs]LLFLLLLFSMSVVVRRKHQLQRVQSS*	VSAVAALLF,AVAALLFLL,LLLLFSMSV,LLLFSMSVV,LLFSMSVVV,HVSAVAALL,SMSVVVRRK,FSMSVVVRR,ALLFLLLLF,LFLLLLFSM,VVRRKHQLQ,LFSMSVVVR,SAVAALLFL,VVVRRKHQL,FHVSAVAAL,VAALLFLLL,HQLQRVQSS,SAVAALLFLL,AVAALLFLLL,LLFLLLLFSM,FLLLLFSMSV,LLLLFSMSVV,LLLFSMSVVV,LLFSMSVVVR,FSMSVVVRRK,AALLFLLLLF,VVRRKHQLQR,HVSAVAALLF,LFSMSVVVRR,SVVVRRKHQL,FHVSAVAALL	CESC
MIER2	c.391C>T	p.L131F	ESEGGDVAPNLPDMTLDKEQIAKDL[p.L131F]FSGEEEEETQSSADDLTPSVTSHEAS	KEQIAKDLF	TGCT
MKI67	c.3241C>A	p.R1081S	REPAGDGKSIRTFKESPKQILDPAA[p.R1081S]SVTGMKKWPRTPKEEAQSLEDLAGFK	AASVTGMKK,DPAASVTGM,SVTGMKKWPR,AASVTGMKKW	LUAD
MKI67	c.4991_4992insCA	p.T1664fs	VGVKEELLAVGKLTQTSGETTHTHT[p.T1664fs]KSQQEMVRA*	HTKSQQEMV,HTHTKSQQEM,HTKSQQEMVR	STAD
MKI67	c.4992_4993insCA	p.T1664fs	VGVKEELLAVGKLTQTSGETTHTHT[p.T1664fs]QSQQEMVRA*	HTQSQQEMV,THTQSQQEM,HTHTQSQQEM,HTQSQQEMVR	UCEC
MKI67	c.6637C>G	p.H2213D	AQPLEDLAGLKELFQTPICTDKPTT[p.H2213D]DEKTTKIACRSPQPDPVGTPTIFKPQ	CTDKPTTDEK	CLL
MKL1	c.920delC	p.P307fs	HHNYQAILPAPPKSAGEALGSSGTP[p.P307fs]QYAASPLPIAAPARAPLGPVGWHVRTAPH*	PLGPVGWHV,QYAASPLPI,GWHVRTAPH,LGSSGTPQY,YAASPLPIA,IAAPARAPL,TPQYAASPL,SPLPIAAPA,LPIAAPARA,ALGSSGTPQY,YAASPLPIAA,APARAPLGPV,PQYAASPLPI,ARAPLGPVGW,APLGPVGWHV	STAD
MKLN1	c.1455C>A	p.F485L	CMLFHSKNRCLYVFGGQRSKTYLND[p.F485L]LFSYDVDSDHVDIISDGTKKDSGMVP	YLNDLFSYD,TYLNDLFSY,RSKTYLNDL,KTYLNDLFS,SKTYLNDLF,KTYLNDLFSY,YLNDLFSYDV,RSKTYLNDLF	UCEC
MKRN3	c.1343C>A	p.P448H	PEGWGDEPPGPGGGSFSAYWHQLVE[p.P448H]HVRMGEGNMLYKSIKKELVVLRLASL	YWHQLVEHV,HVRMGEGNM,HQLVEHVRM,AYWHQLVEHV,HVRMGEGNML,YWHQLVEHVR,SAYWHQLVEH,WHQLVEHVRM	LUAD
MKRN3	c.809G>T	p.G270V	YYASRGVCFRGESCMYLHGDICDMC[p.G270V]VLQTLHPMDAAQREEHMRACIEAHEK	CVLQTLHPM,CDMCVLQTL,MCVLQTLHPM	LUSC
MLL2	c.1939_1940insC	p.P647fs	ASRLSPPPEDSPMSPPPEESPMSPP[p.P647fs]T*	EESPMSPPT	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
MLL2	c.1940delC	p.P647fs	EASRLSPPPEDSPMSPPPEESPMSP[p.P647fs]HLRYRAYPPCLWCHACLHRLRNLPCPHRLRSLPRPLHLRLHASPHHLRTPPHPHHLRTHLLPHHRRTRSCPCRWRSHPCCHYLRSRNSAPGPRGRTCHPGLRSRTCPPGLRSHTYLRRLRSHTCPPSLRSHAYALCLRSHTCPPRLRDHICPLSLRNCTCPPRLRSRTCLLCLRSHACPPNLRNHTCPPSLRSHACPPGLRNRICPLSLRSHPCPLGLKSPLRSQANALHLRSCPCSLPLGNHPYLPCLESQPCLSLGNHLCPLCPRSCRCPHLGSHPCRLS*	RLHASPHHL,SLRSHAYAL,RLRDHICPL,SLGNHLCPL,RLRSRTCLL,GLRNRICPL,SLRSHPCPL,HLRSCPCSL,HLGSHPCRL,HLRTHLLPH,GLRSHTYLR,RTHLLPHHR,SQANALHLR,RYRAYPPCL,HLRYRAYPP,RLRNLPCPH,RLRSLPRPL,RSLPRPLHL,HLRLHASPH,HLRTPPHPH,RTPPHPHHL,RTRSCPCRW,RWRSHPCCH,RSHPCCHYL,HYLRSRNSA,RSRNSAPGP,RGRTCHPGL,RSRTCPPGL,RSHTYLRRL,HTYLRRLRS,RLRSHTCPP,RSHTCPPSL,RSHAYALCL,RSHTCPPRL,RSRTCLLCL,RSHACPPNL,RNHTCPPSL,RSHACPPGL,RNRICPLSL,RSHPCPLGL,RSQANALHL,RSCPCSLPL,SPMSPHLRY,SLPLGNHPY,ESPMSPHLR,PMSPHLRYR,NLPCPHRLR,SLPRPLHLR,LLPHHRRTR,SHAYALCLR,DHICPLSLR,MSPHLRYRA,SPHLRYRAY,LPRPLHLRL,RPLHLRLHA,SPHHLRTPP,HPHHLRTHL,LPHHRRTRS,APGPRGRTC,CPLGLKSPL,LPLGNHPYL,CPRSCRCPH,CPHLGSHPC,YLRSRNSAP,NLRNHTCPP,WRSHPCCHY,RDHICPLSL,LESQPCLSL,EESPMSPHL,PPSLRSHAY,CPPRLRDHI,CPPGLRNRI,ESPMSPHLRY,CSLPLGNHPY,SLPLGNHPYL,SLPRPLHLRL,GLKSPLRSQA,YLPCLESQPC,RLRNLPCPHR,RLRSLPRPLH,RLHASPHHLR,GLRSHTYLRR,RSHAYALCLR,CLRSHTCPPR,SLRNCTCPPR,RSRTCLLCLR,RSHPCPLGLK,RSLPRPLHLR,RTHLLPHHRR,RSHPCCHYLR,RTCHPGLRSR,RSHTCPPSLR,RSHTCPPRLR,CTCPPRLRSR,RSHACPPNLR,RSHACPPGLR,RSQANALHLR,RYRAYPPCLW,LWCHACLHRL,HLRYRAYPPC,RNLPCPHRLR,HLRLHASPHH,HLRTPPHPHH,RTPPHPHHLR,HLRTHLLPHH,HLLPHHRRTR,RTRSCPCRWR,RSCPCRWRSH,RWRSHPCCHY,RSRNSAPGPR,RGRTCHPGLR,GLRSRTCPPG,RSRTCPPGLR,RSHTYLRRLR,HTYLRRLRSH,RLRSHTCPPS,SLRSHAYALC,RLRDHICPLS,RLRSRTCLLC,RNHTCPPSLR,SLRSHACPPG,GLRNRICPLS,RNRICPLSLR,SLRSHPCPLG,KSPLRSQANA,MSPHLRYRAY,SPMSPHLRYR,CLWCHACLHR,CPHRLRSLPR,HPCCHYLRSR,HACPPGLRNR,LPCPHRLRSL,RPLHLRLHAS,SPHHLRTPPH,HPHHLRTHLL,LPHHRRTRSC,PPRLRSRTCL,SPLRSQANAL,CPRSCRCPHL,YLRSRNSAPG,YLRRLRSHTC,HAYALCLRSH,LRYRAYPPCL,RAYPPCLWCH,HRLRSLPRPL,LRSLPRPLHL,LHLRLHASPH,LRLHASPHHL,LRTPPHPHHL,HHLRTHLLPH,WRSHPCCHYL,CHYLRSRNSA,LRSHTYLRRL,LRSHTCPPSL,LRSHAYALCL,LRSHTCPPRL,LRNCTCPPRL,LRSHACPPNL,LRNHTCPPSL,LRSHACPPGL,LRNRICPLSL,LSLRSHPCPL,LRSQANALHL,SQANALHLRS,LHLRSCPCSL,LRSCPCSLPL,LSLGNHLCPL,CPPGLRSHTY,CPPSLRSHAY	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
MLL2	c.1966delC	p.L656fs	EDSPMSPPPEESPMSPPPEVSRLSP[p.L656fs]CLWCHACLHRLRNLPCPHRLRSLPRPLHLRLHASPHHLRTPPHPHHLRTHLLPHHRRTRSCPCRWRSHPCCHYLRSRNSAPGPRGRTCHPGLRSRTCPPGLRSHTYLRRLRSHTCPPSLRSHAYALCLRSHTCPPRLRDHICPLSLRNCTCPPRLRSRTCLLCLRSHACPPNLRNHTCPPSLRSHACPPGLRNRICPLSLRSHPCPLGLKSPLRSQANALHLRSCPCSLPLGNHPYLPCLESQPCLSLGNHLCPLCPRSCRCPHLGSHPCRLS*	RLHASPHHL,SLRSHAYAL,RLRDHICPL,SLGNHLCPL,RLRSRTCLL,GLRNRICPL,SLRSHPCPL,HLRSCPCSL,HLGSHPCRL,HLRTHLLPH,GLRSHTYLR,RTHLLPHHR,SQANALHLR,RLRNLPCPH,RLRSLPRPL,RSLPRPLHL,HLRLHASPH,HLRTPPHPH,RTPPHPHHL,RTRSCPCRW,RWRSHPCCH,RSHPCCHYL,HYLRSRNSA,RSRNSAPGP,RGRTCHPGL,RSRTCPPGL,RSHTYLRRL,HTYLRRLRS,RLRSHTCPP,RSHTCPPSL,RSHAYALCL,RSHTCPPRL,RSRTCLLCL,RSHACPPNL,RNHTCPPSL,RSHACPPGL,RNRICPLSL,RSHPCPLGL,RSQANALHL,RSCPCSLPL,SLPLGNHPY,NLPCPHRLR,SLPRPLHLR,LLPHHRRTR,SHAYALCLR,DHICPLSLR,EVSRLSPCL,LPRPLHLRL,RPLHLRLHA,SPHHLRTPP,HPHHLRTHL,LPHHRRTRS,APGPRGRTC,CPLGLKSPL,LPLGNHPYL,CPRSCRCPH,CPHLGSHPC,YLRSRNSAP,NLRNHTCPP,VSRLSPCLW,WRSHPCCHY,RDHICPLSL,LESQPCLSL,PPSLRSHAY,CPPRLRDHI,CPPGLRNRI,CSLPLGNHPY,RLSPCLWCHA,SLPLGNHPYL,SLPRPLHLRL,GLKSPLRSQA,YLPCLESQPC,RLRNLPCPHR,RLRSLPRPLH,RLHASPHHLR,GLRSHTYLRR,RSHAYALCLR,CLRSHTCPPR,SLRNCTCPPR,RSRTCLLCLR,RSHPCPLGLK,RSLPRPLHLR,RTHLLPHHRR,RSHPCCHYLR,RTCHPGLRSR,RSHTCPPSLR,RSHTCPPRLR,CTCPPRLRSR,RSHACPPNLR,RSHACPPGLR,RSQANALHLR,LWCHACLHRL,RNLPCPHRLR,HLRLHASPHH,HLRTPPHPHH,RTPPHPHHLR,HLRTHLLPHH,HLLPHHRRTR,RTRSCPCRWR,RSCPCRWRSH,RWRSHPCCHY,RSRNSAPGPR,RGRTCHPGLR,GLRSRTCPPG,RSRTCPPGLR,RSHTYLRRLR,HTYLRRLRSH,RLRSHTCPPS,SLRSHAYALC,RLRDHICPLS,RLRSRTCLLC,RNHTCPPSLR,SLRSHACPPG,GLRNRICPLS,RNRICPLSLR,SLRSHPCPLG,KSPLRSQANA,CLWCHACLHR,CPHRLRSLPR,HPCCHYLRSR,HACPPGLRNR,LPCPHRLRSL,RPLHLRLHAS,SPHHLRTPPH,HPHHLRTHLL,LPHHRRTRSC,PPRLRSRTCL,SPLRSQANAL,CPRSCRCPHL,YLRSRNSAPG,YLRRLRSHTC,HAYALCLRSH,HRLRSLPRPL,LRSLPRPLHL,LHLRLHASPH,LRLHASPHHL,LRTPPHPHHL,HHLRTHLLPH,WRSHPCCHYL,CHYLRSRNSA,LRSHTYLRRL,LRSHTCPPSL,LRSHAYALCL,LRSHTCPPRL,LRNCTCPPRL,LRSHACPPNL,LRNHTCPPSL,LRSHACPPGL,LRNRICPLSL,LSLRSHPCPL,LRSQANALHL,SQANALHLRS,LHLRSCPCSL,LRSCPCSLPL,LSLGNHLCPL,CPPGLRSHTY,CPPSLRSHAY	STAD
MLL2	c.7061delC	p.P2354fs	APLTPRASQVEPQSPGLGLRPQEPP[p.P2354fs]LPRLWHLLLQVTQTSFALAPTLTHMLSPH*	RLWHLLLQV,ALAPTLTHM,LQVTQTSFA,VTQTSFALA,QVTQTSFAL,QTSFALAPT,LPRLWHLLL,LLQVTQTSF,GLRPQEPPL,TQTSFALAP,TSFALAPTL,FALAPTLTH,RLWHLLLQVT,ALAPTLTHML,LLQVTQTSFA,LQVTQTSFAL,LLLQVTQTSF,QVTQTSFALA,QTSFALAPTL,RPQEPPLPRL,FALAPTLTHM,TQTSFALAPT	STAD
MLL3	c.1066C>A	p.Q356K	IDQAPERSKEDANCAVCDSPGDLLD[p.Q356K]KFFCTTCGQHYHGMCLDIAVTPLKRA	LLDKFFCTT,SPGDLLDKF,SPGDLLDKFF	LUAD
MLL3	c.1179C>A	p.N393K	GMCLDIAVTPLKRAGWQCPECKVCQ[p.N393K]KCKQSGEDSKMLVCDTCDKGYHTFCL	KCKQSGEDSK	LUAD
MLL3	c.13488delT	p.F4496fs	TSGCHRFRCTNIYHFTCAIKAQCMF[p.F4496fs]LRTKLCFAPCTNQREFMSKN*	FLRTKLCFA,AIKAQCMFL,AQCMFLRTK,MFLRTKLCF,RTKLCFAPC,CFAPCTNQR,AIKAQCMFLR,KAQCMFLRTK,CTNQREFMSK,CMFLRTKLCF,RTKLCFAPCT,FLRTKLCFAP,AQCMFLRTKL,FAPCTNQREF	STAD
MLL5	c.197A>G	p.Y66C	YPHQLYTSSSHHSHSYIGLPYADHN[p.Y66C]CGARPPPTPPASPPPSVLISKNEVGI	LPYADHNCGA	TGCT
MLXIPL	c.2368A>C	p.S790R	NWKFWVFSILIRPLFESFNGMVSTA[p.S790R]RVHTLRQTSLAWLDQYCSLPALRPTV	STARVHTLR,RVHTLRQTS,GMVSTARVH,VSTARVHTL,MVSTARVHTL,VSTARVHTLR,RVHTLRQTSL,SFNGMVSTAR	KIRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
MMAA	c.976C>T	p.R326C	RIQAEYVSALKLLRKRSQVWKPKVI[p.R326C]CISARSGEGISEMWDKMKDFQDLMLA	CISARSGEGI	CRC
MMP3	c.190delA	p.I64fs	ENYYDLKKDVKQFVRRKDSGPVVKK[p.I64fs]SEKCRSSLDWR*	KSEKCRSSL,KCRSSLDWR,KKSEKCRSSL,SEKCRSSLDW	STAD
MMRN1	c.2751C>A	p.F917L	QALQLQVLNSRFKALEAKSIHLSIN[p.F917L]LFSLNKTLHEVLTMCHNASTSVSELN	HLSINLFSL,NLFSLNKTL,SINLFSLNK,SIHLSINLF,KSIHLSINL,LSINLFSLNK,KSIHLSINLF,AKSIHLSINL,IHLSINLFSL	UCEC
MMRN1	c.3037G>T	p.A1013S	RSLPGSLANVVKSQKQVKSLPKKIN[p.A1013S]SLKKPTVNLTTVLIGRTQRNTDNIIY	SLPKKINSL,SLKKPTVNL,KSLPKKINS,LPKKINSLK,SLPKKINSLK,KSLPKKINSL,KINSLKKPTV	LUAD
MMS19	c.3013G>A	p.D1005N	ALTRLPTPVLLPYKPQVIRALAKPL[p.D1005N]NDKKRLVRKEAVSARGEWFLLGSPGS	ALAKPLNDK,LAKPLNDKK,RALAKPLNDK,ALAKPLNDKK	TGCT
MN1	c.1415C>T	p.S472L	APPYMNVAKRPRFDFPGSAGVDRCA[p.S472L]LWNGSMHNGALDNHLSPSAYPGLPGE	RCALWNGSM	BLCA
MOCOS	c.2545T>C	p.S849P	NQHVFQKLSESRETKVNFGMYLMHA[p.S849P]PLDLSSPCFLSVGSQVLPVLKENVEG	GMYLMHAPL,YLMHAPLDL,FGMYLMHAPL,YLMHAPLDLS,MYLMHAPLDL,APLDLSSPCF,LMHAPLDLSS	KIRC
MOCS2	c.65delC	p.P22fs	MSSLEISSSCFSLETKLPLSP[p.P22fs]H*	LETKLPLSPH	STAD
MOGAT2	c.197_198insG	p.Q66fs	TRFWLLTVLYAAWWYLDRDKPRQGG[p.Q66fs]PAHPGHQVLDYMEVHEGLFPHLAGQDC*	HQVLDYMEV,GLFPHLAGQ,DYMEVHEGL,KPRQGGPAH,GPAHPGHQV,RQGGPAHPG,YMEVHEGLF,HPGHQVLDY,EVHEGLFPH,HEGLFPHLA,DYMEVHEGLF,EVHEGLFPHL,GPAHPGHQVL,RQGGPAHPGH,AHPGHQVLDY,HQVLDYMEVH,LDYMEVHEGL,MEVHEGLFPH,HPGHQVLDYM	LUAD
MORC1	c.337G>T	p.D113Y	KRLSTLKFIGQYGNGLKSGSMRIGK[p.D113Y]YFILFTKKEETMTCVFFSQTFCEEES	SMRIGKYFI,RIGKYFILF,KYFILFTKK,SGSMRIGKY,MRIGKYFIL,GSMRIGKYF,IGKYFILFTK,MRIGKYFILF,GSMRIGKYFI,SMRIGKYFIL,KSGSMRIGKY,SGSMRIGKYF	CRC
MORC2	c.2219G>A	p.R740H	SDSAGEEDSADLKRAQKDKGLHVEV[p.R740H]HVNREWYTGRVTAVEVGKHVVRWKVK	VEVHVNREW,HVNREWYTGR,VEVHVNREWY	CRC
MPDZ	c.2410C>A	p.L804I	VRIGVAKPLPLSPEEGYVSAKEDSF[p.L804I]IYPPHSCEEAGLADKPLFRADLALVG	SAKEDSFIY,KEDSFIYPP,VSAKEDSFIY,YVSAKEDSFI	CRC
MPDZ	c.4745delA	p.K1582fs	KLTIHAENPDSQAVPSAAGAASGEK[p.K1582fs]RTAPSL*	GEKRTAPSL	STAD
MPRIP	c.1052delC	p.A351fs	SSDTRQGRSEKRAFPRKRDFTNEAP[p.A351fs]QLLSQTPRLPPCLHTEEPSHWTGGPRSPP*	FTNEAPQLL,QLLSQTPRL,SQTPRLPPC,RDFTNEAPQL,SQTPRLPPCL,CLHTEEPSHW,NEAPQLLSQT	STAD
MR1	c.137C>T	p.S46L	DSRTHSLRYFRLGVSDPIHGVPEFI[p.S46L]LVGYVDSHPITTYDSVTRQKEPRAPW	VPEFILVGY,GVPEFILVGY,VPEFILVGYV	CRC
MRPL47	c.700C>A	p.L234I	LRLEREKRARIKARKENLERKKAKI[p.L234I]ILKKFPHLAEAQKSSLV*	ILKKFPHLA,RKKAKIILK,IILKKFPHL,KAKIILKKF,RKKAKIILKK,KIILKKFPHL,LERKKAKIIL,KKAKIILKKF	CRC
MRPS25	c.355_357delGAG	p.E119del	SNKEIMEHIRKILGKNEETLREEEE[p.E119del]KKQLSHPANFGPRKYCLRECICEVEGQV	REEEEKKQL	TGCT
MS4A4A	c.295G>A	p.V99M	ALMSLSMGITMMCMASNTYGSNPIS[p.V99M]MYIGYTIWGSVMFIISGSLSIAAGIR	ISMYIGYTI,TYGSNPISM,SMYIGYTIW,MYIGYTIWG,YGSNPISMY,NPISMYIGY,ISMYIGYTIW,MYIGYTIWGS,TYGSNPISMY,NTYGSNPISM	BRCA
MS4A8B	c.8C>T	p.S3L	MN[p.S3L]LMTSAVPVANSVLVVAPHNGYPVTPG	NLMTSAVPV,LMTSAVPVA,NLMTSAVPVA,MNLMTSAVPV	CRC,UCEC
MSH4	c.1392G>T	p.K464N	KNCNTPLLRAYYGSLEDKRFGIILE[p.K464N]NIKTVINDDARYMKGCLNMRTQKCYA	IILENIKTV,RFGIILENI,GIILENIKTV,RFGIILENIK,KRFGIILENI	CRC
MSH4	c.2188G>A	p.E730K	YVPAEYSSFRIAKQIFTRISTDDDI[p.E730K]KTNSSTFMKEMKEIAYILHNANDKSL	KTNSSTFMK,IKTNSSTFM	UCEC

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MSH6	c.1727A>C	p.D576A	GHTRAYGVCFVDTSLGKFFIGQFSD[p.D576A]ARHCSRFRTLVAHYPPVQVLFEKGNL	FSDARHCSR,DARHCSRFR,GQFSDARHC,SDARHCSRF,FSDARHCSRF,KFFIGQFSDA,FFIGQFSDAR,QFSDARHCSR,GQFSDARHCS,ARHCSRFRTL	TGCT
MSH6	c.3254_3255insC	p.T1085fs	LANYSRGGDGPMCRPVILLPEDTPP[p.T1085fs]LLRA*	LLPEDTPPL,LPEDTPPLL,ILLPEDTPPL,LLPEDTPPLL	CRC,STAD
MSH6	c.3284G>A	p.R1095H	GDGPMCRPVILLPEDTPPFLELKGS[p.R1095H]HHPCITKTFFGDDFIPNDILIGCEEE	GSHHPCITK,KGSHHPCITK,ELKGSHHPCI,SHHPCITKTF,LELKGSHHPC	CRC
MSLNL	c.202A>C	p.T68P	MTSARRRTDVGPRVAFTYPCTQLSP[p.T68P]PRAHRHLPVHTVTYPCTQLSPTRAHS	QLSPPRAHR,SPPRAHRHL,TQLSPPRAH,PPRAHRHLPV	PRAD
MST1	c.1304delA	p.N435fs	AETPHKPQFTFTSEPHAQLEENFCR[p.N435fs]TQMGIAMGPGATRWTQGPHSTTVPCDAALMTSRHQSWTPQTRCSLRSVARGWIGWISGVPSCAWLGAIRATHPGQSACGIGRASISAGGL*	GWIGWISGV,WISGVPSCA,RTQMGIAMG,QTRCSLRSV,RCSLRSVAR,AIRATHPGQ,HQSWTPQTR,HPGQSACGI,EENFCRTQM,CRTQMGIAM,SLRSVARGW,ISGVPSCAW,RATHPGQSA,SLRSVARGWI,SVARGWIGWI,QTRCSLRSVA,RGWIGWISGV,AIRATHPGQS,WTPQTRCSLR,VPSCAWLGAI,FCRTQMGIAM,LEENFCRTQM,CSLRSVARGW,RSVARGWIGW,WISGVPSCAW	KIRP
MST1R	c.1390A>G	p.M464V	FNGLLGPVQVTALYVTRLDNVTVAH[p.M464V]VGTMDGRILQVELVRSLNYLLYVSNF	VTVAHVGTM,RLDNVTVAHV	KIRC
MTG1	c.315delA	p.L105fs	LNKMDLADLTEQQKIMQHLEGEGLK[p.L105fs]MSFLPTV*	HLEGEGLKM,LKMSFLPTV,GEGLKMSFL,GLKMSFLPTV,LEGEGLKMSF	STAD
MTG1	c.981delC	p.H327fs	DFLQTFRRGLLGSVMLDLDVLRGHP[p.H327fs]RLRLCPELVRVGRAGGMWPPRPPDLGG*	RLCPELVRV,RLRLCPELV,RAGGMWPPR,MWPPRPPDL,VLRGHPRLR,RGHPRLRLC,LVRVGRAGG,HPRLRLCPE,RVGRAGGMW,GMWPPRPPDL,RLRLCPELVR,VLRGHPRLRL,LVRVGRAGGM,DLDVLRGHPR,DVLRGHPRLR,HPRLRLCPEL	STAD
MTIF2	c.326delA	p.N109fs	STKSKKVVEVWIGMTIEELARAMEK[p.N109fs]TQIMYMKLY*	AMEKTQIMY,KTQIMYMKL,RAMEKTQIM,TQIMYMKLY,MEKTQIMYM,KTQIMYMKLY,RAMEKTQIMY,MEKTQIMYMK,ARAMEKTQIM,AMEKTQIMYM	STAD
MTMR9	c.577delA	p.K193fs	DEALRKVATFRHGGRFPVLSYYHKK[p.K193fs]MGW*	SYYHKKMGW,VLSYYHKKM,LSYYHKKMGW	KICH
MTOR	c.4379T>C	p.L1460P	YAMKHFGELEIQATWYEKLHEWEDA[p.L1460P]PVAYDKKMDTNKDDPELMLGRMRCLE	APVAYDKKM,HEWEDAPVA,KLHEWEDAPV,HEWEDAPVAY	KIRC
MTOR	c.4448G>T	p.C1483F	DALVAYDKKMDTNKDDPELMLGRMR[p.C1483F]FLEALGEWGQLHQQCCEKWTLVNDET	LMLGRMRFL,RFLEALGEW,LGRMRFLEA,RMRFLEALG,ELMLGRMRF,GRMRFLEAL,MLGRMRFLEA,RMRFLEALGE,ELMLGRMRFL,LGRMRFLEAL,MRFLEALGEW	KIRC
MTOR	c.6644C>A	p.S2215Y	EDLRQDERVMQLFGLVNTLLANDPT[p.S2215Y]YLRKNLSIQRYAVIPLSTNSGLIGWV	LLANDPTYL,LANDPTYLR,TYLRKNLSI,TLLANDPTY,TLLANDPTYL,LLANDPTYLR,LANDPTYLRK,NTLLANDPTY,YLRKNLSIQR	UCEC
MTUS2	c.3013C>T	p.R1005W	YPKQRTAAARNGFPPKPDPQAREAE[p.R1005W]WQLVLRLKERCEQQTRQLGVAQGELK	EAEWQLVLR,REAEWQLVL,AEWQLVLRL,DPQAREAEW,AEWQLVLRLK	STAD
MUC16	c.15355C>T	p.P5119S	LPNFSSTSDKILATSKDSKDTKEIF[p.P5119S]SSINTEETNVKANNSGHESHSPALAD	DTKEIFSSI,KEIFSSINT,KDTKEIFSSI	SKCM
MUC16	c.18466G>A	p.A6156T	PDISPEASSSHSNSPPLTISTHKTI[p.A6156T]TTQTGPSGVTSLGQLTLDTSTIATSA	TTQTGPSGV,ITTQTGPSGV	STAD
MUC16	c.25817G>A	p.R8606H	ESISSSPHPVTALLTLGPVKTTDML[p.R8606H]HTSSEPETSSPPNLSSTSAEILATSE	MLHTSSEPET	CRC
MUC16	c.31355_31356insC	p.P10452fs	GIMEHITKIPNEAAHRGTIRPVKGP[p.P10452fs]SDIHFACQS*	RPVKGPSDI,VKGPSDIHF	KICH
MUC16	c.33014C>T	p.T11005I	VLPEVPGMVTSLVASSRAVTSTTLP[p.T11005I]ILTLSPGEPETTPSMATSHGAEASST	AVTSTTLPI,LPILTLSPG,RAVTSTTLPI	CLL
MUC16	c.33778C>G	p.P11260A	IDSWVAHPGTEASSVVPTLTVSTGE[p.P11260A]AFTNISLVTHPAESSTLPRTTSRFS	STGEAFTNI,EAFTNISLV,LTVSTGEAF,GEAFTNISL,TLTVSTGEAF,GEAFTNISLV	KIRC

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MUC16	c.34782C>A	p.N11594K	YEPETTATWLTHPAETSTTVSGTIP[p.N11594K]KFSHRGSDTAPSMVTSPGVDTRSGVP	TTVSGTIPK,GTIPKFSHR,STTVSGTIPK,TTVSGTIPKF	LUSC
MUC16	c.38321G>A	p.R12774H	SGCRLTLLRSEKDGAATGVDAICTH[p.R12774H]HLDPKSPGVDREQLYWELSQLTNGIK	HLDPKSPGV,AICTHHLDPK	HNSC
MUC17	c.13244G>A	p.R4415H	LVYGLVGAGVVLMLIILVALLMLVF[p.R4415H]HSKREVKRQKYRLSQLYKWQEEDSGP	LLMLVFHSK,VFHSKREVK,LMLVFHSKR,MLVFHSKREV,ALLMLVFHSK,LVFHSKREVK,HSKREVKRQK,LLMLVFHSKR,VFHSKREVKR	BRCA
MUC17	c.229G>A	p.V77M	CQQLSQHVRTGSAANTATGTTSTNV[p.V77M]MEPRMYLSCSTNPEMTSIESSVTSDT	NVMEPRMYL,TSTNVMEPR,MEPRMYLSC,STNVMEPRMY,TTSTNVMEPR,NVMEPRMYLS,ATGTTSTNVM	GBM
MUC17	c.3680_3681insC	p.R1227fs	PTAEVTSMPTSTPGERSTPLTSMPV[p.R1227fs]STHASGQF*	TSMPVSTHA,VSTHASGQF,MPVSTHASG,LTSMPVSTHA,MPVSTHASGQ	KIRC
MUC17	c.3683delA	p.H1228fs	TAEVTSMPTSTPGERSTPLTSMPVR[p.H1228fs]PRQWPVLRLAPFQHLPLTPAHL*	FQHLPLTPA,HLPLTPAHL,LTSMPVRPR,PVRPRQWPV,RPRQWPVLR,RQWPVLRLA,WPVLRLAPF,LRLAPFQHL,LAPFQHLPL,RLAPFQHLPL,VLRLAPFQHL,QWPVLRLAPF,PVRPRQWPVL,MPVRPRQWPV,RPRQWPVLRL,FQHLPLTPAH,TSMPVRPRQW,RQWPVLRLAP	KIRC
MUC17	c.6836C>A	p.T2279N	STEATSSPTTAEGTSIPTSTLSEGT[p.T2279N]NPLTSIPVSHTLVANSEVSTLSTTPV	TLSEGTNPL,TLSEGTNPLT,GTNPLTSIPV,STLSEGTNPL,SEGTNPLTSI,NPLTSIPVSH	TGCT
MUC2	c.4703C>T	p.T1568M	TTTVTPTPTPTGTQTPTTTPITTTTT[p.T1568M]MVTPTPTPTGTQTPTSTPITTTTTVT	TTPITTTTTM,TPITTTTTMV,TTTTMVTPT,TTMVTPTPT,MVTPTPTPT,TTTPITTTTM,TTPITTTTMV,TMVTPTPTPT,TPITTTTMVT	TGCT
MUC2	c.4739C>A	p.T1580N	TQTPTTTPITTTTTVTPTPTPTGTQ[p.T1580N]NPTSTPITTTTTVTPTPTPTGTQTPT	TQNPTSTPI,TQNPTSTPIT	TGCT
MUC2	c.4745C>G	p.T1582R	TPTTTPITTTTTVTPTPTPTGTQTP[p.T1582R]RSTPITTTTTVTPTPTPTGTQTPTTT	TQTPRSTPI,GTQTPRSTPI,TPRSTPITTT	KIRP
MUC2	c.4790C>T	p.T1597I	TPTPTGTQTPTSTPITTTTTVTPTP[p.T1597I]IPTGTQTPTTTPITTTTTVTPTPTPT	TTTVTPTPI,TTTTVTPTPI,TTVTPTPIPT	TGCT
MUC2	c.5111C>T	p.T1704I	TTTTTVTPTPTPTGTQTPTSTPITT[p.T1704I]ITTVTPTPTPTGTQTPTPTPISTTTT	TTITTVTPT,TPITTITTV,STPITTITTV,TPITTITTVT,TPTSTPITTI	TGCT
MUC2	c.5117C>T	p.T1706M	TTTVTPTPTPTGTQTPTSTPITTTT[p.T1706M]MVTPTPTPTGTQTPTPTPISTTTTVT	TPITTTTMV,TTTTMVTPT,TTMVTPTPT,MVTPTPTPT,STPITTTTMV,TSTPITTTTM,TMVTPTPTPT,TPITTTTMVT	TGCT
MUC2	c.5143G>A	p.G1715S	PTGTQTPTSTPITTTTTVTPTPTPT[p.G1715S]STQTPTPTPISTTTTVTPTPTPTGTQ	STQTPTPTPI	TGCT
MUC2	c.5165C>T	p.T1722I	TSTPITTTTTVTPTPTPTGTQTPTP[p.T1722I]IPISTTTTVTPTPTPTGTQTPTTTPI	IPISTTTTV,TQTPTPIPI,TPIPISTTT,TPIPISTTTT,IPISTTTTVT	KIRP
MUC5B	c.2041A>G	p.S681G	YMGIFLVIETHGMAVSWDRKTSVFI[p.S681G]GLHQDYKGRVCGLCGNFDDNAINDFA	KTSVFIGLH,FIGLHQDYK,VFIGLHQDY,RKTSVFIGL,GLHQDYKGRV,VFIGLHQDYK,SVFIGLHQDY	ACC
MUC5B	c.2045A>G	p.D682G	MGIFLVIETHGMAVSWDRKTSVFIR[p.D682G]RHQDYKGRVCGLCGNFDDNAINDFAT	FIRRHQDYK,KTSVFIRRH,VFIRRHQDY,VFIRRHQDYK,SVFIRRHQDY	ACC,KIRP

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MUC6	c.4707_4708insA	p.P1569fs	ITPNPTSTRTRTPVAHTNSATSSRP[p.P1569fs]TTTLHHTLPTYREQSLLFHRSHDGNILQDHHYLSNPITPSDHTSHSRSTFLHLFGDSKYSHSHHPYPCTDGHFCLHPLNANRHDSSTDNAQGHRVHPHSANNDADHQRDQPSPELIKHSQNLYIPTFTHFLHTPC*	CTDGHFCLH,YLSNPITPS,YIPTFTHFL,FLHLFGDSK,CLHPLNANR,TYREQSLLF,SRSTFLHLF,KYSHSHHPY,SQNLYIPTF,LYIPTFTHF,SSRPTTTLH,TSHSRSTFL,HSRSTFLHL,RSTFLHLFG,RVHPHSANN,TLHHTLPTY,LHLFGDSKY,LIKHSQNLY,FTHFLHTPC,LPTYREQSL,HPHSANNDA,ELIKHSQNL,HTSHSRSTF,TSSRPTTTL,HRSHDGNIL,GNILQDHHY,HHYLSNPIT,SKYSHSHHP,AQGHRVHPH,IKHSQNLYI,HPYPCTDGH,IPTFTHFLH,TTLHHTLPTY,STDNAQGHRV,LIKHSQNLYI,TLHHTLPTYR,TSHSRSTFLH,TFLHLFGDSK,PTYREQSLLF,HSRSTFLHLF,HSQNLYIPTF,NLYIPTFTHF,LYIPTFTHFL,ATSSRPTTTL,SSRPTTTLHH,HTSHSRSTFL,RVHPHSANND,HQRDQPSPEL,FLHLFGDSKY,SKYSHSHHPY,ELIKHSQNLY,RPTTTLHHTL,LPTYREQSLL,HPYPCTDGHF,EQSLLFHRSH,FHRSHDGNIL,SHSRSTFLHL,HLFGDSKYSH,YSHSHHPYPC,KHSQNLYIPT,SQNLYIPTFT,YPCTDGHFCL,REQSLLFHRS,QDHHYLSNPI,IPTFTHFLHT	KIRC
MUC6	c.5930C>A	p.P1977H	AHTTSASSSRLPTPFTTHSPPTGSS[p.P1977H]HFSSTGPMTATSFQTTTTYPTPSHPQ	SHFSSTGPM,SSHFSSTGPM,HSPPTGSSHF,SHFSSTGPMT	TGCT
MUC6	c.6000C>G	p.H2000Q	SSPFSSTGPMTATSFQTTTTYPTPS[p.H2000Q]QPQTTLPTHVPPFSTSLVTPSTHTVI	TPSQPQTTL,SQPQTTLPT,SQPQTTLPTH,QPQTTLPTHV	TGCT
MUC6	c.6387_6389delCTC	p.2129_2130SS>S	SPITTQLPHLSSATTPVSTTNQLSS[p.2129_2130SS>S]FSPSPSAPSTVSSYVPSSHSSPQTSSPS	STTNQLSSF,NQLSSFSPS,VSTTNQLSSF,NQLSSFSPSP	STAD
MUC7	c.1007C>T	p.S336L	PNSSPTTLAPDTSETSAAPTHQTTT[p.S336L]LVTTQTTTTKQPTSAPGQNKISRFLL	APTHQTTTL,HQTTTLVTT,LVTTQTTTTK,APTHQTTTLV,HQTTTLVTTQ	UCEC
MVK	c.412delC	p.P138fs	YLSICRKQRALPSLDIVVWSELPPG[p.P138fs]RAWAPAPPTRCVWQQPS*	RAWAPAPPT,APAPPTRCV,SELPPGRAW,RAWAPAPPTR,VVWSELPPGR,WAPAPPTRCV,LPPGRAWAPA,APAPPTRCVW,SELPPGRAWA	STAD
MXRA5	c.970G>T	p.D324Y	EEDGGSQLILEKFQLPQWSISLNMT[p.D324Y]YEHGNMVNLVCDIKKPMDVYKIHLNQ	WSISLNMTY,MTYEHGNMV,NMTYEHGNM,YEHGNMVNL,NMTYEHGNMV,TYEHGNMVNL,QWSISLNMTY,LNMTYEHGNM,YEHGNMVNLV	LUAD
MYB	c.1443delA	p.R481fs	ESSLDPPKVLPPARHSTIPLVILRK[p.R481fs]NGARPAP*	VILRKNGAR,ILRKNGARPA,LVILRKNGAR	STAD
MYBPC2	c.1937G>A	p.R646H	TNPVGEDVASIFLQVVDVPDPPEAV[p.R646H]HITSVGEDWAILVWEPPMYDGGKPVT	PEAVHITSV,VPDPPEAVHI	UCEC
MYD88	c.719T>C	p.M240T	TCVWSIASELIEKRLARRPRGGCRR[p.M240T]TVVVVSDDYLQSKECDFQTKFALSLS	TVVVVSDDY,RPRGGCRRT,RTVVVVSDDY,TVVVVSDDYL,RPRGGCRRTV	CLL
MYD88	c.752G>A	p.S251N	EKRLARRPRGGCRRMVVVVSDDYLQ[p.S251N]NKECDFQTKFALSLSPGAHQKRLIPI	YLQNKECDF,VVSDDYLQNK,NKECDFQTKF	DLBCL
MYD88	c.818T>C	p.L273P	YLQSKECDFQTKFALSLSPGAHQKR[p.L273P]PIPIKYKAMKKEFPSILRFITVCDYT	HQKRPIPIK,RPIPIKYKA,QKRPIPIKY,AHQKRPIPIK,QKRPIPIKYK,HQKRPIPIKY,SPGAHQKRPI,RPIPIKYKAM	CLL,DLBCL
MYEF2	c.967A>G	p.K323E	LFDRPMHVKMDDKSVPHEEYRSHDG[p.K323E]ETPQLPRGLGGIGMGLGPGGQPISAS	ETPQLPRGL,RSHDGETPQL,GETPQLPRGL	TGCT
MYEOV	c.807delG	p.L269fs	CSTWGLPLRVAGSWLTVVTVEALGG[p.L269fs]GAWELGGLARWGPLCTHPQCQVLLLSSSTTSSSSSSSSSSLVEDVLCAKWFICPASFNPQNDSMR*	ALGGGAWEL,SLVEDVLCA,GLARWGPLC,LVEDVLCAK,KWFICPASF,SSSSSSSLV,CAKWFICPA,DVLCAKWFI,HPQCQVLLL,VEALGGGAW,WELGGLARW,CQVLLLSSS,SFNPQNDSM,SLVEDVLCAK,SSSSSSSSLV,SFNPQNDSMR,VTVEALGGGA,EALGGGAWEL,LARWGPLCTH,CQVLLLSSST,AKWFICPASF,ASFNPQNDSM,WELGGLARWG	STAD
MYEOV	c.905T>A	p.L302H	RRTGQVGPTMHPPPVSGASPLLLHH[p.L302H]HLLLLLIIILTC*	LLLHHHLLL,LLHHHLLLL,SPLLLHHHL,LHHHLLLLL,LLLHHHLLL,LLHHHLLLLL,SPLLLHHHLL,LHHHLLLLI,HHHLLLLLII	TGCT
MYH10	c.3271_3272insC	p.L1091fs	MISDLEERLKKEEKTRQELEKAKRK[p.L1091fs]PRRGDDRPAGPDRRAAGAD*	KAKRKPRRG,RPAGPDRRA,KPRRGDDRPA,RPAGPDRRAA	LUAD

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MYH11	c.2977G>A	p.E993K	EEEAARQKLQLEKVTAEAKIKKLED[p.E993K]KILVMDDQNNKLSKERKLLEERISDL	KLEDKILVM,KKLEDKILVM	HNSC
MYH11	c.3787_3789delAAG	p.K1263del	KENADLAGELRVLGQAKQEVEHKKK[p.K1263del]LEAQVQELQSKCSDGERARAELNDKVHK	VEHKKKLEA,KQEVEHKKKL	STAD
MYH13	c.931G>A	p.D311N	HIFYQIMSNKKPELIDLLLISTNPF[p.D311N]NFPFVSQGEVTVASIDDSEELLATDN	LISTNPFNF,STNPFNFPF,TNPFNFPFV,NPFNFPFVS,STNPFNFPFV,LLISTNPFNF,ISTNPFNFPF	CRC
MYH4	c.2369C>T	p.T790M	TKVFFKAGLLGTLEEMRDEKLAQLI[p.T790M]MRTQAICRGFLMRVEFRKMMERRESI	KLAQLIMRT,QLIMRTQAI,IMRTQAICR,AQLIMRTQA,DEKLAQLIM,LIMRTQAICR,IMRTQAICRG,RDEKLAQLIM,AQLIMRTQAI,MRTQAICRGF	LUAD
MYH6	c.2540C>T	p.T847M	AFMGVKNWPWMKLYFKIKPLLKSAE[p.T847M]MEKEMATMKEEFGRIKETLEKSEARR	LLKSAEMEK,KPLLKSAEM,KSAEMEKEM,AEMEKEMAT,EMEKEMATM,IKPLLKSAEM,LKSAEMEKEM,AEMEKEMATM	BRCA
MYH7	c.4459G>A	p.A1487T	ESQSELESSQKEARSLSTELFKLKN[p.A1487T]TYEESLEHLETFKRENKNLQEEISDL	TYEESLEHL,ELFKLKNTY,LKNTYEESL,KLKNTYEESL,NTYEESLEHL,TELFKLKNTY	KIRP
MYH7	c.5065C>T	p.R1689C	NDDLKENIAIVERRNNLLQAELEEL[p.R1689C]CAVVEQTERSRKLAEQELIETSERVQ	AELEELCAV,EELCAVVEQ,AELEELCAVV,EELCAVVEQT	CRC
MYH8	c.2354C>T	p.A785V	KFGHTKVFFKAGLLGLLEEMRDEKL[p.A785V]VQIITRTQAVCRGFLMRVEYQKMLQR	KLVQIITRT,VQIITRTQA,DEKLVQIIT,VQIITRTQAV,EMRDEKLVQI	TGCT
MYH8	c.3016C>A	p.H1006N	LTEEMAGLDETIAKLSKEKKALQET[p.H1006N]NQQTLDDLQAEEDKVNILTKAKTKLE	LQETNQQTL,ALQETNQQTL	LUAD
MYH8	c.3143G>A	p.R1048Q	LTKAKTKLEQQVDDLEGSLEQEKKL[p.R1048Q]QMDLERAKRKLEGDLKLAQESTMDME	KLQMDLERA,LEQEKKLQM,LQMDLERAK,QEKKLQMDL,KLQMDLERAK	CRC
MYH8	c.3349C>T	p.R1117C	NLISKIEDEQAVEIQLQKKIKELQA[p.R1117C]CIEELGEEIEAERASRAKAEKQRSDL	KIKELQACI,KKIKELQAC,KKIKELQACI,KELQACIEEL	LUAD
MYO18A	c.627delC	p.P209fs	PRPGHRSRAPELVTKKFPVDLRLPP[p.P209fs]WCPCPHLPSGSWSCNDGPLETLASPCGAQPCWIGAPRARPVGVWSTLLSLVQAPRTWPWGWCQEIDWWRLMGTMWRASPGMRLWR*	GVWSTLLSL,RLMGTMWRA,TMWRASPGM,VWSTLLSLV,VQAPRTWPW,WWRLMGTMW,RARPVGVWS,GTMWRASPG,MWRASPGMR,QPCWIGAPR,CWIGAPRAR,LLSLVQAPR,ETLASPCGA,CPHLPSGSW,APRARPVGV,RPVGVWSTL,SLVQAPRTW,QEIDWWRLM,WRASPGMRL,RASPGMRLW,LPPWCPCPH,SPCGAQPCW,WPWGWCQEI,GVWSTLLSLV,WIGAPRARPV,TMWRASPGMR,TLLSLVQAPR,RASPGMRLWR,TWPWGWCQEI,DWWRLMGTMW,MWRASPGMRL,RARPVGVWST,GTMWRASPGM,WWRLMGTMWR,FPVDLRLPPW,APRARPVGVW,RPVGVWSTLL,GSWSCNDGPL,VGVWSTLLSL,LSLVQAPRTW,LVQAPRTWPW,CQEIDWWRLM,IDWWRLMGTM,WRASPGMRLW,LETLASPCGA,LPPWCPCPHL	STAD
MYO1D	c.326C>T	p.T109M	AAYKAMKRRSKDTCIVISGESGAGK[p.T109M]MEASKYIMQYIAAITNPSQRAEVERV	GAGKMEASK,AGKMEASKY,GKMEASKYI,KMEASKYIM,SGAGKMEASK,GAGKMEASKY,MEASKYIMQY,GKMEASKYIM,GESGAGKMEA	GBM
MYO1D	c.736G>A	p.E246K	LQKSLSSYNYIIHVGAQLKSSINDAA[p.E246K]KFRVVADAMKVIGFKPEEIQTVYKIL	KSSINDAAK,SINDAAKFR,KFRVVADAM,DAAKFRVVA,SSINDAAKF,SINDAAKFRV,SSINDAAKFR,AAKFRVVADA,KFRVVADAMK,KSSINDAAKF,AKFRVVADAM	CRC
MYO3A	c.1573A>C	p.N525H	AVVGAQISEYLLEKSRVIHQAIGEK[p.N525H]HFHIFYYIYAGLAEKKKLAHYKLPEN	AIGEKHFHI,IGEKHFHIF,KHFHIFYYI,HFHIFYYIY,HQAIGEKHF,GEKHFHIFY,EKHFHIFYY,HFHIFYYIY,HFHIFYYIYA,IGEKHFHIFY,GEKHFHIFYY,KHFHIFYYIY,QAIGEKHFHI,IHQAIGEKHF,AIGEKHFHIF	CRC
MYO3A	c.1574A>G	p.N525S	AVVGAQISEYLLEKSRVIHQAIGEK[p.N525S]SFHIFYYIYAGLAEKKKLAHYKLPEN	AIGEKSFHI,KSFHIFYYI,GEKSFHIFY,SFHIFYYIY,HQAIGEKSF,IGEKSFHIF,EKSFHIFYY,KSFHIFYYIY,SFHIFYYIYA,IGEKSFHIFY,GEKSFHIFYY,QAIGEKSFHI,IHQAIGEKSF,HQAIGEKSFH,AIGEKSFHIF	KIRC,OV

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
MYO5B	c.1214C>T	p.A405V	KLVTTSETYVKTMSLQQVINARNAL[p.A405V]VKHIYAQLFGWIVEHINKALHTSLKQ	VINARNALV,LVKHIYAQL,RNALVKHIY,VKHIYAQLF,ALVKHIYAQL,QVINARNALV,VINARNALVK,RNALVKHIYA,LVKHIYAQLF,ARNALVKHIY	BRCA
MYO5B	c.2123G>T	p.R708L	VLETIRISAAGYPSRWAYHDFFNRY[p.R708L]LVLVKKRELANTDKKAICRSVLENLI	FFNRYLVLV,DFFNRYLVL,FNRYLVLVK,HDFFNRYLV,AYHDFFNRYL,HDFFNRYLVL	LUAD
MYO6	c.2742_2743insA	p.Q914fs	EQIQKEYDALVKSSEELLSALQKKK[p.Q914fs]TAGRGSRKAEAYSRRNGKGKKKT*	KTAGRGSRK,LQKKKTAGR,GSRKAEAYS,EAYSRRNGK,YSRRNGKGK,RGSRKAEAY,KTAGRGSRKA,GSRKAEAYSR,AYSRRNGKGK,YSRRNGKGKK	GBM
MYO6	c.3538G>A	p.D1180N	IPARQREIEMNRQQRFFRIPFIRPA[p.D1180N]NQYKDPQSKKKGWWYAHFDGPWIARQ	FIRPANQYK,IPFIRPANQY	CRC
MYO7B	c.6119C>A	p.P2040H	KQTSEPSYPDVILIAINRHGVLLIH[p.P2040H]HKTKDLLTTYPFTKISSWSSGSTYFH	VLLIHHKTK,LLIHHKTKDL,GVLLIHHKTK,RHGVLLIHHK,HKTKDLLTTY	LUAD
MYO9A	c.500G>A	p.R167Q	QPQQKDFDDLCSLPDLNEKTLLENL[p.R167Q]QNRFKHEKIYTYVGSILIVINPFKFL	LQNRFKHEK,TLLENLQNR,LLENLQNRF,KTLLENLQNR,TLLENLQNRF,LQNRFKHEKI	CRC
MYO9A	c.6536G>A	p.R2179Q	FLRAMGLQERKETIRGVYSVIDQLS[p.R2179Q]QTHLNTLERLIFHLVRIALQEDTNRM	SVIDQLSQT,QTHLNTLER,LSQTHLNTL,QLSQTHLNTL	CRC
MYO9B	c.281G>T	p.R94L	KESGGEEWVLDANDSPVHRVLLWPR[p.R94L]LAQDEHPQEDGYYFLLQERNADGTIK	RVLLWPRLA,HRVLLWPRL	LUAD
MYOCD	c.1478C>T	p.T493M	AGSLPDTFNDASPSFGLHPSPVHVC[p.T493M]MEESLMSSLNGGSVPSELDGLDSEKD	HPSPVHVCM,MEESLMSSL,CMEESLMSSL,VHVCMEESLM	HNSC
MYOCD	c.678delC	p.G226fs	ENDRNDSASQPSHQSDAGKQGLGPP[p.G226fs]APP*	GKQGLGPPA	STAD
MYOCD	c.910_912delCAG	p.Q310del	AYARLLQQQQLFLQLQILSQQQQQQ[p.Q310del]HRFSYLGMHQAQLKEPNEQMVRNPNSSS	SQQQQQQHRF	PRAD
MYOF	c.495_496insG	p.G165fs	PGMGGDGEEDEGDEDRLDNAVRGPG[p.G165fs]AQGASWDGVGSSACSEAHQSKEQPADAVK*	GPGAQGASW,SACSEAHQSK,AVRGPGAQGA	LUAD
MYOM1	c.188G>A	p.R63Q	VYTQGSTAYSSRSSAAHRRESEAFR[p.R63Q]QASASSSQQQASQHALSSEVSRKAAS	AFRQASASS,RESEAFRQA,SEAFRQASA,RQASASSSQ,AFRQASASSS,RESEAFRQAS,RQASASSSQQ,SEAFRQASAS	HNSC
MYOM2	c.2962G>A	p.D988N	DHSKLYLKNPDKEDLGTYSVSVSDT[p.D988N]NGVSSSFVLDPEELERLMALSNEIKN	VSVSDTNGV,DTNGVSSSF,NGVSSSFVL,SVSVSDTNGV,DTNGVSSSFV,SDTNGVSSSF	CESC
MYOZ2	c.751G>A	p.E251K	LSGRRSFNRTPKGWISENIPIVITT[p.E251K]KPTDDTTVPESEDL*	TTKPTDDTTV	CRC
MYT1	c.676G>A	p.E226K	AAEGAASEEGEKGLFIQPEDAEEVV[p.E226K]KVTTERSQDLCPQSLEDAASEESSKQ	EVVKVTTER,AEEVVKVTT	CRC
MYT1L	c.1052C>A	p.P351Q	SLECLRNQCFDLARKLSETNPQERN[p.P351Q]QQQNMNIRQHVRPEEDFPGRTPDRNY	QERNQQQNM,QQQNMNIRQH	LUAD
N4BP2L2	c.1516C>T	p.R506C	STKNKKRRKKRIFNLVPNFDLLGQS[p.R506C]CIGVKEREKCDLLTKNHGLKITLGEE	LLGQSCIGV,FDLLGQSCI,LLGQSCIGVK	UCEC
NAA11	c.551C>A	p.T184K	RRQMDLKKGGYVVLGSRENQETQGS[p.T184K]KLSDSEEACQQKNPATEESGSDSKEP	NQETQGSKL	LUAD
NAA16	c.1542delT	p.H514fs	CISAYQRLGRYGDALKKCHEVERHF[p.H514fs]LR*	HEVERHFLR	STAD
NAA25	c.2420C>A	p.S807Y	DIYELDTSGLEDTMEIQERIENSFK[p.S807Y]YLLDQLKDVFSKCKGDLLEVKDGNLK	YLLDQLKDV,RIENSFKYL,IENSFKYLL,KYLLDQLKDV,YLLDQLKDVF,SFKYLLDQLK,QERIENSFKY,NSFKYLLDQL	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
NAB1	c.216G>C	p.L72F	EEFLEIMALVGMASKPLHVRRLQKA[p.L72F]FRDWVTNPGLFNQPLTSLPVSSIPIY	RLQKAFRDW,HVRRLQKAF,LQKAFRDWV,RLQKAFRDWV,HVRRLQKAFR,LHVRRLQKAF,RRLQKAFRDW,LQKAFRDWVT	LUAD
NANOS3	c.548C>T	p.S183L	KTQDTGHRRGGGGGAGFRGAGKSEP[p.S183L]LPSCSPSMST*	RGAGKSEPL,EPLPSCSPSM,FRGAGKSEPL	HNSC
NAP1L3	c.1058C>G	p.P353R	MIQKYDEPILKFLSDVSLKFSKPGQ[p.P353R]RVSYTFEFHFLPNPYFRNEVLVKTYI	RVSYTFEFH,PGQRVSYTF,QRVSYTFEF,SKPGQRVSY,RVSYTFEFHF,SLKFSKPGQR,FSKPGQRVSY,KPGQRVSYTF,GQRVSYTFEF,LKFSKPGQRV	TGCT
NAP1L4	c.854_855CC>AA	p.P285Q	VTVKTIKKKQKHKGRGTVRTITKQV[p.P285Q]QNESFFNFFNPLKASGDGESLDEDSEF	VQNESFFNF,KQVQNESFF,TKQVQNESF,QVQNESFFNF,VQNESFFNFF,ITKQVQNESF,TKQVQNESFF	SKCM
NAPSA	c.362G>A	p.R121Q	DTGSSNLWVPSRRCHFFSVPCWLHH[p.R121Q]QFDPKASSSFQANGTKFAIQYGTGRV	WLHHQFDPK,VPCWLHHQF,HQFDPKASS,WLHHQFDPKA,CWLHHQFDPK,SVPCWLHHQF,QFDPKASSSF,HQFDPKASSS	UCEC
NARS2	c.719C>G	p.P240R	AFLTVSGQLHLEVMSGAFTQVFTFG[p.P240R]RTFRAENSQSRRHLAEFYMIEAEISF	FTFGRTFRA,FTQVFTFGR,VFTFGRTFR,QVFTFGRTF,QVFTFGRTFR,AFTQVFTFGR,TQVFTFGRTF	BRCA
NAT10	c.1178T>C	p.I393T	IQYIHPADAVKLGQAELVVIDEAAA[p.I393T]TPLPLVKSLLGPYLVFMASTINGYEG	AAATPLPLV,AATPLPLVK,EAAATPLPL,TPLPLVKSL,IDEAAATPL,DEAAATPLP,VIDEAAATPL,AAATPLPLVK,EAAATPLPLV,TPLPLVKSLL,DEAAATPLPL	TGCT
NBPF1	c.2428G>A	p.E810K	SSSHVEWEDAVHIIPENESDDEEEE[p.E810K]KKGPVSPRNLQESEEEEVPQESWDEG	KKGPVSPRNL	MM
NBPF14	c.73C>T	p.R25C	MVVSAGPWSSEKAEMNILEINEKL[p.R25C]CPQLAENKQQFGNLKERCFVTQLAGF	KLCPQLAENK	PAAD
NBPF16	c.1347delT	p.D449fs	RELLDEKEPEVLQDSLDRCYSTPSD[p.D449fs]ILNCLT*	RCYSTPSDI,TPSDILNCL,STPSDILNCL,RCYSTPSDIL	PAAD
NBPF3	c.1472A>T	p.D491V	QEEEEDQGPPCPRLSRELPEVVEPE[p.D491V]VLQDSLDRWYSTPFSYPELPDSCQPY	LPEVVEPEV,ELPEVVEPEV	KIRC
NCAM2	c.2092G>T	p.G698C	GYSEPTVYEFSMPPKPNIIKDTLFN[p.G698C]CLGLGAVIGLGVAALLLILVVTDVSC	DTLFNCLGL,TLFNCLGLGA,IIKDTLFNCL,KDTLFNCLGL	LUAD
NCAPD2	c.659G>T	p.R220L	VSLVTGCCYRLLENPTINHQKNRPT[p.R220L]LEAITHLLGVALTRYNHMLSATVKII	TLEAITHLL,KNRPTLEAI,LEAITHLLG,HQKNRPTLEA,RPTLEAITHL,INHQKNRPTL,QKNRPTLEAI,LEAITHLLGV	LUAD
NCAPD3	c.2725delC	p.Q909fs	ASSADADHSPSSQGSSEAPASQPPP[p.Q909fs]RSEVLSCPL*	QPPPRSEVL,RSEVLSCPL,EAPASQPPPR,SQPPPRSEVL	STAD
NCAPH	c.1398delA	p.T466fs	HWRFRPRRKQDAPSQSENKKKSTKK[p.T466fs]ILKLTLKMILTLMYILEKQRLLLF*	KMILTLMYI,MILTLMYIL,YILEKQRLL,ILKLTLKMI,TLKMILTLM,LTLMYILEK,MYILEKQRL,KKSTKKILK,KILKLTLKM,LKMILTLMY,LMYILEKQR,LKLTLKMIL,LTLKMILTL,LEKQRLLLF,KLTLKMILTL,KMILTLMYIL,YILEKQRLLL,ILTLMYILEK,MYILEKQRLL,ILEKQRLLLF,KKKSTKKILK,STKKILKLTL,TLKMILTLMY,TLMYILEKQR,ILKLTLKMIL,KKSTKKILKL,KKILKLTLKM,LTLKMILTLM,LKMILTLMYI,LMYILEKQRL	STAD
NCOA3	c.3759_3760delGC	p.Q1253fs	RSRELLSHHFRQQRVAMMMQQQQQQ[p.Q1253fs]TAAAAAAAAATATATATAATAANPGLQPTS*	QTAAAAAAA,MQQQQQQTA,QQQQQQTAA,QQQQQTAA,QQQQTAAAA,QQQTAAAAA,QQTAAAAAA,MMMQQQQQQT,MMQQQQQQTA,ATATATATAA,ATATATAATA,QTAAAAAAAA,TAATAANPGL,MQQQQQQTAA,QQQQQQTAAA,QQQQQTAAAA,QQQQTAAAAA,QQQTAAAAAA,QQTAAAAAAA	PAAD
NCOA4	c.1685G>A	p.R562Q	ADWVLPGKKMGNLSQLSSGEDKWLL[p.R562Q]QKKAQEVLLNSPLQEEHNFPPDHYGL	LLQKKAQEV,LQKKAQEVL,WLLQKKAQEV,LLQKKAQEVL,LQKKAQEVLL	CRC
NCOA7	c.1107G>T	p.E369D	DSRPIVPLEKSTGHTPTKPSGSSVS[p.E369D]DKLKKLDSSRETSHGSPTVTKLSKEP	SSVSDKLKK,GSSVSDKLKK	UCEC
NCOR1	c.4682G>A	p.R1561Q	PGVDPVVSHSPFDPHHRGSTAGEVY[p.R1561Q]QSHLPTHLDPAMPFHRALDPAAAAYL	YQSHLPTHL,EVYQSHLPT,VYQSHLPTHL,EVYQSHLPTH,GEVYQSHLPT	HNSC

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NCR1	c.772C>T	p.R258W	TYLLTTETGLQKDHALWDHTAQNLL[p.R258W]WMGLAFLVLVALVWFLVEDWLSRKRT	LLWMGLAFL,WMGLAFLVL,AQNLLWMGL,LWMGLAFLV,HTAQNLLWM,NLLWMGLAF,NLLWMGLAFL,LLWMGLAFLV,WMGLAFLVL,AQNLLWMGLA,LWMGLAFLVL,QNLLWMGLAF	UCEC
NDST3	c.1279G>A	p.V427I	LNKKFALEHGIPTDMGYAVAPHHSG[p.V427I]IYPVHVQLYEAWKKVWNIKITSTEEY	GIYPVHVQL,AVAPHHSGI,IYPVHVQLY,VAPHHSGIY,GIYPVHVQLY,AVAPHHSGIY,YAVAPHHSGI,APHHSGIYPV,SGIYPVHVQL	LUAD
NEDD4L	c.570_572delTCC	p.P194del	DMEHGWEVVDSNDSASQHQEELPPP[p.P194del]LPPGWEEKVDNLGRTYYVNHNNRTTQWH	HQEELPPPL,LPPPLPPGW	CLL
NEDD9	c.2392G>A	p.A798T	RNKVMNSSNQLCEQLKTIVMATKMA[p.A798T]TLHYPSTTALQEMVHQVTDLSRNAQL	VMATKMATL,TLHYPSTTA,ATKMATLHY,KMATLHYPS,MATKMATLHY,IVMATKMATL,KMATLHYPST,TLHYPSTTAL,ATKMATLHYP,ATLHYPSTTA,VMATKMATLH,TKMATLHYPS	CRC
NEDD9	c.946G>A	p.A316T	ARRHQSLSPNHPPPQLGQSVGSQND[p.A316T]TYDVPRGVQFLEPPAETSEKANPQER	SVGSQNDTY,DTYDVPRGV,TYDVPRGVQF,QSVGSQNDTY	CRC
NEFH	c.1933G>A	p.E645K	SPVKEEAKSPAEVKSPEKAKSPTKE[p.E645K]KAKSPEKAKSPEKEEAKSPEKAKSPV	KAKSPTKEK,KSPTKEKAK,KEKAKSPEK,KAKSPTKEKA,KEKAKSPEKA	KIRP
NEFH	c.1993_1994insAGGAAG	p.665_666insEE	PTKEEAKSPEKAKSPEKEEAKSPEK[p.665_666insEE]EEAKSPVKAEAKSPEKAKSPVKAEAKSPEKA	EEAKSPVKA,KEEAKSPVKA	ACC,KIRP
NEFH	c.2009T>A	p.V670E	EAKSPEKAKSPEKEEAKSPEKAKSP[p.V670E]EKAEAKSPEKAKSPVKAEAKSPEKAK	KSPEKAEAK,KAKSPEKAEA	TGCT
NEFM	c.638C>T	p.A213V	RFEEEARLRDDTEAAIRALRKDIEE[p.A213V]VSLVKVELDKKVQSLQDEVAFLRSNH	ALRKDIEEV,EVSLVKVEL,RKDIEEVSL,IEEVSLVKV,VSLVKVELDK,EEVSLVKVEL	STAD
NEK1	c.1822C>T	p.R608C	EVYLARLRQIRLQNFNERQQIKAKL[p.R608C]CGEKKEANHSEGQEGSEEADMRRKKI	KAKLCGEKK,QIKAKLCGEK	CRC
NEK11	c.1121G>A	p.R374Q	KLQAADEKARKLKKIVEEKYEENSK[p.R374Q]QMQELRSRNFQQLSVDVLHEKTHLKG	NSKQMQELR,QMQELRSRNF,EKYEENSKQM,KQMQELRSRN	UCEC
NEK2	c.715C>A	p.R239S	PPFTAFSQKELAGKIREGKFRRIPY[p.R239S]SYSDELNEIITRMLNLKDYHRPSVEE	KFRRIPYSY,SYSDELNEI,IPYSYSDEL,SYSDELNEII,KFRRIPYSYS,GKFRRIPYSY,YSYSDELNEI	LUAD
NEK8	c.2070delC	p.V690fs	VTSVSCCHGNTLLAVRSVTDEPVPP[p.V690fs]EAPGFTSGPP*	EPVPPEAPGF	STAD
NELL2	c.509G>A	p.G170D	QTHLNSGVILSIHHLDHRYLELESS[p.G170D]DHRNEVRLHYRSGSHRPHTEVFPYIL	ESSDHRNEV,ESSDHRNEVR,LESSDHRNEV	TGCT
NES	c.1831G>C	p.V611L	LKSLEKENKELLKDVEVVRPLEKEA[p.V611L]LGQLKPTGKEDTQTLQSLQKENQELM	LEKEALGQL,ALGQLKPTGK,KEALGQLKPT	KIRC
NF1	c.2027_2028insC	p.T676fs	PGASLRKGKGNSSMDSAAGCSGTPP[p.T676fs]DLPTSPDQTRSGPVHVSVEP*	QTRSGPVHV,RSGPVHVSV,SPDQTRSGPV	STAD
NF1	c.4974_4977delTCTC	p.F1658fs	AKPYEIVVDLTHTGPSNRFKTDFLS[p.F1658fs]GLLFFLALLTTTSPQSISITVTPGSGSTPSIMSGC*	KTDFLSGLL,FLSGLLFFL,GLLFFLALL,FLALLTTTS,DFLSGLLFF,RFKTDFLSG,TTSPQSISI,STPSIMSGC,SPQSISITV,FKTDFLSGL,TDFLSGLLF,SGLLFFLAL,GSGSTPSIM,KTDFLSGLLF,FLSGLLFFLA,LLFFLALLTT,FLALLTTTSP,LLTTTSPQSI,DFLSGLLFFL,RFKTDFLSGL,TTTSPQSISI,TSPQSISITV,TPGSGSTPSI,FKTDFLSGLL,TDFLSGLLFF,LSGLLFFLAL	GBM
NFASC	c.766G>A	p.V256I	QFEEDQFQPGVWHDHSKYPGSVNSA[p.V256I]ILRLSPYVNYQFRVIAINEVGSSHPS	AILRLSPYV,GSVNSAILR,SAILRLSPY,YPGSVNSAI,NSAILRLSPY,SAILRLSPYV,KYPGSVNSAI,ILRLSPYVNY,YPGSVNSAIL	CRC
NFAT5	c.2716C>G	p.Q906E	QQQQQQQQVMESSAAMVMEMQQSIC[p.Q906E]EAAAQIQSELFPSTASANGNLQQSPV	EMQQSICEA,SICEAAAQI,MQQSICEAA,CEAAAQIQS,QSICEAAAQI,EAAAQIQSEL,MEMQQSICEA,MQQSICEAAA	KIRC

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NFE2L2	c.100C>G	p.R34G	PGLPSQQDMDLIDILWRQDIDLGVS[p.R34G]GEVFDFSQRRKEYELEKQKKLEKERQ	IDLGVSGEVF,LGVSGEVFDF	BLCA
NFE2L2	c.101G>A	p.R34Q	PGLPSQQDMDLIDILWRQDIDLGVS[p.R34Q]QEVFDFSQRRKEYELEKQKKLEKERQ	IDLGVSQEVF,LGVSQEVFDF	LUSC
NFE2L2	c.235G>A	p.E79K	LEKERQEQLQKEQEKAFFAQLQLDE[p.E79K]KTGEFLPIQPAQHIQSETSGSANYSQ	QLDEKTGEFL,LQLDEKTGEF,DEKTGEFLPI	BLCA,HNSC
NFE2L2	c.235G>C	p.E79Q	LEKERQEQLQKEQEKAFFAQLQLDE[p.E79Q]QTGEFLPIQPAQHIQSETSGSANYSQ	AQLQLDEQT,QLDEQTGEF,EQTGEFLPI,QLDEQTGEFL,LQLDEQTGEF,DEQTGEFLPI	HNSC,LUSC
NFE2L2	c.241G>A	p.G81S	KERQEQLQKEQEKAFFAQLQLDEET[p.G81S]SEFLPIQPAQHIQSETSGSANYSQVA	QLDEETSEF,EETSEFLPI,SEFLPIQPA,QLDEETSEFL,LQLDEETSEF,DEETSEFLPI,SEFLPIQPAQ	LUSC
NFE2L2	c.85G>C	p.D29H	LELPPPGLPSQQDMDLIDILWRQDI[p.D29H]HLGVSREVFDFSQRRKEYELEKQKKL	ILWRQDIHL,HLGVSREVF,DIHLGVSREV,IHLGVSREVF	CESC,HNSC,LUSC
NFE2L2	c.88C>T	p.L30F	ELPPPGLPSQQDMDLIDILWRQDID[p.L30F]FGVSREVFDFSQRRKEYELEKQKKLE	ILWRQDIDF,IDFGVSREV,IDFGVSREVF,FGVSREVFDF	LUSC
NFE2L2	c.92G>C	p.G31A	LPPPGLPSQQDMDLIDILWRQDIDL[p.G31A]AVSREVFDFSQRRKEYELEKQKKLEK	DLAVSREVF,WRQDIDLAV,AVSREVFDF,ILWRQDIDLA,IDLAVSREVF,LAVSREVFDF	LUSC
NFIA	c.882G>C	p.L294F	SVTELVRVSQTPIAAGTGPNFSLSD[p.L294F]FESSSYYSMSPGAMRRSLPSTSSTSS	LSDFESSSY,SDFESSSYY,FESSSYYSM,GPNFSLSDF,LSDFESSSYY,SLSDFESSSY,FESSSYYSMS	LUAD
NHEJ1	c.326G>A	p.R109Q	LKDAAHPSEATFSCDCVADALILRV[p.R109Q]QSELSGLPFYWNFHCMLASPSLVSQH	RVQSELSGL,QSELSGLPF,QSELSGLPFY,ALILRVQSEL,VQSELSGLPF,LRVQSELSGL	UCEC
NHLRC1	c.612delT	p.F204fs	DVTITNDCHVVVTDAGDRSIKVFDF[p.F204fs]LARSSLSLEANSPYLGVWRPPLRMGLW*	LSLEANSPY,FLARSSLSL,SLEANSPYL,YLGVWRPPL,RSIKVFDFL,SIKVFDFLA,LGVWRPPLR,EANSPYLGV,FDFLARSSL,ANSPYLGVW,SIKVFDFLAR,DFLARSSLSL,PYLGVWRPPL,RSIKVFDFLA,LARSSLSLEA,VWRPPLRMGL,SLSLEANSPY,YLGVWRPPLR,LSLEANSPYL,LEANSPYLGV,LGVWRPPLRM,EANSPYLGVW	STAD
NHP2L1	c.250C>T	p.R84C	DAEPLEIILHLPLLCEDKNVPYVFV[p.R84C]CSKQALGRACGVSRPVIACSVTIKEG	YVFVCSKQAL,NVPYVFVCSK,FVCSKQALGR	GBM
NHS	c.4681G>A	p.D1561N	ATEILKSPILPKPPGELTAESPQST[p.D1561N]NDAHQGSQGAEALSPLSPCSPRVNAE	AESPQSTNDA	TGCT
NID2	c.3103delC	p.R1035fs	EPTQRPPTICERWRENLLEHYGGTP[p.R1035fs]GMTSTCPSAMTWATSSPCSATERATSAGVWTKMAERCRAPAPSQAPPLRVYPPSLHPWSGPRPGQM*	GMTSTCPSA,ATSAGVWTK,SLHPWSGPR,GVWTKMAER,VYPPSLHPW,RVYPPSLHP,MTSTCPSAM,SQAPPLRVY,WTKMAERCR,MTWATSSPC,TSAGVWTKM,HPWSGPRPG,PLRVYPPSL,LEHYGGTPG,EHYGGTPGM,STCPSAMTW,AMTWATSSP,TERATSAGV,CPSAMTWAT,AERCRAPAP,KMAERCRAPA,GMTSTCPSAM,AMTWATSSPC,TSSPCSATER,RATSAGVWTK,RVYPPSLHPW,WTKMAERCRA,RCRAPAPSQA,MTSTCPSAMT,MTWATSSPCS,TSAGVWTKMA,APAPSQAPPL,APSQAPPLRV,LEHYGGTPGM,TERATSAGVW,ATSAGVWTKM,SQAPPLRVYP,CPSAMTWATS,AERCRAPAPS,TSTCPSAMTW	STAD
NINL	c.4096C>T	p.R1366C	VRALQATEEKQRGAEKQSRLLEEKV[p.R1366C]CALNKLVSRIAPAALSV*	LLEEKVCAL,KVCALNKLV,CALNKLVSR,RLLEEKVCAL	CRC
NKD1	c.856_857insC	p.P286fs	AGIENYTSQFGPGSPSVAQKSELPP[p.P286fs]PHLQSHSISLP*	HLQSHSISL,AQKSELPPP,LQSHSISLP,AQKSELPPPH,QKSELPPPHL	STAD
NKD2	c.1315_1317delCAC	p.H447del	GYAVPViQRHEHHHHHEHHHHHHHH[p.H447del]FHPS*	EHHHHHHHHF	TGCT

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NLK	c.570delT	p.C190fs	KKMPNVFQNLVSCKRVFRELKMLCF[p.C190fs]LSMIMYSLPLTYSNLHTLTILKKYMLSQN*	IMYSLPLTY,YSNLHTLTI,KMLCFLSMI,FLSMIMYSL,SMIMYSLPL,MIMYSLPLT,LTYSNLHTL,SLPLTYSNL,NLHTLTILK,HTLTILKKY,LTILKKYML,MLCFLSMIM,RELKMLCFL,LKMLCFLSM,LCFLSMIMY,SNLHTLTIL,LPLTYSNLH,MIMYSLPLTY,KMLCFLSMIM,SMIMYSLPLT,IMYSLPLTYS,FLSMIMYSLP,MLCFLSMIMY,NLHTLTILKK,SNLHTLTILK,CFLSMIMYSL,YSLPLTYSNL,TYSNLHTLTI,ELKMLCFLSM,LSMIMYSLPL,LKMLCFLSMI,YSNLHTLTIL,LHTLTILKKY,RELKMLCFLS,LPLTYSNLHT	STAD
NLRC4	c.1225G>A	p.E409K	SDFIRSLDHCGDLALEGVFSHKFDF[p.E409K]KLQDVSSVNEDVLLTTGLLCKYTAQR	VFSHKFDFK,FSHKFDFKL,FKLQDVSSV,GVFSHKFDFK,VFSHKFDFKL,HKFDFKLQDV	CRC
NLRC4	c.1777G>A	p.D593N	KSALSQEFEAFFQGKSLYINSGNIP[p.D593N]NYLFDFFEHLPNCASALDFIKLDFYG	NIPNYLFDF,INSGNIPNY,IPNYLFDFF,SGNIPNYLF,NSGNIPNYLF,GNIPNYLFDF,NIPNYLFDFF,NYLFDFFEHL,YINSGNIPNY	CRC
NLRC4	c.862C>T	p.R288W	ALIKENHRFKNMVIVTTTTECLRHI[p.R288W]WQFGALTAEVGDMTEDSAQALIREVL	ECLRHIWQF,RHIWQFGAL,WQFGALTAE,WQFGALTAEV,CLRHIWQFGA,TECLRHIWQF,LRHIWQFGAL,RHIWQFGALT,HIWQFGALTA	BRCA
NLRP3	c.469C>T	p.R157C	MKKDYRKKYRKYVRSRFQCIEDRNA[p.R157C]CLGESVSLNKRYTRLRLIKEHRSQQE	RNACLGESV,CLGESVSLNK	LUAD
NLRP4	c.685G>A	p.V229I	LISREWPDPAAPITEIVSQPERLLF[p.V229I]IIDSFEELQGGLNEPDSDLCGDLMEK	SQPERLLFI,FIIDSFEEL,RLLFIIDSF,QPERLLFII,SQPERLLFII,LFIIDSFEEL	CRC
NLRP5	c.1175G>A	p.R392H	LGSVLNNDTKLCKDWAEKQPPFTLI[p.R392H]HSLLRKVLLPESFLIVTVRDVGTEKL	LIHSLLRKV,TLIHSLLRK,FTLIHSLLR,PFTLIHSLL,HSLLRKVLL,PPFTLIHSL,KQPPFTLIH,TLIHSLLRKV,FTLIHSLLRK,QPPFTLIHSL,LIHSLLRKVL	CRC
NLRP5	c.2209C>T	p.R737W	LPINQNLDLIASSFCLQHCPYLRKI[p.R737W]WVDVKGIFPRDESAEACPVVPLWMRD	YLRKIWVDV,IWVDVKGIF,CPYLRKIWV,YLRKIWVDVK,PYLRKIWVDV,WVDVKGIFPR,RKIWVDVKGI,KIWVDVKGIF	GBM
NLRP6	c.1832A>G	p.E611G	CPGVAPEVTEGAKGLEDTEEPEEEE[p.E611G]GGEEPNYPLELLYCLYETQEDAFVRQ	EEGGEEPNY,EEEGGEEPNY	THCA
NME9	c.223G>A	p.E75K	QKMRIEVGLDLLHFALAEADRLDVL[p.E75K]KKYRGKCEPTFLFYAGGELVAVVRGA	KKYRGKCEPT	CRC
NMU	c.53C>A	p.A18E	MLRTESCRPRSPAGQVA[p.A18E]EASPLLLLLLLLAWCAGACRGAPILP	QVAEASPLL,EASPLLLLL,GQVAEASPL,AEASPLLLL,QVAEASPLLL,EASPLLLLLL,GQVAEASPLL,AEASPLLLLL	ACC
NMU	c.56C>A	p.A19E	MLRTESCRPRSPAGQVAA[p.A19E]ESPLLLLLLLLAWCAGACRGAPILPQ	QVAAESPLL,GQVAAESPL,VAAESPLLL,AESPLLLLL,QVAAESPLLL,GQVAAESPLL,VAAESPLLLL,AESPLLLLLL	ACC
NNMT	c.697G>A	p.E233K	EQKFSSLPLGREAVEAAVKEAGYTI[p.E233K]KWFEVISQSYSSTMANNEGLFSLVAR	YTIKWFEVI,GYTIKWFEV,KEAGYTIKW,AVKEAGYTIK,GYTIKWFEVI,KWFEVISQSY,KEAGYTIKWF	UCEC
NOL9	c.172T>G	p.S58A	PRRRLGSLRWCGRRRLRWRLLQAQA[p.S58A]AGVDWREGARQVSRAAAARRPNTATP	WRLLQAQAA,RWRLLQAQAA	ACC
NOLC1	c.1283C>T	p.T428M	VTTKSPAVKPAAAPKQPVGGGQKLL[p.T428M]MRKADSSSSEEESSSSEEEKTKKMVA	LMRKADSSS,LMRKADSSSS	CRC
NOM1	c.70C>G	p.R24G	MAASRSAGEAGPGGSQGRVVRMK[p.R24G]GRGGRGPRRGPAGGGEKALKRLKLAV	RMKGRGGRG,KGRGGRGPR,QGRVVRMKGR,VVRMKGRGGR,KGRGGRGPRR	ACC
NOS1AP	c.901_903delCAG	p.Q306del	LGTETPLSTHHQMQLLQQLLQQQQQ[p.Q306del]TQVAVAQVHLLKDQLAAEAAARLEAQAR	LQQQQQTQV,LLQQQQQTQV,LQQQQQTQVA	BLCA
NOTCH1	c.7541_7542delCT	p.P2514fs	SYSSPVDNTPSHQLQVPEHPFLTPS[p.P2514fs]RVP*	HPFLTPSRV	CLL

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NOTCH2	c.17_18delCC	p.P6fs	MPALR[p.P6fs]RSAVGAAGALAVLRGPRACIAVSRWL*	ALRRSAVGA,AAGALAVLR,RSAVGAAGA,VLRGPRACI,ALAVLRGPR,MPALRRSAV,SAVGAAGAL,LRRSAVGAA,GAAGALAVL,RACIAVSRW,ALRRSAVGAA,AVGAAGALAV,ALAVLRGPRA,RSAVGAAGAL,GALAVLRGPR,VLRGPRACIA,RACIAVSRWL,MPALRRSAVG,VGAAGALAVL	BLCA
NOTCH2	c.57C>G	p.C19W	MPALRPALLWALLALWLC[p.C19W]WAAPAHALQCRDGYEPCVNEGMCVTY	LLALWLCWA,CWAAPAHAL,ALLALWLCW,WLCWAAPAH,ALLALWLCWA,LLALWLCWAA,ALWLCWAAPA,WLCWAAPAHA,WALLALWLCW,LCWAAPAHAL	ACC
NOTCH2	c.6314G>T	p.R2105L	LSPVICGPNRSFLSLKHTPMGKKSR[p.R2105L]LPSAKSTMPTSLPNLAKEAKDAKGSR	KSRLPSAKS,TPMGKKSRL,RLPSAKSTM,MGKKSRLPSA,KSRLPSAKST,LPSAKSTMPT,SRLPSAKSTM	LUAD
NOTCH2	c.6892C>T	p.R2298W	APAEGTHPGIAPQSRPPEGKHITTP[p.R2298W]WEPLPPIVTFQLIPKGSIAQPAGAPQ	HITTPWEPL,TPWEPLPPI,WEPLPPIVT,TTPWEPLPPI,KHITTPWEPL,WEPLPPIVTF,TPWEPLPPIV	CESC
NOX3	c.1210_1211delTG	p.C404fs	SLPRLAVDGPFGTALTDVFHYPVCV[p.C404fs]RCRGDRSHSLRCSSEIYMVQMQ*	RSHSLRCSS,SLRCSSEIY,VFHYPVCVR,HSLRCSSEI,LRCSSEIYM,SLRCSSEIYM,CVRCRGDRSH,RSHSLRCSSE,HSLRCSSEIY,DVFHYPVCVR,RCRGDRSHSL,CSSEIYMVQM	PRAD
NOX5	c.1401delT	p.P467fs	AVCIMEVNLLPSKVTHLLIKRPPFF[p.P467fs]TIDLVTTCI*	FTIDLVTTC,RPPFFTIDL,IKRPPFFTI,PPFFTIDLV,LLIKRPPFFT,FTIDLVTTCI,LIKRPPFFTI	STAD
NOXA1	c.18C>G	p.D6E	MASLG[p.D6E]ELVRAWHLGAQAVDRGDWARALHLFS	SLGELVRAW,GELVRAWHL,ELVRAWHLGA,ASLGELVRAW,GELVRAWHLG	ACC
NOXO1	c.8_9insG	p.G3fs	MAGP[p.G3fs]PIPSFSARGSPGADQEAPNVCLLCALVRRQRHLRAQELGRIQAAQEDPQGDLPGGGGPAAEI*	FSARGSPGA,LVRRQRHLR,RQRHLRAQE,HLRAQELGR,CLLCALVRR,NVCLLCALV,LPGGGGPAA,ALVRRQRHL,QRHLRAQEL,MAGPPIPSF,QEAPNVCLL,AQELGRIQA,QELGRIQAA,HLRAQELGRI,SFSARGSPGA,LVRRQRHLRA,RQRHLRAQEL,RAQELGRIQA,NVCLLCALVR,LLCALVRRQR,ALVRRQRHLR,APNVCLLCAL,CALVRRQRHL,AQELGRIQAA	KIRC
NPAS2	c.602A>G	p.Q201R	DSITPLLGHLPSDVMDQNLLNFLPE[p.Q201R]REHSEVYKILSSHMLVTDSPSPEYLK	NLLNFLPER,PEREHSEVY,REHSEVYKI,LPEREHSEV,FLPEREHSEV,LPEREHSEVY,REHSEVYKIL	OV
NPC1	c.1351G>A	p.E451K	GADVPFGPPLDIQILHQVLDLQIAI[p.E451K]KNITASYDNETVTLQDICLAPLSPYN	AIKNITASY,LQIAIKNIT,QVLDLQIAIK,IAIKNITASY,LQIAIKNITA	CRC
NPIP	c.812C>T	p.A271V	QPPPPTQQHSIIDNSLSLKTPSELS[p.A271V]VHSPSTLSSTLSG*	LKTPSELSV,SELSVHSPS,LSVHSPSTL,SLKTPSELSV,LKTPSELSVH,SELSVHSPST	PRAD
NPM1	c.859_860insTCTG	p.L287fs	KVEAKFINYVKNCFRMTDQEAIQDL[p.L287fs]CLAVEEVSLRK*	AIQDLCLAV,AVEEVSLRK,EAIQDLCLA,QEAIQDLCL,LAVEEVSLRK,EAIQDLCLAV,QEAIQDLCLA	LAML
NPM1	c.861_862insCTGC	p.L287fs	KVEAKFINYVKNCFRMTDQEAIQDL[p.L287fs]LLAVEEVSLRK*	AIQDLLLAV,LLAVEEVSL,AVEEVSLRK,EAIQDLLLA,QEAIQDLLL,LLLAVEEVSL,LAVEEVSLRK,EAIQDLLLAV,QEAIQDLLLA	LAML
NPM1	c.863_864insTCTG	p.W288fs	KVEAKFINYVKNCFRMTDQEAIQDL[p.W288fs]CLAVEEVSLRK*	AIQDLCLAV,AVEEVSLRK,EAIQDLCLA,QEAIQDLCL,LAVEEVSLRK,EAIQDLCLAV,QEAIQDLCLA	LAML
NPR3	c.412T>C	p.Y138H	LFSLVDRVAAARGAKPDLILGPVCE[p.Y138H]HAAAPVARLASHWDLPMLSAGALAAG	ILGPVCEHA,HAAAPVARL,CEHAAAPVA,GPVCEHAAA,ILGPVCEHAA,HAAAPVARLA	STAD
NPSR1	c.704G>A	p.R235Q	YMTIVAFLVYFIPLTIISIMYGIVI[p.R235Q]QTIWIKSKTYETVISNCSDGKLCSSY	IMYGIVIQT,IVIQTIWIK,MYGIVIQTI,QTIWIKSKT,YGIVIQTIW,IMYGIVIQTI,SIMYGIVIQT,VIQTIWIKSK,GIVIQTIWIK,MYGIVIQTIW,QTIWIKSKTY	CRC
NPTX1	c.787G>A	p.A263T	YMYAKVKKSLPEMYAFTVCMWLKSS[p.A263T]TTPGVGTPFSYAVPGQANELVLIEWG	LKSSTTPGV,WLKSSTTPGV,STTPGVGTPF	GBM
NPY1R	c.1111G>A	p.A371T	DYETIAMSTMHTDVSKTSLKQASPV[p.A371T]TFKKINNNDDNEKI*	KQASPVTFK,QASPVTFKK,LKQASPVTF,KQASPVTFKK,SLKQASPVTF	UCEC
NR2C1	c.809G>T	p.S270I	HPSGVKTESAVLMTSDKAESCQGDL[p.S270I]ITLANVVTSLANLGKTKDLSQNSNEM	AESCQGDLI,ITLANVVTSL,GDLITLANVV,AESCQGDLIT	KIRC
NR4A2	c.941G>T	p.R314L	RTVQKNAKYVCLANKNCPVDKRRRN[p.R314L]LCQYCRFQKCLAVGMVKEVVRTDSLK	RNLCQYCRF,KRRRNLCQY,NLCQYCRFQK,CPVDKRRRNL,RRNLCQYCRF	LUAD

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NR5A2	c.238G>A	p.E80K	SHGEQGQMPENMQVSQFKMVNYSYD[p.E80K]KDLEELCPVCGDKVSGYHYGLLTCES	KMVNYSYDK,KDLEELCPV,YSYDKDLEEL	CESC
NRAP	c.979G>A	p.E327K	YEEHRGKGSFPAMITPAYQNAKKAH[p.E327K]KLASDIKYRQDFNKMKGAAHYHSLPA	YQNAKKAHK,KAHKLASDI,KLASDIKYR,HKLASDIKY,YQNAKKAHKL,KAHKLASDIK,AYQNAKKAHK,KKAHKLASDI,AHKLASDIKY	CRC
NRAS	c.181C>A	p.Q61K	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61K]KEEYSAMRDQYMRTGEGFLCVFAINN	LDTAGKEEY,AGKEEYSAM,ILDTAGKEEY,DTAGKEEYSA	CRC,LAML,MM,SKCM,THCA
NRAS	c.182A>G	p.Q61R	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61R]REEYSAMRDQYMRTGEGFLCVFAINN	LDTAGREEY,AGREEYSAM,ILDTAGREEY,AGREEYSAMR,DTAGREEYSA	CLL,MM,OV,SKCM,TGCT,THCA,UCEC
NRAS	c.182A>T	p.Q61L	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61L]LEEYSAMRDQYMRTGEGFLCVFAINN	LDTAGLEEY,AGLEEYSAM,ILDTAGLEEY,LLDILDTAGL,DTAGLEEYSA	CRC,LUAD,MM,SKCM
NRAS	c.183A>C	p.Q61H	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61H]HEEYSAMRDQYMRTGEGFLCVFAINN	LDTAGHEEY,AGHEEYSAM,ILDTAGHEEY,DTAGHEEYSA	MM
NRAS	c.183A>T	p.Q61H	IEDSYRKQVVIDGETCLLDILDTAG[p.Q61H]HEEYSAMRDQYMRTGEGFLCVFAINN	LDTAGHEEY,AGHEEYSAM,ILDTAGHEEY,DTAGHEEYSA	LAML
NRAS	c.34G>T	p.G12C	MTEYKLVVVGA[p.G12C]CGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGACGV,VVGACGVGK,KLVVVGACGV,VVVGACGVGK	CRC
NRAS	c.35G>A	p.G12D	MTEYKLVVVGA[p.G12D]DGVGKSALTIQLIQNHFVDEYDPTIE	LVVVGADGV,VVGADGVGK,KLVVVGADGV,VVVGADGVGK	CRC,LAML,MM
NRAS	c.37G>C	p.G13R	MTEYKLVVVGAG[p.G13R]RVGKSALTIQLIQNHFVDEYDPTIED	VVGAGRVGK,RVGKSALTI,KLVVVGAGR,AGRVGKSAL,KLVVVGAGRV,VVVGAGRVGK,GRVGKSALTI	CRC,MM
NRAS	c.38G>A	p.G13D	MTEYKLVVVGAG[p.G13D]DVGKSALTIQLIQNHFVDEYDPTIED	VVGAGDVGK,KLVVVGAGDV,VVVGAGDVGK	LAML
NRG1	c.1441G>T	p.V481L	VSSMTVSMPSMAVSPFMEEERPLLL[p.V481L]LTPPRLREKKFDHHPQQFSSFHHNPA	LLLLTPPRL,LTPPRLREK,LLLTPPRLR,EEERPLLLL,EERPLLLLT,LLTPPRLREK,MEEERPLLLL	LUAD
NRG2	c.737C>T	p.T246M	LKKEVGKILCTDCATRPKLKKMKSQ[p.T246M]MGQVGEKQSLKCEAAAGNPQPSYRWF	KMKSQMGQV,SQMGQVGEK,KLKKMKSQM,MKSQMGQVG,KSQMGQVGEK,KLKKMKSQMG,KMKSQMGQVG,KKMKSQMGQV	CRC
NRG4	c.63_64insG	p.G21fs	ANRSRRALWSQSQVVLPEWGA[p.G21fs]VVM*	VLPEWGAVV,LPEWGAVVM,VVLPEWGAVV,VLPEWGAVVM,QVVLPEWGAV	CLL
NRXN3	c.307C>T	p.R103C	FETPEAYISLPKWNTKRMGSISFDF[p.R103C]CTTEPNGLILFTHGKPQERKDARSQK	CTTEPNGLI	LUAD
NRXN3	c.68C>A	p.P23H	MLGSDDFFYVGGSPSTADLPGS[p.P23H]HVSNNFMGCLKEVVYKNNDIRLELSR	GSHVSNNFM,STADLPGSH,STADLPGSHV,HVSNNFMGCL,LPGSHVSNNF	LUAD
NSMCE1	c.730G>A	p.D244N	YFQSNAEPRCPHCNDYWPHEIPKVF[p.D244N]NPEKERESGVLKSNKKSLRSRQH*	KVFNPEKER,HEIPKVFNP,HEIPKVFNPE	UCEC
NSMCE2	c.91_92insA	p.Q31fs	SNSGSTGFISFSGVESALSSLKNFQ[p.Q31fs]SLYQLWYGHSF*	FQSLYQLWY,YQLWYGHSF,SLKNFQSLY,SSLKNFQSL,NFQSLYQLW,KNFQSLYQL,SLYQLWYGH,SSLKNFQSLY,KNFQSLYQLW,LYQLWYGHSF,NFQSLYQLWY,LSSLKNFQSL,LKNFQSLYQL	KIRC
NT5C3	c.7G>C	p.A3P	MR[p.A3P]PPSMDRAAVARVGAVASASVCALVAG	RPPSMDRAA,PPSMDRAAV,RPPSMDRAAV	TGCT
NT5M	c.616delC	p.P206fs	AEPTPSWEHVLFTACHNQHLQLQPP[p.P206fs]AAGCTRGRTTGRPFWTASGPAELDCASGSSVGL*	LQLQPPAAG,NQHLQLQPPA	STAD
NTM	c.997G>T	p.G333C	IMLFEVKTTALTPWKGPGAVSEVSN[p.G333C]CTSRRAGCVWLLPLLVLHLLLKF*	EVSNCTSRR	LUAD

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NTN4	c.175G>A	p.E59K	CNPRMGNLALGRKLWADTTCGQNAT[p.E59K]KLYCFYSENTDLTCRQPKCDKCNAAY	TTCGQNATK,ATKLYCFYS,CGQNATKLY,NATKLYCFY,KLYCFYSENT,QNATKLYCFY,DTTCGQNATK,GQNATKLYCF	CRC
NUAK1	c.517G>T	p.G173C	RRLSERETRHFFRQIVSAVHYCHKN[p.G173C]CVVHRDLKLENILLDDNCNIKIADFG	AVHYCHKNCV,KNCVVHRDLK,VHYCHKNCVV,HKNCVVHRDL	LUAD
NUB1	c.1118G>A	p.R373Q	RLVHIKGNCGKEKVLFLRLYLLQGI[p.R373Q]QNYHSGNDVEAYEYLNKARQLFKELY	YLLQGIQNY,IQNYHSGNDV	CRC
NUDT15	c.248C>A	p.S83Y	ECAQRETWEEAALHLKNVHFASVVN[p.S83Y]YFIEKENYHYVTILMKGEVDVTHDSE	FASVVNYFI,SVVNYFIEK,HFASVVNYF,VHFASVVNY,ASVVNYFIEK,VHFASVVNYF,HFASVVNYFI,YFIEKENYHY,NVHFASVVNY,VNYFIEKENY	CRC
NUDT21	c.39_40insG	p.W13fs	MSVVPPNRSQTGW[p.W13fs]APGGHSVRQQVHPADEAPHPGAHHQPVPSYQLYFWYKRAPLREGQLCCSQISAHEGRI*	QLYFWYKRA,SYQLYFWYK,YQLYFWYKR,YFWYKRAPL,RSQTGWAPG,SVRQQVHPA,FWYKRAPLR,AHHQPVPSY,PSYQLYFWY,HPGAHHQPV,QPVPSYQLY,HQPVPSYQL,DEAPHPGAH,VPSYQLYFW,YQLYFWYKRA,PSYQLYFWYK,SYQLYFWYKR,LYFWYKRAPL,GAHHQPVPSY,HQPVPSYQLY,YFWYKRAPLR,VPSYQLYFWY,RQQVHPADEA,HHQPVPSYQL,QPVPSYQLYF,REGQLCCSQI,GQLCCSQISA,SQISAHEGRI,DEAPHPGAHH	KIRC
NUF2	c.1019C>T	p.S340L	KESLNLEDQIESDESELKKLKTEEN[p.S340L]LFKRLMIVKKEKLATAQFKINKKHED	NLFKRLMIV,KTEENLFKR,LFKRLMIVK,KKLKTEENL,KLKTEENLF,EENLFKRLM,TEENLFKRL,KLKTEENLFK,NLFKRLMIVK,LFKRLMIVKK,KKLKTEENLF,TEENLFKRLM,EENLFKRLMI	CRC
NUFIP2	c.670delA	p.R224fs	TNGYMGKGADNDGSGSESGYTTPKK[p.R224fs]GKLGAIVPRVVKTLI*	KLGAIVPRV,GAIVPRVVK,VPRVVKTLI,KKGKLGAIV,KLGAIVPRVV,AIVPRVVKTL,SGYTTPKKGK,KGKLGAIVPR,LGAIVPRVVK,TPKKGKLGAI	STAD
NUFIP2	c.86_88delAGC	p.Q29del	KPGQPQPQHHHSHHHPHHHPQQQQQ[p.Q29del]PHHHHHYYFYNHSHNHHHHHHHQQPHQY	HPQQQQQPH	GBM
NUP210	c.403delC	p.L135fs	DAIVDLIHDIQIVSTTRELYLEDSP[p.L135fs]WS*	ELYLEDSPW,RELYLEDSPW	STAD
NUP88	c.905C>T	p.A302V	FLTYISLLHSPGNIGKLLGPLPMHP[p.A302V]VAEDNYGYDACAVLCLPCVPNILVIA	PVAEDNYGY,LLGPLPMHPV,PMHPVAEDNY,HPVAEDNYGY	CRC
NUP93	c.40G>A	p.E14K	MDTEGFGELLQQA[p.E14K]KQLAAETEGISELPHVERNLQEIQQA	LQQAKQLAA,KQLAAETEG,KQLAAETEGI,LLQQAKQLAA,GELLQQAKQL	BRCA
NYAP1	c.1438C>T	p.P480S	DKAVSYTMVYSAVKVTTHSVLPAGP[p.P480S]SLGAGEPKTEKEISVLHGMLCTSSRP	SVLPAGPSL,LPAGPSLGA,VLPAGPSLGA,HSVLPAGPSL	TGCT
NYAP2	c.1310C>T	p.P437L	SSPPPPSTLYRTQSPHGYPKSHSTS[p.P437L]LSPVSMGRSLTPLSLKRPPPYDAVHS	SLSPVSMGR,KSHSTSLSP,YPKSHSTSL,SHSTSLSPV,STSLSPVSM,TSLSPVSMGR,KSHSTSLSPV,HSTSLSPVSM	LUAD
NYAP2	c.590G>A	p.R197Q	RTEASAKPRPHSDEYSKKIPPPKPK[p.R197Q]QNPNTQLSTSFDETYIKKHGPRRTSL	KQNPNTQLS,KPKQNPNTQL,KQNPNTQLST	CESC
NYNRIN	c.339delC	p.G113fs	AFLGAQGLFLDCLCWSTLAYLVPGP[p.G113fs]LAP*	LAYLVPGPL,TLAYLVPGPL	STAD
OBSCN	c.13546C>T	p.R4516W	LLLRSAQPHHAGEVTFACRDAVASA[p.R4516W]WLTVLGLPDPPEDAEVVARSSHTVTL	AVASAWLTV,VASAWLTVL,SAWLTVLGL,AVASAWLTVL,DAVASAWLTV,ACRDAVASAW,ASAWLTVLGL	ACC
OBSCN	c.2721_2722TG>CA	p.A908T	VSEPKVVFAKEQLARRKLQAEAGAS[p.A908T]TTLSCEVAQAQTEVTWYKDGKKLSSSS	LQAEAGAST,AEAGASTTL,LQAEAGASTT,QAEAGASTTL,AEAGASTTLS	TGCT
OBSCN	c.2989_2990insG	p.G997fs	LDVKEPKVVFAKDQVAHSEVQAEAG[p.G997fs]GQCHAELRGGPGPDGGDVVQRWEEAELQLESACRGQGLQTEAGGAAGRQDRCRGLQLRGQGPEGLLPPAHHRAQDDVCKGAVSA*	LLPPAHHRA,AEAGGQCHA,VQRWEEAEL,LQTEAGGAA,EEAELQLES,AELRGGPGP,AELQLESAC,GLLPPAHHRA,VQAEAGGQCH,QRWEEAELQL,LESACRGQGL,LQTEAGGAAG,RQDRCRGLQL,LQLRGQGPEG,EEAELQLESA	STAD
OBSL1	c.4924G>A	p.E1642K	RCAARLIVREVPVTIVRGPHDLEVT[p.E1642K]KGDTATFECELSQALADVTWEKDGNA	VTKGDTATF,LEVTKGDTA,EVTKGDTATF	CESC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ODF2L	c.1221delA	p.K407fs	TTLAALKDEVVSVENELSELQEVEK[p.K407fs]NRKPLLKCIKLRYKSCKKQLK*	KLRYKSCKK,RYKSCKKQL,LLKCIKLRY,ELQEVEKNR,KPLLKCIKL,CIKLRYKSC,VEKNRKPLL,LLKCIKLRYK,VEKNRKPLLK,KNRKPLLKCI,CIKLRYKSCK,RYKSCKKQLK,QEVEKNRKPL,LRYKSCKKQL	KICH
ODF2L	c.880G>A	p.E294K	DQEAKLSETISASNAWKSHYEKIVI[p.E294K]KKTELEVQIETMKKQIINLLEDLKKM	KKTELEVQI,YEKIVIKKT,IVIKKTELEV,KSHYEKIVIK	MM
ODF4	c.181C>T	p.R61C	TGELGQDGRLLSSTLSLSSNRSLGQ[p.R61C]CQNSPLPFQWRITHSFRWMAQVLASE	QCQNSPLPF,SLGQCQNSPL,GQCQNSPLPF,CQNSPLPFQW	GBM
ODZ1	c.1097G>T	p.R366M	HLFGLTWQLQPVEGELYANGVSKGN[p.R366M]MGTESMDTTYSPIGGKVSDKSEKKVF	KGNMGTESM,MGTESMDTTY,YANGVSKGNM,SKGNMGTESM	HNSC
ODZ1	c.7666C>T	p.R2556W	KGIKFAIKDGIVTADIIGVANEDSR[p.R2556W]WLAAILNNAHYLENLHFTIEGRDTHY	WLAAILNNA,NEDSRWLAA,RWLAAILNNA,WLAAILNNAH,NEDSRWLAAI	CRC
ODZ2	c.1882_1883insG	p.W628fs	KAACPVLCSGNGQYSKGTCQCYSGW[p.W628fs]ERCRVRRAHESVHRSFLRGPRLLH*	SFLRGPRLL,RVRRAHESV,SVHRSFLRG,RSFLRGPRL,CYSGWERCR,SGWERCRVR,ESVHRSFLR,AHESVHRSF,HESVHRSFL,WERCRVRRA,RVRRAHESVH,RAHESVHRSF,VHRSFLRGPR,RSFLRGPRLL,SGWERCRVRR,WERCRVRRAH	KIRC
ODZ3	c.653C>A	p.P218Q	SAQHHPSITSLNRNSLTNRRNQSPA[p.P218Q]QPAALPAELQTTPESVQLQDSWVLGS	QPAALPAEL,NQSPAQPAA,SPAQPAALPA,RRNQSPAQPA,NQSPAQPAAL,AQPAALPAEL	LUAD
OGDH	c.233delT	p.I78fs	NYVEEMYCAWLENPKSVHKSWDIFF[p.I78fs]ATRMPEPHRALPTRVPFP*	RMPEPHRAL,RALPTRVPF,ATRMPEPHR,SWDIFFATR,WDIFFATRM,FATRMPEPH,KSWDIFFATR,ATRMPEPHRA,RALPTRVPFP,FATRMPEPHR,MPEPHRALPT,TRMPEPHRAL,HRALPTRVPF,EPHRALPTRV	GBM
OGDH	c.2844_2845insC	p.Y948fs	VAITRIEQLSPFPFDLLLKEVQKYP[p.Y948fs]QC*	KEVQKYPQC	STAD
OGDHL	c.1279G>A	p.A427T	TKAEQFYRGDAQGKKVMSILVHGDA[p.A427T]TFAGQGVVYETFHLSDLPSYTTNGTV	LVHGDATFA,ATFAGQGVV,TFAGQGVVY,DATFAGQGV,ILVHGDATF,ATFAGQGVVY,ILVHGDATFA,SILVHGDATF	CRC
OGDHL	c.169C>T	p.R57C	RLLPSRLGVQAARLLAAHDVPVFGW[p.R57C]CSRSSGPPATFPSSKGGGGSSYMEEM	CSRSSGPPA,VPVFGWCSR,CSRSSGPPAT,DVPVFGWCSR	UCEC
OGFOD1	c.1430_1431insGTTTTTTT	p.G477fs	SKAEFALDLILYCGCEGWEPEYGGF[p.G477fs]FFLLLTLPKVKMKSC*	FLLLTLPKV,FFLLLTLPK,LTLPKVKMK,EYGGFFFLL,YGGFFFLLL,GFFFLLLTL,LPKVKMKSC,WEPEYGGFF,PEYGGFFFL,EPEYGGFFF,FFFLLLTLPK,GWEPEYGGFF,EYGGFFFLLL,WEPEYGGFFF,GGFFFLLLTL,LLLTLPKVKM,PEYGGFFFLL,EPEYGGFFFL	PAAD
OGFR	c.1670G>C	p.S557T	DEPAESPSETPGPRPAGPAGDEPAE[p.S557T]TPSETPGPRPAGPAGDEPAESPSETP	ETPSETPGPR	ACC
OIT3	c.1522C>A	p.R508S	FVGKDHKEVFLHCRVLVCGVLDERS[p.R508S]SCAQGCHRRMRRGAGGEDSAGLQGQT	VLDERSSCA,RSSCAQGCHR	LUAD
OLFM4	c.396G>T	p.K132N	HVLSQKFEKELSKVREYVQLISVYE[p.K132N]NKLLNLTVRIDIMEKDTISYTELDFE	QLISVYENK,VYENKLLNL,YENKLLNLT,QLISVYENKL,SVYENKLLNL,VQLISVYENK,YENKLLNLTV	CRC
OMA1	c.1334G>A	p.R445Q	MEFVDSLHGQPKMPEWLSTHPSHGN[p.R445Q]QVEYLDRLIPQALKIREMCNCPPLSN	NQVEYLDRL,PSHGNQVEY,STHPSHGNQV,HPSHGNQVEY,NQVEYLDRLI	UCEC
ONECUT1	c.1270T>A	p.L424M	TLHAIFKENKRPSKELQITISQQLG[p.L424M]MELSTVSNFFMNARRRSLDKWQDEGS	QLGMELSTV,ITISQQLGM,MELSTVSNF,ISQQLGMEL,QQLGMELST,QQLGMELSTV,GMELSTVSNF,MELSTVSNFF,SQQLGMELST	KIRC
OOEP	c.301C>T	p.R101C	TSQALLTVDIVDSGNLVEITVFGRP[p.R101C]CVQNRVKSMLLCLAWFHREHRARAEK	ITVFGRPCV,CVQNRVKSM,EITVFGRPCV,VEITVFGRPC	LUAD
OPLAH	c.2699C>A	p.A900D	QQEGAVFLSFKLVQGGVFQEEAVTE[p.A900D]DLRAPGKVPNCSGTRNLHDNLSDLRA	QEEAVTEDL,VTEDLRAPGK,FQEEAVTEDL,EEAVTEDLRA	TGCT

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
OPN1LW	c.848C>A	p.P283H	STQKAEKEVTRMVVVMIFAYCVCWG[p.P283H]HYTFFACFAAANPGYAFHPLMAALPA	CVCWGHYTF,VCWGHYTFF,AYCVCWGHY,GHYTFFACF,YCVCWGHYTF,CVCWGHYTFF,FAYCVCWGHY,WGHYTFFACF	LUAD
OPN1MW	c.853G>A	p.A285T	QKAEKEVTRMVVVMVLAFCFCWGPY[p.A285T]TFFACFAAANPGYPFHPLMAALPAFF	CFCWGPYTF,FCWGPYTFF,FCWGPYTFFA,FCFCWGPYTF,CFCWGPYTFF	HNSC
OPRD1	c.80G>T	p.C27F	EPAPSAGAELQPPLFANASDAYPSA[p.C27F]FPSAGANASGPPGARSASSLALAIAI	ASDAYPSAF,AYPSAFPSA,FPSAGANAS,YPSAFPSAG,DAYPSAFPSA,YPSAFPSAGA,NASDAYPSAF,SAFPSAGANA,FPSAGANASG	ACC
OPRM1	c.1058G>A	p.R353H	KICVFIFAFIMPVLIITVCYGLMIL[p.R353H]HLKSVRMLSGSKEKDRNLRRITRMVL	LMILHLKSV,YGLMILHLK,CYGLMILHL,HLKSVRMLS,MILHLKSVR,ILHLKSVRM,LHLKSVRML,GLMILHLKSV,ILHLKSVRML,HLKSVRMLSG,LMILHLKSVR,MILHLKSVRM	CRC
OPRM1	c.1384C>T	p.R462C	NFKRCFREFCIPTSSNIEQQNSTRI[p.R462C]CQNTRDHPSTANTVDRTNHQLENLEA	STRICQNTR,NSTRICQNTR	UCEC
OPTN	c.70delC	p.P24fs	MSHQPLSCLTEKEDSPSESTGNGPP[p.P24fs]TWPTQTWTRLPRRSCCSR*	TQTWTRLPR,QTWTRLPRR,TWPTQTWTR,WPTQTWTRL,PPTWPTQTW,TWPTQTWTRL,RLPRRSCCSR,PTWPTQTWTR,PTQTWTRLPR,TQTWTRLPRR,SESTGNGPPT,ESTGNGPPTW	STAD
OR10A3	c.217T>G	p.F73V	IISLNQSLHVPMYLFLLNLSVVEVS[p.F73V]VSAVITPEMLVVLSTEKTMISFVGCF	NLSVVEVSV,SVVEVSVSA,VEVSVSAVI,VSAVITPEM,SVVEVSVSAV,SVSAVITPEM,VEVSVSAVIT	KIRC
OR10A3	c.278C>A	p.S93Y	VVEVSFSAVITPEMLVVLSTEKTMI[p.S93Y]YFVGCFAQMYFILLFGGTECFLLGAM	LSTEKTMIY,STEKTMIYF,MIYFVGCFA,YFVGCFAQM,KTMIYFVGC,TMIYFVGCF,TEKTMIYFV,TMIYFVGCFA,KTMIYFVGCF,IYFVGCFAQM,VLSTEKTMIY,YFVGCFAQMY,STEKTMIYFV,LSTEKTMIYF	CRC
OR10H4	c.597G>T	p.M199I	VIHHFFCHVLSLLKLACENKTSSVI[p.M199I]IGVMLVCVTALIGCLFLIILSYVFIV	KTSSVIIGV,SVIIGVMLV,IIGVMLVCV,TSSVIIGVM,VIIGVMLVCV,KTSSVIIGVM,SSVIIGVMLV,CENKTSSVII	LUAD
OR10J1	c.470T>A	p.L157Q	DRYVAICNPLRYMVIMNKRLRIQLV[p.L157Q]QGACSIGLIVAITQVTSVFRLPFCAR	QLVQGACSI,RLRIQLVQG,VQGACSIGL,RLRIQLVQGA,IQLVQGACSI,VQGACSIGLI	LUAD
OR10J1	c.731G>A	p.R244Q	VPMGLVFISYVLIISTILKIASVEG[p.R244Q]QKKAFATCASHLTVVIVHYSCASIAY	KIASVEGQK,KIASVEGQKK,ASVEGQKKAF	TGCT
OR10X1	c.892C>A	p.L298I	IVYLKPEASGDDTLIAVPYTVITPF[p.L298I]ISPIIFSLRNKDMKNAFRRMMGNTVA	VITPFISPI,FISPIIFSL,ISPIIFSLR,PYTVITPFI,ITPFISPII,TPFISPIIF,TVITPFISPI,VITPFISPII,FISPIIFSLR,ITPFISPIIF,PFISPIIFSL,VPYTVITPFI	LUAD
OR10Z1	c.615G>C	p.L205F	DTPPVLSLACGDTGPSELRIFILSL[p.L205F]FVLLVSFFFITISYAYILAAILRIPS	RIFILSLFV,FILSLFVLL,ILSLFVLLV,LRIFILSLF,IFILSLFVL,SLFVLLVSF,LFVLLVSFF,FVLLVSFFF,FVLLVSFFI,IFILSLFVLL,LSLFVLLVSF,SLFVLLVSFF,LFVLLVSFFF,ELRIFILSLF	LUAD
OR11H12	c.461A>C	p.H154P	LLTVMAFDQYLAICRPLLYPNIMTG[p.H154P]PLCAKLVILCWVCGFLWFLIPIVLIS	IMTGPLCAK,MTGPLCAKL,YPNIMTGPL,GPLCAKLVI,IMTGPLCAKL,LLYPNIMTGP,NIMTGPLCAK,LYPNIMTGPL,MTGPLCAKLV,GPLCAKLVIL,YPNIMTGPLC	GBM
OR13C2	c.25C>G	p.L9V	MEWENHTI[p.L9V]VVEFFLKGLSGHPRLELLFFVLIFIM	TIVVEFFLK,HTIVVEFFL,MEWENHTIV,IVVEFFLKGL,HTIVVEFFLK,MEWENHTIVV,WENHTIVVEF	CESC
OR13G1	c.773G>A	p.R258H	KAFSTCSSHLTVVTLYYSPVIYTYI[p.R258H]HPASSYTFERDKVVAALYTLVTPTLN	VIYTYIHPA,YIHPASSYT,IHPASSYTF,TYIHPASSY,YTYIHPASS,SPVIYTYIH,YTYIHPASSY,YIHPASSYTF,HPASSYTFER	BRCA
OR14A16	c.478G>T	p.G160C	DRSTCVQRATVSWLYGGLIAVMHTA[p.G160C]CTFSLSYCGSNMVHQFFCDIPQLLAI	TACTFSLSY,HTACTFSLS,AVMHTACTF,MHTACTFSL,HTACTFSLSY,VMHTACTFSL,GLIAVMHTAC,IAVMHTACTF	LUAD
OR1M1	c.205G>A	p.V69I	LIILAISIDSHLHTPMYFFLANLSL[p.V69I]IDFCLATNTIPKMLVSLQTGSKAISY	NLSLIDFCL,SLIDFCLAT,FFLANLSLI,LANLSLIDF,NLSLIDFCLA,FLANLSLIDF,YFFLANLSLI,IDFCLATNTI	PRAD
OR2A25	c.240G>A	p.M80I	HTPMYFFLSHLAVVDIACACSTVPQ[p.M80I]ILVNLLHPAKPISFAGCMTQMFLFLS	ILVNLLHPA,CSTVPQILV,TVPQILVNL,VPQILVNLL,ILVNLLHPAK,STVPQILVNL,TVPQILVNLL	LUAD
OR2A25	c.313A>T	p.S105C	MLVNLLHPAKPISFAGCMTQMFLFL[p.S105C]CFAHTECLLLVVMSYDRYVAICHPLR	QMFLFLCFA,FLFLCFAHT,FLCFAHTEC,TQMFLFLCF,LCFAHTECL,MTQMFLFLCF,TQMFLFLCFA,FLCFAHTECL,CFAHTECLLL,QMFLFLCFAH	CLL
OR2A5	c.212C>T	p.S71L	GLIWLDSRLHTPMYFFLSHLAIIDI[p.S71L]LYASNNVPKMLTNLGLNKRKTISFVP	HLAIIDILY,AIIDILYAS,LYASNNVPK,DILYASNNV,ILYASNNVP,HLAIIDILYA,ILYASNNVPK,LYASNNVPKM,SHLAIIDILY,LSHLAIIDIL,IDILYASNNV	SKCM

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
OR2AG2	c.745G>T	p.G249W	TVLRMPSNEGRKKALVTCSSHLIVV[p.G249W]WMFYGAATFMYVLPSSFHSPKQDNII	IVVWMFYGA,WMFYGAATF,HLIVVWMFY,SHLIVVWMF,SSHLIVVWM,CSSHLIVVW,LIVVWMFYGA,WMFYGAATFM,SSHLIVVWMF,VWMFYGAATF,SHLIVVWMFY,IVVWMFYGAA	LUAD
OR2AK2	c.111G>C	p.W37C	LVSAMKTGNQSFGTDFLLVGLFQYG[p.W37C]CINSLLFVVIATLFTVALTGNIMLIH	FQYGCINSL,CINSLLFVV,QYGCINSLL,YGCINSLLF,FQYGCINSLL,CINSLLFVVI,QYGCINSLLF	LUAD
OR2AK2	c.133G>A	p.V45I	NQSFGTDFLLVGLFQYGWINSLLFV[p.V45I]IIATLFTVALTGNIMLIHLIRLNTRL	WINSLLFVI,SLLFVIIAT,LLFVIIATL,VIIATLFTV,IIATLFTVA,LFVIIATLF,WINSLLFVII,SLLFVIIATL,FVIIATLFTV,VIIATLFTVA,IIATLFTVAL,GWINSLLFVI,LLFVIIATLF	BRCA
OR2B11	c.29G>T	p.G10V	MKSDNHSFL[p.G10V]VDSPKAFILLGVSDRPWLELPLFVVL	KSDNHSFLV,FLVDSPKAF,HSFLVDSPK,FLVDSPKAFI,SFLVDSPKAF,MKSDNHSFLV	LUSC
OR2H1	c.859G>A	p.V287I	NPYAQGRGKFFGLFYAVGTPSLNPL[p.V287I]IYTLRNKEIKRALRRLLGKERDSRES	IYTLRNKEI	GBM
OR2H2	c.615G>C	p.L205F	PALIRLSCEDTSYNEIQVAVASVFI[p.L205F]FVVPLSLILVSYGAITWAVLRINSAK	AVASVFIFV,SVFIFVVPL,FIFVVPLSL,FVVPLSLIL,VAVASVFIF,IFVVPLSLI,VASVFIFVV,VAVASVFIV,AVASVFIFV,FIFVVPLSLI,FVVPLSLILV,VFIFVVPLSL,IFVVPLSLIL,QVAVASVFIF,ASVFIFVVPL	LUAD
OR2J2	c.700G>T	p.G234W	LIPLILILTTYGAIARAVLSMQSTT[p.G234W]WLQKVFRTCGAHLMVVSLFFIPVMCM	MQSTTWLQK,TTWLQKVFR,QSTTWLQKV,VLSMQSTTW,LSMQSTTWL,STTWLQKVF,VLSMQSTTWL,MQSTTWLQKV,SMQSTTWLQK,STTWLQKVFR,AVLSMQSTTW,QSTTWLQKVF	LUAD
OR2L13	c.318G>T	p.M106I	AYNFLSGQKGISFLGCGVQSFFFLT[p.M106I]IACSEGLLLTSMAYDRYLAICHSLYY	VQSFFFLTI,QSFFFLTIA,LTIACSEGL,IACSEGLLL,FLTIACSEGL,GVQSFFFLTI,LTIACSEGLL,VQSFFFLTIA	LUAD
OR2L13	c.724A>G	p.T242A	CGRVLFAVYHMHSKEGRKKAFTTIS[p.T242A]AHLTVVIFYYAPFVYTYLRPRNLRSP	TISAHLTVV,KAFTTISAH,AHLTVVIFY,FTTISAHLT,TTISAHLTV,SAHLTVVIF,KKAFTTISA,ISAHLTVVI,FTTISAHLTV,TTISAHLTVV,TISAHLTVVI,ISAHLTVVIF,RKKAFTTISA,KAFTTISAHL,SAHLTVVIFY,AHLTVVIFYY,KKAFTTISAH	LUAD
OR2L3	c.199C>A	p.L67I	LSMILLIFLDTHLHTPMYFLLSQLS[p.L67I]IIDLNYISTIVPKMASDFLSGNKSIS	QLSIIDLNY,FLLSQLSII,LLSQLSIIDL,QLSIIDLNYI,YFLLSQLSII,SQLSIIDLNY	LUAD
OR2L3	c.3G>T	p.M1I	[p.M1I]IENYNQTSTDFILLGFFPPSRIGLFL	IENYNQTST	LUAD
OR2L3	c.881A>G	p.K294R	EDKVLAVFYTTLTPMLNPIIYSLRN[p.K294R]REVMGALTRVSQRICSGKM*	IIYSLRNREV,RNREVMGALT,REVMGALTRV	TGCT
OR2L8	c.361C>T	p.R121C	CGIQSFFFLALGGAEALLLASMAYD[p.R121C]CYIAICFPLHYLIRMSKRVCVLMITG	ASMAYDCYI,SMAYDCYIA,MAYDCYIAI,CYIAICFPL,SMAYDCYIAI,AYDCYIAICF,CYIAICFPLH	LUAD
OR2L8	c.513G>T	p.R171S	GSWIIGSINACAHTVYVLHIPYCRS[p.R171S]SAINHFFCDVPAMVTLACMDTWVYEG	RSSAINHFF,IPYCRSSAI,CRSSAINHF,HIPYCRSSAI,SAINHFFCDV,RSSAINHFFC,YCRSSAINHF,LHIPYCRSSA,CRSSAINHFF	LUAD
OR2L8	c.603_604delTG	p.S201fs	FCDVPAMVTLACMDTWVYEGTVFLS[p.S201fs]HHLSRVSLHWYFMFLWPGSLCCLPHEICRREEESLFDLQHPPHCSNFLLCTFCLHLSTSKIPAISNRGQGSGCLLHHPHPNAQPHHL*	FLSHHLSRV,SLHWYFMFL,FMFLWPGSL,FLWPGSLCC,SLCCLPHEI,LLCTFCLHL,SLFDLQHPP,CLHLSTSKI,HLSTSKIPA,LLHHPHPNA,SRVSLHWYF,VSLHWYFMF,WYFMFLWPG,CSNFLLCTF,NFLLCTFCL,VFLSHHLSR,RVSLHWYFM,LSRVSLHWY,HPPHCSNFL,HPHPNAQPH,HPNAQPHHL,YEGTVFLSH,SHHLSRVSL,HLSRVSLHW,CRREEESLF,REEESLFDL,LQHPPHCSN,RGQGSGCLL,GQGSGCLLH,EESLFDLQH,LHWYFMFLW,HLSRVSLHWY,VSLHWYFMFL,FMFLWPGSLC,FLWPGSLCCL,FLLCTFCLHL,HLSTSKIPAI,CLLHHPHPNA,FLSHHLSRVS,TVFLSHHLSR,TFCLHLSTSK,VFLSHHLSRV,RVSLHWYFMF,SLHWYFMFLW,YFMFLWPGSL,TSKIPAISNR,HPPHCSNFLL,LSRVSLHWYF,LQHPPHCSNF,SLFDLQHPPH,YEGTVFLSHH,LSHHLSRVSL,HHLSRVSLHW,SRVSLHWYFM,ICRREEESLF,HCSNFLLCTF,LHLSTSKIPA,GQGSGCLLHH,WPGSLCCLPH	KIRP

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
OR2M2	c.284delC	p.A95fs	DLMLICTTVPKMAFNYLSGSKSISM[p.A95fs]VVVSHKFSSIYHCLALNVFFWLLWLMTAILLFATL*	VSHKFSSIY,LALNVFFWL,ALNVFFWLL,NVFFWLLWL,WLLWLMTAI,LLWLMTAIL,LMTAILLFA,VVSHKFSSI,ISMVVVSHK,SMVVVSHKF,KFSSIYHCL,IYHCLALNV,CLALNVFFW,VFFWLLWLM,LWLMTAILL,WLMTAILLF,GSKSISMVV,FSSIYHCLA,MTAILLFAT,TAILLFATL,SSIYHCLAL,SKSISMVVV,HKFSSIYHC,YHCLALNVF,HCLALNVFF,SIYHCLALNV,CLALNVFFW,LALNVFFWL,NVFFWLLWLM,WLLWLMTAIL,LLWLMTAILL,WLMTAILLFA,LMTAILLFAT,MTAILLFATL,VVVSHKFSSI,SISMVVVSHK,VSHKFSSIYH,ISMVVVSHKF,IYHCLALNVF,YHCLALNVFF,FWLLWLMTAI,LWLMTAILLF,GSKSISMVVV,KFSSIYHCLA,VVSHKFSSIY,KSISMVVVSH,HKFSSIYHCL,FSSIYHCLAL	HNSC
OR2M2	c.531C>A	p.F177L	GSTDGIIDAVATFSFSFCGSREIAH[p.F177L]LFCEFPSLLILSCNDTSIFEEVIFIC	HLFCEFPSL,GSREIAHLF,EIAHLFCEF,REIAHLFCE,HLFCEFPSLL,REIAHLFCEF,LFCEFPSLLI,GSREIAHLFC,CGSREIAHLF,AHLFCEFPSL	LUAD
OR2M2	c.967T>C	p.F323L	TRAFMKILGKGKSESELPHKLYVLL[p.F323L]LAKFFFLISIFFYDVKILALIMYIA	LLLAKFFFL,LLAKFFFLI,KLYVLLLAK,LYVLLLAKF,VLLLAKFFF,VLLLAKFFFL,LLLAKFFFLI,KLYVLLLAKF,LYVLLLAKFF,YVLLLAKFFF,LAKFFFLISI,LPHKLYVLLL	LUAD
OR2M3	c.704G>A	p.R235H	PVAIIIASYARVILAVIHMGSGEGR[p.R235H]HKAFTTCSSHLLVVGMYYGAALFMYI	SGEGRHKAF,HMGSGEGRHK,GSGEGRHKAF,HKAFTTCSSH,GEGRHKAFTT	CRC
OR2M3	c.819G>T	p.M273I	VGMYYGAALFMYIRPTSDRSPTQDK[p.M273I]IVSVFYTILTPMLNPLIYSLRNKEVT	KIVSVFYTI,TQDKIVSVF,TQDKIVSVFY,KIVSVFYTIL,SPTQDKIVSV	HNSC
OR2M5	c.613G>T	p.V205L	DFPSLLILSCNDTSIFEKVLFICCI[p.V205L]LMIVFPVAIIIASYARVILAVIHMGS	FICCILMIV,CILMIVFPV,ILMIVFPVA,LMIVFPVAI,LFICCILMI,KVLFICCIL,VLFICCILM,VLFICCILMI,ILMIVFPVAI,LMIVFPVAII,KVLFICCILM,FICCILMIVF	LUAD
OR2T12	c.551G>A	p.R184H	VATLSFPYCGAHEIDHFFCEAPVLV[p.R184H]HLACADTSVFENAMYICCVLMLLVPF	HLACADTSV,EAPVLVHLA,CEAPVLVHL,HLACADTSVF,CEAPVLVHLA	GBM
OR2T12	c.772A>T	p.M258L	KKAFATCSSHVAVVGLFYGAGIFTY[p.M258L]LRPKSHRSTNHDKVVSAFYTMFTPLL	YGAGIFTYL,GIFTYLRPK,GAGIFTYLR,TYLRPKSHR,YLRPKSHRS,AGIFTYLRPK,FTYLRPKSHR,FYGAGIFTYL,YGAGIFTYLR,YLRPKSHRST	LUAD
OR2T2	c.37T>G	p.F13V	MGMEGLLQNSTN[p.F13V]VVLTGLITHPAFPGLLFAIVFSIFVV	GLLQNSTNV,LLQNSTNVV,STNVVLTGL,LQNSTNVVL,GLLQNSTNVV,LLQNSTNVVL,NSTNVVLTGL,STNVVLTGLI,LQNSTNVVLT	LUSC
OR2T27	c.31G>T	p.D11Y	MEQSNYSVYA[p.D11Y]YFILLGLFSNARFPWLLFALILLVFL	QSNYSVYAY,SVYAYFILL,YAYFILLGL,SNYSVYAYF,NYSVYAYFI,YSVYAYFIL,VYAYFILLG,AYFILLGLF,YSVYAYFILL,NYSVYAYFIL,VYAYFILLGL,YAYFILLGLF,EQSNYSVYAY,QSNYSVYAYF,SNYSVYAYFI	LUAD
OR2T33	c.358C>A	p.R120S	CGVQIFFLPTLGGGECFLLAAMAYD[p.R120S]SYAAVCHPLRYPTLMSWQLCLRMTMS	AMAYDSYAA,MAYDSYAAV,AAMAYDSYA,SYAAVCHPL,LAAMAYDSY,FLLAAMAYDS,AMAYDSYAAV,AAMAYDSYAA,LLAAMAYDSY,SYAAVCHPLR,LAAMAYDSYA,DSYAAVCHPL,MAYDSYAAVC	HNSC
OR2T33	c.494C>A	p.P165Q	LRMTMSCWLLGAADGLLQAVVTLSF[p.P165Q]QYCGAHEIDHFFCETPVLVRLACADT	FQYCGAHEI,TLSFQYCGA,AVVTLSFQY,LSFQYCGAH,SFQYCGAHEI,QAVVTLSFQY,FQYCGAHEID	LUAD
OR2T34	c.737G>T	p.C246F	SSYTLILHLIHRMNSAAGRRKALAT[p.C246F]FSSHMIIVLLLFGASFYTYMLRSSYH	ALATFSSHM,KALATFSSH,ATFSSHMII,GRRKALATF,RKALATFSS,FSSHMIIVL,LATFSSHMI,ALATFSSHMI,ATFSSHMIIV,FSSHMIIVLL,TFSSHMIIVL,KALATFSSHM,AGRRKALATF,RKALATFSSH,LATFSSHMII	LUAD
OR2T4	c.408_409CG>TC	p.V137L	KMLLDQVMGVNKISAPECGMQMFFY[p.V137L]LTLAGSEFFLLATMAYDRYVAICHPLR	GMQMFFYLT,MQMFFYLTL,CGMQMFFYL,GMQMFFYLTL,MQMFFYLTLA,FYLTLAGSEF	LIHC
OR2T6	c.637G>T	p.V213L	ACGDKTTYETVMYVCCVAMLLIPFS[p.V213L]LVTASYTRILITVHQMTSAEGRKKAF	AMLLIPFSL,MLLIPFSLV,LLIPFSLVT,LIPFSLVTA,LVTASYTRI,SLVTASYTR,PFSLVTASY,IPFSLVTAS,AMLLIPFSLV,LLIPFSLVTA,SLVTASYTRI,FSLVTASYTR,IPFSLVTASY,VAMLLIPFSL	LUAD
OR4C12	c.744C>A	p.F248L	LKNNSLEGRCKALSTCISHIIVVVL[p.F248L]LFVPCIFVYLRSVTTLPIDKAVAVFY	IIVVVLLFV,LLFVPCIFV,HIIVVVLLF,VLLFVPCIF,LFVPCIFVY,HIIVVVLLFV,VLLFVPCIFV,LLFVPCIFVY,SHIIVVVLLF,VVLLFVPCIF,LFVPCIFVYL,ISHIIVVVLL	UCEC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
OR4C12	c.837G>T	p.M279I	FVYLRSVTTLPIDKAVAVFYTMVVP[p.M279I]ILNPVVYTLRNAEVKSAIRKLWRKKV	MVVPILNPV,ILNPVVYTL,VFYTMVVPI,FYTMVVPIL,VPILNPVVY,AVFYTMVVPI,TMVVPILNPV,MVVPILNPVV,ILNPVVYTLR,VFYTMVVPIL,VVPILNPVVY	LUAD
OR4C12	c.925G>T	p.D309Y	VYTLRNAEVKSAIRKLWRKKVTSDN[p.D309Y]Y	RKKVTSDNY,WRKKVTSDNY	LUAD
OR4C16	c.188A>T	p.Y63F	LGNLLIIISVKTSQALKNPMFFFLF[p.Y63F]FLSLSDTCLSTSITPRMIVDALLKKT	PMFFFLFFL,FLSLSDTCL,FFFLFFLSL,NPMFFFLFF,FLFFLSLSDT,FLSLSDTCLS,KNPMFFFLFF,MFFFLFFLSL,NPMFFFLFFL	CLL
OR4C16	c.403A>C	p.S135R	IFILILTAVDRYVDICKPLHYMTII[p.S135R]RQWVCGVLMAVAWVGSCVHSLVQIFL	YMTIIRQWV,IIRQWVCGV,HYMTIIRQW,RQWVCGVLM,TIIRQWVCGV,RQWVCGVLMA,HYMTIIRQWV,LHYMTIIRQW,IRQWVCGVLM	STAD
OR4C16	c.484C>A	p.L162M	WVCGVLMAVAWVGSCVHSLVQIFLA[p.L162M]MSLPFCGPNVINHCFCDLQPLLKQAC	SLVQIFLAM,VQIFLAMSL,FLAMSLPFC,IFLAMSLPF,MSLPFCGPNV,FLAMSLPFCG,QIFLAMSLPF,HSLVQIFLAM,VQIFLAMSLP	LUAD
OR4C3	c.389_390insT	p.H130fs	IADSLYEGRTISYECCMAQLFGAHF[p.H130fs]FGRC*	AQLFGAHFF,LFGAHFFGR,QLFGAHFFGR,MAQLFGAHFF	LUAD
OR4E2	c.677G>A	p.R226Q	TNSGTISLSCFLAVVTSYMVILVSL[p.R226Q]QKHSAEGRQKALSTCSAHFMVVALFF	MVILVSLQK,ILVSLQKHSA,YMVILVSLQK	SKCM
OR4K2	c.761G>T	p.C254F	SSRGSSKALSTCTAHFIVVFLFFGP[p.C254F]FIFIYMWPLSSFLTDKILSVFYTIFT	FLFFGPFIF,FIFIYMWPL,VFLFFGPFI,LFFGPFIFI,FFGPFIFIY,VVFLFFGPF,GPFIFIYMW,VVFLFFGPFI,FLFFGPFIFI,IVVFLFFGPF,VFLFFGPFIF,FFGPFIFIYM,FGPFIFIYMW,PFIFIYMWPL,LFFGPFIFIY	LUSC
OR4K5	c.529delT	p.F177fs	VHTLSQLSFTVNLPFCGPNVVDSFF[p.F177fs]VIFLESPNLPAWTLTSLKY*	NVVDSFFVI,FLESPNLPA,PAWTLTSLK,AWTLTSLKY,SPNLPAWTL,LPAWTLTSL,VVDSFFVIF,LESPNLPAW,VVDSFFVIFL,FVIFLESPNL,NLPAWTLTSL,PAWTLTSLKY,ESPNLPAWTL,NVVDSFFVIF,FLESPNLPAW,LESPNLPAWT	STAD
OR4M1	c.122G>A	p.G41E	GLSQTREVQLVLFVIFLSFYLFILP[p.G41E]ENILIICTIRLDPHLTSPMYFLLANL	YLFILPENI,FILPENILI,ILPENILII,YLFILPENIL,FILPENILII,FYLFILPENI,LFILPENILI,ENILIICTIR	SKCM
OR4M2	c.355G>T	p.A119S	FDGCIAQLFFLHFAGASEMFLLTVM[p.A119S]SFDLYTAICRPLHYATIMNQRLCCIL	LTVMSFDLY,LLTVMSFDL,VMSFDLYTA,MSFDLYTAI,MFLLTVMSF,TVMSFDLYT,LLTVMSFDLY,FLLTVMSFDL,TVMSFDLYTA,VMSFDLYTAI,EMFLLTVMSF,MSFDLYTAIC,SEMFLLTVMS	LUAD
OR4M2	c.481G>T	p.A161S	MNQRLCCILVALSWRGGFIHSIIQV[p.A161S]SLIVRLPFCGPNELDSYFCDITQVVR	SIIQVSLIV,IQVSLIVRL,SLIVRLPFC,VSLIVRLPF,HSIIQVSLI,IHSIIQVSL,FIHSIIQVSL,SIIQVSLIVR,HSIIQVSLIV,QVSLIVRLPF	LUAD
OR4M2	c.803C>T	p.S268F	YSHITIVVLMFGPSIYIYARPFDSF[p.S268F]FLDKVVSVFNTLIFPLRNPIIYTLRN	FFLDKVVSV,FLDKVVSVF,YARPFDSFF,IYARPFDSFF,FFLDKVVSVF,YARPFDSFFL,RPFDSFFLDK	SKCM
OR4N2	c.122G>A	p.G41E	GLTQSQDIQLLVFVLVLIFYFIILP[p.G41E]ENFLIIFTIKSDPGLTAPLYFFLGNL	FIILPENFL,IILPENFLI,ILPENFLII,YFIILPENF,ENFLIIFTI,LPENFLIIF,FIILPENFLI,IILPENFLII,FYFIILPENF,YFIILPENFL,ILPENFLIIF,PENFLIIFTI	SKCM
OR4N2	c.448_449insT	p.L150fs	ICRPLHYPTVMNPRTCYAMMLALWL[p.L150fs]WGFCPLHYPGGPHPPLAFLWPKPAGQLLL*	MLALWLWGF,AMMLALWLW,LWLWGFCPL,LWGFCPLHY,YPGGPHPPL,GPHPPLAFL,WPKPAGQLL,LHYPGGPHP,LAFLWPKPA,MMLALWLWGF,MLALWLWGFC,ALWLWGFCPL,FLWPKPAGQL,YAMMLALWLW,HYPGGPHPPL,LWPKPAGQLL,WLWGFCPLHY,WPKPAGQLLL,LHYPGGPHPP,GPHPPLAFLW	BLCA,KIRC
OR4N4	c.448_449insT	p.L150fs	ICRPLHCSTVMNPRACYAMMLALWL[p.L150fs]WGFCPLHYPGGPHPPLAFLWPKPAGQLLL*	MLALWLWGF,AMMLALWLW,LWLWGFCPL,LWGFCPLHY,YPGGPHPPL,GPHPPLAFL,WPKPAGQLL,LHYPGGPHP,LAFLWPKPA,MMLALWLWGF,MLALWLWGFC,ALWLWGFCPL,FLWPKPAGQL,YAMMLALWLW,HYPGGPHPPL,LWPKPAGQLL,WLWGFCPLHY,WPKPAGQLLL,LHYPGGPHPP,GPHPPLAFLW	CLL
OR51A7	c.371T>G	p.L124R	AQEFFIHGFTVMESSVLLIMSLDRF[p.L124R]RAIHNPLRYSSILTSNRVAKMGLILA	IMSLDRFRA,LIMSLDRFR,RFRAIHNPL,MSLDRFRAI,RAIHNPLRY,IMSLDRFRAI,LIMSLDRFRA,MSLDRFRAIH,RFRAIHNPLR,FRAIHNPLRY,LLIMSLDRFR	STAD
OR51B2	c.488C>T	p.S163L	RVIALGVGVFLRGFVSILPVILRLF[p.S163L]LFSYCKSHVITRAFCLHQEIMRLACA	RLFLFSYCK,PVILRLFLF,ILRLFLFSY,LPVILRLFL,FLFSYCKSH,FLFSYCKSHV,ILPVILRLFL,VILRLFLFSY,LPVILRLFLF	SKCM

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
OR51B5	c.197_213delCCACAGACCTGGGGCTG	p.A66fs	GTLLLLIKEDHNLHEPMYFFLAMLA[p.A66fs]GPDHNAHGAGSPLAGSQGDWKCGLLFPGLLYTLTFLSRVWHSACHGL*	MLAGPDHNA,LLFPGLLYT,GLLYTLTFL,LLYTLTFLS,YTLTFLSRV,FLSRVWHSA,GLLFPGLLY,LFPGLLYTL,VWHSACHGL,LYTLTFLSR,NAHGAGSPL,SQGDWKCGL,GDWKCGLLF,FPGLLYTLT,AMLAGPDHNA,GLLFPGLLYT,LLFPGLLYTL,FLSRVWHSAC,RVWHSACHGL,LLYTLTFLSR,LYTLTFLSRV,YTLTFLSRVW,LSRVWHSACH,CGLLFPGLLY,HNAHGAGSPL,FPGLLYTLTF,MLAGPDHNAH,SQGDWKCGLL,WKCGLLFPGL,SPLAGSQGDW	KIRC
OR51F2	c.200G>C	p.R67P	SIPFCLLYVVAVSGNSMILFVVLCE[p.R67P]PSLHKPMYYFLSMLSATDLSLSLCTL	VLCEPSLHK,PSLHKPMYY,CEPSLHKPM,VVLCEPSLHK,LCEPSLHKPM,EPSLHKPMYY	LUSC
OR51S1	c.476G>A	p.R159Q	ICRPLHYPALLTNGVISKISLAISF[p.R159Q]QCLGLHLPLPFLLAYMPYCLPQVLTH	SLAISFQCL,SFQCLGLHL,ISFQCLGLH,FQCLGLHLPL,ISLAISFQCL,LAISFQCLGL,ISFQCLGLHL	LUSC
OR51V1	c.892C>A	p.P298T	FGKHLSPVAHVLIGNIYILFPPLMN[p.P298T]TIIYSVKTQQIHTRMLRLFSLKRY	ILFPPLMNT,LMNTIIYSV,LFPPLMNTI,MNTIIYSVK,NTIIYSVKT,PPLMNTIIY,FPPLMNTII,ILFPPLMNTI,PLMNTIIYSV,LMNTIIYSVK,LFPPLMNTII,FPPLMNTIIY	LUAD
OR52W1	c.397C>T	p.R133C	FVHALTAMESGVLLAMACDRAAAIG[p.R133C]CPLHYPVLVTKACVGYAALALALKAV	RAAAIGCPL,AAIGCPLHY,CPLHYPVLV,AIGCPLHYPV,RAAAIGCPLH,AAAIGCPLHY,IGCPLHYPVL	CRC
OR5AK2	c.267G>T	p.K89N	QHLAFVDICYTSAITPKMLQSFTEE[p.K89N]NNLMLFQGCVIQFLVYATFATSDCYL	FTEENNLML,TEENNLMLF,FTEENNLMLF,LQSFTEENNL,QSFTEENNLM	UCEC
OR5AS1	c.117G>T	p.M39I	FVGFTDYLPLRVTLFLVFLLVYTLT[p.M39I]IVGNILLIILVNINSSLQIPMYYFLS	FLLVYTLTI,LLVYTLTIV,YTLTIVGNI,TIVGNILLI,LTIVGNILL,FLLVYTLTIV,VFLLVYTLTI,VYTLTIVGNI,YTLTIVGNIL,LTIVGNILLI	LUAD
OR5AU1	c.935G>A	p.R312H	KAFSTCASHLTAICLFFGTTLFMYL[p.R312H]HPRSSYSLTQDRTVAVIYTVVIPVLN	FMYLHPRSS,YLHPRSSYS,TLFMYLHPR,GTTLFMYLH,MYLHPRSSY,HPRSSYSLT,LHPRSSYSL,YLHPRSSYSL,FMYLHPRSSY,TTLFMYLHPR	CRC
OR5B12	c.865A>T	p.S289C	HFMGTDKMASVFYAIVIPMLNPLVY[p.S289C]CLRNKEVKSAFKKTVGKAKASIGFIF	MLNPLVYCL,LVYCLRNKEV,MLNPLVYCLR,CLRNKEVKSA	LUAD
OR5B17	c.488G>A	p.R163H	VCACLAIGCYVIGFLNASIQIGDTF[p.R163H]HLSFCMSNVIHHFFCDKPAVITLTCS	IQIGDTFHL,HLSFCMSNV,DTFHLSFCM,IGDTFHLSF,HLSFCMSNVI,DTFHLSFCMS,QIGDTFHLSF	CRC
OR5B17	c.798G>T	p.M266I	SHLIAIFLFYITVIIMYIRPSSSHS[p.M266I]IDTDKIASVFYTMIIPMLSPIVYTLR	SSHSIDTDK,SIDTDKIASV,YIRPSSSHSI,SSSHSIDTDK,RPSSSHSIDT,IDTDKIASVF	LUAD
OR5D13	c.706C>T	p.R236C	SSLIIILTSYMLIFTTIMKMRSASG[p.R236C]CQKTFSTCASHLTAITIFHGTILFLY	KMRSASGCQ,SASGCQKTF,CQKTFSTCA,KMRSASGCQK,RSASGCQKTF,CQKTFSTCAS	GBM
OR5D14	c.736C>A	p.H246N	VFIFVTVLKIRSVSGRHKAFSTWAS[p.H246N]NLTSITIFHGTILFLYCVPNSKNSRQ	TWASNLTSI,KAFSTWASN,ASNLTSITI,SNLTSITIF,STWASNLTSI,KAFSTWASNL,WASNLTSITI,ASNLTSITIF	LUAD
OR5D16	c.790C>A	p.P264T	VFSTCASHLTAITIFHGTILFLYCV[p.P264T]TNSKNSRHTVKVASVFYTVVIPLLNP	FLYCVTNSK,CVTNSKNSR,LFLYCVTNSK	LUAD
OR5D18	c.812C>A	p.T271K	LTAITIFHGTILFLYCVPNSKNSRH[p.T271K]KVKVASVFYTVVIPMLNPLIYSLRNK	KVKVASVFY,RHKVKVASV,HKVKVASVF,NSKNSRHKVK,KVKVASVFYT,RHKVKVASVF,HKVKVASVFY	LUSC
OR5F1	c.131G>T	p.G44V	DTLELQIILFLFFLVIYTLTVLGNL[p.G44V]VMILLIRIDSQLHTPMYFFLANLSFV	VLGNLVMIL,TLTVLGNLV,TVLGNLVMI,LTVLGNLVM,YTLTVLGNLV,VLGNLVMILL,NLVMILLIRI,TLTVLGNLVM	LUAD
OR5J2	c.106G>T	p.A36S	EFILLGLTDHAELKAVLFVVFLVIY[p.A36S]SITLLRNLGMILLIQITSKLHTPMYF	VVFLVIYSI,FLVIYSITL,LVIYSITLL,VIYSITLLR,YSITLLRNL,FVVFLVIYSI,FLVIYSITLL,LVIYSITLLR,VFLVIYSITL,IYSITLLRNL	LUAD
OR5L1	c.824C>A	p.T275N	VFHGTVLSIYCRPSSGNSGDADKVA[p.T275N]NVFYTVVIPMLNSVIYSLRNKDVKEA	KVANVFYTV,ANVFYTVVI,DADKVANVF,DADKVANVFY,KVANVFYTVV,NVFYTVVIPM,GDADKVANVF,VANVFYTVVI	LUAD
OR5M3	c.265delA	p.T89fs	LSFVDVWFSSNVTPKMLENLLSDKK[p.T89fs]QLLMLVV*	LSDKKQLLM,LLSDKKQLL,KKQLLMLVV,LSDKKQLLML,LLSDKKQLLM	STAD
OR5P2	c.299C>T	p.A100V	PNMLVNFLVERNTVSYLGCAIQLGS[p.A100V]VAFFATVECVLLAAMAYDRFVAICSP	QLGSVAFFA,GSVAFFATV,IQLGSVAFF,AIQLGSVAF,CAIQLGSVA,IQLGSVAFFA,VAFFATVECV,CAIQLGSVAF,AIQLGSVAFF	GBM
OR6C65	c.460_461insT	p.I154fs	TTIMSNKVCNWLVISSWLAGFLIIF[p.I154fs]SPRDYGPPTGFL*	DYGPPTGFL,GFLIIFSPR,LIIFSPRDY,SPRDYGPPT,RDYGPPTGF,WLAGFLIIFS,AGFLIIFSPR,FLIIFSPRDY,RDYGPPTGFL	LUAD
OR6C75	c.280G>T	p.G94W	ISFTSVCIPRFLVTVVTGNRTISYN[p.G94W]WCVAQLFFFIFLGVTEFYLLAAMSYD	RTISYNWCV,SYNWCVAQL,YNWCVAQLF,NWCVAQLFF,SYNWCVAQLF,YNWCVAQLFF,NWCVAQLFFF,RTISYNWCVA,ISYNWCVAQL	LUAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
OR6K2	c.236C>A	p.P79Q	HLHTPMYTFISALSFLEIWYTTATI[p.P79Q]QKMLSSLLSERSISFNGCLLQMYFFH	TIQKMLSSL,IQKMLSSLL,YTTATIQKM,TTATIQKML,ATIQKMLSSL,TIQKMLSSLL,IWYTTATIQK,WYTTATIQKM,YTTATIQKML,IQKMLSSLLS	LUAD
OR6K6	c.931T>C	p.F311L	YLRFSATYSVFWDTAIAVTFVILAP[p.F311L]LFNPIIYSLKNKDMKEAIGRLFHYQK	VTFVILAPL,ILAPLFNPI,TFVILAPLF,APLFNPIIY,VILAPLFNPI,ILAPLFNPII,AVTFVILAPL,LFNPIIYSLK,VTFVILAPLF,LAPLFNPIIY	TGCT,THCA
OR6N2	c.877C>T	p.R293C	LTLDRTLAIVYSVLTPMVNPIIYSL[p.R293C]CNKEIIKAIKRTIFQKGDKASLAHL	SLCNKEIIK,PIIYSLCNK,IYSLCNKEI,YSLCNKEII,IIYSLCNKEI,YSLCNKEIIK,IYSLCNKEII,CNKEIIKAIK,MVNPIIYSLC	GBM
OR6V1	c.744delC	p.I248fs	VLRIPSASSCQKAFSTCGSHLTLVF[p.I248fs]MATVVPSFCMSGLAKLTLCKSGRSWPW*	LTLVFMATV,TLVFMATVV,FMATVVPSF,FCMSGLAKL,GLAKLTLCK,SFCMSGLAK,GSHLTLVFM,VPSFCMSGL,MSGLAKLTL,TLCKSGRSW,CKSGRSWPW,HLTLVFMATV,LTLVFMATVV,FMATVVPSFC,VVPSFCMSGL,CMSGLAKLTL,PSFCMSGLAK,SGLAKLTLCK,VFMATVVPSF,MATVVPSFCM,LTLCKSGRSW	HNSC
OR7C1	c.311delT	p.F104fs	PKMLLNILTQNKFITYAGCLSQIFF[p.F104fs]SLHLDAWTIYS*	CLSQIFFSL,SQIFFSLHL,SLHLDAWTI,FFSLHLDAW,LHLDAWTIY,FSLHLDAWTI,IFFSLHLDAW,SLHLDAWTIY,LSQIFFSLHL	KIRC
OR7C1	c.535delT	p.C179fs	MGSLLETLTVLRLSFCTEMEIPHFF[p.C179fs]VIYLKS*	MEIPHFFVI,EMEIPHFFV,IPHFFVIYL,MEIPHFFVIY,IPHFFVIYLK,TEMEIPHFFV,EMEIPHFFVI,EIPHFFVIYL	STAD
OR7E24	c.21_22insT	p.L7fs	MSYFPILFFFF[p.L7fs]PQKVSELHRATESHRCLRIPPPGTLRGSRTAAGPRWAVPVHVPGHGAGEPAHHPGCQL*	ILFFFFPQK,LFFFFPQKV,ATESHRCLR,GSRTAAGPR,RTAAGPRWA,TAAGPRWAV,TLRGSRTAA,RATESHRCL,LRIPPPGTL,FPQKVSELH,ILFFFFPQKV,RTAAGPRWAV,PILFFFFPQK,FFFPQKVSEL,RATESHRCLR,CLRIPPPGTL,GTLRGSRTAA,RGSRTAAGPR,ELHRATESHR,GPRWAVPVHV,EPAHHPGCQL,SELHRATESH,HRATESHRCL,GSRTAAGPRW,FPILFFFFPQ	PRAD
OR8D2	c.917G>T	p.R306M	IIPMLNPLIYSLRNKDVKNALKKMT[p.R306M]MGRQSS	ALKKMTMGR,KNALKKMTM,KKMTMGRQS,KMTMGRQSS,NALKKMTMGR,VKNALKKMTM,KKMTMGRQSS	LUAD
OR8H2	c.498G>T	p.L166F	CLALITGPYVIGFIDSFVNVVSMSR[p.L166F]FHFYDSNVIHHFFCDTSPILALSCTD	VSMSRFHFY,VVSMSRFHF,MSRFHFYDS,RFHFYDSNV,VNVVSMSRF,FHFYDSNVI,VVSMSRFHFY,RFHFYDSNVI,MSRFHFYDSN,FVNVVSMSRF,NVVSMSRFHF,SRFHFYDSNV,FHFYDSNVIH	LUSC
OR8J3	c.479C>T	p.S160L	VVSRRLCLLLVSLTYLYGFSTAIVV[p.S160L]LPCIFSVSYCSSNIINHFYCDIAPLL	VVLPCIFSV,TAIVVLPCI,LPCIFSVSY,AIVVLPCIF,IVVLPCIFSV,VLPCIFSVSY,STAIVVLPCI,YGFSTAIVVL,TAIVVLPCIF	LUSC
OR8K3	c.705G>T	p.K235N	SLLIVLLSYLLILVAILRMNSAGRQ[p.K235N]NAFSTCGAHLTVVIVFYGTLLFMYVQ	NSAGRQNAF,NAFSTCGAH,RQNAFSTCG,RMNSAGRQNA,RQNAFSTCGA,MNSAGRQNAF,NAFSTCGAHL	LUSC
OR8S1	c.296C>T	p.A99V	SSVIVPKMLENLLSQRKTISVEGCL[p.A99V]VQVFFVFVTAGTEACLLSGMAYDRHA	LVQVFFVFV,TISVEGCLV,CLVQVFFVF,VEGCLVQVF,VQVFFVFVT,CLVQVFFVFV,VQVFFVFVTA,KTISVEGCLV,GCLVQVFFVF,EGCLVQVFFV,SVEGCLVQVF,VEGCLVQVFF	CRC
OR9A2	c.865C>T	p.R289W	VEYNKIVSLLVSVLTPFLNPFIFTL[p.R289W]WNDKVKEALRDGMKRCCQLLKD*	FIFTLWNDK,FTLWNDKVK,LNPFIFTLW,FIFTLWNDKV,TLWNDKVKEA,FLNPFIFTLW	LUAD
OR9G9	c.506G>T	p.R169L	VAVSYCGGFINSSIITKKTFSFNFC[p.R169L]LENIIDDFFCDLLPLVELACGEKGGY	KTFSFNFCL,SFNFCLENI,FNFCLENII,LENIIDDFF,FSFNFCLENI,SFNFCLENII,KTFSFNFCLE,KKTFSFNFCL	LUAD
OSBP	c.2163G>C	p.Q721H	FSELALTLNAWESGTAPTDSRLRPD[p.Q721H]HRLMENGRWDEANAEKQRLEEKQRLS	RLRPDHRLM,DSRLRPDHR,RLRPDHRLME,SRLRPDHRLM	CESC
OSBP2	c.1881_1882insC	p.H627fs	ETFELDRLDDMGLRSLCEQVSHHPP[p.H627fs]LSCALRVLQAWLEPLAGDHHLQQVPGKIHLHHAARCHPLRIPGQWESLRVEEEHLNCSQHHRGQALDRPVRGHRDCEP*	VLQAWLEPL,ALRVLQAWL,KIHLHHAAR,HAARCHPLR,AARCHPLRI,HLNCSQHHR,SQHHRGQAL,HHAARCHPL,EQVSHHPPL,CALRVLQAW,LQAWLEPLA,LQQVPGKIH,QQVPGKIHL,GKIHLHHAA,GQWESLRVE,EPLAGDHHL,HPLRIPGQW,RVLQAWLEPL,VLQAWLEPLA,KIHLHHAARC,HHAARCHPLR,CEQVSHHPPL,SHHPPLSCAL,LQAWLEPLAG,LQQVPGKIHL,QQVPGKIHLH,LHHAARCHPL,LRIPGQWESL,WESLRVEEEH,LEPLAGDHHL,HPPLSCALRV,IPGQWESLRV	STAD
OSBPL6	c.1730G>A	p.R577Q	SEDNTSVADNISRQILNGELTGGAF[p.R577Q]QNGRRACLPAPCPDTSNINLWNILRN	FQNGRRACL,LTGGAFQNGR	UCEC
OSTN	c.344G>A	p.R115Q	PLDRLSAGSVDHKGKQRKVVDHPKR[p.R115Q]QFGIPMDRIGRNRLSNSRG	RQFGIPMDR,PKRQFGIPM,RQFGIPMDRI,HPKRQFGIPM,KVVDHPKRQF	CRC

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OTOF	c.1163C>T	p.T388M	DDISSGLKGYVKCDVAVVGKGDNIK[p.T388M]MPHKANETDEDDIEGNLLLPEGVPPE	KGDNIKMPHK	BRCA
OTOF	c.3910G>A	p.E1304K	KLETMVKLDATSEAVVKVDVAEEEK[p.E1304K]KKKKKKKGTAEEPEEEEPDESMLDWW	KVDVAEEEKK	STAD
OTOL1	c.1291G>A	p.V431I	VAQNKKQFKSRETLYGQEIDQASLL[p.V431I]IILKLSAGDQVWLEVSKDWNGVYVSA	QASLLIILK,IDQASLLII,DQASLLIIL,QEIDQASLLI,IDQASLLIIL	CRC
OTOP1	c.310_318delCTGCTGTGG	p.LLW104del	AWAVHAAGVSKSDLLCFLTALMLLQ[p.LLW104del]MLWYVGRSSAHRRLFRLKDTHAGAGWLRGSITLF	MLLQMLWYV,LQMLWYVGR,LMLLQMLWY,LTALMLLQM,ALMLLQMLW,FLTALMLLQM,LMLLQMLWYV,ALMLLQMLWY,LLQMLWYVGR,TALMLLQMLW	ACC
OTUD3	c.830G>T	p.R277I	VQNLEAENYNIESAIIAVLRMNQGK[p.R277I]INNAEENLEPSGRVLKQCGPLWEEGG	RMNQGKINNA,GKINNAEENL	CRC
OTUD4	c.2726C>T	p.T909I	ALASIPPVAEGKAHPPTQILNRERE[p.T909I]IVPVELEPKRTIQSLKEKTEKVKDPK	ILNREREIV,REREIVPVE,LNREREIVPV,TQILNREREI,REREIVPVEL,REIVPVELEP	BLCA,PRAD,THCA
OTUD4	c.458_460delCTG	p.A153del	VADEDNSEISDSEDDSCKSKTAAAA[p.A153del]DVNGFKPLSGNEQLKNNGNSTSLPLSRK	KSKTAAAAD,KSKTAAAADV,TAAAADVNGF	PRAD
OTX2	c.130delC	p.R44fs	TSGMDLLHPSVGYPGPWASCPAATP[p.R44fs]GNSAGRGRRSLGRS*	RGRRSLGRS,SAGRGRRSL,AGRGRRSLGR,CPAATPGNSA,NSAGRGRRSL	STAD
OXR1	c.364G>A	p.E122K	GTIEYTVESRDSLNSIALKFDTTPN[p.E122K]KLVQLNKLFSRAVVTGQVLYVPDPEY	KLVQLNKLF,ALKFDTTPNK,DTTPNKLVQL,LKFDTTPNKL,NKLVQLNKLF	UCEC
P2RX1	c.58delC	p.R20fs	MARRFQEELAAFLFEYDTP[p.R20fs]AWCWCVIRRWALSSD*	FLFEYDTPA,DTPAWCWCV,TPAWCWCVI,WCVIRRWAL,FLFEYDTPAW,AWCWCVIRRW,CWCVIRRWAL,TPAWCWCVIR,DTPAWCWCVI,FEYDTPAWCW	STAD
P2RX7	c.425C>A	p.P142Q	RLCPEYPTRRTLCSSDRGCKKGWMD[p.P142Q]QQSKGIQTGRCVVYEGNQKTCEVSAW	WMDQQSKGI,KGWMDQQSK	LUAD
PABPC1	c.1223A>T	p.Y408F	MQRMASVRAVPNPVINPYQPAPPSG[p.Y408F]FFMAAIPQTQNRAAYYPPSQIAQLRP	YQPAPPSGF,QPAPPSGFF,PYQPAPPSGF,YQPAPPSGFF,QPAPPSGFFM,APPSGFFMAA,PPSGFFMAAI	KIRC
PABPC1	c.280C>T	p.R94C	LDTMNFDVIKGKPVRIMWSQRDPSL[p.R94C]CKSGVGNIFIKNLDKSIDNKALYDTF	SQRDPSLCK,CKSGVGNIF,SLCKSGVGNI,WSQRDPSLCK,LCKSGVGNIF	DLBCL
PABPC1	c.467_468insG	p.E156fs	DENGSKGYGFVHFETQEAAERAIEK[p.E156fs]NEWNAPK*	AERAIEKNEW	KIRC
PABPC1	c.541G>A	p.A181T	EKMNGMLLNDRKVFVGRFKSRKERE[p.A181T]TELGARAKEFTNVYIKNFGEDMDDER	SRKERETEL,KERETELGA,RETELGARA,KSRKERETEL,TELGARAKEF	KIRC
PABPC1	c.761_762insT	p.K254fs	KSKGFGFVSFERHEDAQKAVDEMNG[p.K254fs]NGAQWKTNLCWSSSEKGGTADGT*	NLCWSSSEK,KTNLCWSSS,AQWKTNLCW,DEMNGNGAQ,TNLCWSSSEK,AQWKTNLCWS,DEMNGNGAQW	CLL
PABPC1	c.999delA	p.K333fs	LRKEFSPFGTITSAKVMMEGGRSKG[p.K333fs]LVLYVSPPQKKPLKQLQK*	VLYVSPPQK,RSKGLVLYV,GRSKGLVLY,MMEGGRSKGL,LVLYVSPPQK,VLYVSPPQKK,RSKGLVLYVS,VSPPQKKPLK,GGRSKGLVLY	KIRC
PABPC3	c.975_979delTATGA	p.V325fs	LDDGIDDERLRKAFSPFGTITSAKV[p.V325fs]GRWSQQRVWFCMFLLPRRSH*	RVWFCMFLL,KVGRWSQQR,RWSQQRVWF,QQRVWFCMF,TITSAKVGR,WFCMFLLPR,GRWSQQRVW,SQQRVWFCM,GTITSAKVGR,VWFCMFLLPR,SQQRVWFCMF,KVGRWSQQRV,QQRVWFCMFL,WFCMFLLPRR,VGRWSQQRVW,GRWSQQRVWF,WSQQRVWFCM,CMFLLPRRSH	TGCT
PABPC3	c.997delA	p.K333fs	LRKAFSPFGTITSAKVMMEGGRSKG[p.K333fs]LVLYVSPPQKKPLKQLQK*	VLYVSPPQK,RSKGLVLYV,GRSKGLVLY,MMEGGRSKGL,LVLYVSPPQK,VLYVSPPQKK,RSKGLVLYVS,VSPPQKKPLK,GGRSKGLVLY	BLCA
PACSIN1	c.1075G>A	p.E359K	AVESTSQAGDRGSVSSYDRGQPYAT[p.E359K]KWSDDESGNPFGGSETNGGANPFEDD	RGQPYATKW	HNSC

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PACSIN2	c.993G>C	p.Q331H	ADLNRTLSRREKKKATDGVTLTGIN[p.Q331H]HTGDQSLPSKPSSTLNVPSNPAQSAQ	INHTGDQSL,HTGDQSLPSK	BRCA
PADI2	c.340A>C	p.T114P	SSDKVTVNYYDEEGSIPIDQAGLFL[p.T114P]PAIEISLDVDADRDGVVEKNNPKKAS	GLFLPAIEI,FLPAIEISL,DQAGLFLPA,LFLPAIEISL,DQAGLFLPAI,LPAIEISLDV,IDQAGLFLPA	MM
PAFAH1B1	c.904delA	p.K302fs	VECISWAPESSYSSISEATGSETKK[p.K302fs]VVNLGHSCCLDPETRLLRCGMSVLACAL*	RLLRCGMSV,GMSVLACAL,LLRCGMSVL,SETKKVVNL,RLLRCGMSVL,LLRCGMSVLA,CGMSVLACAL	STAD
PALB2	c.839delA	p.N280fs	DSGSSQHLEHIPPKGSSELTTHDLK[p.N280fs]TLDLLHL*	LKTLDLLHL,SELTTHDLKT	STAD
PALLD	c.2986G>A	p.A996T	DSAHKMLVRENGVHSLIIEPVTSRD[p.A996T]TGIYTCIATNRAGQNSFSLELVVAAK	VTSRDTGIY,RDTGIYTCI,PVTSRDTGIY	KIRC
PALM2-AKAP2	c.3213_3214insGAAGCT	p.1075_1076insEA	KAVSKTSRDGAEQQGPEATVEEAEA[p.1075_1076insEA]EAAAFGSEKPQSMFEPPQVSSPVQEKRDVLP	EAEAEAAAF,VEEAEAEAA,AEAEAAAFG,EEAEAEAAAF,AEAEAAAFGS,VEEAEAEAAA	KIRC
PALM2-AKAP2	c.3354_3355insC	p.G1118fs	VQEKRDVLPKILPAEDRALRERGPP[p.G1118fs]PATASCAAQWPD*	RERGPPPAT,ALRERGPPPA,RERGPPPATA	KIRC
PALM2-AKAP2	c.895G>A	p.A299T	KLEMVHKSRKDHSSGNPGQQAQAPS[p.A299T]TAGPEANLDQPVTMIFMGYQNIEDEE	STAGPEANL,APSTAGPEA,GQQAQAPST,QQAQAPSTA,GQQAQAPSTA,QQAQAPSTAG	BRCA
PAMR1	c.302delG	p.G101fs	CDSCLIHPGCTIFENCKSCRNGSWG[p.G101fs]VPWMTSM*	WGVPWMTSM,RNGSWGVPW,KSCRNGSWGV,CRNGSWGVPW,RNGSWGVPWM,SWGVPWMTSM	STAD
PANK1	c.1199delA	p.K400fs	DSVGFNGKPECYYFENPTNPELCQK[p.K400fs]SRTALITHTLCCWLTWAQVSAF*	TLCCWLTWA,WLTWAQVSA,RTALITHTL,HTLCCWLTW,CQKSRTALI,KSRTALITH,LTWAQVSAF,LCQKSRTAL,LITHTLCCWL,KSRTALITHT,HTLCCWLTWA,ELCQKSRTAL,WLTWAQVSAF,SRTALITHTL,ALITHTLCCW	STAD
PANK2	c.1251delT	p.T417fs	VSILAVYSKDNYKRVTGTSLGGGTF[p.T417fs]LVSAVFLLAVPLLKKLLKWHLVEIAPKWIN*	SLGGGTFLV,FLVSAVFLL,AVFLLAVPL,LLKWHLVEI,LVSAVFLLA,FLLAVPLLK,LLAVPLLKK,TFLVSAVFL,VFLLAVPLL,GTFLVSAVF,VSAVFLLAV,LKWHLVEIA,HLVEIAPKW,FLVSAVFLLA,LVSAVFLLAV,AVFLLAVPLL,LLAVPLLKKL,KLLKWHLVEI,LLKKLLKWHL,LLKWHLVEIA,HLVEIAPKWI,FLLAVPLLKK,VFLLAVPLLK,AVPLLKKLLK,TFLVSAVFLL,GTFLVSAVFL,KWHLVEIAPK,TSLGGGTFLV,SAVFLLAVPL,GGTFLVSAVF,VPLLKKLLKW	PRAD
PANK2	c.377G>C	p.G126A	AAEEARRNPTLGGLLGRQRLLLRMG[p.G126A]AGRLGAPMERHGRASATSVSSAGEQA	LLRMGAGRL,RMGAGRLGA,LLLRMGAGR,GAGRLGAPM,RQRLLLRMGA,RLLLRMGAGR,AGRLGAPMER,MGAGRLGAPM,LRMGAGRLGA	ACC
PANK3	c.779G>T	p.R260I	LEMASKGDSTQADKLVRDIYGGDYE[p.R260I]IFGLPGWAVASSFGNMIYKEKRESVS	IYGGDYEIF,IFGLPGWAV,DIYGGDYEI,EIFGLPGWA,YEIFGLPGW,EIFGLPGWAV,DIYGGDYEIF,RDIYGGDYEI,YEIFGLPGWA	CRC
PAOX	c.319C>T	p.H107Y	QLAAEYGLLGEKELSQENQLVETGG[p.H107Y]YVGLPSVSYASSGASVSLQLVAEMAT	QLVETGGYV,NQLVETGGY,YVGLPSVSY,VETGGYVGL,YVGLPSVSYA,GYVGLPSVSY	CESC
PAPD4	c.675_676insT	p.C225fs	SLNGFGTRSSDGDLCLVVKEEPCFF[p.C225fs]SGKSED*	KEEPCFFSG	STAD
PAPPA2	c.2749C>A	p.P917T	QYVHTASSRRVCDSSGYWTPEEAVG[p.P917T]TPDVDQPCEPSLQAWSPEVHLYHMNM	EEAVGTPDV	LUAD
PAPPA2	c.5049delC	p.I1683fs	NSVEYKCEQGYGIGAVCSPLCVIPP[p.I1683fs]VTP*	SPLCVIPPV,CSPLCVIPPV	STAD
PAPPA2	c.5117C>A	p.P1706H	CVIPPSDPVMLPENITADTLEHWME[p.P1706H]HVKVQSIVCTGRRQWHPDPVLVHCIQ	TLEHWMEHV,MEHVKVQSI,WMEHVKVQSI,TLEHWMEHVK,DTLEHWMEHV,MEHVKVQSIV,LEHWMEHVKV	LUAD
PARD6A	c.252_253insC	p.G84fs	TDAHGDLLPLTNDDSLHRALASGPP[p.G84fs]ATAPTGAEAGRS*	ALASGPPAT,RALASGPPA,ALASGPPATA,RALASGPPAT,HRALASGPPA	KIRC

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PARG	c.1750G>A	p.A584T	KYNVAYSKKWDFTALIDFWDKVLEE[p.A584T]TEAQHLYQSILPDMVKIALCLPNICT	EETEAQHLY,LEETEAQHL,TEAQHLYQS,LEETEAQHLY,TEAQHLYQSI	KIRP,PRAD
PARP15	c.1381delA	p.K461fs	PSLKTVKVVIFQPELLNIFYDSMKK[p.K461fs]ETSLHH*	SMKKETSLH,DSMKKETSL,MKKETSLHH,SMKKETSLHH	STAD
PARP4	c.2541delA	p.K847fs	SSLDSSGFSLHIGLSAAYLPRMWVE[p.K847fs]NIQKKKARLACLSFNPISMSTSLT*	RMWVENIQK,IQKKKARLA,KARLACLSF,LPRMWVENI,NPISMSTSL,NIQKKKARL,KKKARLACL,LACLSFNPI,CLSFNPISM,YLPRMWVENI,RLACLSFNPI,RMWVENIQKK,KARLACLSFN,KKARLACLSF,ACLSFNPISM	STAD
PASD1	c.685_687delGCT	p.A236del	SSQGQRGHTSMKAVYVEPAAAAAAA[p.A236del]ISDDQIDIAEVEQYGPQENVHMFVDSDS	EPAAAAAAAI	GBM
PASK	c.185C>T	p.T62I	PSRSFSSAHRHLSRRNGLSRLCQSR[p.T62I]IALSEDRWSSYCLSSLAAQNICTSKL	RLCQSRIAL,LSRLCQSRI,GLSRLCQSRI,LSRLCQSRIA,SRLCQSRIAL	KIRC
PAX2	c.1183delC	p.P395fs	YSHPQYTAYNEAWRFSNPALLMPPP[p.P395fs]VRPCRCCRCL*	PVRPCRCCR,MPPPVRPCR,RPCRCCRCL,LLMPPPVRPC,LMPPPVRPCR,NPALLMPPPV	STAD
PAX3	c.1271C>T	p.T424M	HGGVPHQPQTDYALSPLTGGLEPTT[p.T424M]MVSASCSQRLDHMKSLDSLPTSQSYC	MVSASCSQR,LEPTTMVSA,MVSASCSQRL,TMVSASCSQR	CRC
PAX3	c.590C>T	p.S197L	LERKEAEESEKKAKHSIDGILSERA[p.S197L]LAPQSDEGSDIDSEPDLPLKRKQRRS	SERALAPQS	BLCA
PAX6	c.1124delC	p.P375fs	QTSSYSCMLPTSPSVNGRSYDTYTP[p.P375fs]HICRHT*	RSYDTYTPH,SYDTYTPHI,DTYTPHICR,RSYDTYTPHI	STAD
PBLD	c.164C>A	p.P55Q	LDEDMHQKIAREMNLSETAFIRKLH[p.P55Q]QTDNFAQSSCFGLRWFTPASEVPLCG	KLHQTDNFA,RKLHQTDNF,IRKLHQTDNF,HQTDNFAQSS	LUAD
PBX2	c.208G>A	p.E70K	PGGRGKQDIGDILQQIMTITDQSLD[p.E70K]KAQAKKHALNCHRMKPALFSVLCEIK	TITDQSLDK,QSLDKAQAK,SLDKAQAKK,KAQAKKHAL,MTITDQSLDK,QSLDKAQAKK	BLCA
PBX2	c.785A>T	p.Y262F	LRSRFLDARRKRRNFSKQATEVLNE[p.Y262F]FFYSHLSNPYPSEEAKEELAKKCGIT	QATEVLNEF,TEVLNEFFY,NEFFYSHLS,ATEVLNEFFY,VLNEFFYSHL,KQATEVLNEF,FFYSHLSNPY,NEFFYSHLSN	KIRP,LUSC,TGCT
PBXIP1	c.2186_2188delACC	p.H729del	KKDKHSQSPRAAGPREGHSHSHHHH[p.H729del]RG*	HSHSHHHHR	BLCA
PCBP1	c.305T>A	p.L102Q	DKLEEDINSSMTNSTAASRPPVTLR[p.L102Q]QVVPATQCGSLIGKGGCKIKEIRIEST	RPPVTLRQV,RQVVPATQC,RPPVTLRQVV,RQVVPATQCG	CRC
PCCA	c.689G>A	p.R230H	AVRIAREIGYPVMIKASAGGGGKGM[p.R230H]HIAWDDEETRDGFRLSSQEAASSFGD	HIAWDDEETR	STAD
PCDH10	c.1429G>A	p.V477M	QVSDVNDNAPRFSQPVYDVYVTENN[p.V477M]MPGAYIYAVSATDRDEGANAQLAYSI	NMPGAYIYA,TENNMPGAY,NNMPGAYIY,MPGAYIYAV,VTENNMPGAY,YVTENNMPGA,NMPGAYIYAV,YDVYVTENNM,MPGAYIYAVS,TENNMPGAYI	CRC
PCDH10	c.1759C>A	p.R587S	ILIVDQNDNAPAIVAPLPGRNGTPA[p.R587S]SEVLPRSAEPGYLLTRVAAVDADDGE	GTPASEVLPR,RNGTPASEVL	LUAD
PCDH10	c.2956G>T	p.V986L	SDGRQAADYRSNLHVPGMDSVPDTE[p.V986L]LFETPEAQPGAERSFSTFGKEKALHS	TELFETPEA,GMDSVPDTEL,MDSVPDTELF	LUAD
PCDH10	c.354_355insC	p.N118fs	EVFLENPLELFQVEIEVLDINDNPP[p.N118fs]LFPGARPDGGNL*	VLDINDNPPL,LDINDNPPLF	STAD
PCDH10	c.673_674insC	p.P225fs	TAVDGGGGGGVGEGGGGGGGAGLPP[p.P225fs]PAAAHRHGPTHHPSAGLQ*	AAHRHGPTH,GPTHHPSAGL,RHGPTHHPSA	STAD
PCDH11X	c.1457C>T	p.T486M	DNAPVFTQSFVTVSIPENNSPGIQL[p.T486M]MKVSAMDADSGPNAKINYLLGPDAPP	IQLMKVSAM,QLMKVSAMDA	GBM
PCDH11X	c.3029G>T	p.R1010I	SSDPYSVSDCGYPVTTFEVPVSVHT[p.R1010I]IPPMKEVVRSCTPMKESTTMEIWIHP	SVHTIPPMK,EVPVSVHTI,HTIPPMKEV,VSVHTIPPM,VSVHTIPPMK,TIPPMKEVVR,HTIPPMKEVV,FEVPVSVHTI	LUAD

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PCDH15	c.4655G>T	p.R1552I	DDLSAHNPLYKENISQVSTNSDISQ[p.R1552I]ITDFVDPFSPKIQAKSKSLRGPREKI	DISQITDFV,QITDFVDPF,SDISQITDF,SQITDFVDPF	CRC
PCDH15	c.5138G>T	p.C1713F	VELKSEPNVISSPAECSLELSPSRP[p.C1713F]FVLHSSLSRRETPICMLPIETERNIF	ELSPSRPFV,FVLHSSLSR,RPFVLHSSL,LELSPSRPF,FVLHSSLSRR,SLELSPSRPF,LELSPSRPFV	KIRC
PCDH19	c.1588G>A	p.E530K	YVSINPNSGDIYALRSFNHEQTKAF[p.E530K]KFKVLAKDGGLPSLQSNATVRVIILD	QTKAFKFKV,KAFKFKVLA,AFKFKVLAK,TKAFKFKVL,HEQTKAFKF,KAFKFKVLAK,QTKAFKFKVL	UCEC
PCDH19	c.856C>T	p.R286C	NASDPDEGTNGQVVYSFYGYVNDRT[p.R286C]CELFQIDPHSGLVTVTGALDYEEGHV	YVNDRTCEL,YVNDRTCELF	BRCA
PCDHAC2	c.1555G>A	p.A519T	LVERRVGERALSNYVSVHAESGKVY[p.A519T]TLQPLDHEELELLQFQVSARDAGVPP	AESGKVYTL,GKVYTLQPL,TLQPLDHEEL,KVYTLQPLDH,SGKVYTLQPL,HAESGKVYTL	CRC
PCDHAC2	c.2207C>T	p.A736V	ALSTVSFIFLLTIIILSIIKCYRYT[p.A736V]VYGTACCGGFCGVRERSPAELYKQAN	IIKCYRYTV,YTVYGTACC,IKCYRYTVY,YRYTVYGTA,SIIKCYRYTV,VYGTACCGGF,IIKCYRYTVY,CYRYTVYGTA,YRYTVYGTAC	CRC
PCDHAC2	c.2225C>T	p.A742V	TALRCSAAPTEGACGPVKPTLVCSS[p.A742V]VVGSWSYSQQRRQRVCSGEGLPKADL	SSVVGSWSY,KPTLVCSSV,CSSVVGSWSY,KPTLVCSSVV,LVCSSVVGSW	LUAD
PCDHAC2	c.414G>T	p.K138N	PLQVFHVDVEVKDINDNPPVFPATQ[p.K138N]NNLFIAESRPLDSRFPLEGASDADIG	VFPATQNNL,NNLFIAESR,FPATQNNLF,VFPATQNNLF,FPATQNNLFI	UCEC
PCDHAC2	c.467C>T	p.A156V	RFSRQEQRLFILESRMPDSRFPLEG[p.A156V]VSDLDIGANAQLRYRLNPNEYFDLDV	DSRFPLEGV,FPLEGVSDL	CRC
PCDHAC2	c.568G>A	p.E190K	NALLSYKLSSSEFFFLDIQANDELS[p.E190K]KSLSLVLGKSLDREETAEVNLLLVAT	ELSKSLSLV,KSLSLVLGK,LSKSLSLVL,DELSKSLSL,DELSKSLSLV	CRC
PCDHAC2	c.796G>A	p.A266T	AFERTIYKVRLLENAPNGTLVVTVN[p.A266T]TTDLDEGVNKDIAYSFNTDMSADILS	NTTDLDEGV,TTDLDEGVNK	CRC
PCDHAC2	c.811G>A	p.E271K	SYKVVLSENVQNDTRVIQLNASDPD[p.E271K]KGLNGEISYGIKMILPVSEKCMFSIN	QLNASDPDK,KGLNGEISY	CRC
PCDHB1	c.1704C>G	p.N568K	SSQVTVRVVVLDDNDNRPMILYPLQ[p.N568K]KGTLPCNDLVPRSAEAGYLVTKVVAV	ILYPLQKGT,PMILYPLQK,ILYPLQKGTL,RPMILYPLQK,YPLQKGTLPC	LUSC
PCDHB12	c.865C>T	p.R289C	VSAWDLDSGTNSELSYTFSHASEDI[p.R289C]CKTFEINQKSGDITLTAPLDFEAIES	ASEDICKTF,FSHASEDICK,HASEDICKTF,SEDICKTFEI	UCEC
PCDHB13	c.662C>T	p.P221L	VLDKALDREEEAELRLTLTALDGGS[p.P221L]LPRSGTAQVYIEVLDVNDNAPEFEQP	LPRSGTAQV,SLPRSGTAQV,TALDGGSLPR,LPRSGTAQVY	GBM
PCDHB4	c.763_764CC>TT	p.P255F	LIMDINDNAPEFVHTPYGVQVLENS[p.P255F]FLDSPIVRVLARDIDAGNFGSVSYGLF	FLDSPIVRV,SFLDSPIVR,NSFLDSPIV,GVQVLENSF,VQVLENSFL,FLDSPIVRVL,NSFLDSPIVR,YGVQVLENSF,LENSFLDSPI	TGCT
PCDHB5	c.151G>T	p.D51Y	AGSEAVRYSIPEETESGYSVANLAK[p.D51Y]YLGLGVGELATRGARMHYKGNKELLQ	YSVANLAKY,YLGLGVGEL,AKYLGLGVG,NLAKYLGLGV,YLGLGVGELA,KYLGLGVGEL,GYSVANLAKY,YSVANLAKYL	CRC
PCDHB5	c.1945C>T	p.P649S	RTARLLSERDAAKHRLVVLVKDNGE[p.P649S]SPRSATATLHVLLVDGFSQPYLPLPE	SPRSATATL,GESPRSATA,LVKDNGESPR,ESPRSATATL,GESPRSATAT	LUAD
PCDHB8	c.703G>A	p.D235N	RLTLTALDGGSPPRSGTAQVYIEVV[p.D235N]NVNDNAPEFEQPFYRVQISEDSPISF	QVYIEVVNV,EVVNVNDNA,NVNDNAPEF,AQVYIEVVNV,VNVNDNAPEF,IEVVNVNDNA	CRC
PCDHGC5	c.1796G>T	p.G599V	GVELAPRSAERGYLVTKVVAVDRDS[p.G599V]VQNAWLSYRLLKASEPGLFSVGLHTG	SVQNAWLSY,VQNAWLSYR,VVAVDRDSV,VQNAWLSYRL,SVQNAWLSYR,DSVQNAWLSY,VDRDSVQNAW	KIRC
PCDHGC5	c.1984G>A	p.V662M	ALKQSLVVAVQDHGQPPLSATVTLT[p.V662M]MAVADSIPEVLADLGSLEPSDGPYNY	LSATVTLTM,ATVTLTMAV,LTMAVADSI,TVTLTMAVA,MAVADSIPEV,TLTMAVADSI,SATVTLTMAV,PLSATVTLTM	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
PCDHGC5	c.1990G>A	p.D664N	RLLVAVRDGGQPPLSATATLHLVFA[p.D664N]NSLQEVLPDITDRPDPSDLQAELQFY	VFANSLQEV,LHLVFANSL,FANSLQEVL,LVFANSLQEV,TLHLVFANSL,VFANSLQEVL	BRCA
PCDHGC5	c.2051C>A	p.P684H	TVTVAVADRIPDILADLGSIKTPID[p.P684H]HEDLDLTLYLVVAVAAVSCVFLAFVI	HEDLDLTLY,IDHEDLDLTL,TPIDHEDLDL,HEDLDLTLYL	LUAD
PCDHGC5	c.208G>A	p.A70T	SVVGNLAKDLGLSVLDVSARKLRVS[p.A70T]TEKLHFSVDAESGDLLVKNRIDREQI	SARKLRVST,RKLRVSTEK,KLRVSTEKL,STEKLHFSV,RVSTEKLHF,KLRVSTEKLH,VSTEKLHFSV,RKLRVSTEKL,LRVSTEKLHF,TEKLHFSVDA	UCEC
PCDHGC5	c.36G>T	p.K12N	MAALQKLPHCR[p.K12N]NLVLLCFLLATLWEARAGQIRYSVRE	KLPHCRNLV,NLVLLCFLL,LPHCRNLVL,QKLPHCRNL,KLPHCRNLVL,LPHCRNLVLL,LQKLPHCRNL,HCRNLVLLCF	LUAD
PCDHGC5	c.866C>T	p.S289L	LTATDPDEGINGKLTYSFRNEEEKI[p.S289L]LETFQLDSNLGEISTLQSLDYEESRF	EEEKILETF,NEEEKILETF,LETFQLDSNL	CRC
PCDHGC5	c.877C>T	p.R293C	DPDEGANGEVTYSFHNVDHRVAQIF[p.R293C]CLDSYTGEISNKEPLDFEEYKMYSME	CLDSYTGEI,AQIFCLDSY,HRVAQIFCL,VAQIFCLDSY,AQIFCLDSYT	SKCM
PCGF3	c.189delC	p.H63fs	SCLVKYLEENNTCPTCRIVIHQSHP[p.H63fs]CSTSVMTEPCKILFTNWYQASKKRK*	ILFTNWYQA,FTNWYQASK,TSVMTEPCK,HQSHPCSTS,QSHPCSTSV,SHPCSTSVM,VMTEPCKIL,MTEPCKILF,CKILFTNWY,KILFTNWYQA,HQSHPCSTSV,ILFTNWYQAS,FTNWYQASKK,STSVMTEPCK,VMTEPCKILF,LFTNWYQASK,QSHPCSTSVM,EPCKILFTNW	STAD
PCLO	c.11836C>A	p.P3946T	PYQTQPTFQAVATMSFTPQVQPTPT[p.P3946T]TQPSYQLPSQMMVIQQKPRQTTLYLE	PTPTTQPSY,TPTTQPSYQL,QPTPTTQPSY	LUAD
PCLO	c.12397C>T	p.R4133C	VKAEEDPMEDPYELKLLKHQIKQEF[p.R4133C]CRGTESLDHLAGLSHYYHADTSYRHF	HQIKQEFCR,QEFCRGTES,QEFCRGTESL	SKCM
PCMTD1	c.812G>T	p.R271M	LARIYIRRTLRNFINDEMQAKGIPQ[p.R271M]MAPPKRKRKRVKQRINTYVFVGNQLI	MQAKGIPQM,GIPQMAPPK,MAPPKRKRK,QMAPPKRKR,MQAKGIPQMA,KGIPQMAPPK,QMAPPKRKRK,MAPPKRKRK,EMQAKGIPQM	LUAD
PCMTD1	c.842T>C	p.V281A	RNFINDEMQAKGIPQRAPPKRKRKR[p.V281A]AKQRINTYVFVGNQLIPQPLDSEEDE	RAKQRINTY,RAKQRINTYV,KRAKQRINTY,AKQRINTYVF	TGCT
PCNXL2	c.404G>A	p.R135Q	GEHITNHRNPSNNRQIHNGKKEEAS[p.R135Q]QNLSTPPLRCSSRGQSITSHHSSGPL	SQNLSTPPL,KKEEASQNL,SQNLSTPPLR,GKKEEASQNL,ASQNLSTPPL,KEEASQNLST	CRC
PCOLCE2	c.1043C>T	p.A348V	ITTITRDGSLHATVSIINIYKEGNL[p.A348V]VIQQAGKNMSARLTVVCKQCPLLRRG	NIYKEGNLV,IYKEGNLVI,LVIQQAGKNM,KEGNLVIQQA	CRC
PCOLCE2	c.260G>A	p.R87H	KITVPEGKVVVLNFRFIDLESDNLC[p.R87H]HYDFVDVYNGHANGQRIGRFCGTFRP	LESDNLCHY,CHYDFVDVY,SDNLCHYDF,ESDNLCHYDF,NLCHYDFVDV,LCHYDFVDVY	CRC
PCP4L1	c.191A>G	p.K64R	DLTAPETEKAALAIQGKFRRFQKRK[p.K64R]RDPSS*	KFRRFQKRKR	TGCT
PDE4B	c.1250C>T	p.S417L	MMTLEDHYHSDVAYHNSLHAADVAQ[p.S417L]LTHVLLSTPALDAVFTDLEILAAIFA	HAADVAQLT,DVAQLTHVL,LHAADVAQL,AQLTHVLLS,SLHAADVAQL,DVAQLTHVLL,LTHVLLSTPA,HAADVAQLTH,ADVAQLTHVL,AQLTHVLLST	CRC
PDGFRA	c.685G>A	p.E229K	NVYALKATSELDLEMEALKTVYKSG[p.E229K]KTIVVTCAVFNNEVVDLQWTYPGEVK	KTIVVTCAV,TVYKSGKTI,YKSGKTIVV,ALKTVYKSGK,KTIVVTCAVF,KTVYKSGKTI,TVYKSGKTIV,YKSGKTIVVT	GBM
PDGFRB	c.1949C>T	p.S650L	SQATMKVAVKMLKSTARSSEKQALM[p.S650L]LELKIMSHLGPHLNVVNLLGACTKGG	KQALMLELK,EKQALMLEL,ALMLELKIM,LELKIMSHL,MLELKIMSHL,RSSEKQALML,SEKQALMLEL,KQALMLELKI,LMLELKIMSH	GBM
PDIA6	c.168T>G	p.N56K	PCSPTSPAHSLSRKSPIMYPSTTMA[p.N56K]KAPGLVSCTFFLAVNGLYSSSDDVIE	TMAKAPGLV,MYPSTTMAK,TTMAKAPGL,YPSTTMAKA,TTMAKAPGLV,IMYPSTTMAK,MYPSTTMAKA,KAPGLVSCTF	TGCT
PDILT	c.1498G>A	p.E500K	LYKGEHTLKGFSDFLESHIKTKIED[p.E500K]KDELLSVEQNEVIEEEVLAEEKEVPM	HIKTKIEDK,IEDKDELLSV	CESC
PDPR	c.2377G>T	p.G793W	TMFILDDHDSDLDLWPWWGEPIYRN[p.G793W]WQYVGKTTSSAYSYSLERHVCLGFVH	EPIYRNWQY,WQYVGKTTS,WWGEPIYRNW,IYRNWQYVGK,EPIYRNWQYV,WQYVGKTTSS	LUAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
PDS5A	c.3927G>C	p.L1309F	KNDDLNKPINKGRKRAAVGQESPGG[p.L1309F]FEAGNAKAPKLQDLAKKAAPAERQID	QESPGGFEA,GQESPGGFEA	TGCT
PDYN	c.571G>T	p.G191W	EDPKEQVKRYGGFLRKYPKRSSEVA[p.G191W]WEGDGDSMGHEDLYKRYGGFLRRIRP	YPKRSSEVAW,VAWEGDGDSM	LUAD
PDZD2	c.1693C>A	p.R565S	RKHSLPQLLDSSSASQEYHIVKKST[p.R565S]SSLSTTQVESPWRLIRPSVISIIGLY	IVKKSTSSL,TSSLSTTQV,KKSTSSLST,HIVKKSTSSL,STSSLSTTQV,IVKKSTSSLS,KKSTSSLSTT	LUAD
PDZD2	c.302_303insG	p.R101fs	DTETVGLSFGNIPVFGDYGEKRRGG[p.R101fs]QEEENPPGSCAGCGLHLGDRAEEEQPSREEWEGPTAG*	REEWEGPTA,EEQPSREEW,EEWEGPTAG,EENPPGSCA	STAD
PELI2	c.589delG	p.G197fs	AKWKNPDGHMDGLTTNGVLVMHPRG[p.G197fs]ASPRSPSPGSGARSLSVEMCTPCEKPGRPSNEESWWKVRPTSCRTAPSLTCVGPLSSGEQQMGFFILQLRST*	RTAPSLTCV,QMGFFILQL,VLVMHPRGA,MGFFILQLR,GARSLSVEM,KVRPTSCRT,SPGSGARSL,RPTSCRTAP,VMHPRGASP,SSGEQQMGF,GEQQMGFFI,EQQMGFFIL,RPSNEESWW,QQMGFFILQL,VMHPRGASPR,SVEMCTPCEK,QMGFFILQLR,RSPSPGSGAR,KVRPTSCRTA,WWKVRPTSCR,HPRGASPRSP,RPTSCRTAPS,APSLTCVGPL,GPLSSGEQQM,SGARSLSVEM,LSSGEQQMGF,GEQQMGFFIL,EESWWKVRPT	STAD
PEX1	c.1108delA	p.I370fs	QSKTKQNVLSPEKEKQMSEPLDQKK[p.I370fs]LGQIIMKKMRRPVCYK*	KLGQIIMKK,KMRRPVCYK,IMKKMRRPV,QIIMKKMRR,MKKMRRPVC,QKKLGQIIM,KKMRRPVCY,IIMKKMRRPV,KKMRRPVCYK,IMKKMRRPVC,DQKKLGQIIM,KLGQIIMKKM,MKKMRRPVCY	BLCA,PRAD
PFKM	c.352C>A	p.R118S	TSGGDAQGMNAAVRAVVRVGIFTGA[p.R118S]SVFFVHEGYQGLVDGGDHIKEATWES	FTGASVFFV,SVFFVHEGY,IFTGASVFF,GIFTGASVF,VGIFTGASV,RVGIFTGASV,ASVFFVHEGY,IFTGASVFFV,VGIFTGASVF,GIFTGASVFF	LUAD
PFKP	c.1779delG	p.M593fs	SGTKRRVFIIETMGGYCGYLANMGG[p.M593fs]SRPELMPHTFSKSPSTSGICSPTWST*	ELMPHTFSK,GSRPELMPH,HTFSKSPST,YLANMGGSR,STSGICSPT,RPELMPHTF,NMGGSRPEL,SKSPSTSGI,TSGICSPTW,MPHTFSKSPS,ANMGGSRPEL,NMGGSRPELM,SRPELMPHTF,FSKSPSTSGI,STSGICSPTW	STAD
PGAM1	c.719G>A	p.R240H	PIVYELDKNLKPIKPMQFLGDEETV[p.R240H]HKAMEAVAAQGKAKK*	TVHKAMEAV,ETVHKAMEA,HKAMEAVAA,DEETVHKAM,ETVHKAMEAV,EETVHKAMEA	CRC
PGAP1	c.1694T>G	p.F565C	QAPSSTEISLKLHIAQPENNTHVAL[p.F565C]CKMYTSSDCRYEVTVKTSFSQILGQV	THVALCKMY,NTHVALCKMY	OV
PGM5	c.1277_1278insC	p.G426fs	VWLSIIAARKQSVEEIVRDHWAKFG[p.G426fs]PPLLLQV*	HWAKFGPPL,AKFGPPLLL,HWAKFGPPLL,KFGPPLLLQV	KIRC
PGM5	c.292A>G	p.I98V	RTAIEIVVQMAAANGIGRLIIGQNG[p.I98V]VLSTPAVSCIIRKIKAAGGIIILTASH	RLIIGQNGV,VLSTPAVSCI,RLIIGQNGVL,GQNGVLSTPA	STAD
PGPEP1L	c.490_491insA	p.R164fs	KGCAALIHVPPLSRGLPASLLGRAL[p.R164fs]KSHHPGNAGRGGKAQAQSPVRRKLNHGPSSQRELTGGLLL*	SQRELTGGL,ASLLGRALK,RALKSHHPG,KSHHPGNAG,KAQAQSPVR,QAQSPVRRK,GKAQAQSPV,AQSPVRRKL,RKLNHGPSS,RELTGGLLL,ALKSHHPGNA,KLNHGPSSQR,KSHHPGNAGR,KAQAQSPVRR,AQAQSPVRRK,SQRELTGGLL	KIRC
PHACTR1	c.752_753insG	p.V251fs	LPCLPVKLSPPLPPKKVMICMPVGG[p.V251fs]ARPLTGVLHSPEEWPAGCGPAPPHCPALPDPAPAAVRQPRPAPPLHHRLPPHAPLGLQNDRRAQQNAGHDHAEAGKL*	ALPDPAPAA,AVRQPRPAP,RQPRPAPPL,MICMPVGGA,MPVGGARPL,GARPLTGVL,GPAPPHCPA,LPDPAPAAV,LPPHAPLGL,HRLPPHAPL,AQQNAGHDH,WPAGCGPAP,VMICMPVGGA,VLHSPEEWPA,ALPDPAPAAV,RLPPHAPLGL,CMPVGGARPL,MICMPVGGAR,GARPLTGVLH,AVRQPRPAPP,AGHDHAEAGK,MPVGGARPLT,GPAPPHCPAL,CPALPDPAPA,RPAPPLHHRL,HHRLPPHAPL,EEWPAGCGPA,VRQPRPAPPL,RQPRPAPPLH,AQQNAGHDHA,WPAGCGPAPP	LAML
PHACTR1	c.753delG	p.V251fs	LPCLPVKLSPPLPPKKVMICMPVGG[p.V251fs]QTSHWCPTQPRRVASRVWPSTTTLSCPPRSSTSCSTAATASTSPPPPAPSPCTPRAAE*	RVWPSTTTL,TTTLSCPPR,RVASRVWPS,ASRVWPSTT,RSSTSCSTA,HWCPTQPRR,TQPRRVASR,CPTQPRRVA,QPRRVASRV,WPSTTTLSC,GQTSHWCPT,SRVWPSTTT,MPVGGQTSH,TSHWCPTQPR,STTTLSCPPR,RVASRVWPST,ASRVWPSTTT,RSSTSCSTAA,STSCSTAATA,PTQPRRVASR,CPTQPRRVAS,QPRRVASRVW,APSPCTPRAA,MPVGGQTSHW,SRVWPSTTTL	STAD
PHACTR2	c.711_712insA	p.S237fs	APVPPPKPASRNTTREAAGSSHSKK[p.S237fs]NNWL*	SSHSKKNNWL	STAD

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PHACTR4	c.1061delC	p.S354fs	DEREKSTCSMGSELLPMISPRSPSP[p.S354fs]HCLLIYLQSLHAPLHSLLRLFKLCQKLSFHHP*	CLLIYLQSL,YLQSLHAPL,SLHAPLHSL,RLFKLCQKL,LIYLQSLHA,RSPSPHCLL,LHSLLRLFK,HAPLHSLLR,SPSPHCLLI,SPHCLLIYL,APLHSLLRL,LQSLHAPLH,LHAPLHSLL,FKLCQKLSF,LLIYLQSLHA,SLHAPLHSLL,PLHSLLRLFK,LLRLFKLCQK,RSPSPHCLLI,IYLQSLHAPL,LFKLCQKLSF,SPSPHCLLIY,SPRSPSPHCL,APLHSLLRLF,YLQSLHAPLH,QSLHAPLHSL	STAD
PHC3	c.104_106delCCA	p.T35del	STAMDTEPNPGTSSVSTTTSSTTTT[p.T35del]ITTSSSRMQQPQISVYSGSDRHAVQVIQ	TTSSTTTTI,TTTSSTTTTI	GBM
PHGDH	c.517_518GG>TT	p.G173L	LGILGLGRIGREVATRMQSFGMKTI[p.G173L]LYDPIISPEVSASFGVQQLPLEEIWPL	KTILYDPII,SFGMKTILY,QSFGMKTIL,MKTILYDPI,GMKTILYDPI,QSFGMKTILY,LYDPIISPEV,MQSFGMKTIL,MKTILYDPII	SKCM
PHIP	c.5043C>G	p.I1681M	KKRGRKPKKLQYAKPEDLEQNNVHP[p.I1681M]MRDEVLPSSTCNFLSETNNVKEDLLQ	EQNNVHPMR,NVHPMRDEV,LEQNNVHPM,HPMRDEVLPS	LUSC
PHOSPHO1	c.95_97delCCT	p.S32del	PWPANQPLPGGLLPRPLSLAPSSSS[p.S32del]CCSPPCSQDGRMAAQGAPRFLLTFDFDE	SLAPSSSSC,SLAPSSSSCC	PRAD
PI15	c.64G>T	p.V22F	MIAISAVSSALLFSLLCEAST[p.V22F]FVLLNSTDSSPPTNNFTDIEAALKAQ	LLCEASTFV,SLLCEASTF,CEASTFVLL,SLLCEASTFV,LLCEASTFVL,FSLLCEASTF	LUAD
PIAS2	c.1556C>T	p.S519L	SETQSSPTKGVLMYQPSSVRVPSVT[p.S519L]LVDPAAIPPSLTDYSVPFHHTPISSM	SVRVPSVTL,SVRVPSVTLV,SSVRVPSVTL	CRC
PIAS3	c.1378G>A	p.D460N	GGDPSENKKKVEVIDLTIESSSDEE[p.D460N]NLPPTKKHCSVTSAAIPALPGSKGVL	IESSSDEENL	CESC
PIAS3	c.348delC	p.H116fs	LAPIPPTLLAPGTLLGPKREVDMHP[p.H116fs]LCPSLCTLMSP*	KREVDMHPL,REVDMHPLC,DMHPLCPSL,HPLCPSLCTL,VDMHPLCPSL,REVDMHPLCP	STAD
PIGM	c.674G>T	p.R225L	NDKSLRQFRYTFQACLYELLKRLCN[p.R225L]LAVLLFVAVAGLTFFALSFGFYYEYG	RLCNLAVLL,NLAVLLFVA,LLKRLCNLA,LAVLLFVAV,ELLKRLCNL,LKRLCNLAV,KRLCNLAVL,LCNLAVLLF,NLAVLLFVAV,LLKRLCNLAV,RLCNLAVLLF,YELLKRLCNL,LKRLCNLAVL,KRLCNLAVLL	LUAD
PIGO	c.2361delC	p.P787fs	VTVLVKAGAGAPRTRTVLTPFSGPP[p.P787fs]LLKLTWIMWSLKSTDTCRRSSGAG*	KLTWIMWSL,WIMWSLKST,LTWIMWSLK,SLKSTDTCR,TPFSGPPLL,LLKLTWIMW,VLTPFSGPPL,KLTWIMWSLK,SLKSTDTCRR,LKLTWIMWSL	STAD
PIGR	c.548T>G	p.V183G	NAQKRKSLYKQIGLYPVLVIDSSGY[p.V183G]GNPNYTGRIRLDIQGTGQLLFSVVIN	SSGYGNPNY,DSSGYGNPNY	TGCT
PIGT	c.1037delC	p.A346fs	TAMINNSRNLNIQLKWKRPPENEAP[p.A346fs]QCPSCMPSGT*	NEAPQCPSCM	STAD
PIK3C2B	c.4419C>G	p.F1473L	EELNGYIWHLIHAPPEVAECDLVYT[p.F1473L]LFHPLPRDEKAMGTSPAPKSSDGTWA	LVYTLFHPL,YTLFHPLPR,AECDLVYTL,DLVYTLFHPL,LFHPLPRDEK,VYTLFHPLPR,AECDLVYTLF	KIRC

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PIK3C2B	c.859delC	p.R287fs	PLDFSKDTSGKPVARSKTMPPQVPP[p.R287fs]APMPPAMATERMRRLARTAGFLQPRWAPGPTLLPMAMSCLRSQKREMRRLLHFATCWISFDLALTSKTTSSLAMSGVLSPLAQSTSGMRST*	TMPPQVPPA,LLHFATCWI,AMSGVLSPL,RLARTAGFL,FLQPRWAPG,LLPMAMSCL,EMRRLLHFA,WISFDLALT,VLSPLAQST,AMATERMRR,AMSCLRSQK,RTAGFLQPR,RWAPGPTLL,REMRRLLHF,HFATCWISF,CWISFDLAL,RMRRLARTA,RSQKREMRR,TSKTTSSLA,LPMAMSCLR,MSCLRSQKR,LTSKTTSSL,TSSLAMSGV,PPQVPPAPM,VPPAPMPPA,PPAPMPPAM,APMPPAMAT,QPRWAPGPT,APGPTLLPM,GPTLLPMAM,MATERMRRL,CLRSQKREM,RRLARTAGF,PRWAPGPTL,SQKREMRRL,QKREMRRLL,RLLHFATCW,SKTTSSLAM,SSLAMSGVL,LAMSGVLSP,TLLPMAMSCL,RLLHFATCWI,LAMSGVLSPL,AMSGVLSPLA,KTMPPQVPPA,AMATERMRRL,ALTSKTTSSL,TTSSLAMSGV,MAMSCLRSQK,ISFDLALTSK,ATERMRRLAR,RMRRLARTAG,CLRSQKREMR,RSQKREMRRL,SQKREMRRLL,TSKTTSSLAM,RTAGFLQPRW,LLPMAMSCLR,AMSCLRSQKR,QVPPAPMPPA,FATCWISFDL,LTSKTTSSLA,MPPQVPPAPM,VPPAPMPPAM,MPPAMATERM,QPRWAPGPTL,SPLAQSTSGM,MRRLARTAGF,EMRRLLHFAT,RRLARTAGFL,WAPGPTLLPM,KREMRRLLHF,REMRRLLHFA,RRLLHFATCW,LHFATCWISF,AQSTSGMRST,LPMAMSCLRS	GBM
PIK3CA	c.1035T>A	p.N345K	GETSTKSLWVINSALRIKILCATYV[p.N345K]KVNIRDIDKIYVRTGIYHGGEPLCDN	ILCATYVKV,KILCATYVK,KVNIRDIDK,ATYVKVNIR,KILCATYVKV,TYVKVNIRDI,CATYVKVNIR	BRCA,CRC,STAD,UCEC
PIK3CA	c.1049A>G	p.D350G	KSLWVINSALRIKILCATYVNVNIR[p.D350G]GIDKIYVRTGIYHGGEPLCDNVNTQR	YVNVNIRGI,NVNIRGIDK,NIRGIDKIY,TYVNVNIRGI,VNIRGIDKIY	CRC
PIK3CA	c.113G>A	p.R38H	IHLMPPRILVECLLPNGMIVTLECL[p.R38H]HEATLITIKHELFKEARKYPLHQLLQ	VTLECLHEA,LECLHEATL,CLHEATLITI,HEATLITIKH,LECLHEATLI	UCEC
PIK3CA	c.115G>A	p.E39K	HLMPPRILVECLLPNGMIVTLECLR[p.E39K]KATLITIKHELFKEARKYPLHQLLQD	IVTLECLRK,LRKATLITI,LECLRKATL,CLRKATLITI,MIVTLECLRK,RKATLITIKH,LECLRKATLI	UCEC
PIK3CA	c.1258T>C	p.C420R	DLPRAARLCLSICSVKGRKGAKEEH[p.C420R]RPLAWGNINLFDYTDTLVSGKMALNL	KEEHRPLAW,GAKEEHRPLA,RPLAWGNINL,AKEEHRPLAW	BRCA,UCEC
PIK3CA	c.1338_1364delGCCAGTACCTCATGGATTAGAAGATTT	p.PVPHGLEDL447del	LAWGNINLFDYTDTLVSGKMALNLW[p.PVPHGLEDL447del]LNPIGVTGSNPNKETPCLELEFDWFSSVVKFPDMSVIEEHANWSVSREAGFS	ALNLWLNPI,NLWLNPIGV,GKMALNLWL,MALNLWLNPI	BRCA
PIK3CA	c.1357G>A	p.E453K	NLFDYTDTLVSGKMALNLWPVPHGL[p.E453K]KDLLNPIGVTGSNPNKETPCLELEFD	GLKDLLNPI,LWPVPHGLK,VPHGLKDLL,NLWPVPHGLK,WPVPHGLKDL,HGLKDLLNPI	BRCA
PIK3CA	c.1364_1365insG	p.L455fs	DYTDTLVSGKMALNLWPVPHGLEDL[p.L455fs]AEPYWCYWIKSK*	GLEDLAEPY,DLAEPYWCY,AEPYWCYWI,LAEPYWCYW,HGLEDLAEPY	BRCA
PIK3CA	c.1624G>A	p.E542K	LARDNELRENDKEQLKAISTRDPLS[p.E542K]KITEQEKDFLWSHRHYCVTIPEILPK	ISTRDPLSK,STRDPLSKI,LSKITEQEK,AISTRDPLSK,SKITEQEKDF	BLCA,BRCA,CESC,CRC,HNSC,LUAD,LUSC,STAD,UCEC
PIK3CA	c.1633G>A	p.E545K	DNELRENDKEQLKAISTRDPLSEIT[p.E545K]KQEKDFLWSHRHYCVTIPEILPKLLL	SEITKQEKDF,KQEKDFLWSH	BLCA,BRCA,CESC,CRC,GBM,HNSC,KIRC,LUAD,LUSC,STAD,TGCT,UCEC,UCS
PIK3CA	c.1634A>C	p.E545A	DNELRENDKEQLKAISTRDPLSEIT[p.E545A]AQEKDFLWSHRHYCVTIPEILPKLLL	TAQEKDFLW,SEITAQEKDF,AQEKDFLWSH,ITAQEKDFLW	BRCA,CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
PIK3CA	c.1634A>G	p.E545G	DNELRENDKEQLKAISTRDPLSEITE[p.E545G]GQEKDFLWSHRHYCVTIPEILPKLLL	SEITGQEKDF,GQEKDFLWSH	CRC
PIK3CA	c.1636C>A	p.Q546K	NELRENDKEQLKAISTRDPLSEITE[p.Q546K]KEKDFLWSHRHYCVTIPEILPKLLLS	KEKDFLWSH,TEKEKDFLW,SEITEKEKDF	BRCA,CRC,UCEC
PIK3CA	c.1637A>C	p.Q546P	NELRENDKEQLKAISTRDPLSEITE[p.Q546P]PEKDFLWSHRHYCVTIPEILPKLLLS	EITEPEKDFL,SEITEPEKDF,EPEKDFLWSH	UCEC
PIK3CA	c.1637A>G	p.Q546R	NELRENDKEQLKAISTRDPLSEITE[p.Q546R]REKDFLWSHRHYCVTIPEILPKLLLS	REKDFLWSH,TEREKDFLW,SEITEREKDF	BRCA,UCEC
PIK3CA	c.1A>G	p.M1V	[p.M1V]VPPRPSSGELWGIHLMPPRILVECLL	VPPRPSSGEL	GBM
PIK3CA	c.2176G>A	p.E726K	HLNRQVEAMEKLINLTDILKQEKKD[p.E726K]KTQKVQMKFLVEQMRRPDFMDALQGF	KTQKVQMKF,KDKTQKVQMK,KTQKVQMKFL,KKDKTQKVQM	BRCA,CESC,LUSC
PIK3CA	c.263G>A	p.R88Q	QDESSYIFVSVTQEAEREEFFDETR[p.R88Q]QLCDLRLFQPFLKVIEPVGNREEKIL	RQLCDLRLF,ETRQLCDLR,EEFFDETRQL	BRCA,CRC,GBM,STAD,UCEC
PIK3CA	c.278G>A	p.R93Q	YIFVSVTQEAEREEFFDETRRLCDL[p.R93Q]QLFQPFLKVIEPVGNREEKILNREIG	QLFQPFLKV,LQLFQPFLK,RRLCDLQLF,CDLQLFQPF,LQLFQPFLKV,QLFQPFLKVI,DLQLFQPFLK,TRRLCDLQLF,LCDLQLFQPF,CDLQLFQPFL	UCEC
PIK3CA	c.3012G>A	p.M1004I	RFQEMCYKAYLAIRQHANLFINLFS[p.M1004I]IMLGSGMPELQSFDDIAYIRKTLALD	NLFINLFSI,FINLFSIML,LFINLFSIM,FSIMLGSGM,IMLGSGMPEL,NLFINLFSIM,LFINLFSIML,LFSIMLGSGM	BRCA
PIK3CA	c.3127A>G	p.M1043V	DIAYIRKTLALDKTEQEALEYFMKQ[p.M1043V]VNDAHHGGWTTKMDWIFHTIKQHALN	ALEYFMKQV,FMKQVNDAH,MKQVNDAHH,EALEYFMKQV,FMKQVNDAHH	GBM,HNSC,UCEC
PIK3CA	c.3129G>A	p.M1043I	DIAYIRKTLALDKTEQEALEYFMKQ[p.M1043I]INDAHHGGWTTKMDWIFHTIKQHALN	FMKQINDAH,KQINDAHHG,EALEYFMKQI,FMKQINDAHH,KQINDAHHGG	BRCA,UCEC
PIK3CA	c.3130A>T	p.N1044Y	IAYIRKTLALDKTEQEALEYFMKQM[p.N1044Y]YDAHHGGWTTKMDWIFHTIKQHALN*	MYDAHHGGW,FMKQMYDAH,LEYFMKQMY,MKQMYDAHH,KQMYDAHHG,ALEYFMKQMY,FMKQMYDAHH,QMYDAHHGGW,KQMYDAHHGG	BRCA
PIK3CA	c.3132T>A	p.N1044K	IAYIRKTLALDKTEQEALEYFMKQM[p.N1044K]KDAHHGGWTTKMDWIFHTIKQHALN*	FMKQMKDAH,KQMKDAHHG,MKDAHHGGW,ALEYFMKQMK,FMKQMKDAHH,KQMKDAHHGG,QMKDAHHGGW	KIRC
PIK3CA	c.3140A>G	p.H1047R	IRKTLALDKTEQEALEYFMKQMNDA[p.H1047R]RHGGWTTKMDWIFHTIKQHALN*	FMKQMNDAR,KQMNDARHG,RHGGWTTKM,YFMKQMNDAR,FMKQMNDARH,KQMNDARHGG,QMNDARHGGW,ARHGGWTTKM	BRCA,CRC,GBM,HNSC,LIHC,LUSC,STAD,UCEC,UCS
PIK3CA	c.3140A>T	p.H1047L	IRKTLALDKTEQEALEYFMKQMNDA[p.H1047L]LHGGWTTKMDWIFHTIKQHALN*	FMKQMNDAL,ALHGGWTTK,KQMNDALHG,LHGGWTTKM,ALHGGWTTKM,YFMKQMNDAL,DALHGGWTTK,FMKQMNDALH,KQMNDALHGG,QMNDALHGGW	BRCA,HNSC,UCEC
PIK3CA	c.317G>T	p.G106V	EFFDETRRLCDLRLFQPFLKVIEPV[p.G106V]VNREEKILNREIGFAIGMPVCEFDMV	FLKVIEPVV,KVIEPVVNR	UCS
PIK3CA	c.323G>A	p.R108H	FDETRRLCDLRLFQPFLKVIEPVGN[p.R108H]HEEKILNREIGFAIGMPVCEFDMVKD	HEEKILNREI	UCEC
PIK3CA	c.325_327delGAA	p.E110del	ETRRLCDLRLFQPFLKVIEPVGNRE[p.E110del]KILNREIGFAIGMPVCEFDMVKDPEVQD	REKILNREI	BRCA,UCEC
PIK3CA	c.331A>G	p.K111E	TRRLCDLRLFQPFLKVIEPVGNREE[p.K111E]EILNREIGFAIGMPVCEFDMVKDPEV	REEEILNREI,EEILNREIGF	UCEC
PIK3CA	c.331_333delAAG	p.K111del	TRRLCDLRLFQPFLKVIEPVGNREE[p.K111del]ILNREIGFAIGMPVCEFDMVKDPEVQDF	REEILNREI,EEILNREIGF	BRCA

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PIK3CD	c.1141T>C	p.C381R	CFALYAVIEKAKKARSTKKKSKKAD[p.C381R]RPIAWANLMLFDYKDQLKTGERCLYM	KSKKADRPI,RPIAWANLM,KKADRPIAW,KSKKADRPIA,RPIAWANLML,KKSKKADRPI,SKKADRPIAW,ADRPIAWANL	TGCT
PIK3CG	c.493G>A	p.V165I	RHPPSEESQAFQRQLTALIGYDVTD[p.V165I]ISNVHDDELEFTRRGLVTPRMAEVAS	LIGYDVTDI,ALIGYDVTDI	LUAD
PIK3R1	c.1126G>A	p.G376R	ADGTFLVRDASTKMHGDYTLTLRKG[p.G376R]RNNKLIKIFHRDGKYGFSDPLTFSSV	TLRKGRNNK,KGRNNKLIK,YTLTLRKGR,RNNKLIKIF,LTLRKGRNNK,TLRKGRNNKL,KGRNNKLIKI,GRNNKLIKIF	GBM
PIK3R1	c.1137A>T	p.K379N	TFLVRDASTKMHGDYTLTLRKGGNN[p.K379N]NLIKIFHRDGKYGFSDPLTFSSVVEL	KGGNNNLIK,NNLIKIFHR,RKGGNNNLI,GNNNLIKIF,TLRKGGNNNL,NNNLIKIFHR,GGNNNLIKIF	GBM
PIK3R1	c.1697_1708delTTAAACCAGACC	p.KPDL567del	RRRLEEDLKKQAAEYREIDKRMNSI[p.KPDL567del]IQLRKTRDQYLMWLTQKGVRQKKLNEWLGNENTEDQY	RMNSIIQLR,MNSIIQLRK,SIIQLRKTR,KRMNSIIQL,RMNSIIQLRK,NSIIQLRKTR	BRCA
PIK3R5	c.1112T>G	p.L371R	LLSTSSLASHDSTLSLASSQASGPA[p.L371R]RSRHLLTSFVSGLSDGMDSGYVEDSE	SSQASGPAR,RSRHLLTSF,GPARSRHLL,ASSQASGPAR,RSRHLLTSFV,ARSRHLLTSF	KIRC
PILRA	c.872_873insC	p.S291fs	VYASLALSSSTSPRAPPSHRPLKSP[p.S291fs]PERDPVLCLKGLTNGQPSQD*	SPPERDPVL	LUAD
PIM1	c.490C>T	p.L164F	LQEELARSFFWQVLEAVRHCHNCGV[p.L164F]FHRDIKDENILIDLNRGELKLIDFGS	RHCHNCGVF,HCHNCGVFHR,VRHCHNCGVF	DLBCL
PIM1	c.550C>T	p.L184F	HNCGVLHRDIKDENILIDLNRGELK[p.L184F]FIDFGSGALLKDTVYTDFDGTRVYSP	FIDFGSGAL,RGELKFIDF,FIDFGSGALL,IDLNRGELKF,LKFIDFGSGA,KFIDFGSGAL,GELKFIDFGS	DLBCL
PIP4K2A	c.656G>A	p.R219K	IVTRNVFSHRLSVYRKYDLKGSTVA[p.R219K]KEASDKEKAKELPTLKDNDFINEGQK	TVAKEASDK,KEASDKEKA,STVAKEASDK,VAKEASDKEK	KIRP
PIP4K2C	c.611G>A	p.R204H	NTLLPQFLGMYRVSVDNEDSYMLVM[p.R204H]HNMFSHRLPVHRKYDLKGSLVSREAS	VMHNMFSHR,LVMHNMFSH,SYMLVMHNM,YMLVMHNMF,MHNMFSHRL,VMHNMFSHRL,LVMHNMFSHR,SYMLVMHNMF,DSYMLVMHNM,HNMFSHRLPV,MLVMHNMFSH	CRC
PITPNM1	c.884delC	p.P295fs	PPGKPSTEARSAASNTGTPDGPEAP[p.P295fs]QAQMPPPMPALGSSGPHPPVPPTHPNMEGLCLPRACLSGACRTLPETLRTAPRKSSLMPTKASRTVRRSSPRR*	AQMPPPMPA,QMPPPMPAL,CLSGACRTL,TLPETLRTA,RTVRRSSPR,ETLRTAPRK,RTAPRKSSL,RKSSLMPTK,KSSLMPTKA,SLMPTKASR,ASRTVRRSS,TVRRSSPRR,NMEGLCLPR,GPEAPQAQM,HPNMEGLCL,LPRACLSGA,MPTKASRTV,PQAQMPPPM,MEGLCLPRA,AQMPPPMPAL,CLPRACLSGA,SLMPTKASRT,LMPTKASRTV,RTVRRSSPRR,SSLMPTKASR,RTLPETLRTA,RTAPRKSSLM,PTKASRTVRR,APQAQMPPPM,MPALGSSGPH,LPRACLSGAC,APRKSSLMPT,LRTAPRKSSL,RKSSLMPTKA	STAD
PIWIL1	c.2095G>A	p.V699M	GLKVCLQAALRAWNSCNEYMPSRII[p.V699M]MYRDGVGDGQLKTLVNYEVPQFLDCL	RIIMYRDGV,EYMPSRIIM,YMPSRIIMY,MPSRIIMYR,YMPSRIIMYR,NEYMPSRIIM	HNSC
PKD1	c.2813C>T	p.T938M	VENSASRANLSLRVTAEEPICGLRA[p.T938M]MPSPEARVLQGVLVRYSPVVEAGSDM	AMPSPEARV,RAMPSPEAR,EPICGLRAM,MPSPEARVL,GLRAMPSPEA,RAMPSPEARV,AMPSPEARVL,EEPICGLRAM	TGCT
PKD2	c.1457A>T	p.Y486F	KLIRYVTTFDFFLAACEIIFCFFIF[p.Y486F]FYVVEEILEIRIHKLHYFRSFWNCLD	FCFFIFFYV,IIFCFFIFF,CFFIFFYVV,IFFYVVEEI,FFYVVEEIL,IFCFFIFFY,FCFFIFFYVV,FIFFYVVEEI,IIFCFFIFFY,IFCFFIFFYV,IFFYVVEEIL,FYVVEEILEI,EIIFCFFIFF	CLL
PKHD1L1	c.5568C>A	p.F1856L	PPVASLSPTSGSIGGGTTLVITGNG[p.F1856L]LYPGNTTVTIGDEPCQIISINPNEVY	LVITGNGLY,GLYPGNTTV,TLVITGNGL,GLYPGNTTVT,LYPGNTTVTI,TLVITGNGLY,TTLVITGNGL	CRC
PKN2	c.226delA	p.K76fs	KREIRKELKIKEGAENLRKVTTDKK[p.K76fs]VWLM*	TTDKKVWLM,RKVTTDKKVW	STAD
PLA2G15	c.689delG	p.W230fs	FLQRQPQAWKDKYIRAFVSLGAPWG[p.W230fs]AWPRPCASWLQETTTGSQSSGP*	WLQETTTGS,AWPRPCASW,GAPWGAWPR,WPRPCASWL,SLGAPWGAW,FVSLGAPWGA,LGAPWGAWPR,VSLGAPWGAW,GAWPRPCASW	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
PLA2G1B	c.157_158insTG	p.L53fs	KMIKCVIPGSDPFLEYNNYGCYCGL[p.L53fs]WGAQAPPWMNWTSAARHMTTAMTRPRSWTAVNFCWTTRTPTPIHTRALARQSPVAAKTKSVRPSFATATATLPSAFQKLHITRHTRTWTPRSIVRVEYHLSKASPLSASSHTVLSNKAPC*	ALARQSPVA,SVRPSFATA,TLPSAFQKL,PLSASSHTV,ATLPSAFQK,SSHTVLSNK,MTTAMTRPR,AVNFCWTTR,NYGCYCGLW,LWGAQAPPW,SWTAVNFCW,SFATATATL,AARHMTTAM,RHMTTAMTR,MTRPRSWTA,RSWTAVNFC,TTRTPTPIH,RTPTPIHTR,HTRALARQS,RALARQSPV,LARQSPVAA,KTKSVRPSF,KLHITRHTR,ITRHTRTWT,HTRTWTPRS,RTWTPRSIV,RSIVRVEYH,RVEYHLSKA,LSKASPLSA,WMNWTSAAR,AFQKLHITR,TWTPRSIVR,WTSAARHMT,WTAVNFCWT,WTTRTPTPI,WTPRSIVRV,RPRSWTAVN,TPIHTRALA,RPSFATATA,YHLSKASPL,ATATLPSAF,AQAPPWMNW,TAMTRPRSW,RQSPVAAKT,FQKLHITRH,HITRHTRTW,SKASPLSAS,LSASSHTVL,VEYHLSKAS,AMTRPRSWTA,MTRPRSWTAV,ALARQSPVAA,ATATATLPSA,HLSKASPLSA,RTWTPRSIVR,IVRVEYHLSK,ASSHTVLSNK,TAVNFCWTTR,TATLPSAFQK,SAFQKLHITR,RSWTAVNFCW,CWTTRTPTPI,AARHMTTAMT,TTRTPTPIHT,RTPTPIHTRA,HTRALARQSP,RALARQSPVA,LARQSPVAAK,RQSPVAAKTK,KTKSVRPSFA,KSVRPSFATA,SVRPSFATAT,KLHITRHTRT,ITRHTRTWTP,HTRTWTPRSI,RSIVRVEYHL,SSHTVLSNKA,PWMNWTSAAR,HMTTAMTRPR,TPIHTRALAR,TSAARHMTTA,WTAVNFCWTT,APPWMNWTSA,SAARHMTTAM,RPRSWTAVNF,TPTPIHTRAL,SPVAAKTKSV,RPSFATATAT,LPSAFQKLHI,SPLSASSHTV,MNWTSAARHM,TATATLPSAF,GLWGAQAPPW,WMNWTSAARH,AKTKSVRPSF,PSFATATATL,FQKLHITRHT,LHITRHTRTW,KASPLSASSH,TPRSIVRVEY	STAD
PLA2G3	c.602G>A	p.R201Q	GPDLCCREHDRCPQNISPLQYNYGI[p.R201Q]QNYRFHTISHCDCDTRFQQCLQNQHD	IQNYRFHTI,NYGIQNYRF,QYNYGIQNY,YNYGIQNYR,LQYNYGIQN,YNYGIQNYRF,LQYNYGIQNY,QYNYGIQNYR,IQNYRFHTIS,QNYRFHTISH	UCEC
PLAG1	c.551delA	p.K184fs	FESTGVLLEHLKSHAGKSSGGVKEK[p.K184fs]STSANIVIAGSTPERMSGDTWWCTLEERTSSVSIVHRDLGERIT*	RMSGDTWWC,TLEERTSSV,VIAGSTPER,RTSSVSIVH,TSSVSIVHR,GVKEKSTSA,KSTSANIVI,TWWCTLEER,IVHRDLGER,STSANIVIA,KEKSTSANI,EERTSSVSI,RMSGDTWWCT,CTLEERTSSV,IVIAGSTPER,RTSSVSIVHR,KSTSANIVIA,DTWWCTLEER,SIVHRDLGER,KEKSTSANIV,MSGDTWWCTL,LEERTSSVSI,EERTSSVSIV,TPERMSGDTW	STAD
PLAGL2	c.30delC	p.P10fs	MTTFFTSVPP[p.P10fs]GFKMQSRRRKWAGN*	FTSVPPGFK,FFTSVPPGF,TSVPPGFKM,KMQSRRRKW,FFTSVPPGFK,TFFTSVPPGF,GFKMQSRRRK,KMQSRRRKWA,FTSVPPGFKM,FKMQSRRRKW	STAD
PLAU	c.602_603insG	p.R201fs	IIGGEFTTIENQPWFAAIYRRHRGG[p.R201fs]LCHLRVWRQPHQPLLGDQRHTLLH*	LLGDQRHTL,VWRQPHQPL,HLRVWRQPH,GLCHLRVWR,RHRGGLCHL,WRQPHQPLL,LLGDQRHTLL,VWRQPHQPLL,AIYRRHRGGL,RHRGGLCHLR,HLRVWRQPHQ,RVWRQPHQPL,RRHRGGLCHL,RGGLCHLRVW	STAD
PLCD3	c.1495delG	p.E499fs	KGRVLVKGKKLPAARSEDGRALSDR[p.E499fs]RRRRRMTRRKKRRWRLQRRGGWPSRSPRSCRPWLCTATPPA*	WLCTATPPA,RALSDRRRR,RRRRRRMTR,RRRRRMTRR,RRRRMTRRK,RRRMTRRKK,RMTRRKKRR,KKRRWRLQR,KRRWRLQRR,RWRLQRRGG,GGWPSRSPR,WPSRSPRSC,SPRSCRPWL,RRKKRRWRL,LQRRGGWPS,RSPRSCRPW,RALSDRRRRR,ALSDRRRRRR,RRRRRRMTRR,RRRRRMTRRK,RRRRMTRRKK,MTRRKKRRWR,RKKRRWRLQR,KKRRWRLQRR,RWRLQRRGGW,LQRRGGWPSR,RGGWPSRSPR,RSPRSCRPWL,RSCRPWLCTA,RPWLCTATPP,TRRKKRRWRL,RMTRRKKRRW,SRSPRSCRPW	CLL
PLCE1	c.1315G>T	p.G439C	NTVGSLLHFLTKLPASETAHGRISV[p.G439C]CPCLKQCVRDTVCEYRATLQRTSISQ	RISVCPCLK,GRISVCPCL,HGRISVCPCL	LUSC
PLCE1	c.1690G>T	p.G564C	LMEQEQTIYRRVLPVDYLCFLTRDL[p.G564C]CTPECQSSLPCLKASISASILTTQNG	CTPECQSSL	LUAD
PLCL1	c.1692G>T	p.M564I	VKGKKLPSDPDVLEGEVTDEDEEAE[p.M564I]ISRRMSVDYNGEQKQIRLCRELSDLV	ISRRMSVDY,AEISRRMSV,EEAEISRRM,EISRRMSVDY,DEEAEISRRM	LUAD
PLEC	c.4157G>A	p.R1386Q	QDARRRQEQIQAMPLADSQAVREQL[p.R1386Q]QQEQALLEEIERHGEKVEECQRFAKQ	EQLQQEQAL,REQLQQEQA,REQLQQEQAL,EQLQQEQALL,QQEQALLEEI	ACC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
PLEKHA6	c.329G>T	p.R110L	VDRCLFYYKDEKEESILGSIPLLSF[p.R110L]LVAAVQPSDNISRKHTFKAEHAGVRT	SIPLLSFLV,LLSFLVAAV,FLVAAVQPS,IPLLSFLVA,GSIPLLSFL,GSIPLLSFLV,PLLSFLVAAV,IPLLSFLVAA	LUAD
PLEKHA6	c.982delG	p.V328fs	TNPDKIAQRKSSMNQLQQWVNLRRG[p.V328fs]YPRLKTFGVPLGSILCLAGSLSTMAPTPPSTPMIISTTRQECGRRASVPCRPMIGSARPGPWRTSAMPSAMGVALPTSCESGRSPPATGGRMPPSGSQAPPGSQSIMMSWMPPLAPCAACPCSPAPTLCPAHPARAPTAVPAFTPLSAHPVPVLSGCHLAVRTSMLTLLPM*	RLKTFGVPL,CLAGSLSTM,SAMPSAMGV,IMMSWMPPL,MMSWMPPLA,WMPPLAPCA,FTPLSAHPV,PLSAHPVPV,VLSGCHLAV,NLRRGYPRL,TMAPTPPST,AMPSAMGVA,RMPPSGSQA,HLAVRTSML,RGYPRLKTF,RAPTAVPAF,LRRGYPRLK,STMAPTPPS,RASVPCRPM,SARPGPWRT,RTSAMPSAM,AVRTSMLTL,QWVNLRRGY,VNLRRGYPR,TPMIISTTR,STTRQECGR,TLCPAHPAR,CAACPCSPA,TAVPAFTPL,YPRLKTFGV,APTPPSTPM,RPGPWRTSA,MPSAMGVAL,SPPATGGRM,APPGSQSIM,MPPLAPCAA,CPCSPAPTL,SPAPTLCPA,HPARAPTAV,VPAFTPLSA,VPVLSGCHL,SQSIMMSWM,TSMLTLLPM,FGVPLGSIL,RQECGRRAS,IGSARPGPW,WRTSAMPSA,SAMGVALPT,CESGRSPPA,SQAPPGSQS,GSQSIMMSW,MSWMPPLAP,ARAPTAVPA,LSAHPVPVL,CHLAVRTSM,VRTSMLTLL,VPLGSILCL,QECGRRASV,TPPSTPMII,RTSMLTLLPM,CLAGSLSTMA,AMPSAMGVAL,SIMMSWMPPL,IMMSWMPPLA,WMPPLAPCAA,KTFGVPLGSI,SQAPPGSQSI,TLCPAHPARA,HLAVRTSMLT,AVRTSMLTLL,NLRRGYPRLK,WVNLRRGYPR,STPMIISTTR,RGYPRLKTFG,RLKTFGVPLG,STMAPTPPST,CGRRASVPCR,RASVPCRPMI,SARPGPWRTS,PWRTSAMPSA,RTSAMPSAMG,SWMPPLAPCA,QQWVNLRRGY,PTLCPAHPAR,VLSGCHLAVR,MAPTPPSTPM,TSAMPSAMGV,YPRLKTFGVP,APTPPSTPMI,RPMIGSARPG,RPGPWRTSAM,APPGSQSIMM,APTLCPAHPA,CPAHPARAPT,TPLSAHPVPV,RRGYPRLKTF,LCLAGSLSTM,RQECGRRASV,RRASVPCRPM,MIGSARPGPW,WRTSAMPSAM,SAMPSAMGVA,RMPPSGSQAP,MMSWMPPLAP,ARAPTAVPAF,GCHLAVRTSM,CHLAVRTSML,LAVRTSMLTL,MPSAMGVALP,MPPLAPCAAC,SPAPTLCPAH,VPAFTPLSAH,HPVPVLSGCH,CESGRSPPAT,VPLGSILCLA,VPVLSGCHLA	CRC,STAD
PLEKHB1	c.436T>C	p.S146P	TALLEANSTPAPAGATVPPRSRRVC[p.S146P]PKVRCVTRSWSPCKVERRIWVRVYSP	RSRRVCPKV,RVCPKVRCV,CPKVRCVTR,RSRRVCPKVR	CLL
PLEKHG4B	c.1150G>A	p.E384K	AIIFLQNSFCSLNTHRTPRTAQEVA[p.E384K]KLIDQHETMMKLVLEDPLLVSLRLEG	KLIDQHETM,RTAQEVAKL,KLIDQHETMM,AKLIDQHETM	CRC
PLEKHM1	c.2684C>T	p.A895V	RIIHNWDLTKRPICRQALKFLTQIR[p.A895V]VQPLINLQMVNASLYEHVERMHLIGR	TQIRVQPLI,LTQIRVQPL,LKFLTQIRV,IRVQPLINL,VQPLINLQM,FLTQIRVQPL,ALKFLTQIRV,QIRVQPLINL,RVQPLINLQM	TGCT
PLEKHM2	c.1376C>T	p.S459L	DQSFRTGSPGDAPERPPLCDFSEGL[p.S459L]LAPMDFYRFTVESPSTVTSGGGHHDP	LLAPMDFYR,LAPMDFYRF,GLLAPMDFY,FSEGLLAPM,LLAPMDFYRF,GLLAPMDFYR,SEGLLAPMDF,DFSEGLLAPM	BLCA
PLEKHO1	c.761delC	p.T254fs	QPSADRASSLSRPWEKTDKGATYTP[p.T254fs]RHPRS*	ATYTPRHPR,ATYTPRHPRS,GATYTPRHPR	STAD
PLEKHO2	c.1051G>C	p.E351Q	GEMQASGPPAPGTVQVSVNGMDDSP[p.E351Q]QPAKPSQAEGTPGTPPKDATTSTALP	GMDDSPQPA,GMDDSPQPAK,SPQPAKPSQA	CESC
PLIN5	c.916C>T	p.R306W	LETLVLSRSLTQELQGTVEALESSV[p.R306W]WGLPAGAQEKVAEVRRSVDALQTAFA	ALESSVWGL,ESSVWGLPA,SVWGLPAGA,VEALESSVW,EALESSVWGL,SSVWGLPAGA,LESSVWGLPA	ACC
PLK1	c.698A>G	p.D233G	KKTLCGTPNYIAPEVLSKKGHSFEV[p.D233G]GVWSIGCIMYTLLVGKPPFETSCLKE	SFEVGVWSI,KGHSFEVGV,GVWSIGCIM,FEVGVWSIG,GVWSIGCIMY,HSFEVGVWSI,EVGVWSIGCI,KGHSFEVGVW,VGVWSIGCIM,FEVGVWSIGC	CRC
PLOD3	c.888_889insC	p.P296fs	GWTPEGGCGFCNQDRRTLPGGQPPP[p.P296fs]PGVSGRVCGTAYSVSAPLPAAAATPGLSPRQGHPFPAQQRGLP*	RVCGTAYSV,SVSAPLPAA,SGRVCGTAY,AATPGLSPR,TAYSVSAPL,YSVSAPLPA,APLPAAAAT,LPAAAATPG,LSPRQGHPF,RQGHPFPAQ,VSGRVCGTAY,GTAYSVSAPL,SVSAPLPAAA,AAATPGLSPR,YSVSAPLPAA,LPAAAATPGL,SPRQGHPFPA,HPFPAQQRGL,GLSPRQGHPF,GRVCGTAYSV	STAD

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PLOD3	c.889delC	p.R297fs	GWTPEGGCGFCNQDRRTLPGGQPPP[p.R297fs]GCFWPCLWNSLLRFCPASCSGCYSWTIPPTGSPFSCTTTRSSMNPTSLTPGRSSRTTSQL*	FWPCLWNSL,CLWNSLLRF,NSLLRFCPA,TTRSSMNPT,RSSMNPTSL,RSSRTTSQL,SPFSCTTTR,SLTPGRSSR,TIPPTGSPF,CPASCSGCY,ASCSGCYSW,SCTTTRSSM,SMNPTSLTP,WPCLWNSLL,CFWPCLWNSL,FWPCLWNSLL,WTIPPTGSPF,TTRSSMNPTS,RSSMNPTSLT,TSLTPGRSSR,MNPTSLTPGR,FSCTTTRSSM,TRSSMNPTSL,SMNPTSLTPG,GRSSRTTSQL	CRC,STAD
PLSCR3	c.229G>A	p.E77K	FPSPGPVALGSAAPFLPLPGVPSGL[p.E77K]KFLVQIDQILIHQKAERVETFLGWET	KFLVQIDQI,VPSGLKFLV,GVPSGLKFLV,KFLVQIDQIL,LPGVPSGLKF,LKFLVQIDQI	CRC
PLXNA1	c.3046delC	p.P1016fs	LTPPGQSPGSAPIIININRAQLTNP[p.P1016fs]R*	INRAQLTNPR	STAD
PLXNA1	c.3883G>A	p.E1295K	ALECKEAFAELQTDIHELTNDLDGA[p.E1295K]SIPFLDYRTYAMRVLFPGIEDHPVLK	ASIPFLDYR,GASIPFLDY,DLDGASIPF,GASIPFLDYR,SIPFLDYRTY,LTNDLDGASI,NDLDGASIPF	UCEC
PLXNA2	c.1392_1393insCC	p.P464fs	YNGYSVVFVGTKSGKLKKIRADGPP[p.P464fs]PMVGSSTRWSLCSRTEAPSSGTWPSPLISATCTSCLRDRSPGSPWSHVSSIRLVGSA*	STRWSLCSR,KIRADGPPP,SATCTSCLR,WPSPLISAT,SPWSHVSSI,IRADGPPPM,PMVGSSTRW,VGSSTRWSL,TEAPSSGTW,ISATCTSCL,RDRSPGSPW,WSHVSSIRL,SPGSPWSHV,LISATCTSCL,SSTRWSLCSR,ISATCTSCLR,KIRADGPPPM,STRWSLCSRT,RWSLCSRTEA,MVGSSTRWSL,RTEAPSSGTW,WPSPLISATC,PPMVGSSTRW	STAD
PLXNA3	c.172C>T	p.P58S	LTHLAVHRVTGEVFVGAVNRVFKLA[p.P58S]SNLTELRAHVTGPVEDNARCYPPPSM	KLASNLTEL,RVFKLASNL,LASNLTELR,KLASNLTELR,RVFKLASNLT,FKLASNLTEL	HNSC
PLXNC1	c.1385C>T	p.S462L	IYIYLTAGKEVRRIRVANCNKHKSC[p.S462L]LECLTATDPHCGWCHSLQRCTFQGDC	NKHKSCLECL	CRC
PLXNC1	c.2455C>T	p.R819C	NINVSEYCVATYCGFLAPSLKSSKV[p.R819C]CTNVTVKLRVQDTYLDCGTLQYREDP	KVCTNVTVK,CTNVTVKLR,KSSKVCTNV,SKVCTNVTV,SSKVCTNVTV	CRC
PLXND1	c.1100G>T	p.R367L	GLQCAGGAGRGDLYSRLVSVFPARE[p.R367L]LLFAVFERPQGSPAARAAPAALCAFR	VFPARELLF,SVFPARELL,ELLFAVFER,ARELLFAVF,FPARELLFA,RELLFAVFE,SVFPARELLF,FPARELLFAV,PARELLFAVF	TGCT
PMEPA1	c.624delC	p.P208fs	RAPPNRTIFDSDLMDSARLGGPCPP[p.P208fs]AVTRASAPRATAAAGAWRGRRPPTARSSATTRGPPSSTSRAVGRPPCWRGPGSTTHTSRP*	RLGGPCPPA,AVTRASAPR,ATAAAGAWR,SSTSRAVGR,AVGRPPCWR,VTRASAPRA,RASAPRATA,AWRGRRPPT,RGRRPPTAR,TARSSATTR,AAGAWRGRR,SAPRATAAA,APRATAAAG,RPPTARSSA,RPPCWRGPG,RATAAAGAW,RAVGRPPCW,RLGGPCPPAV,VTRASAPRAT,RASAPRATAA,ASAPRATAAA,RATAAAGAWR,AWRGRRPPTA,RGRRPPTARS,TSRAVGRPPC,RAVGRPPCWR,TAAAGAWRGR,AAAGAWRGRR,CPPAVTRASA,APRATAAAGA,RPPTARSSAT,GPPSSTSRAV,ARLGGPCPPA	STAD
PMS2	c.1952A>G	p.K651R	AKRIKQLHHEAQQSEGEQNYRKFRA[p.K651R]RICPGENQAAEDELRKEISKTMFAEM	NYRKFRARI,KFRARICPG,RARICPGEN,QNYRKFRAR,KFRARICPGE,RARICPGENQ,EQNYRKFRAR,RKFRARICPG	TGCT
PNKP	c.520G>T	p.G174W	NLEKLLVFTAAGVKPQGKVAGFDLD[p.G174W]WTLITTRSGKVFPTGPSDWRILYPEI	AGFDLDWTL,WTLITTRSGK,DLDWTLITTR,GKVAGFDLDW	LUAD
PNLIP	c.110C>T	p.T37M	GAVAGKEVCYERLGCFSDDSPWSGI[p.T37M]MERPLHILPWSPKDVNTRFLLYTNEN	GIMERPLHI,SPWSGIMER,IMERPLHIL,GIMERPLHIL,DSPWSGIMER,MERPLHILPW	MM
PNPLA4	c.668T>C	p.L223P	LDLYVNIAKQDIMLSLANLVRLNQA[p.L223P]PFPPSKRKMESLYQCGFDDTVKFLLK	NQAPFPPSK,LVRLNQAPF,LNQAPFPPSK,NQAPFPPSKR,APFPPSKRKM,NLVRLNQAPF,RLNQAPFPPS	TGCT

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PNPLA7	c.3597delC	p.P1199fs	LAYVCCVRQLEVVKSSDYCEYLRPP[p.P1199fs]STATAPWTSASSTRSAKWATSTGARCLTSGAAAACWRRCSATSRGRARSPRVRSSPVPTPPSRTLPKLCLALSPPSPPWWMTNLTTRRSTRRSCWTSPGMHTQTSRAPQPSRAQTWRTSPHCGIDTPVWLSQNCLRAPLTRTGRGLC*	YLRPPSTAT,CLTSGAAAA,TLPKLCLAL,GMHTQTSRA,WLSQNCLRA,SQNCLRAPL,SASSTRSAK,STRSAKWAT,KWATSTGAR,GARCLTSGA,AACWRRCSA,RGRARSPRV,RARSPRVRS,RVRSSPVPT,RTLPKLCLA,TTRRSTRRS,STRRSCWTS,RSCWTSPGM,TSRAPQPSR,LTRTGRGLC,SATSRGRAR,WWMTNLTTR,WMTNLTTRR,NLTTRRSTR,LTTRRSTRR,VWLSQNCLR,RAPLTRTGR,TATAPWTSA,ATAPWTSAS,APWTSASST,SPRVRSSPV,VPTPPSRTL,SPPWWMTNL,APQPSRAQT,RSAKWATST,AKWATSTGA,ALSPPSPPW,AQTWRTSPH,PPSTATAPW,CEYLRPPST,YLRPPSTATA,TSASSTRSAK,RTLPKLCLAL,STATAPWTSA,STRSAKWATS,SAKWATSTGA,GARCLTSGAA,AAACWRRCSA,CWRRCSATSR,TSRGRARSPR,RGRARSPRVR,RARSPRVRSS,RSPRVRSSPV,RVRSSPVPTP,RSSPVPTPPS,TTRRSTRRSC,STRRSCWTSP,TSRAPQPSRA,RAQTWRTSPH,TWRTSPHCGI,CSATSRGRAR,WWMTNLTTRR,TNLTTRRSTR,NLTTRRSTRR,QTSRAPQPSR,PVWLSQNCLR,WTSASSTRSA,RPPSTATAPW,TPPSRTLPKL,APQPSRAQTW,SPHCGIDTPV,TPVWLSQNCL,APLTRTGRGL,CEYLRPPSTA,SASSTRSAKW,WATSTGARCL,LALSPPSPPW,ALSPPSPPWW,RRSCWTSPGM,AQTWRTSPHC,LSQNCLRAPL,SQNCLRAPLT,LTSGAAAACW	STAD
PNRC1	c.217C>T	p.R73C	PRALPPTLFLPHFLGGDGPCLTPQP[p.R73C]CAPAALPNRSLAVAGGTPRAAPKKRR	LTPQPCAPA,TPQPCAPAA,CLTPQPCAPA,TPQPCAPAAL	CESC
PODN	c.903delC	p.I301fs	RHVPKHLPPALYKLHLKNNKLEKIP[p.I301fs]RGPSAS*	LEKIPRGPSA	STAD
PODNL1	c.449C>T	p.A150V	QLQHLCVAHNKLSVAPQFLPRSLRV[p.A150V]VDLAANQVMEIFPLTFGEKPALRSVY	FLPRSLRVV,RSLRVVDLA,VDLAANQVM,RVVDLAANQV,RSLRVVDLAA,LPRSLRVVDL	GBM
PODXL	c.486_487insC	p.S162fs	TATAKPNTTSSQNGAEDTTNSGGKS[p.S162fs]QPQCDHRPHIH*	QPQCDHRPHI,SQPQCDHRPH	GBM
POGZ	c.223G>T	p.G75W	SAPVPIAAHASVAGHLSTSTTVSSS[p.G75W]WAQNSDSTKKTLVTLIANNNAGNPLV	TSTTVSSSW,STSTTVSSSW	LUAD
POLA1	c.1809G>T	p.E603D	PFQSHFCVVSKPKDCIFPYAFKEVI[p.E603D]DKKNVKVEVAATERTLLGFFLAKVHK	YAFKEVIDK,AFKEVIDKK,YAFKEVIDKK,EVIDKKNVKV	CRC
POLE	c.1231G>T	p.V411L	EIGFQKDSQGEYKAPQCIHMDCLRW[p.V411L]LKRDSYLPVGSHNLKAAAKAKLGYDP	HMDCLRWLK,RWLKRDSYL,IHMDCLRWL,LRWLKRDSY,LKRDSYLPV,WLKRDSYLPV,IHMDCLRWLK,CLRWLKRDSY,HMDCLRWLKR,LRWLKRDSYL	CRC,UCEC
POLE	c.1376C>T	p.S459F	YDPVELDPEDMCRMATEQPQTLATY[p.S459F]FVSDAVATYYLYMKYVHPFIFALCTI	FVSDAVATY,ATYFVSDAV,QPQTLATYF,FVSDAVATYY,TLATYFVSDA,ATYFVSDAVA,YFVSDAVATY,LATYFVSDAV,EQPQTLATYF,QPQTLATYFV	CRC
POLE	c.1718G>T	p.R573L	ESGVFRSDIPCRFRMNPAAFDFLLQ[p.R573L]LVEKTLRHALEEEEKVPVEQVTNFEE	FLLQLVEKT,DFLLQLVEK,AAFDFLLQL,AAFDFLLQLV,FLLQLVEKTL,QLVEKTLRHA,LQLVEKTLRH	LUAD
POLE	c.857C>G	p.P286R	DDLVERPDPVVLAFDIETTKLPLKF[p.P286R]RDAETDQIMMISYMIDGQGYLITNRE	TTKLPLKFR,RDAETDQIM,KFRDAETDQI,ETTKLPLKFR,RDAETDQIMM	UCEC
POLM	c.290delC	p.P97fs	EETSAEEAVSWQERRMAAAPPGCTP[p.P97fs]QLCWT*	APPGCTPQL	STAD
POLQ	c.2579G>A	p.R860Q	NAVPFKSARKAVDEEEEAVEERRNM[p.R860Q]QTIWVTGRKGLTEREAAALIVEEARM	QTIWVTGRK,MQTIWVTGR,RNMQTIWVT,MQTIWVTGRK,NMQTIWVTGR,RNMQTIWVTG,EERRNMQTIW	CRC
POLR1C	c.994A>C	p.K332Q	IFSVESTGVLPPDVLVSEAIKVLMG[p.K332Q]QCRRFLDELDAVQMD*	KVLMGQCRR,VLMGQCRRF,LMGQCRRFL,VLMGQCRRFL,AIKVLMGQCR,KVLMGQCRRF,GQCRRFLDEL	KIRC
POLR3B	c.1114C>T	p.L372F	GDNKVDDRDYYGNKRLELAGQLLSL[p.L372F]FFEDLFKKFNSEMKKIADQVIPKQRA	LLSLFFEDL,SLFFEDLFK,LFFEDLFKK,LSLFFEDLF,FFEDLFKKF,LAGQLLSLF,AGQLLSLFF,QLLSLFFEDL,LSLFFEDLFK,SLFFEDLFKK,LFFEDLFKKF,ELAGQLLSLF,LAGQLLSLFF,LLSLFFEDLF	BLCA

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POM121L12	c.691C>A	p.P231T	GRRNLQPRPSAFKPLSKNGAVASFV[p.P231T]TRPGPLKPSLGPWSLSFCDDAWPSVL	FVTRPGPLK,GAVASFVTR,SFVTRPGPL,SFVTRPGPLK,ASFVTRPGPL,NGAVASFVTR	LUAD
POM121L12	c.725C>A	p.P242H	FKPLSKNGAVASFVPRPGPLKPSLG[p.P242H]HWSLSFCDDAWPSVLVQPAPSAIWDF	SLGHWSLSF,KPSLGHWSL,PSLGHWSLSF,LKPSLGHWSL,GPLKPSLGHW	LUAD
PON1	c.917G>A	p.R306Q	WVGCHPNGMKIFFYDSENPPASEVL[p.R306Q]QIQNILTEEPKVTQVYAENGTVLQGS	SEVLQIQNI,LQIQNILTE,PPASEVLQI,SEVLQIQNIL,NPPASEVLQI	UCEC
POP1	c.2248delA	p.K750fs	VASSPNGKESDLRRSEVPCAPMPKK[p.K750fs]LISHLMKWAHP*	LISHLMKWA,KLISHLMKW,KKLISHLMK,APMPKKLIS,MPKKLISHL,ISHLMKWAH,KLISHLMKWA,APMPKKLISH,MPKKLISHLM,KKLISHLMKW	STAD
POSTN	c.1522C>T	p.R508C	GAIHIFREIIKPAEKSLHEKLKQDK[p.R508C]CFSTFLSLLEAADLKELLTQPGDWTL	KQDKCFSTF,CFSTFLSLL,KCFSTFLSL,KQDKCFSTFL,LKQDKCFSTF,KCFSTFLSLL	CRC
POTEC	c.1519A>G	p.K507E	EEQNTGISQDEILTNKQKQIEVAEK[p.K507E]EMNSELSLSHKKEEDLLRENSMLQEE	AEKEMNSEL,KEMNSELSL,KEMNSELSLS,AEKEMNSELS	GBM,PRAD
POTEE	c.496G>A	p.V166M	DKLHRAAWWGKVPRKDLIVMLRDTD[p.V166M]MNKKDKQKRTALHLASANGNSEVVKL	MLRDTDMNKK	GBM
POTEE	c.862G>A	p.V288M	ADIESKNKHGLTPLLLGVHEQKQQV[p.V288M]MKFLIKKKANLNALDRYGRTALILAV	QVMKFLIKK,VMKFLIKKK,KQQVMKFLI,QQVMKFLIK,VHEQKQQVM,EQKQQVMKF,QVMKFLIKKK,KQQVMKFLIK,QQVMKFLIKK,GVHEQKQQVM,HEQKQQVMKF	LUAD
POTEE	c.908G>T	p.R303I	LGVHEQKQQVVKFLIKKKANLNALD[p.R303I]IYGRTALILAVCCGSASIVSLLLEQN	IYGRTALIL,DIYGRTALI,KANLNALDI,ANLNALDIY,LDIYGRTAL,ALDIYGRTAL,IYGRTALILA,KANLNALDIY,NLNALDIYGR,KKANLNALDI	UCEC
POTEF	c.2022G>T	p.K674N	STLREEIAMLRLELDTMKHQSQLRE[p.K674N]NKYLEDIESVKKRNDNLLKALQLNEL	SQLRENKYL,RENKYLEDI,KHQSQLRENK,HQSQLRENKY,NKYLEDIESV	UCEC
POTEF	c.334A>G	p.S112G	DDSAMKTLRNKMGKWCCHCFPCCRG[p.S112G]GSKSKVGAWGDYDDSAFMEPRYHVRG	CCRGGSKSK	TGCT
POTEG	c.151G>A	p.D51N	KWCRHCFPWCRGSGKSNVGTSGDHD[p.D51N]NSAMKTLRSKMGKWCRHCFPWCRGSS	DNSAMKTLR,NSAMKTLRSK	SKCM
POTEG	c.407G>A	p.R136H	GSGKSKVGPWGDYDDSAFMEPRYHV[p.R136H]HREDLDKLHRAAWWGKVPRKDLIVML	HVHREDLDK,FMEPRYHVH,FMEPRYHVHR	GBM
POU2F2	c.715A>G	p.T239A	RIKLGFTQGDVGLAMGKLYGNDFSQ[p.T239A]ATISRFEALNLSFKNMCKLKPLLEKW	ATISRFEAL,DFSQATISR,FSQATISRF,KLYGNDFSQA,SQATISRFEA,DFSQATISRF,YGNDFSQATI	DLBCL
POU2F2	c.715A>T	p.T239S	RIKLGFTQGDVGLAMGKLYGNDFSQ[p.T239S]STISRFEALNLSFKNMCKLKPLLEKW	STISRFEAL,FSQSTISRF,DFSQSTISR,DFSQSTISRF,YGNDFSQSTI,SQSTISRFEA	DLBCL
POU3F3	c.961G>T	p.D321Y	GGGGGAGPGLNSHDPHSDEDTPTSD[p.D321Y]YLEQFAKQFKQRRIKLGFTQADVGLA	YLEQFAKQF,DEDTPTSDY,TSDYLEQFAK,DYLEQFAKQF,TPTSDYLEQF	LUAD
PPARGC1B	c.403delC	p.P135fs	AFPALDGGDALSCTSASPAPSSAPP[p.P135fs]ALPRRSPRPQPLRWTSSHCCRSSSWPHPTQHQALTPRRKGPPGARQASDLKVNGLVLRRTAPKTRRLP*	KVNGLVLRR,LVLRRTAPK,SSAPPALPR,RSPRPQPLR,SSHCCRSSS,HQALTPRRK,GARQASDLK,RTAPKTRRL,PALPRRSPR,TQHQALTPR,APSSAPPAL,RPQPLRWTS,WPHPTQHQA,RRSPRPQPL,SHCCRSSSW,SPRPQPLRW,ASDLKVNGLV,GLVLRRTAPK,SSAPPALPRR,VLRRTAPKTR,RTAPKTRRLP,DLKVNGLVLR,SPAPSSAPPA,SPRPQPLRWT,RPQPLRWTSS,WPHPTQHQAL,TPRRKGPPGA,SSHCCRSSSW,SDLKVNGLVL	STAD
PPIL4	c.1146T>A	p.S382R	PKQDTKYDLILDEQAEDSKSSHSHT[p.S382R]RKKHKKKTHHCSEEKEDEDYMPIKNT	KSSHSHTRK,SSHSHTRKK,HSHTRKKHK,HTRKKHKKK,KSSHSHTRKK,HSHTRKKHKK,DSKSSHSHTR	CLL

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PPL	c.1362delC	p.P454fs	GESWELMDSAGNKLIAPAVCFVIPP[p.P454fs]QTLRPWLWLTAWAASTGACGRRQLGANARCSSGMRC*	TLRPWLWLT,WLWLTAWAA,WLTAWAAST,FVIPPQTLR,CFVIPPQTL,PQTLRPWLW,NARCSSGMR,TAWAASTGA,RPWLWLTAW,RQLGANARC,ANARCSSGM,IPPQTLRPW,TLRPWLWLTA,LTAWAASTGA,CGRRQLGANA,CFVIPPQTLR,WAASTGACGR,IPPQTLRPWL,RPWLWLTAWA,RQLGANARCS,GANARCSSGM	STAD
PPL	c.976C>T	p.H326Y	DWKEYLNLLICEESHLKYMEDYHQF[p.H326Y]YEDVKDAQELLRKVDSDLNQKYGPDF	YMEDYHQFY,KYMEDYHQFY,HQFYEDVKDA,YEDVKDAQEL	BLCA
PPM1E	c.931C>T	p.R311W	IHLHVNLVRQEMFPHDPAEALCRAF[p.R311W]WVTDERFVQKAARESLRCGTTGVVTF	RAFWVTDER,AFWVTDERF,EALCRAFWV,AEALCRAFW,WVTDERFVQK,RAFWVTDERF,AEALCRAFWV	KIRC
PPM1H	c.678delC	p.P226fs	NSRTLTRAASLRGGVGAPGSPSTPP[p.P226fs]HASLPRRRFPMSAWSSERLKVHSRKWTYR*	SLPRRRFPM,SAWSSERLK,ASLPRRRFP,RLKVHSRKW,KVHSRKWTY,PMSAWSSER,MSAWSSERL,FPMSAWSSE,LPRRRFPMS,HASLPRRRF,RRRFPMSAW,MSAWSSERLK,KVHSRKWTYR,STPPHASLPR,ASLPRRRFPM,SERLKVHSRK,RLKVHSRKWT,FPMSAWSSER,SPSTPPHASL,LPRRRFPMSA,RRFPMSAWSS,LKVHSRKWTY	STAD
PPP1R12C	c.1116delC	p.P372fs	LSSREKISLQDLSKERRPGGAGGPP[p.P372fs]SRTRMRGKKVPPNHPLQNPEPSMASPPRRTPALRVPCSLKRPPSPGALAS*	ALRVPCSLK,PSRTRMRGK,RTRMRGKKV,RMRGKKVPP,RGKKVPPNH,ASPPRRTPA,SLKRPPSPG,SPPRRTPAL,RPPSPGALA,KKVPPNHPL,LQNPEPSMA,SLKRPPSPGA,PSRTRMRGKK,RTRMRGKKVP,RMRGKKVPPN,MASPPRRTPA,ALRVPCSLKR,RPGGAGGPPS,HPLQNPEPSM,TPALRVPCSL,LKRPPSPGAL,GKKVPPNHPL,LQNPEPSMAS	STAD
PPP2R1A	c.536C>G	p.P179R	CYPRVSSAVKAELRQYFRNLCSDDT[p.P179R]RMVRRAAASKLGEFAKVLELDNVKSE	TRMVRRAAA,RMVRRAAAS,NLCSDDTRMV,RMVRRAAASK,RNLCSDDTRM	UCEC,UCS
PPP2R1A	c.547C>T	p.R183W	VSSAVKAELRQYFRNLCSDDTPMVR[p.R183W]WAAASKLGEFAKVLELDNVKSEIIPM	MVRWAAASK,DTPMVRWAA,TPMVRWAAA,VRWAAASKL,CSDDTPMVRW,MVRWAAASKL,DTPMVRWAAA,TPMVRWAAAS,WAAASKLGEF	CRC,UCS
PPP2R1A	c.656C>T	p.S219L	KVLELDNVKSEIIPMFSNLASDEQD[p.S219L]LVRLLAVEACVNIAQLLPQEDLEALV	DEQDLVRLL,NLASDEQDLV,DEQDLVRLLA	UCS
PPP2R1A	c.767C>T	p.S256F	IAQLLPQEDLEALVMPTLRQAAEDK[p.S256F]FWRVRYMVADKFTELQKAVGPEITKT	KFWRVRYMV,FWRVRYMVA,QAAEDKFWR,RQAAEDKFW,DKFWRVRYM,KFWRVRYMVA,QAAEDKFWRV,TLRQAAEDKF,AEDKFWRVRY	UCEC
PPP2R2B	c.977C>T	p.P326L	SKGTIRLCDMRASALCDRHTKFFEE[p.P326L]LEDPSNRSFFSEIISSISDVKFSHSG	RHTKFFEEL,LEDPSNRSF,ELEDPSNRSF,LEDPSNRSFF	CRC
PPP2R3B	c.1165delA	p.T389fs	RKVQKEGKISYADFVWFLISEEDKK[p.T389fs]HRPASSTGSAAWTWTGTAPCPCSSSSTSTRSSAEGWTAWPSRPCPSRTASARCWTWSSRGLKGRSRCRT*	WTWSSRGLK,CSSSSTSTR,STGSAAWTW,SSTSTRSSA,RTASARCWT,SARCWTWSS,EGWTAWPSR,WTWTGTAPC,WTAWPSRPC,RPASSTGSA,RPCPSRTAS,SSAEGWTAW,KKHRPASST,ASSTGSAAW,RSSAEGWTA,AEGWTAWPS,TASARCWTW,RTASARCWTW,SSSTSTRSSA,SARCWTWSSR,CWTWSSRGLK,SSRGLKGRSR,RGLKGRSRCR,TWSSRGLKGR,SAAWTWTGTA,RPASSTGSAA,RPCPSRTASA,SSTGSAAWTW,RSSAEGWTAW,RCWTWSSRGL,SEEDKKHRPA	STAD
PPP2R3B	c.930C>A	p.F310L	ELRRSSFLQNVALLEEEADINQLTE[p.F310L]LFSYEHFYVIYCKFWELDTDHDLLID	LTELFSYEH,NQLTELFSY,ELFSYEHFY,ADINQLTEL,TELFSYEHF,ELFSYEHFYV,LFSYEHFYVI,INQLTELFSY,ADINQLTELF,LTELFSYEHF,TELFSYEHFY	UCEC
PPP2R5C	c.776C>A	p.S259Y	GFALPLKEEHKIFLLKVLLPLHKVK[p.S259Y]YLSVYHPQLAYCVVQFLEKDSTLTEP	YLSVYHPQL,KYLSVYHPQ,KVKYLSVYH,LPLHKVKYL,LHKVKYLSV,HKVKYLSVY,YLSVYHPQLA,LLPLHKVKYL,KYLSVYHPQL,KVKYLSVYHP,VLLPLHKVKY,LHKVKYLSVY,HKVKYLSVYH	CRC
PPP4R1	c.1791G>C	p.L597F	DSVPLISDAVENMDSTLHYIHSDSD[p.L597F]FSNNSSFSPDEERRTKVQDVVPQALL	HYIHSDSDF,SDFSNNSSF,LHYIHSDSDF	CESC
PPP6C	c.901C>T	p.R301C	LVHEGYKFMFDEKLVTVWSAPNYCY[p.R301C]CCGNIASIMVFKDVNTREPKLFRAVP	CYCCGNIASI,YCCGNIASIM	SKCM

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PPT2	c.794G>T	p.R265L	WQSSFFGFYDANETVLEMEEQLVYL[p.R265L]LDSFGLKTLLARGAIVRCPMAGISHT	YLLDSFGLK,VYLLDSFGL,QLVYLLDSF,MEEQLVYLL,LVYLLDSFGL,YLLDSFGLKT,LLDSFGLKTL,EQLVYLLDSF	LUAD
PRAM1	c.802G>A	p.A268T	QPEFSEAAQTPLWKPQSSEPKRDSS[p.A268T]TFPKKASQPPLSDFPKKPPQPELGDL	RDSSTFPKK,EPKRDSSTF,SEPKRDSSTF	UCEC
PRAMEF11	c.251G>C	p.C84S	KLQVLDLQDVCENFWMVWSEAMAHG[p.C84S]SFLNAKRNKTPVQDCPRMRERQPLTV	MAHGSFLNA,SFLNAKRNK,HGSFLNAKR,EAMAHGSFL,SEAMAHGSF,AMAHGSFLNA,MAHGSFLNAK,GSFLNAKRNK,WSEAMAHGSF,SEAMAHGSFL	SKCM
PRAMEF11	c.311G>A	p.R104Q	AMAHGCFLNAKRNKTPVQDCPRMRE[p.R104Q]QQPLTVFVELWLKNRTLDEYLTCLLL	RMREQQPLT,EQQPLTVFV,REQQPLTVF,RMREQQPLTV,CPRMREQQPL,MREQQPLTVF,REQQPLTVFV	CLL
PRAMEF4	c.743G>A	p.R248H	LTQFTPYLGHMRNLQKLILSHMDVS[p.R248H]HYVSPEQKKEIVTQFTTQFLKLRCLQ	LSHMDVSHY,SHMDVSHYV,VSHYVSPEQK,ILSHMDVSHY,LSHMDVSHYV	CRC
PRAMEF8	c.1342A>G	p.I448V	ALCWGRFAELGAELMKTPRDLRQPK[p.I448V]VIVFCTVPCPRCGIRASYDLEPSHCL	LRQPKVIVF,TPRDLRQPKV,DLRQPKVIVF,QPKVIVFCTV	TGCT
PRAMEF8	c.956G>A	p.R319H	LEMVVMTDCLLSESDLKHLSWCPSI[p.R319H]HQLKELDLRGVTLTHFSPEPLTGLLE	SWCPSIHQL,HLSWCPSIH,SWCPSIHQLK,CPSIHQLKEL,LSWCPSIHQL	PRAD
PRB1	c.820delC	p.R274fs	KPQGPPPPGKPQGPPAQGGSKSQSA[p.R274fs]DLLQESHKDHPNKKATILKVPHLQQEAIPSSLRHLLLDSPRDHHALLKGADLPDLPSDSLPSHLGFNDRK*	HPNKKATIL,VPHLQQEAI,IPSSLRHLL,SPRDHHALL,LPDLPSDSL,DSLPSHLGF,SKSQSADLL,LQQEAIPSS,QQEAIPSSL,LPSDSLPSH,LQQEAIPSSL,AIPSSLRHLL,LLKGADLPDL,SADLLQESHK,SPRDHHALLK,EAIPSSLRHL,IPSSLRHLLL,LPSDSLPSHL,KKATILKVPH,LKVPHLQQEA,SDSLPSHLGF	HNSC
PRDM1	c.1763C>G	p.S588C	PYPLKKQNGKIKYECNVCAKTFGQL[p.S588C]CNLKVHLRVHSGERPFKCQTCNKGFT	KTFGQLCNL,GQLCNLKVH,KTFGQLCNLK,QLCNLKVHLR,AKTFGQLCNL,GQLCNLKVHL	MM
PRDM16	c.3107C>T	p.P1036L	HLCNRCFGQQTNLDRHLKKHEHENA[p.P1036L]LVSQHPGVLTNHLGTSASSPTSESDN	ALVSQHPGV,KKHEHENAL,HEHENALVS,HENALVSQH,ALVSQHPGVL,LKKHEHENAL,KKHEHENALV	LUAD
PRDM16	c.811G>C	p.E271Q	RRHKKYTCGSVGAALYEGLAEELKP[p.E271Q]QGLGGGSGQAHECKDCERMFPNKYSL	AEELKPQGL	BLCA
PRDM4	c.2404T>A	p.*802K	DSVGTEDCRINSAVYSADESLSAHK[p.*802K]KKEKKQAILDENANGKIHITSYLL*	KIHITSYLL,SAHKKKEKK,NGKIHITSY,GKIHITSYL,ILDENANGKI,SLSAHKKKEK,AILDENANGK,ANGKIHITSY,NGKIHITSYL,GKIHITSYLL	CLL
PRDM7	c.1159A>C	p.M387L	GQELGIRSSIEPAESLGQAVNCWSG[p.M387L]LGMSMARNWASSGAASGRKSSWQGEN	SGLGMSMAR,QAVNCWSGL,VNCWSGLGM,CWSGLGMSM,LGMSMARNW,GQAVNCWSGL,AVNCWSGLGM,NCWSGLGMSM	PRAD
PRELP	c.601G>T	p.D201Y	LRLSQNHISRIPPGVFSKLENLLLL[p.D201Y]YLQHNRLSDGVFKPDTFHGLKNLMQL	KLENLLLLY,LLYLQHNRL,LLLYLQHNR,LENLLLLYL,KLENLLLLYL,LLLYLQHNRL,SKLENLLLLY,LLLLYLQHNR	LUAD
PREP	c.1407C>A	p.F469L	SKDGTKIPMFIVHKKGIKLDGSHPA[p.F469L]LLYGYGGFNISITPNYSVSRLIFVRH	KLDGSHPAL,SHPALLYGY,ALLYGYGGF,KLDGSHPALL,LLYGYGGFNI,GSHPALLYGY,LDGSHPALLY,IKLDGSHPAL	CESC
PREX1	c.2191G>A	p.V731I	AKEIIKIPDQPDTLCFQIRGAAPPY[p.V731I]IYAVGRGSEAMAAGLCAGQCILKVNG	AAPPYIYAV,RGAAPPYIY,GAAPPYIYAV,QIRGAAPPYI,RGAAPPYIYA,IRGAAPPYIY	CRC
PREX1	c.3736G>A	p.E1246K	CLEHLFNQVDSINALLKGPVMSRAF[p.E1246K]KETKHFPMNHSLQEFKQKEECTIRGR	MSRAFKETK,FKETKHFPM,RAFKETKHF,VMSRAFKETK,KGPVMSRAFK,MSRAFKETKH,AFKETKHFPM,SRAFKETKHF	UCEC
PREX2	c.1088G>A	p.R363Q	WFVCMAKTPEEKHEWFEAILKERER[p.R363Q]QKGLKLGMEQDTWVMISEQGEKLYKM	ILKERERQK,RQKGLKLGM,KERERQKGL,RERQKGLKL,AILKERERQK,KERERQKGLK	BRCA
PREX2	c.1686_1687insT	p.R562fs	CDNGFMHHVLEKSEFKDEPLLFRFF[p.R562fs]FG*	EPLLFRFFF,DEPLLFRFFF	STAD
PRG4	c.2023A>C	p.N675H	PTTPEEPTPTTPEEPAPTTPKAAAP[p.N675H]HTPKEPAPTTPKEPAPTTPKEPAPTT	KAAAPHTPK,APHTPKEPA	CLL

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PRIC285	c.3865G>C	p.E1289Q	LFWVQIVLWRQGFYYPLGIVREVLP[p.E1289Q]QASTWEQGLRILGLEYSLRVPPSDQA	IVREVLPQA,REVLPQAST,EVLPQASTW,GIVREVLPQA,QASTWEQGLR,REVLPQASTW	BLCA
PRKAA2	c.1220G>A	p.R407Q	CPLDALNTTKPKSLAVKKAKWHLGI[p.R407Q]QSQSKPYDIMAEVYRAMKQLDFEWKV	GIQSQSKPY,KAKWHLGIQS,LGIQSQSKPY,IQSQSKPYDI	CRC
PRKAB1	c.311C>A	p.P104H	PTVFRWTGGGKEVYLSGSFNNWSKL[p.P104H]HLTRSHNNFVAILDLPEGEHQYKFFV	NWSKLHLTR,HLTRSHNNF,FNNWSKLHL,SKLHLTRSH,HLTRSHNNFV,SFNNWSKLHL,NNWSKLHLTR,LHLTRSHNNF	CLL
PRKAR2B	c.926C>T	p.S309L	ERLKVVDVIGTKVYNDGEQIIAQGD[p.S309L]LADSFFIVESGEVKITMKRKGKSEVE	DLADSFFIV,AQGDLADSF,GDLADSFFI,AQGDLADSFF,IAQGDLADSF,GEQIIAQGDL,GDLADSFFIV	CRC
PRKCD	c.1294delG	p.G432fs	FLTHLICTFQTKDHLFFVMEFLNGG[p.G432fs]T*	FVMEFLNGGT	GBM
PRKCE	c.470_471insG	p.Q157fs	SSGEAPKDNEERVFRERMRPRKRQG[p.Q157fs]GRQAQGPSGQRPQVHGHLSSAAHLLLPLQRLHLGCHRKAGIPVSSLHLRGPQAVPRAHNHKVCWVKEAGDPRPGGLPAVQRQHAPQVRYPQLQGPYLLRSLWVPALGTLAAGFAV*	HLSSAAHLL,YLLRSLWVP,GTLAAGFAV,QVHGHLSSA,SLHLRGPQA,LLRSLWVPA,RLHLGCHRK,AVPRAHNHK,PYLLRSLWV,LWVPALGTL,RPRKRQGGR,HNHKVCWVK,VQRQHAPQV,RQHAPQVRY,RSLWVPALG,RYPQLQGPY,WVKEAGDPR,QLQGPYLLR,SAAHLLLPL,GPSGQRPQV,RPQVHGHLS,VPRAHNHKV,DPRPGGLPA,APQVRYPQL,YPQLQGPYL,VPALGTLAA,ALGTLAAGF,RKRQGGRQA,GQRPQVHGH,HGHLSSAAH,GHLSSAAHL,LSSAAHLLL,LQRLHLGCH,CHRKAGIPV,KAGIPVSSL,LHLRGPQAV,RAHNHKVCW,PQLQGPYLL,GPYLLRSLW,LRSLWVPAL,HLSSAAHLL,LLLPLQRLHL,SLHLRGPQAV,YLLRSLWVPA,LLRSLWVPAL,SLWVPALGTL,ALGTLAAGFA,AAHLLLPLQR,RYPQLQGPYL,RMRPRKRQGG,LQRLHLGCHR,RLHLGCHRKA,SSLHLRGPQA,HLRGPQAVPR,QAVPRAHNHK,RAHNHKVCWV,VQRQHAPQVR,VRYPQLQGPY,SSAAHLLLPL,RPQVHGHLSS,VPRAHNHKVC,DPRPGGLPAV,YPQLQGPYLL,GPYLLRSLWV,HLGCHRKAGI,GQRPQVHGHL,HGHLSSAAHL,GHLSSAAHLL,RKAGIPVSSL,AGIPVSSLHL,RQHAPQVRYP,LQGPYLLRSL,VPALGTLAAG	KIRC
PRKCG	c.1033C>T	p.R345C	SSSPIPSPSPSPTDPKRCFFGASPG[p.R345C]CLHISDFSFLMVLGKGSFGKVMLAER	CLHISDFSF,CLHISDFSFL,SPGCLHISDF,GCLHISDFSF	STAD
PRKCI	c.1438C>T	p.R480C	IVGSSDNPDQNTEDYLFQVILEKQI[p.R480C]CIPRSLSVKAASVLKSFLNKDPKERL	KQICIPRSL,CIPRSLSVK,KQICIPRSLS,LEKQICIPRS	CRC
PRKCQ	c.971C>T	p.A324V	GMNVHHRCQTKVANLCGINQKLMAE[p.A324V]VLAMIESTQQARCLRDTEQIFREGPV	KLMAEVLAM,LMAEVLAMI,NQKLMAEVL,AEVLAMIES,GINQKLMAEV,KLMAEVLAMI,QKLMAEVLAM,AEVLAMIEST	UCEC
PRKDC	c.10702C>G	p.Q3568E	DTSTGHKNKEFVARIKSKLDQGGVI[p.Q3568E]EDFINALDQLSNPELLFKDWSNDVRA	GVIEDFINA,GVIEDFINAL	CESC
PRKRA	c.366G>T	p.K122N	NILKANASICFAVPDPLMPDPSKQP[p.K122N]NNQLNPIGSLQELAIHHGWRLPEYTL	QPNNQLNPI,KQPNNQLNPI	CRC
PRMT8	c.84delC	p.S28fs	SSRCLLLRRKMAENAAESTEVNSPP[p.S28fs]PSPPSPSSLLSPCNASIMCPLNPAAQDGARCPSC*	LLSPCNASI,SIMCPLNPA,IMCPLNPAA,SPPSPSSLL,LSPCNASIM,SLLSPCNASI,SIMCPLNPAA,LLSPCNASIM,PPSPPSPSSL	STAD
PRMT8	c.91T>C	p.S31P	SSRCLLLRRKMAENAAESTEVNSPP[p.S31P]PQPPQPVVPAKPVQCVHHVSTQPSCP	SPPPQPPQPV	BLCA
PRODH	c.1579C>G	p.L527V	TVRFALRRMEELGLHPADHRVYFGQ[p.L527V]VLGMCDQISFPLGQAGYPVYKYVPYG	VYFGQVLGM,RVYFGQVLG,HRVYFGQVL,RVYFGQVLGM,VLGMCDQISF,GQVLGMCDQI	TGCT
PROKR2	c.889G>A	p.V297I	KTVLVLMCILTAYVLCWAPFYGFTI[p.V297I]IRDFFPTVFVKEKHYLTAFYVVECIA	IIRDFFPTV,GFTIIRDFF,TIIRDFFPT,APFYGFTII,YGFTIIRDF,IRDFFPTVF,TIIRDFFPTV,FYGFTIIRDF,YGFTIIRDFF,APFYGFTIIR,FTIIRDFFPT,IIRDFFPTVF	GBM

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PROX1	c.1774delT	p.F592fs	SPYSGSAMQEGLSPNHLKKAKLMFF[p.F592fs]IPVIPAPIC*	KLMFFIPVI,FIPVIPAPI,KAKLMFFIP,MFFIPVIPA,KKAKLMFFI,AKLMFFIPV,LMFFIPVIPA,FFIPVIPAPI,KAKLMFFIPV,AKLMFFIPVI	STAD
PROX1	c.674T>A	p.V225D	PRESYRENKRKQKLPQQQQQSFQQL[p.V225D]DSARKEQKREERRQLKQQLEDMQKQL	SFQQLDSAR,QSFQQLDSAR	KIRC
PRPF31	c.865C>T	p.R289W	STSVLPHTGYIYHSDIVQSLPPDLR[p.R289W]WKAARLVAAKCTLAARVDSFHESTEG	RWKAARLVA,DLRWKAARL,WKAARLVAA,LRWKAARLV,LPPDLRWKA,SLPPDLRWKA,QSLPPDLRWK,RWKAARLVAA,DLRWKAARLV,VQSLPPDLRW,LRWKAARLVA,LPPDLRWKAA	TGCT
PRPF6	c.2288G>T	p.R763L	KCPHSTPLWLLLSRLEEKIGQLTRA[p.R763L]LAILEKSRLKNPKNPGLWLESVRLEY	QLTRALAIL,KIGQLTRAL,GQLTRALAI,ALAILEKSRL,LTRALAILEK,KIGQLTRALA,RALAILEKSR,EKIGQLTRAL,GQLTRALAIL	LUAD
PRRC2C	c.5647C>A	p.P1883T	SASIPILASALASTSAPTPAPAASS[p.P1883T]TAAPVITAPTIPASAPTASVPLAPAS	AASSTAAPV,STAAPVITA,TPAPAASST,APAASSTAA,ASSTAAPVI,TAAPVITAPT,TPAPAASSTA,APAASSTAAP,AASSTAAPVI	KIRC
PRRX1	c.587C>T	p.A196V	DVTAVEQPIVPRPAPRPTDYLSWGT[p.A196V]VSPYSAMATYSATCANNSPAQGINMA	LSWGTVSPY,YLSWGTVSP,TVSPYSAMA,GTVSPYSAM,TDYLSWGTV,PTDYLSWGTV,YLSWGTVSPY,VSPYSAMATY,WGTVSPYSAM	BRCA
PRSS1	c.319G>A	p.D107N	EGNEQFINAAKIIRHPQYDRKTLNN[p.D107N]NIMLIKLSSRAVINARVSTISLPTAP	TLNNNIMLI,KTLNNNIML,RKTLNNNIM,KTLNNNIMLI,TLNNNIMLIK,NIMLIKLSSR,RKTLNNNIML	HNSC
PRSS36	c.2038delC	p.L680fs	LPQGHQVSRLVISIRLPQHLGLRPP[p.L680fs]WPSWS*	GLRPPWPSW,QHLGLRPPW,PQHLGLRPPW,LGLRPPWPSW	STAD
PRSS57	c.115G>C	p.E39Q	TVATALMLPVKPPAGSWGAQIIGGH[p.E39Q]QVTPHSRPYMASVRFGGQHHCGGFLL	AQIIGGHQV,QVTPHSRPY,HQVTPHSRPY,AQIIGGHQVT	LUSC
PSD2	c.766delG	p.G256fs	NVLSRLSLMAMPNGFHEDGPQGPGG[p.G256fs]MRMMMRRTRTSC*	GGMRMMMRR,GMRMMMRRT,RMMMRRTRT,MMMRRTRTS,MMRRTRTSC,GPGGMRMMM,PQGPGGMRM,MMMRRTRTSC,GMRMMMRRTR,RMMMRRTRTS,GPQGPGGMRM,PQGPGGMRMM	STAD
PSD3	c.1687A>C	p.T563P	PEIAFWGSNAGVKTTRLEAHSEMGS[p.T563P]PEILEKETPENLSNGTSSNVEAAKRL	MGSPEILEK,SEMGSPEIL,EMGSPEILEK,AHSEMGSPEI	KIRC
PSG8	c.1189C>T	p.R397C	FQLSGQKLFIPQITTKHSGLYACSV[p.R397C]CNSATGKESSKSMTVKVSGKRIPVSL	SVCNSATGK,GLYACSVCNS,CSVCNSATGK	CRC
PSG8	c.958C>T	p.R320C	LILPSVTRNETGPYQCEIRDQYGGI[p.R320C]CSYPVTLNVLYGPDLPRIYPSFTYYR	DQYGGICSY,CSYPVTLNV,QYGGICSYPV,RDQYGGICSY,GGICSYPVTL,CSYPVTLNVL	CRC
PSG9	c.1210G>A	p.E404K	LFIPQITRNHSGLYACSVHNSATGK[p.E404K]KISKSMTVKVSGPCHGDLTESQS*	KISKSMTVK,SATGKKISK,KKISKSMTV,KISKSMTVKV,SVHNSATGKK	SKCM
PSMD11	c.14C>T	p.A5V	MAAA[p.A5V]VVVEFQRAQSLLSTDREASIDILHSI	MAAAVVVEF,AAAVVVEFQR	TGCT
PSMD12	c.602G>A	p.R201Q	SMEKKERVEFILEQMRLCLAVKDYI[p.R201Q]QTQIISKKINTKFFQEENTEKLKLKY	YIQTQIISK,IQTQIISKK,KDYIQTQII,AVKDYIQTQI,YIQTQIISKK,IQTQIISKKI	CRC
PSME3	c.691C>T	p.R231W	IAKYPHVEDYRRTVTEIDEKEYISL[p.R231W]WLIISELRNQYVTLHDMILKNIEKIK	SLWLIISEL,KEYISLWLI,EYISLWLII,DEKEYISLW,SLWLIISELR,KEYISLWLII,ISLWLIISEL,DEKEYISLWL	CESC
PSME4	c.1483A>G	p.N495D	GGRWFPEGPTHMLPLLMRALPGVDP[p.N495D]DDFSKCMITFQFIATFSTLVPLVDCS	GVDPDDFSK,LPGVDPDDF,DDFSKCMITF,DPDDFSKCMI	TGCT
PSPH	c.433G>A	p.V145I	IRELVSRLQERNVQVFLISGGFRSI[p.V145I]IEHVASKLNIPATNVFANRLKFYFNG	SIIEHVASK,ISGGFRSII,SIIEHVASKL,LISGGFRSII,RSIIEHVASK,GFRSIIEHVA,IEHVASKLNI	GBM
PTCH1	c.2066C>A	p.P689H	LRTEYDPHTHVYYTTAEPRSEISVQ[p.P689H]HVTVTQDTLSCQSPESTSSTRDLLSQ	EISVQHVTV,SEISVQHVT,SEISVQHVTV,VQHVTVTQDT	KIRC

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PTCH1	c.3921delC	p.P1307fs	RQQPHLDSGSLPPGRQGQQPRRDPP[p.P1307fs]EKACGHPPTDRAETLLKFLLKGILALAIGPAGALAGPVLTTLGTQRPLPWAAPCPATASPSPL*	FLLKGILAL,LLKGILALA,ILALAIGPA,ALAIGPAGA,LLKFLLKGI,AIGPAGALA,ALAGPVLTT,ETLLKFLLK,KFLLKGILA,TQRPLPWAA,WAAPCPATA,LAIGPAGAL,RPLPWAAPC,LPWAAPCPA,LKFLLKGIL,LKGILALAI,AGALAGPVL,LAGPVLTTL,LGTQRPLPW,AETLLKFLL,TLLKFLLKGI,FLLKGILALA,LLKGILALAI,ALAIGPAGAL,ALAGPVLTTL,KFLLKGILAL,HPPTDRAETL,GPAGALAGPV,CPATASPSPL,LLKFLLKGIL,TDRAETLLKF,LKFLLKGILA,TQRPLPWAAP,LPWAAPCPAT	STAD
PTCHD3	c.1764delT	p.F588fs	KKFCCFPFGSVPDEHGTDIHPISLF[p.F588fs]LETILAPFSQGVSPSIL*	SLFLETILA,FLETILAPF,ILAPFSQGV,DIHPISLFL,ISLFLETIL,FSQGVSPSI,SQGVSPSIL,HPISLFLET,LETILAPFS,TILAPFSQGV,LFLETILAPF,HPISLFLETI,FSQGVSPSIL	STAD
PTEN	c.388C>G	p.R130G	CEDLDQWLSEDDNHVAAIHCKAGKG[p.R130G]GTGVMICAYLLHRGKFLKAQEALDFY	GTGVMICAY,GGTGVMICAY,KAGKGGTGVM	UCEC
PTEN	c.389G>A	p.R130Q	CEDLDQWLSEDDNHVAAIHCKAGKG[p.R130Q]QTGVMICAYLLHRGKFLKAQEALDFY	QTGVMICAY,GKGQTGVMI,GQTGVMICAY,KAGKGQTGVM	CESC,CRC,UCEC
PTEN	c.389G>C	p.R130P	CEDLDQWLSEDDNHVAAIHCKAGKG[p.R130P]PTGVMICAYLLHRGKFLKAQEALDFY	PTGVMICAY,GKGPTGVMI,GPTGVMICAY,KAGKGPTGVM	UCEC
PTEN	c.389G>T	p.R130L	CEDLDQWLSEDDNHVAAIHCKAGKG[p.R130L]LTGVMICAYLLHRGKFLKAQEALDFY	LTGVMICAY,GLTGVMICA,KAGKGLTGV,GKGLTGVMI,GLTGVMICAY,KAGKGLTGVM	UCEC
PTEN	c.407G>A	p.C136Y	WLSEDDNHVAAIHCKAGKGRTGVMI[p.C136Y]YAYLLHRGKFLKAQEALDFYGEVRTR	GVMIYAYLL,VMIYAYLLH,RTGVMIYAY,KGRTGVMIY,VMIYAYLLHR,GVMIYAYLLH,KGRTGVMIYA,RTGVMIYAYL,GKGRTGVMIY,GRTGVMIYAY	GBM
PTEN	c.509G>A	p.S170N	FLKAQEALDFYGEVRTRDKKGVTIP[p.S170N]NQRRYVYYYSYLLKNHLDYRPVALLF	VTIPNQRRY,NQRRYVYYY,IPNQRRYVY,GVTIPNQRRY,TIPNQRRYVY,VTIPNQRRYV,IPNQRRYVY	GBM
PTEN	c.518G>A	p.R173H	AQEALDFYGEVRTRDKKGVTIPSQR[p.R173H]HYVYYYYSYLLKNHLDYRPVALLFHKM	TIPSQRHYV,HYVYYYSYL,SQRHYVYYY,RHYVYYYSY,VTIPSQRHY,IPSQRHYVY,PSQRHYVYY,PSQRHYVYYY,VTIPSQRHYV,RHYVYYYSYL,HYVYYYSYLL,SQRHYVYYYS,GVTIPSQRHY,TIPSQRHYVY,QRHYVYYYSY,IPSQRHYVYY	GBM
PTEN	c.701G>T	p.R234L	GTCNPQFVVCQLKVKIYSSNSGPTR[p.R234L]LEDKFMYFEFPQPLPVCGDIKVEFFH	RLEDKFMYF,YSSNSGPTRL,TRLEDKFMYF,LEDKFMYFEF	LUAD
PTEN	c.795delA	p.L265fs	EFPQPLPVCGDIKVEFFHKQNKMLK[p.L265fs]RTKCFTFG*	KMLKRTKCF,MLKRTKCFT,LKRTKCFTF,MLKRTKCFTF,KQNKMLKRTK,KMLKRTKCFT,NKMLKRTKCF	STAD
PTEN	c.830C>T	p.T277I	DIKVEFFHKQNKMLKKDKMFHFWVN[p.T277I]IFFIPGPEETSEKVENGSLCDQEIDS	KMFHFWVNI,MFHFWVNIF,FHFWVNIFF,HFWVNIFFI,KMFHFWVNIF,MFHFWVNIFF,FHFWVNIFFI	GBM
PTGR1	c.119A>C	p.E40A	GYPTNSDFELKTAELPPLKNGEVLL[p.E40A]AALFLTVDPYMRVAAKRLKEGDTMMG	VLLAALFLT,LLAALFLTV,EVLLAALFL,GEVLLAALF,VLLAALFLTV,AALFLTVDPY,LKNGEVLLAA,GEVLLAALFL	TGCT
PTH2	c.64C>G	p.L22V	METRQVSRSPRVRLLLLLLLL[p.L22V]VVVPWGVRTASGVALPPVGVLSLRPP	LLLLLLVVV,LLVVVPWGV,LVVVPWGVR,LLLLVVVPW,RLLLLLLLV,LLLLLLLVVV,LLLVVVPWGV,LLVVVPWGVR,LLLLLVVVPW	PRAD
PTPDC1	c.1288C>T	p.R430W	AVAADFDNRGMIFSNEQQFDPLWKR[p.R430W]WNVECLQPLTHLKRRLSYSDSDLKRA	WKRWNVECL,WNVECLQPL,LWKRWNVECL,RWNVECLQPL,QQFDPLWKRW	CRC
PTPN11	c.1508G>T	p.G503V	IIREKGVDCDIDVPKTIQMVRSQRS[p.G503V]VMVQTEAQYRFIYMAVQHYIETLQRR	QMVRSQRSV,MVRSQRSVM,RSVMVQTEA,VMVQTEAQY,SQRSVMVQT,IQMVRSQRSV,SVMVQTEAQY,MVRSQRSVMV,QMVRSQRSVM	LUAD
PTPN11	c.226G>A	p.E76K	VTHIKIQNTGDYYDLYGGEKFATLA[p.E76K]KLVQYYMEHHGQLKEKNGDVIELKYP	KLVQYYMEH,ATLAKLVQY,LAKLVQYYM,TLAKLVQYY,EKFATLAKL,TLAKLVQYYM,ATLAKLVQYY,FATLAKLVQY,GEKFATLAKL,KLVQYYMEHH	MM
PTPN12	c.2294G>A	p.R765Q	PPTFSDKREQISENPTEATDIGFGN[p.R765Q]QCGKPKGPRDPPSEWT*	IGFGNQCGK	CRC
PTPN13	c.2660C>T	p.S887L	SYQHKFQLQMRARQSNQDAQDIERA[p.S887L]LFRSLNLQAESVRGFNMGRAISTGSL	RALFRSLNL,LFRSLNLQA,AQDIERALF,IERALFRSL,ALFRSLNLQA	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
PTPN13	c.6199G>A	p.E2067K	YIQEDDIYDDSQEAEVIQSLLDVVD[p.E2067K]KEAQNLLNENNAAGYSCGPGTLKMNG	QSLLDVVDK,SLLDVVDKEA	LUAD
PTPN14	c.2147_2149delAGG	p.E716del	QYHHKKTFSDATMLIHSSESEEEEE[p.E716del]APESVPQIPMLREKMEYSAQLQAALARI	SESEEEEEA	GBM
PTPN14	c.856G>A	p.E286K	THNKSTILVELINKEETALFHTDDI[p.E286K]KNAKYISRLFATRHKFYKQNKICTEQ	ALFHTDDIK,HTDDIKNAK,KNAKYISRL,HTDDIKNAKY,TALFHTDDIK,DIKNAKYISR,IKNAKYISRL,KNAKYISRLF	MM
PTPN18	c.1113_1118delGACGGG	p.TG378del	TYAVVQKRGAPAGAGSGTQTGTGTG[p.TG378del]ARSAEEAPLYSKVTPRAQRPGAHAEDARGTL	QTGTGTGAR	UCS
PTPN4	c.957delT	p.N319fs	NLWKACVEHHTFFRLDRPLPPQKNF[p.N319fs]LHIILH*	QKNFLHIIL,RPLPPQKNFL,LPPQKNFLHI	STAD
PTPRB	c.2178A>T	p.Q726H	SLTPGRLYTVTITTRSGKYENHSFS[p.Q726H]HERTVPDKVQGVSVSNSARSDYLRVS	HSFSHERTV,ENHSFSHER,FSHERTVPDK,GKYENHSFSH	TGCT
PTPRB	c.4678G>A	p.D1560N	ENPNSNSKSFNIKLGAEMESLGGKC[p.D1560N]NPTQQKFCDGPLKPHTAYRISIRAFT	KCNPTQQKF,GGKCNPTQQK,GKCNPTQQKF	SKCM
PTPRC	c.2685A>C	p.Q895H	GLEAENKVDVYGYVVKLRRQRCLMV[p.Q895H]HVEAQYILIHQALVEYNQFGETEVNL	RQRCLMVHV,LMVHVEAQY,MVHVEAQYI,VHVEAQYIL,LMVHVEAQYI,RQRCLMVHVE,CLMVHVEAQY,MVHVEAQYIL	STAD
PTPRF	c.3521G>A	p.R1174Q	PRWSTPEELELDELLEAIEQGGEEQ[p.R1174Q]QRRRRQAERLKPYVAAQLDVLPETFT	EQQRRRRQA,QQRRRRQAER	PRAD
PTPRJ	c.1000G>T	p.G334W	HDESLVGPVDPSSGQQSRDTEVLLV[p.G334W]WLEPGTRYNATVYSQAANGTEGQPQA	LVWLEPGTR,RDTEVLLVW,VWLEPGTRY,VLLVWLEPGT,WLEPGTRYNA,LVWLEPGTRY,RDTEVLLVWL	LUAD
PTPRT	c.2783G>T	p.R928L	SWDTAKEDENRNKNRYGNIISYDHS[p.R928L]LVRLLVLDGDPHSDYINANYIDGYHR	IISYDHSLV,NIISYDHSL,ISYDHSLVR,SYDHSLVRL,HSLVRLLVL,YDHSLVRLL,NIISYDHSLV,IISYDHSLVR,SYDHSLVRLL,ISYDHSLVRL,YDHSLVRLLV	LUAD
PTPRT	c.3224delC	p.P1075fs	WPDHGVPCYATGLLGFVRQVKFLNP[p.P1075fs]RKLGP*	RQVKFLNPR,QVKFLNPRK,VKFLNPRKL,RQVKFLNPRK	STAD
PTPRU	c.1675C>T	p.P559S	VNVPGPRRTISKLRNETYHVFSNLH[p.P559S]SGTTYLFSVRARTGKGFGQAALTEIT	NLHSGTTYL,LHSGTTYLF,SNLHSGTTY,FSNLHSGTTY,NLHSGTTYLF,SGTTYLFSVR,HVFSNLHSGT,HSGTTYLFSV,SNLHSGTTYL	LUAD
PTPRU	c.4300G>A	p.D1434N	FFAAKTLRNYKPNMVETMDQYHFCY[p.D1434N]NVALEYLEGLESR*	CYNVALEYL,FCYNVALEY,DQYHFCYNV,YHFCYNVAL,QYHFCYNVAL,HFCYNVALEY,NVALEYLEGL,DQYHFCYNVA,MDQYHFCYNV	CRC
PUF60	c.1187C>T	p.S396L	VMAAQAPGVITGVTPARPPIPVTIP[p.S396L]LVGVVNPILASPPTLGLLEPKKEKEE	VTIPLVGVV,PLVGVVNPI,PPIPVTIPL,RPPIPVTIPL,IPLVGVVNPI,PPIPVTIPLV,IPVTIPLVGV	BLCA
PVRL4	c.1072G>A	p.A358T	LDPQEDSGKQVDLVSASVVVVGVIA[p.A358T]TLLFCLLVVVVVLMSRYHRRKAQQMT	VIATLLFCL,ATLLFCLLV,TLLFCLLVV,VVVGVIATL,VGVIATLLF,GVIATLLFCL,VIATLLFCLL,ATLLFCLLVV,TLLFCLLVVV,VVVGVIATLL,VVGVIATLLF	UCEC
PWWP2B	c.251delC	p.S84fs	PVNDSHGRAPEEGDAEVMQLGSSSP[p.S84fs]LLPAGFSPPRPPAPSHPRPSCRRCPPEACPRTLPTSKAPPSLTRCGSGTRTSCGCPSRRPGPSSARGGVCPATATRGASSSAPSACGRARCSVRSARAR*	MQLGSSSPL,QLGSSSPLL,RTSCGCPSR,GVCPATATR,SSAPSACGR,GFSPPRPPA,LTRCGSGTR,SARGGVCPA,ATRGASSSA,CGRARCSVR,RARCSVRSA,TSCGCPSRR,APSHPRPSC,HPRPSCRRC,RPSCRRCPP,GPSSARGGV,CPATATRGA,LPAGFSPPR,VMQLGSSSPL,MQLGSSSPLL,TSKAPPSLTR,RTSCGCPSRR,SSSAPSACGR,AGFSPPRPPA,RTLPTSKAPP,GTRTSCGCPS,PSRRPGPSSA,RGASSSAPSA,RARCSVRSAR,SSSPLLPAGF,LLPAGFSPPR,RPSCRRCPPE,CPRTLPTSKA,LPTSKAPPSL,CPATATRGAS	STAD
PXDNL	c.3935C>T	p.T1312M	IPKVDLRVWQDCCADCRSRGQFRAV[p.T1312M]MQESQKKRSAQYSYPVDKDMELSHLR	RAVMQESQK,AVMQESQKK,SRGQFRAVM,RSRGQFRAVM,RAVMQESQKK,GQFRAVMQES	CRC
PXDNL	c.4366C>A	p.P1456T	CPPAPCPSPELVKGTCCPVCRDRGM[p.P1456T]TSDSPEKR*	GMTSDSPEK,MTSDSPEKR,RGMTSDSPEK	LUAD

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PYGO2	c.448delC	p.Q150fs	GPQPLRRQPPPFPPNPMGPAFNMPP[p.Q150fs]RVLATHPQAT*	NMPPRVLAT,VLATHPQAT,RVLATHPQA,MPPRVLATH,AFNMPPRVLA,RVLATHPQAT,MGPAFNMPPR,GPAFNMPPRV	STAD
PYHIN1	c.443G>C	p.G148A	NRLTAKGAEETLGPQKRKKPSEEET[p.G148A]ATKRSKMSKEQTRPSCSAGASTSTAM	ATKRSKMSK,TATKRSKMSK	LUSC
QRSL1	c.677C>T	p.S226L	AHCGLVGFKPSYGLVSRHGLIPLVN[p.S226L]LMDVPGILTRCVDDAAIVLGALAGPD	GLIPLVNLM,NLMDVPGIL,IPLVNLMDV,NLMDVPGILT,LVNLMDVPGI	CRC
QSOX1	c.1202G>T	p.R401L	DDRKEGAVLAKKVNWIGCQGSEPHF[p.R401L]LGFPCSLWVLFHFLTVQAARQNVDHS	HFLGFPCSL,CQGSEPHFL,GSEPHFLGF,EPHFLGFPC,FLGFPCSLWV,HFLGFPCSLW,QGSEPHFLGF,LGFPCSLWVL,SEPHFLGFPC	LUAD
QSOX2	c.2048G>T	p.R683L	SLDMSLCVVLYVASSLFLMVMYFFF[p.R683L]LVRSRRWKVKHHHPAV*	LMVMYFFFL,MVMYFFFLV,VMYFFFLVR,FLVRSRRWK,FFLVRSRRW,LVRSRRWKV,YFFFLVRSR,FFFLVRSRR,FLMVMYFFFL,LMVMYFFFLV,FLVRSRRWKV,MVMYFFFLVR,FFFLVRSRRW,MYFFFLVRSR,FFLVRSRRWK,LVRSRRWKVK,YFFFLVRSRR	LUAD
R3HDM2	c.1763G>A	p.S588N	MPNQQQAAYQGMIGVQQPQNQGLLS[p.S588N]NQRSSMGGQMQGLVVQYTPLPSYQVP	LLSNQRSSM,NQRSSMGGQM,GLLSNQRSSM	CLL
R3HDM2	c.1774A>G	p.S592G	QQAAYQGMIGVQQPQNQGLLSSQRS[p.S592G]GMGGQMQGLVVQYTPLPSYQVPVGSD	GMGGQMQGL,LLSSQRSGM,QRSGMGGQM,GMGGQMQGLV,SQRSGMGGQM,GLLSSQRSGM	CLL
R3HDM2	c.616C>T	p.R206W	EFINDNNNQFKKFPQMTSYHRMLLH[p.R206W]WVAAYFGMDHNVDQTGKAVIINKTSN	RMLLHWVAA,MLLHWVAAY,SYHRMLLHW,HWVAAYFGM,LLHWVAAYF,HRMLLHWVA,MLLHWVAAYF,RMLLHWVAAY,SYHRMLLHWV,YHRMLLHWVA,TSYHRMLLHW,HRMLLHWVAA,LHWVAAYFGM	CLL
RAB11FIP4	c.1787C>T	p.S596L	SLYEAKNLFAAQTKAQSLAAEIDTA[p.S596L]LRDELMEALKEQEEINFRLRQYMDKI	ALRDELMEA,LAAEIDTAL,SLAAEIDTAL,ALRDELMEAL,LAAEIDTALR	BLCA
RAB11FIP5	c.509G>A	p.R170H	WYKLHSKPGKKEKERGEIEVTIQFT[p.R170H]HNNLSASMFDLSMKDKPRSPFSKIRD	IEVTIQFTH,IQFTHNNLS,THNNLSASM,HNNLSASMF,IQFTHNNLSA,FTHNNLSASM,VTIQFTHNNL,THNNLSASMF	GBM
RAB13	c.500G>T	p.R167L	EHGIRFFETSAKSSMNVDEAFSSLA[p.R167L]LDILLKSGGRRSGNGNKPPSTDLKTC	SLALDILLK,DEAFSSLAL,FSSLALDIL,SSLALDILLK,EAFSSLALDI,VDEAFSSLAL	LUAD
RAB7L1	c.235C>T	p.R79W	YEIVRLQLWDIAGQERFTSMTRLYY[p.R79W]WDASACVIMFDVTNATTFSNSQRWKQ	RLYYWDASA,TSMTRLYYW,YYWDASACV,MTRLYYWDA,WDASACVIM,SMTRLYYWDA,RLYYWDASAC,FTSMTRLYYW,LYYWDASACV,YYWDASACVI,MTRLYYWDAS,YWDASACVIM,WDASACVIMF	CRC
RAB8A	c.58G>T	p.G20W	MAKTYDYLFKLLLIGDSGV[p.G20W]WKTCVLFRFSEDAFNSTFISTIGIDF	LIGDSGVWK,GVWKTCVLF,VWKTCVLFR,LLIGDSGVW,WKTCVLFRF,GVWKTCVLFR,SGVWKTCVLF,VWKTCVLFRF,LLLIGDSGVW	LUAD
RABGAP1	c.2782_2783insA	p.K928fs	LEEESAQLKEMCRRELDKAESEIKK[p.K928fs]KQFYHW*	SEIKKKQFY,IKKKQFYHW,AESEIKKKQF	STAD
RABGAP1	c.2782delA	p.K928fs	LEEESAQLKEMCRRELDKAESEIKK[p.K928fs]TVLSLVTISRFVLS*	SLVTISRFV,KTVLSLVTI,VLSLVTISR,EIKKTVLSL,LSLVTISRF,KKTVLSLVT,AESEIKKTV,SLVTISRFVL,TVLSLVTISR,EIKKTVLSLV,VLSLVTISRF,AESEIKKTVL,SEIKKTVLSL,KKTVLSLVTI	STAD
RABGEF1	c.619A>G	p.N207D	PASADDFLPTLIYIVLKGNPPRLQS[p.N207D]DIQYITRFCNPSRLMTGEDGYYFTNL	RLQSDIQYI,LQSDIQYIT,SDIQYITRF,QSDIQYITRF	TGCT
RAC1	c.101C>G	p.P34R	VGDGAVGKTCLLISYTTNAFPGEYI[p.P34R]RTVFDNYSANVMVDGKPVNLGLWDTA	RTVFDNYSA,YIRTVFDNY,NAFPGEYIR,FPGEYIRTV,FPGEYIRTVF	TGCT
RAC1	c.476C>T	p.A159V	LTPITYPQGLAMAKEIGAVKYLECS[p.A159V]VLTQRGLKTVFDEAIRAVLCPPPVKK	AVKYLECSV,SVLTQRGLK,KYLECSVLT,VKYLECSVL,VLTQRGLKTV,CSVLTQRGLK,AVKYLECSVL	HNSC
RAC1	c.85C>T	p.P29S	IKCVVVGDGAVGKTCLLISYTTNAF[p.P29S]SGEYIPTVFDNYSANVMVDGKPVNLG	TTNAFSGEY,FSGEYIPTV,SGEYIPTVF,YTTNAFSGEY,TTNAFSGEYI,FSGEYIPTVF	SKCM

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
RAD50	c.205G>T	p.D69Y	THECLKYICTGDFPPGTKGNTFVH[p.D69Y]YPKVAQETDVRAQIRLQFRDVNGELI	GNTFVHYPK,NTFVHYPKV,TKGNTFVHY,KGNTFVHYPK,GTKGNTFVHY,NTFVHYPKVA,YPKVAQETDV	LUAD
RAD51AP2	c.946delA	p.T316fs	RDFTNIYWSQNRPDVKKQKLQNDKK[p.T316fs]L*	KQKLQNDKKL	STAD
RAD51C	c.499G>A	p.D167N	VQIPECFGGVAGEAVFIDTEGSFMV[p.D167N]NRVVDLATACIQHLQLIAEKHKGEEH	FMVNRVVDL,MVNRVVDLA,EGSFMVNRV,FMVNRVVDLA,SFMVNRVVDL,DTEGSFMVNR,TEGSFMVNRV	BLCA
RAD51C	c.670T>C	p.Y224H	FTLDNILSHIYYFRCRDYTELLAQV[p.Y224H]HLLPDFLSEHSKVRLVIVDGIAFPFR	ELLAQVHLL,AQVHLLPDF,TELLAQVHL,AQVHLLPDFL,LAQVHLLPDF,HLLPDFLSEH,TELLAQVHLL	BLCA
RAF1	c.770C>T	p.S257L	YSTPHAFTFNTSSPSSEGSLSQRQR[p.S257L]LTSTPNVHMVSTTLPVDSRMIEDAIR	RQRLTSTPN,LTSTPNVHM,SQRQRLTST,RLTSTPNVH,LTSTPNVHMV,RQRLTSTPNV,RLTSTPNVHM,SQRQRLTSTP	CRC
RALGAPA1	c.1192C>T	p.R398C	LTEREPSSSSLCSIDEEHLTDIEIV[p.R398C]CRVFSSKRSNVNFVTEIFRQAFLLPI	IVCRVFSSK,LTDIEIVCRV,EIVCRVFSSK,IVCRVFSSKR,HLTDIEIVCR,TDIEIVCRVF,IEIVCRVFSS	CRC
RALGAPB	c.1136delC	p.T379fs	RSDSAPPTPVNRLSMPQSAAVSTTP[p.T379fs]HITGGTGLLL*	TTPHITGGT,SAAVSTTPH,AAVSTTPHI,TPHITGGTGL,SAAVSTTPHI	STAD
RALGPS1	c.1142G>A	p.R381Q	SKSATFPSEKARHLLDDSVLESRSP[p.R381Q]QRGLALTSSSAVTNGLSLGSSESSEF	RSPQRGLAL,SVLESRSPQR,LESRSPQRGL,SRSPQRGLAL	BLCA
RANBP17	c.2700G>T	p.M900I	HSDLLQYRKLSQSYYPLLECLTQDH[p.M900I]ISFIINLEPPVLMYVLTSISEGLTTL	LTQDHISFI,CLTQDHISF,TQDHISFII,CLTQDHISFI,LLECLTQDHI,LTQDHISFII,QDHISFIINL	TGCT
RANBP2	c.3691C>T	p.R1231C	VESKEWKERGIGNVKILRHKTSGKI[p.R1231C]CLLMRREQVLKICANHYISPDMKLTP	KTSGKICLL,CLLMRREQV,SGKICLLMR,HKTSGKICL,TSGKICLLMR,KTSGKICLLM,SGKICLLMRR,CLLMRREQVL,RHKTSGKICL,HKTSGKICLL	CRC
RANBP3	c.1157T>G	p.L386W	EATPEKESLAESAAAYTKATARKCL[p.L386W]WEKVEVITGEEAESNVLQMQCKLFVF	CLWEKVEVI,TARKCLWEK,KATARKCLW,ATARKCLWEK	KIRC
RANBP6	c.2743C>T	p.R915W	QWGLCIFDDIIEHCSPTSFKYVEYF[p.R915W]WWPMLLNMRDNNPEVRQAAAYGLGVM	YVEYFWWPM,SFKYVEYFW,KYVEYFWWP,EYFWWPMLL,FWWPMLLNM,FKYVEYFWW,VEYFWWPML,YVEYFWWPML,SFKYVEYFWW,KYVEYFWWPM,VEYFWWPMLL,YFWWPMLLNM,FWWPMLLNMR,TSFKYVEYFW	CESC
RANBP6	c.2950A>C	p.I984L	LVKVIKCANSKTKKNVIATENCISA[p.I984L]LGKILKFKPNCVNVDEVLPHWLSWLP	ISALGKILK,ALGKILKFK,SALGKILKF,TENCISALG,CISALGKILK,SALGKILKFK,IATENCISAL,ISALGKILKF	LUSC
RAPGEFL1	c.1067G>T	p.R356L	LPGKFKNLFRKFENLTDPCRNHKSY[p.R356L]LEVISKMKPPVIPFVPLILKDLTFLH	KSYLEVISK,SYLEVISKM,RNHKSYLEV,KSYLEVISKM,SYLEVISKMK,RNHKSYLEVI	LUAD
RARS2	c.16C>T	p.R6C	MACGF[p.R6C]CRAIACQLSRVLNLPPENLITSISAV	MACGFCRAI	BLCA
RASAL3	c.245G>A	p.R82H	VSTQPAPRSIFRRVLSAPPKESRTS[p.R82H]HLRLSKALWGRHKNPPPEPDPEPEQE	RTSHLRLSK,TSHLRLSKA,SHLRLSKAL,HLRLSKALW,RTSHLRLSKA,HLRLSKALWG,KESRTSHLRL,SHLRLSKALW	GBM
RASGEF1C	c.562G>A	p.A188T	LAALRQGPEGLVGADKPISYRTKPP[p.A188T]TSIHRELLGVCSDPYTLAQQLTHVEL	SYRTKPPTS,RTKPPTSIH,YRTKPPTSI,SYRTKPPTSI,RTKPPTSIHR,TSIHRELLGV,KPPTSIHREL	KIRC
RASIP1	c.1801C>T	p.R601C	ATLLALCVQHSARELELGHLPRLLG[p.R601C]CLARLIKEAVWEKIKEIGDRQPENHP	RLLGCLARL,HLPRLLGCL,LLGCLARLI,CLARLIKEA,LPRLLGCLA,RLLGCLARLI,CLARLIKEAV,HLPRLLGCLA,LLGCLARLIK	ACC
RB1	c.948_951delTCTT	p.N316fs	FKNFIPFMNSLGLVTSNGLPEVENL[p.N316fs]NDTKKFILKIKI*	KKFILKIKI,DTKKFILKIK,VENLNDTKKF	GBM
RBBP4	c.988G>A	p.E330K	NLKLKLHSFESHKDEIFQVQWSPHN[p.E330K]KTILASSGTDRRLNVWDLSKIGEEQS	QVQWSPHNK,SPHNKTILA,VQWSPHNKT,FQVQWSPHNK,SPHNKTILAS,VQWSPHNKTI	LAML
RBBP7	c.820G>A	p.E274K	QKLMIWDTRSNTTSKPSHLVDAHTA[p.E274K]KVNCLSFNPYSEFILATGSADKTVAL	LVDAHTAKV,HLVDAHTAK,HTAKVNCLS,TAKVNCLSF,HLVDAHTAKV,KVNCLSFNPY,HTAKVNCLSF	CRC
RBBP7	c.937G>A	p.E313K	LATGSADKTVALWDLRNLKLKLHTF[p.E313K]KSHKDEIFQVHWSPHNETILASSGTD	KLHTFKSHK,KLKLHTFKS,LKLHTFKSH,FKSHKDEIF,NLKLKLHTFK,KLKLHTFKSH,KSHKDEIFQV,HTFKSHKDEI	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
RBFOX2	c.1018G>A	p.A340T	NTYIPLISLPLVPGFPYPTAATTAA[p.A340T]TFRGAHLRGRGRTVYGAVRAVPPTAI	ATFRGAHLR,AATTAATFR,TTAATFRGA,TAATTAATF,TAATTAATFR,TFRGAHLRGR,AATFRGAHLR,YPTAATTAAT,PTAATTAATF	CRC
RBL2	c.379G>A	p.E127K	VSKGTVEGNYVSLTRILKCSEQSLI[p.E127K]KFFNKMKKWEDMANLPPHFRERTERL	SLIKFFNKM,QSLIKFFNK,LIKFFNKMK,KFFNKMKKW,CSEQSLIKF,SEQSLIKFF,SLIKFFNKMK,LIKFFNKMKK,EQSLIKFFNK,KCSEQSLIKF,IKFFNKMKKW	UCEC
RBM14	c.856_876delGCTGCTGCTGCAGCAGCAGCC	p.AAAAAAAAA286del	LTSTSLDPYDRHLLPTSGAAATAAA[p.AAAAAAAA286del]VTAASTSYYGRDRSPLRRATAPVPTVGEGYGYGHESELSQASAAAR	GAAATAAAV,ATAAAVTAA,TAAAVTAAS,SGAAATAAAV,TAAAVTAAST	PAAD
RBM19	c.1168G>T	p.G390W	FREKNVPTTKGAPKNTTKSWQGRIL[p.G390W]WENEEEEDLAESGRLFVRNLPYTSTE	KSWQGRILW,WENEEEEDL,TKSWQGRILW	LUAD
RBM26	c.1930C>G	p.P644A	TTSPKPLVQQPILPVVKQSVKERLG[p.P644A]AVPSSTIEPAEAQSASSDLPQNVTKL	SVKERLGAV,KERLGAVPS,LGAVPSSTI,RLGAVPSSTI,KERLGAVPSS	BLCA
RBM39	c.1058C>T	p.T353I	ERTDASSASSFLDSDELERTGIDLG[p.T353I]ITGRLQLMARLAEGTGLQIPPAAQQA	LGITGRLQL,ITGRLQLMAR,LERTGIDLGI,LGITGRLQLM	UCEC
RBM47	c.1485_1505delGGCCGCAGCCGCCGCAGCCGC	p.495_502AAAAAAAA>A	HTVEHMISPIAVQPDPASAAAAAAA[p.495_502AAAAAAAA>A]VIPTVSTPPPFQGRPITPVYTVAPNVQRIPTAGIYGASYVPFAAPA	ASAAAAAAAV,SAAAAAAAVI	PAAD
RBM6	c.2024T>G	p.V675G	RQDGESKTIMLKRIYRSTPPEVIVE[p.V675G]GLEPYVRLTTANVRIIKNRTGPMGHT	VIVEGLEPY,VIVEGLEPYV,EVIVEGLEPY	MM
RBM6	c.287_288insG	p.R96fs	SYGARDGPHGDYRGGEGPGHDFRGG[p.R96fs]RFFVF*	FRGGRFFVF,HDFRGGRFF,DFRGGRFFVF,HDFRGGRFFV	STAD
RCL1	c.335C>A	p.P112Q	HDCSVLRGIGYYLESLLCLAPFMKH[p.P112Q]QLKIVLRGVTNDQVDPSVDVLKATAL	FMKHQLKIV,QLKIVLRGV,PFMKHQLKI,APFMKHQLK,MKHQLKIVL,CLAPFMKHQL,HQLKIVLRGV,FMKHQLKIVL,LAPFMKHQLK,APFMKHQLKI	LUAD
RDH8	c.593C>T	p.A198V	LLQFNIFISLVEPGPVVTEFEGKLL[p.A198V]VQVSMAEFPGTDPETLHYFRDLYLPA	KLLVQVSMA,LVQVSMAEF,TEFEGKLLV,GKLLVQVSM,FEGKLLVQV,VTEFEGKLLV,LLVQVSMAEF,VQVSMAEFPG,TEFEGKLLVQ,FEGKLLVQVS	GBM
REG1B	c.170G>T	p.W57L	PRISCPEGTNAYRSYCYYFNEDPET[p.W57L]LVDADLYCQNMNSGNLVSVLTQAEGA	ETLVDADLY,YFNEDPETL,YYFNEDPETL	LUAD
REG1B	c.201G>T	p.M67I	AYRSYCYYFNEDPETWVDADLYCQN[p.M67I]INSGNLVSVLTQAEGAFVASLIKESS	CQNINSGNL,NINSGNLVSV,CQNINSGNLV,INSGNLVSVL	LUSC
REG3A	c.449C>T	p.S150L	SDVMNYFAWERNPSTISSPGHCASL[p.S150L]LRSTAFLRWKDYNCNVRLPYVCKFTD	SLLRSTAFL,LLRSTAFLR,SPGHCASLL,ASLLRSTAF,LRSTAFLRW,SLLRSTAFLR,ASLLRSTAFL,CASLLRSTAF,LLRSTAFLRW	LUAD
REG4	c.329G>T	p.G110V	GYQRSQPIWIGLHDPQKRQQWQWID[p.G110V]VAMYLYRSWSGKSMGGNKHCAEMSSN	WIDVAMYLY,QWIDVAMYL,WQWIDVAMY,RQQWQWIDV,QQWQWIDVA,QWQWIDVAM,VAMYLYRSW,WQWIDVAMYL,WIDVAMYLYR,QWQWIDVAMY,QWIDVAMYLY,QQWQWIDVAM,RQQWQWIDVA	LUAD
REN	c.45_47delGCT	p.15_16LL>L	MDGWRRMPRWGLLLL[p.15_16LL>L]WGSCTFGLPTDTTTFKRIFLKRMPSIRE	MPRWGLLLLW	GBM
RERE	c.528G>C	p.K176N	PACSLPVASQPPQHLSEAGRGPVGS[p.K176N]NRDHLLMNVKWYYRQSEVPDSVYQHL	GSNRDHLLM,AGRGPVGSNR,GPVGSNRDHL	BLCA
REV3L	c.88G>T	p.A30S	RIVTADYYMASPLQGLDTCQSPLTQ[p.A30S]SPVKKVPVVRVFGATPAGQKTCLHLH	SPVKKVPVV,CQSPLTQSP,CQSPLTQSPV,TQSPVKKVPV	TGCT
RFC3	c.245T>A	p.I82N	RELYGVGVEKLRIEHQTITTPSKKK[p.I82N]NEISTIASNYHLEVNPSDAGNSDRVV	TPSKKKNEI,KKKNEISTI,KKNEISTIA,NEISTIASNY,SKKKNEISTI	TGCT
RFC3	c.888G>T	p.K296N	LLEVRGRLYELLTHCIPPEIIMKAC[p.K296N]NEESRSCDIF*	IMKACNEESR,NEESRSCDIF	TGCT

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RGMB	c.187A>C	p.S63R	AWTGMGLRAAPSSAAAAAAEVEQRR[p.S63R]RPGLCPPPLELLLLLLFSLGLLHAGD	RPGLCPPPL,VEQRRRPGL,RRPGLCPPPL	ACC
RGS6	c.1097G>T	p.W366L	LKDQVGRDQFLRFLESEFSSENLRF[p.W366L]LLAVQDLKKQPLQDVAKRVEEIWQEF	FLLAVQDLK,LLAVQDLKK,RFLLAVQDL,FSSENLRFL,SENLRFLLA,FLLAVQDLKK,RFLLAVQDLK,FSSENLRFLL,SENLRFLLAV,LRFLLAVQDL	LUSC
RGS7	c.130C>T	p.R44C	PNMLVYRKMEDVIARMQDEKNGIPI[p.R44C]CTVKSFLSKIPSVFSGSDIVQWLIKN	CTVKSFLSK,IPICTVKSF,KNGIPICTVK,CTVKSFLSKI,IPICTVKSFL	SKCM
RGS9BP	c.286G>T	p.A96S	ERAEFERLWVAFSGCLDLLEADMRR[p.A96S]SLELGAAFPLHAPRRPLVRTGVAGAS	RSLELGAAF,LEADMRRSL,ADMRRSLEL,SLELGAAFPL,RRSLELGAAF	ACC
RGSL1	c.664G>A	p.V222I	HTKMTMAKEEACHGLMQEYETRLYS[p.V222I]ICYTHIGGLPLNMSIKKCHHFQKRYS	RLYSICYTH,EYETRLYSI,LYSICYTHI,ETRLYSICY,YETRLYSIC,RLYSICYTHI,SICYTHIGGL,QEYETRLYSI,YETRLYSICY	BRCA
RHBDD3	c.101_102insG	p.G34fs	SPALPLASSVLMLLMSTLWLVGAGP[p.G34fs]RPGPGPGAVAGPLAGAPAADPCPGPHGPARPAPEPAAPAHCGLAAGVPPGHAEIPACLSPARPGFWAAGSAAGRPWAVQCSRQLWIHACPPGHAGWGGTPP*	AVAGPLAGA,GLAAGVPPG,EIPACLSPA,SAAGRPWAV,CSRQLWIHA,WAAGSAAGR,RPWAVQCSR,GPRPGPGPG,RPGPGPGAV,GPGAVAGPL,GPLAGAPAA,GPHGPARPA,APAHCGLAA,SPARPGFWA,CLSPARPGF,AEIPACLSP,GFWAAGSAA,AGSAAGRPW,WAVQCSRQL,VQCSRQLWI,RQLWIHACP,WIHACPPGHA,TLWLVGAGPR,EIPACLSPAR,FWAAGSAAGR,EPAAPAHCGL,GPRPGPGPGA,RPGPGPGAVA,GPARPAPEPA,RPAPEPAAPA,SPARPGFWAA,RPGFWAAGSA,AEIPACLSPA,ACLSPARPGF,AAGSAAGRPW,WAVQCSRQLW,RQLWIHACPP,HACPPGHAGW	KICH
RHEB	c.103T>A	p.Y35N	AILGYRSVGKSSLTIQFVEGQFVDS[p.Y35N]NDPTIENTFTKLITVNGQEYHLQLVD	FVDSNDPTI,GQFVDSNDPT,SNDPTIENTF	KIRC
RHOA	c.118G>C	p.E40Q	ACGKTCLLIVFSKDQFPEVYVPTVF[p.E40Q]QNYVADIEVDGKQVELALWDTAGQED	VFQNYVADI,YVPTVFQNY,VPTVFQNYV,YVPTVFQNYV,FQNYVADIEV,VYVPTVFQNY,TVFQNYVADI,VPTVFQNYVA	HNSC
RHOA	c.125A>G	p.Y42C	GKTCLLIVFSKDQFPEVYVPTVFEN[p.Y42C]CVADIEVDGKQVELALWDTAGQEDYD	VPTVFENCV,YVPTVFENCV,TVFENCVADI,CVADIEVDGK,VYVPTVFENC,FENCVADIEV	STAD
RHOBTB1	c.1391C>T	p.T464M	VLEMFDLRMMVENIMNKEAFMNQEI[p.T464M]MKAFHVRKANRIKECLSKGTFSDVTF	FMNQEIMKA,IMKAFHVRK,AFMNQEIMK,EIMKAFHVR,MNQEIMKAF,MKAFHVRKA,EAFMNQEIM,QEIMKAFHV,FMNQEIMKAF,IMKAFHVRKA,EAFMNQEIMK,EIMKAFHVRK,KEAFMNQEIM	CRC
RHPN2	c.217G>A	p.V73M	LKAVRMRTGAENLLKVATNSKVREQ[p.V73M]MRLELSFVNSDLQMLKEELEGLNISV	QMRLELSFV,KVREQMRLE,NSKVREQMR,EQMRLELSF,SKVREQMRL,VREQMRLEL,REQMRLELS,EQMRLELSFV,KVREQMRLEL,REQMRLELSF	TGCT
RILPL1	c.1074C>A	p.S358R	RIPQPPPIAHPRTSPQPESGIKRLF[p.S358R]RFFSRDKKRLANTQRNVHIQESFGQW	SGIKRLFRF,GIKRLFRFF,KRLFRFFSR,LFRFFSRDK,ESGIKRLFR,RFFSRDKKR,RLFRFFSRDK,SGIKRLFRFF,GIKRLFRFFS,IKRLFRFFSR,LFRFFSRDKK	KICH
RIMBP2	c.2489G>A	p.R830H	FPRGSAGPQRSRPVTVPSIDDYGRD[p.R830H]HLSPDFYEESETDPGAEELPARIFVA	RDHLSPDFY,YGRDHLSPDF	GBM
RIMBP3	c.1187_1189delCGG	p.A396del	HELIKLNWLLAKALWVLARRCYTLQ[p.A396del]ENKQLRRAGCPYQADEKVKRLKVKRAEL	RCYTLQENK,TLQENKQLR,QENKQLRRA,YTLQENKQLR	KIRC
RIMBP3	c.3461A>G	p.Q1154R	YADGLKVCEVADATAGSTLLEFSQL[p.Q1154R]RVPLTWQKVSVRTMSLCGESLDSVPA	LLEFSQLRV,TLLEFSQLR,SQLRVPLTW,LEFSQLRVP,TLLEFSQLRV,QLRVPLTWQK,STLLEFSQLR,FSQLRVPLTW,LEFSQLRVPL	TGCT
RIMS2	c.1203delA	p.V401fs	LGLKVVGGKMTESGRLCAFITKVKK[p.V401fs]EV*	FITKVKKEV	STAD
RIMS2	c.164G>T	p.R55L	EREEYSQYATSDTAMPRSPSDYADR[p.R55L]LSQHEPQFYEDSDHLSYRDSNRRSHR	LSQHEPQFY,SPSDYADRL,RLSQHEPQF,RLSQHEPQFY	LUAD
RIMS2	c.1796G>A	p.R599Q	KRRTKTVKKTLEPKWNQTFIYSPVH[p.R599Q]QREFRERMLEITLWDQARVREEESEF	FIYSPVHQR,HQREFRERM,IYSPVHQREF,TFIYSPVHQR,YSPVHQREFR,HQREFRERML	CRC

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RIN3	c.1345C>G	p.L449V	DTPRESTEQGQDTEVKASDPHSMPE[p.L449V]VPRTAKQPPVPPPRKKRISRQLASTL	SMPEVPRTA,SMPEVPRTAK,HSMPEVPRTA,VPRTAKQPPV	KIRC
RIN3	c.2123C>T	p.S708L	LYKCVLKPLKEAINSCLHQIHSKDG[p.S708L]LLQQLKENQLVILATTTTDLGVTTSV	HQIHSKDGL,SKDGLLQQL,HQIHSKDGLL	CRC
RING1	c.511delG	p.G171fs	QAMHRAQRVRRPIPGSDQTTTMSGG[p.G171fs]KESPGREKGMEKM*	QTTTMSGGK,GGKESPGREK,KESPGREKGM	STAD
RINL	c.1205C>T	p.P402L	RRRQTALRAGAGPPGAQGPGPEGQS[p.P402L]LAPALRSRIHERLAHLHAACAPRRKV	SLAPALRSR,GPGPEGQSL,PEGQSLAPA,SLAPALRSRI,EGQSLAPALR,PEGQSLAPAL	ACC
RINT1	c.321delA	p.L107fs	SKMQLEEQVLTISSEIPKRIRSALK[p.L107fs]MQKNQSNFLISFWSRKLISSAPLTAIC*	MQKNQSNFL,KLISSAPLT,FLISFWSRK,KMQKNQSNF,RIRSALKMQ,ISFWSRKLI,WSRKLISSA,NFLISFWSR,NQSNFLISF,KRIRSALKM,QKNQSNFLI,RKLISSAPL,ISSAPLTAI,KMQKNQSNFL,FLISFWSRKL,KLISSAPLTA,LISSAPLTAI,MQKNQSNFLI,RIRSALKMQK,SNFLISFWSR,KNQSNFLISF,NFLISFWSRK,SRKLISSAPL,LKMQKNQSNF,NQSNFLISFW	STAD
RIT1	c.270G>T	p.M90I	DDEPANLDILDTAGQAEFTAMRDQY[p.M90I]IRAGEGFIICYSITDRRSFHEVREFK	FTAMRDQYI,AMRDQYIRA,YIRAGEGFI,QYIRAGEGF,TAMRDQYIR,IRAGEGFII,YIRAGEGFII,QYIRAGEGFI,AMRDQYIRAG,FTAMRDQYIR,DQYIRAGEGF	LUAD
RIT2	c.254G>T	p.R85L	QVRIDNEPAYLDILDTAGQAEFTAM[p.R85L]LEQYMRGGEGFIICYSVTDRQSFQEA	GQAEFTAML,TAMLEQYMR,FTAMLEQYM,AEFTAMLEQ,FTAMLEQYMR,AEFTAMLEQY	LUAD
RLBP1	c.215C>T	p.A72V	KAKDELNEREETREEAVRELQEMVQ[p.A72V]VQAASGEELAVAVAERVQEKDSGFFL	RELQEMVQV,QEMVQVQAA,VQAASGEEL,LQEMVQVQAA,VQAASGEELA,QEMVQVQAAS	CRC
RLBP1	c.841G>A	p.D281N	PFLKSKLLERVFVHGDDLSGFYQEI[p.D281N]NENILPSDFGGTLPKYDGKAVAEQLF	FYQEINENI,YQEINENIL,NENILPSDF,GFYQEINENI,FYQEINENIL,QEINENILPS	CRC
RLIM	c.1502C>T	p.S501L	SPSSSSGGESSETSSDLFEGSNEGS[p.S501L]LSSGSSGARREGRHRAPVTFDESGSL	SLSSGSSGA,FEGSNEGSL	KIRC
RLN2	c.412A>T	p.S138C	QQHVPVLKDSSLLFEEFKKLIRNRQ[p.S138C]CEAADSSPSELKYLGLDTHSRKKRQL	LIRNRQCEA,RQCEAADSS,CEAADSSPS,KLIRNRQCEA,LIRNRQCEAA,RQCEAADSSP	LUAD
RNASET2	c.380C>T	p.A127V	HSFPNRSRFWKHEWEKHGTCAAQVD[p.A127V]VLNSQKKYFGRSLELYRELDLNSVLL	QVDVLNSQK,VLNSQKKYF,AQVDVLNSQK,QVDVLNSQKK	CRC
RNF111	c.2313delC	p.R771fs	HEVMQRMEVQRRRMMQHPTRAHERP[p.R771fs]HPIHIGCTQTMVMGIIFMCLRLCPHILDRLQRGLPGNWELKLE*	TMVMGIIFM,VMGIIFMCL,HIGCTQTMV,RLCPHILDR,QTMVMGIIF,RGLPGNWEL,RAHERPHPI,MGIIFMCLR,CTQTMVMGI,MVMGIIFMC,CLRLCPHIL,HERPHPIHI,IHIGCTQTM,IGCTQTMVM,FMCLRLCPH,LQRGLPGNW,LPGNWELKL,MVMGIIFMCL,FMCLRLCPHI,RLCPHILDRL,VMGIIFMCLR,RGLPGNWELK,RAHERPHPIH,QTMVMGIIFM,RPHPIHIGCT,HIGCTQTMVM,TQTMVMGIIF,RLQRGLPGNW	STAD
RNF113B	c.515C>T	p.A172V	YRGIHSYLRYLKPKDTSMGNSSSGM[p.A172V]VRKGPIRAPGHLRATVRWDYQPDICK	NSSSGMVRK,SMGNSSSGMV	CRC
RNF149	c.25A>G	p.S9G	MAWRRREA[p.S9G]GVGARGVLALALLALALCVPGARGRA	AWRRREAGV,MAWRRREAG,RRREAGVGAR,MAWRRREAGV,REAGVGARGV	ACC
RNF150	c.623C>T	p.S208L	LERNITVTMYITIGTRNLQKYVSRT[p.S208L]LVVFVSISFIVLMIISLAWLVFYYIQ	RTLVVFVSI,KYVSRTLVV,YVSRTLVVF,VSRTLVVFV,LQKYVSRTL,LVVFVSISF,QKYVSRTLV,YVSRTLVVFV,NLQKYVSRTL,LQKYVSRTLV,LVVFVSISFI,KYVSRTLVVF,RTLVVFVSIS,TLVVFVSISF,QKYVSRTLVV	CRC
RNF150	c.707G>A	p.R236Q	FVSISFIVLMIISLAWLVFYYIQRF[p.R236Q]QYANARDRNQRRLGDAAKKAISKLQI	FYYIQRFQY,YYIQRFQYA,IQRFQYANA,YIQRFQYANA,FYYIQRFQYA,YYIQRFQYAN,IQRFQYANAR,VFYYIQRFQY,FQYANARDRN	CRC
RNF152	c.283C>T	p.P95S	PDDPEVLAVIAIPHTSEHTPVFIKL[p.P95S]SSNGCYMLPLPISKERALLPGDMGCR	KLSSNGCYM,IKLSSNGCY,LSSNGCYML,KLSSNGCYML,FIKLSSNGCY,IKLSSNGCYM,SSNGCYMLPL	SKCM

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RNF17	c.1052C>G	p.S351C	KKYNNKKELSCYDTYPPLEKKKVDM[p.S351C]CVLTSEAPPPPLQPETNDVHLEAKNF	KKKVDMCVL	KIRC
RNF222	c.397G>A	p.A133T	PLAASSPAWRPPPGQARPPGSPGQS[p.A133T]TQLPLDLLPSLPRESQIFVISRHGMP	SPGQSTQLPL,GQSTQLPLDL,TQLPLDLLPS	ACC
RNF39	c.787G>T	p.G263C	HRRLLISADRRSVQLAPPGTPAPPD[p.G263C]CPKRFDQLPAVLGAQGFGAGRHCWEV	GTPAPPDCPK	ACC
RNF43	c.1976delG	p.G659fs	PSTSSLFNLQKSSLSARHPQRKRRG[p.G659fs]VPPSPPLALGPRMQLCTQLARFFPITPPVWHILGPQRHTP*	RMQLCTQLA,TQLARFFPI,RFFPITPPV,FFPITPPVW,ITPPVWHIL,RGVPPSPPL,MQLCTQLAR,HPQRKRRGV,VPPSPPLAL,RKRRGVPPS,LALGPRMQL,QLCTQLARF,FPITPPVWH,RMQLCTQLAR,MQLCTQLARF,CTQLARFFPI,RFFPITPPVW,RGVPPSPPLA,FPITPPVWHI,SPPLALGPRM,GPRMQLCTQL,RRGVPPSPPL,QLCTQLARFF,TQLARFFPIT,ARFFPITPPV	STAD
RNF43	c.348_349insC	p.P116fs	NASDDDNLEPGFISIVKLESPRRAP[p.P116fs]PPLPVTG*	SPRRAPPPL,RRAPPPLPV	STAD
RNF43	c.647C>T	p.S216L	PPAWPDYDVWILMTVVGTIFVIILA[p.S216L]LVLRIRCRPRHSRPDPLQQRTAWAIS	IILALVLRI,IFVIILALV,VIILALVLR,TIFVIILAL,FVIILALVL,TIFVIILALV,VIILALVLRI,IFVIILALVL,LVLRIRCRPR,FVIILALVLR,IILALVLRIR,LALVLRIRCR,GTIFVIILAL	CRC
RNMT	c.1174delA	p.K392fs	PEFLVYFPLLNEMAKKYNMKLVYKK[p.K392fs]HFWNSTKKRLRTMKIKCS*	VYKKHFWNS,KKHFWNSTK,KHFWNSTKK,STKKRLRTM,KKRLRTMKI,RLRTMKIKC,HFWNSTKKR,MKLVYKKHF,YKKHFWNST,STKKRLRTMK,KKHFWNSTKK,KKRLRTMKIK,RLRTMKIKCS,FWNSTKKRLR,NMKLVYKKHF,MKLVYKKHFW	STAD
RNPC3	c.347delA	p.E116fs	LVVEFAKEQDRVHSPCPTSGSEKKK[p.E116fs]GLMTLSKMIKKKKNLVI*	GLMTLSKMI,LMTLSKMIK,MTLSKMIKK,TLSKMIKKK,LSKMIKKKK,MIKKKKNLV,KGLMTLSKM,IKKKKNLVI,KMIKKKKNLV,GLMTLSKMIK,LMTLSKMIKK,MTLSKMIKKK,TLSKMIKKKK,KKKGLMTLSK,MIKKKKNLVI,SKMIKKKKNL,SEKKKGLMTL,KKGLMTLSKM	CESC
ROBO2	c.3052G>A	p.D1018N	SQITQATPYATTQILHSNSIHELAV[p.D1018N]NLPDPQWKSSIQQKTDLMGFGYSLPD	SIHELAVNL,HELAVNLPD,AVNLPDPQWK,NSIHELAVNL,LAVNLPDPQW,HELAVNLPDP	UCEC
ROBO2	c.3238_3239insC	p.P1080fs	KNKNSSKPQKNNGSTWANVPLPPPP[p.P1080fs]SPAPSWHGAGTLCSGTTRKWL*	TLCSGTTRK,GTLCSGTTR,SPAPSWHGA,APSWHGAGT,GTLCSGTTRK,VPLPPPPSPA,SPAPSWHGAG,APSWHGAGTL	STAD
ROBO2	c.3877delA	p.K1293fs	PTSPFSTDSNTSAALSQSQRPRPTK[p.K1293fs]NTREGGWTNNQHCLIEGKE*	WTNNQHCLI,REGGWTNNQH	STAD
ROCK1	c.1552A>T	p.T518S	HRINEYQRKAEQENEKRRNVENEVS[p.T518S]SLKDQLEDLKKVSQNSQLANEKLSQL	EVSSLKDQL,NVENEVSSLK,RNVENEVSSL,NEVSSLKDQL	PRAD
ROR2	c.2014G>A	p.D672N	KLLGNSLLPIRWMAPEAIMYGKFSI[p.D672N]NSDIWSYGVVLWEVFSYGLQPYCGYS	NSDIWSYGV,KFSINSDIW,SINSDIWSY,IMYGKFSIN,GKFSINSDI,FSINSDIWSY,NSDIWSYGVV,IMYGKFSINS,INSDIWSYGV,GKFSINSDIW	CRC
RORB	c.280G>T	p.G94W	NRNRCQHCRLQKCLALGMSRDAVKF[p.G94W]WRMSKKQRDSLYAEVQKHQQRLQEQR	AVKFWRMSK,MSRDAVKFW,AVKFWRMSKK,MSRDAVKFWR,DAVKFWRMSK,GMSRDAVKFW	LUAD
ROS1	c.734G>T	p.R245I	FPGGPILGYNLRLISKNQKLDAGTQ[p.R245I]ITSFQFYSTLPNTIYRFSIAAVNEVG	GTQITSFQF,TQITSFQFY,QKLDAGTQI,GTQITSFQFY,ITSFQFYSTL,NQKLDAGTQI,LDAGTQITSF,AGTQITSFQF	UCEC
RP1	c.5312C>T	p.S1771L	WLLKENHLLRMSSENPGMCGNADTT[p.S1771L]LVDTLLDNNSSEVPYSHFGNLAPGPT	DTTLVDTLL,GMCGNADTTL	LUSC
RPA1	c.92G>A	p.R31H	SEGAIAAIMQKGDTNIKPILQVINI[p.R31H]HPITTGNSPPRYRLLMSDGLNTLSSF	LQVINIHPI,ILQVINIHPI,LQVINIHPIT	HNSC
RPL10L	c.560A>C	p.K187T	RQKIHISKKWGFTKFNADEFEDMVA[p.K187T]TKCLIPDGCGVKYVPSHGPLDKWRVL	DEFEDMVAT,DEFEDMVATK,FEDMVATKCL	LUAD
RPL13AP20	c.319G>C	p.G107R	QTMRGMPPHKTKPGQAALDCLKVFD[p.G107R]RIPPPYDKKKRMVVPAALKVVRLKPA	VFDRIPPPY,RIPPPYDKK,KVFDRIPPP,KVFDRIPPPY,RIPPPYDKKK	UCS

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RPL19	c.451C>T	p.R151C	KVKGNVFKNKRILMEHIHKLKADKA[p.R151C]CKKLLADQAEARRSKTKEARKRREER	KLKADKACK,KLKADKACKK	TGCT
RPL22	c.44delA	p.K15fs	MAPVKKLVVKGGKK[p.K15fs]RSKF*	VVKGGKKRSK,VKGGKKRSKF	UCEC
RPL5	c.172_173delAG	p.R58fs	KRLVIQDKNKYNTPKYRMIVRVTNR[p.R58fs]YHLSDCLCPYRGGYDSLRSVCTRTAKIWCEGWPDKLCCSILYWPAAGPQASQ*	HLSDCLCPY,RSVCTRTAK,MIVRVTNRY,IVRVTNRYH,RVTNRYHLS,RTAKIWCEG,CLCPYRGGY,DSLRSVCTR,VRVTNRYHL,KLCCSILYW,CSILYWPAA,DKLCCSILY,WPAAGPQAS,WPDKLCCSI,SLRSVCTRTA,RMIVRVTNRY,KIWCEGWPDK,HLSDCLCPYR,IWCEGWPDKL,IVRVTNRYHL,RSVCTRTAKI,YHLSDCLCPY,CPYRGGYDSL,WPDKLCCSIL,RTAKIWCEGW	TGCT
RPL6	c.578T>G	p.F193C	LASGLLLVTGPLVLNRVPLRRTHQK[p.F193C]CVIATSTKIDISNVKIPKHLTDAYFK	CVIATSTKI,RTHQKCVIA,KCVIATSTK,HQKCVIATS,RTHQKCVIAT,HQKCVIATST	CRC
RPRD2	c.289C>A	p.R97S	PHRLNLFYLANDVIQNCKRKNAIIF[p.R97S]SESFADVLPEAAALVKDPSVSKSVER	AIIFSESFA,NAIIFSESF,FSESFADVL,IIFSESFADV,IFSESFADVL,NAIIFSESFA,KNAIIFSESF	LUAD
RPS2	c.598A>G	p.R200G	GKPHTVPCKVTGRCGSVLVRLIPAP[p.R200G]GGTGIVSAPVPKKLLMMAGIDDCYTS	RLIPAPGGT,LVRLIPAPG,IPAPGGTGI,LIPAPGGTGI,IPAPGGTGIV	CLL
RPS6KA5	c.496G>A	p.E166K	THLSQRERFTEHEVQIYVGEIVLAL[p.E166K]KHLHKLGIIYRDIKLENILLDSNGHV	VLALKHLHK,LALKHLHKL,LKHLHKLGI,VLALKHLHKL,ALKHLHKLGI,IVLALKHLHK,YVGEIVLALK,KHLHKLGIIY,GEIVLALKHL,LKHLHKLGII	CRC
RPS6KA6	c.1181C>A	p.S394Y	ATSIAEEYKITPITSANVLPIVQIN[p.S394Y]ENAAQFGEVYELKEDIGVGSYSVCKR	ENAAQFGEV,QINENAAQF,VQINENAAQ,VQINENAAQF,ENAAQFGEVY,NENAAQFGEV,LPIVQINENA	UCEC
RPS6KA6	c.327delA	p.K109fs	KKASLKVRDRVRTKMERDILVEVNH[p.K109fs]HLLSNCTMPFRLKGNCT*	ILVEVNHHL,LLSNCTMPF,LSNCTMPFR,HHLLSNCTM,ILVEVNHHLL,LLSNCTMPFR,SNCTMPFRLK,HLLSNCTMPF,NHHLLSNCTM	STAD
RPSA	c.331C>G	p.Q111E	AVLKFAAATGATPIAGRFTPGTFTN[p.Q111E]EIQAAFWEPRLLVVTDPRADHQPLTE	FTNEIQAAF,TPGTFTNEI,FTPGTFTNEI,TFTNEIQAAF,EIQAAFWEPR,NEIQAAFWEP,FTNEIQAAFW	GBM
RPTN	c.1090G>A	p.G364S	QSSHYGQMDRKGQCYHYDQTNRQGQ[p.G364S]SSHYSQPNRQGQSSHYGQPDTQDQSS	SSHYSQPNR,TNRQGQSSHY,GQSSHYSQPN	CLL
RPTN	c.1614G>A	p.M538I	QTDRQGQSFHYGQPDRQGQSSHYSQ[p.M538I]IDRQGQSSHYGQTDRQGQSSHYGQTD	GQSSHYSQI,SSHYSQIDR,SQIDRQGQSS,IDRQGQSSHY	TGCT
RPTN	c.886G>A	p.G296S	CGQSERLGQELGCGQTDRQGQSSHY[p.G296S]SQTDRQDQSYHYGQTDRQGQSSHYSQ	SQTDRQDQSY	PRAD
RRAD	c.833C>A	p.A278E	LRRDSKEANARRQAGTRRRESLGKK[p.A278E]EKRFLGRIVARNSRKMAFRAKSKSCH	KEKRFLGRI,KEKRFLGRIV	KIRC,TGCT
RREB1	c.2348G>T	p.G783V	CGEDLKHYRALRIHMRTHCGRGLGG[p.G783V]VHKGRKPFECKECSAAFAAKRNCIHH	GVHKGRKPF,CGRGLGGVHK	ACC
RRN3	c.25C>T	p.R9C	MAAPLLHT[p.R9C]CLPGDAAASSSAVKKLGASRTGISNM	MAAPLLHTC,LLHTCLPGDA,MAAPLLHTCL,HTCLPGDAAA	KIRP
RRN3	c.31C>T	p.P11S	MAAPLLHTRL[p.P11S]SGDAAASSSAVKKLGASRTGISNMRA	HTRLSGDAA,LLHTRLSGDA,HTRLSGDAAA	KIRP
RRP15	c.642G>T	p.L214F	KEAGSSMRKRAKLISTVSKKDFISV[p.L214F]FRGMDGSTNETASSRKKPKAKQTEVK	SKKDFISVF,VSKKDFISVF,KDFISVFRGM	LUSC
RRS1	c.135delC	p.N45fs	QRITVHKELELQFDLGNLLASDRNP[p.N45fs]RPGCGAPDPRRRPSYRPWRGTTRNCSSTSCGSCPRSAWKRR*	GSCPRSAWK,STSCGSCPR,RRRPSYRPW,SYRPWRGTT,LLASDRNPR,APDPRRRPS,CGSCPRSAW,SSTSCGSCPR,CGSCPRSAWK,GSCPRSAWKR,RRRPSYRPWR,SYRPWRGTTR,NLLASDRNPR,APDPRRRPSY,RPSYRPWRGT,RPWRGTTRNC	STAD
RSBN1	c.1714G>A	p.E572K	SPFKRRRSMNEIKNLQYLPRTSEPR[p.E572K]KVLFEDRTRAHADHVGQGFDWQSTAA	RTSEPRKVL,RTSEPRKVLF,LPRTSEPRKV	UCEC
RSF1	c.1158delA	p.K386fs	HEITEKSTEETEKLKNDQQAKIPLK[p.K386fs]NEKLN*	QAKIPLKNEK,AKIPLKNEKL	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
RSPO2	c.82C>T	p.R28C	FRLFSFALIILNCMDYSHCQGNRWR[p.R28C]CSKRASYVSNPICKGCLSCSKDNGCS	QGNRWRCSK,RWRCSKRAS,RCSKRASYV,WRCSKRASY,CQGNRWRCSK,RWRCSKRASY,QGNRWRCSKR	CRC
RTN1	c.308C>G	p.S103W	ASTGVAGVSSAMDHTFSTTSKDGEG[p.S103W]WCYTSLISDICYPPQEDSTYFTGILQ	EGWCYTSLI,GEGWCYTSL,TSKDGEGWCY,GEGWCYTSLI	LUAD
RTN2	c.938delC	p.P313fs	KTVPILELSPPLWTAIGWVQRGPTP[p.P313fs]LLLSSGFY*	VQRGPTPLL,PLLLSSGFY,WVQRGPTPL,TPLLLSSGF,VQRGPTPLLL,GWVQRGPTPL,TPLLLSSGFY	STAD
RUNX1	c.286_287insG	p.D96fs	LCSVLPTHWRCNKTLPIAFKVVALG[p.D96fs]GCSRWHSGHCDGWQ*	VVALGGCSR,VALGGCSRW,KVVALGGCSR,RWHSGHCDGW	BRCA
RUNX1	c.403A>G	p.R135G	DENYSAELRNATAAMKNQVARFNDL[p.R135G]GFVGRSGRGKSFTLTITVFTNPPQVA	LGFVGRSGR,VARFNDLGF,VARFNDLGFV,RFNDLGFVGR,DLGFVGRSGR,QVARFNDLGF	LAML
RUNX1	c.424_425insA	p.R142fs	LRNATAAMKNQVARFNDLRFVGRSG[p.R142fs]KREKLHSDHHCLHKPTASRHLPQSHQNHSGWAPRTSKTSAETR*	KLHSDHHCL,CLHKPTASR,HSDHHCLHK,SGWAPRTSK,VGRSGKREK,ASRHLPQSH,RTSKTSAET,RFVGRSGKR,QNHSGWAPR,APRTSKTSA,QSHQNHSGW,HQNHSGWAP,HSGWAPRTSK,RTSKTSAETR,KLHSDHHCLH,HQNHSGWAPR,HCLHKPTASR,LHKPTASRHL	BRCA
RUNX2	c.1010G>T	p.R337M	SPSIHSTTPLSSTRGTGLPAITDVP[p.R337M]MRISDDDTATSDFCLWPSTLSKKSQA	AITDVPMRI,LPAITDVPM,GLPAITDVPM	LUAD
RUNX2	c.1397C>A	p.P466H	STPYLYYGTSSGSYQFPMVPGGDRS[p.P466H]HSRMLPPCTTTSNGSTLLNPNLPNQN	RSHSRMLPP,HSRMLPPCT,RSHSRMLPPC,HSRMLPPCTT	KIRC
RUNX2	c.211C>G	p.Q71E	VAAQQQQQQQQQQQQQQQQQQQQQQQ[p.Q71E]EEAAAAAAAAAAAAAAAAAVPRLRPP	QQQQEEAAA,QQQEEAAAA,QQEEAAAAA,QQQQEEAAAA,QQQEEAAAAA,QQEEAAAAAA,QEEAAAAAAA	KIRP,TGCT
RUSC2	c.1456delC	p.P486fs	SSTQAAAAVGPTVLEGQVYTNTSPP[p.P486fs]TSALDVSAPAAMIAACSAALLSAWARWNVC*	AMIAACSAA,MIAACSAAL,AALLSAWAR,ALLSAWARW,NTSPPTSAL,SALDVSAPA,DVSAPAAMI,SAPAAMIAA,IAACSAALL,SAALLSAWA,LSAWARWNV,APAAMIAAC,LDVSAPAAM,CSAALLSAW,AMIAACSAAL,MIAACSAALL,LLSAWARWNV,SAALLSAWAR,YTNTSPPTSA,TSALDVSAPA,DVSAPAAMIA,CSAALLSAWA,ALDVSAPAAM,AAMIAACSAA,ACSAALLSAW,AALLSAWARW	STAD
RUVBL1	c.1291G>A	p.E431K	SVQLLTPANLLAKINGKDSIEKEHV[p.E431K]KEISELFYDAKSSAKILADQQDKYMK	HVKEISELF,VKEISELFY,IEKEHVKEI,HVKEISELFY,KEHVKEISEL,KEISELFYDA	CRC
RUVBL1	c.349C>T	p.R117C	PFCPMVGSEVYSTEIKKTEVLMENF[p.R117C]CRAIGLRIKETKEVYEGEVTELTPCE	VLMENFCRA,EVLMENFCR,NFCRAIGLR,LMENFCRAI,VLMENFCRAI,NFCRAIGLRI,FCRAIGLRIK,ENFCRAIGLR,EVLMENFCRA,MENFCRAIGL	CRC
RWDD2B	c.761G>A	p.R254H	VEGPQSACEEFWSRLRKLNWKRILI[p.R254H]HHREDIPFDGTNDETERQRKFSIFEE	ILIHHREDI,IHHREDIPF,KLNWKRILIH,RILIHHREDI,NWKRILIHHR,LIHHREDIPF	CRC
RXFP1	c.668C>A	p.S223Y	HRLEWLIIEDNHLSRISPPTFYGLN[p.S223Y]YLILLVLMNNVLTRLPDKPLCQHMPR	GLNYLILLV,TFYGLNYLI,FYGLNYLIL,YGLNYLILL,NYLILLVLM,LNYLILLVL,YGLNYLILLV,GLNYLILLVL,TFYGLNYLIL,FYGLNYLILL,LNYLILLVLM,SPPTFYGLNY	UCEC
RXRA	c.1280C>A	p.S427Y	AYCKHKYPEQPGRFAKLLLRLPALR[p.S427Y]YIGLKCLEHLFFFKLIGDTPIDTFLM	LLRLPALRY,LPALRYIGL,LRYIGLKCL,RLPALRYIGL,LLRLPALRYI,ALRYIGLKCL,YIGLKCLEHL,LLLRLPALRY	BLCA
RXRA	c.1280C>T	p.S427F	AYCKHKYPEQPGRFAKLLLRLPALR[p.S427F]FIGLKCLEHLFFFKLIGDTPIDTFLM	LPALRFIGL,LLRLPALRF,LRFIGLKCL,RLPALRFIGL,FIGLKCLEHL,LLRLPALRFI,LLLRLPALRF	BLCA
RYR1	c.2002G>T	p.D668Y	IRPNIFVGRAEGTTQYSKWYFEVMV[p.D668Y]YEVTPFLTAQATHLRVGWALTEGYTP	MVYEVTPFL,KWYFEVMVY,VMVYEVTPF,YEVTPFLTA,FEVMVYEVT,WYFEVMVYEV,VMVYEVTPFL,MVYEVTPFLT,EVMVYEVTPF,SKWYFEVMVY,YEVTPFLTAQ,FEVMVYEVTP	TGCT
RYR1	c.7726G>A	p.A2576T	NRYLCLAVLPLITKCAPLFAGTEHR[p.A2576T]TIMVDSMLHTVYRLSRGRSLTKAQRD	RTIMVDSML,HRTIMVDSM,RTIMVDSMLH,LFAGTEHRTI,FAGTEHRTIM	UCEC
RYR2	c.13002G>T	p.M4334I	ICSLLLGGSLVEGAKKIKVAELLAN[p.M4334I]IPDPTQDEVRGDGEEGERKPLEAALP	KVAELLANI,LLANIPDPT,IPDPTQDEV,NIPDPTQDEV,IKVAELLANI,AELLANIPDP	LUAD

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RYR2	c.2131G>A	p.E711K	VTAEATHLRVGWASTEGYSPYPGGG[p.E711K]KEWGGNGVGDDLFSYGFDGLHLWSGC	KEWGGNGVG,SPYPGGGKEW	LUSC
RYR2	c.6069A>C	p.L2023F	DFHEDLMTHCGIELDEDGSLDGNSD[p.L2023F]FTIRGRLLSLVEKVTYLKKKQAEKPV	GSLDGNSDF,SLDGNSDFTI,FTIRGRLLSL	TGCT
RYR2	c.7239G>C	p.K2413N	IMTFYSALIDLLGRCAPEMHLIHAG[p.K2413N]NGEAIRIRSILRSLIPLGDLVGVISI	LIHAGNGEA,IHAGNGEAI,HLIHAGNGEA,LIHAGNGEAI	LUAD
RYR3	c.5008C>A	p.P1670T	DESKRHGLPGVGLRTCLKPGFRFST[p.P1670T]TCFVVTGEDHQKQSPEIPLESLRTKA	RFSTTCFVV,GFRFSTTCF,FRFSTTCFV,GFRFSTTCFV,PGFRFSTTCF,FRFSTTCFVV	LUAD
RYR3	c.8114G>A	p.R2705Q	LAVGWTVERTKEGEALVQQRENEKL[p.R2705Q]QSVSQANQGNSYSPAPLDLSNVVLSR	RENEKLQSV,RENEKLQSVS,NEKLQSVSQA	CRC
SACS	c.8717G>A	p.R2906Q	FHVNGHFALDSARRNLWRDDNGVGV[p.R2906Q]QSDWNNSLMTALIAPAYVELLIQLKK	QSDWNNSLM,VQSDWNNSL,VQSDWNNSLM	UCEC
SAFB	c.2393delG	p.W798fs	REGQHYPERHGGPERHGRDSRDGWG[p.W798fs]AMALTRG*	DSRDGWGAM,RDGWGAMAL,DGWGAMALTR,RDSRDGWGAM,SRDGWGAMAL	STAD
SAFB	c.2396G>T	p.G799V	EREGQHYPERHGGPERHGRDSRDGW[p.G799V]VGYGSDKRMSEGRGLPPPPRGRRDWG	DSRDGWVGY,VGYGSDKRM,RDSRDGWVGY	TGCT
SAGE1	c.685C>T	p.R229C	HNVCEQKMENVQPAPDNVLLTLRPR[p.R229C]CINMTDTGISPMSTRDPYATITYNVP	TLRPRCINM,RPRCINMTDT,RCINMTDTGI	CRC
SAGE1	c.894C>A	p.H298Q	STGLINVAGAGTPAISTNGLYSTVP[p.H298Q]QNVCEEKMENDQPQPNNVLSTVQPVI	LYSTVPQNV,GLYSTVPQNV	LUAD
SALL3	c.1777C>G	p.L593V	PGLNHVESGVSATAESPQSLLGGPP[p.L593V]VTKAEPVSLPCTNARAGDAPVGAQAS	SLLGGPPVT,LLGGPPVTK,LLGGPPVTKA,SLLGGPPVTK	ACC
SALL4	c.2983delG	p.V995fs	NQYTSMLNGGLAVKTNEISVIQSGG[p.V995fs]FLPSRFPWGPPPL*	FLPSRFPWG,GFLPSRFPW,RFPWGPPPL,ISVIQSGGF,IQSGGFLPS,SGGFLPSRF,SRFPWGPPP,FLPSRFPWGP,QSGGFLPSRF,GGFLPSRFPW,SRFPWGPPPL	STAD
SALL4	c.560G>T	p.R187L	PPTPQDISYLAKGKVANTNVTLQAL[p.R187L]LGTKVAVNQRSADALPAPVPGANSIP	ALLGTKVAV,LQALLGTKV,TLQALLGTK,TLQALLGTKV,VTLQALLGTK,NTNVTLQALL,LQALLGTKVA	LUAD
SAMD3	c.618G>T	p.Q206H	DMTKYLEGSLYPSTQQYNDVVNALL[p.Q206H]HAHPFLDEDGCGFFLWKRALKDRFKY	ALLHAHPFL,NALLHAHPF,VNALLHAHPF	LUSC
SAMD4B	c.1429C>T	p.R477W	APAPTDGSEPAPAPVADGDIPSQFT[p.R477W]WVMGKVCTQLLVSRPDEENITSYLQL	SQFTWVMGK,DIPSQFTWV,IPSQFTWVM,GDIPSQFTW,SQFTWVMGKV,WVMGKVCTQL,PSQFTWVMGK,DIPSQFTWVM	UCS
SBF1	c.3228delC	p.P1076fs	SRNLVKNAKKTIGRQHVTRKKYNPP[p.P1076fs]AGSTGASRPLRTRRTRSQCRRSWSPAR*	STGASRPLR,ASRPLRTRR,RTRRTRSQC,RTRSQCRRS,RSQCRRSWS,VTRKKYNPPA,ASRPLRTRRT,RTRRTRSQCR,RTRSQCRRSW,RSQCRRSWSP,QCRRSWSPAR,RPLRTRRTRS,KKYNPPAGST,SQCRRSWSPA	STAD
SBNO1	c.3415_3416insA	p.N1139fs	EVHQQNALFQYFADTLTAVVQNAKK[p.N1139fs]KWKI*	AVVQNAKKK,VQNAKKKWK,VVQNAKKKWK	STAD
SBSPON	c.397G>T	p.G133W	GGAPCPPLEERAGCLEYSTPQGQDC[p.G133W]WHTYVPAFITTSAFNKERTRQATSPH	GQDCWHTYV,CWHTYVPAF,QGQDCWHTY,CWHTYVPAFI,PQGQDCWHTY,YSTPQGQDCW	LUAD
SCAF1	c.624_625insC	p.P208fs	PPPAPSSASSSPSPSPSSSSPSPPP[p.P208fs]TPTAPCTPSPTCPPIRYL*	SPSPPPTPT,TPSPTCPPI,SPTCPPIRY,CTPSPTCPPI,SPSPPPTPTA,SPTCPPIRYL	KIRC
SCAF11	c.2776_2777delGA	p.E926fs	SSPGEKSRSQSRERESDRDGQRRER[p.E926fs]KENQKVV*	RERKENQKV,RERKENQKVV	GBM,KIRP
SCAF8	c.2218G>T	p.G740C	LVQPSLSMTPETVKDVGFGSLVIPG[p.G740C]CSVASNLATSALPAGNVFNAPTKQAE	SLVIPGCSV,LVIPGCSVA,SLVIPGCSVA,IPGCSVASNL	LUAD

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SCAPER	c.1097G>A	p.R366Q	AEKTQFTVSTLDDVKNSGSIRDNYV[p.R366Q]QTSEISAVHIDTECVSVMLQAGTPPL	VQTSEISAV,YVQTSEISAV,QTSEISAVHI,RDNYVQTSEI,VQTSEISAVH	UCEC
SCARF1	c.1841G>A	p.R614Q	SVSFAEGTKFAPQSRRSSGELSSPL[p.R614Q]QKPKRLSRGAQSGPEGREAEESTGPE	LSSPLQKPK,LQKPKRLSR,SPLQKPKRL	STAD
SCFD2	c.1633C>T	p.R545W	TDWDSSINLTFHKSKIAVDELFTSL[p.R545W]WDIAGARSLLKQFKSVYVPGNHTHQA	ELFTSLWDI,SLWDIAGAR,TSLWDIAGA,WDIAGARSL,FTSLWDIAGA,ELFTSLWDIA,TSLWDIAGAR,WDIAGARSLL,DELFTSLWDI	CRC
SCLT1	c.327delA	p.K109fs	MKLQLENVIKENERLHSELKDAVEK[p.K109fs]NWRPFPWAQR*	KNWRPFPWA,AVEKNWRPF,EKNWRPFPW,NWRPFPWAQR,VEKNWRPFPW,DAVEKNWRPF	STAD
SCML4	c.581G>A	p.R194Q	GKQHLRSLPVVNSIGYVLRFLAKLC[p.R194Q]QSLLCDDLFSHQPFPRGCSASEKVQE	FLAKLCQSL,FLAKLCQSLL,RFLAKLCQSL,CQSLLCDDLF	CRC
SCML4	c.783G>T	p.L261F	YLVNPVGMNRYSVDTSASTFNHRGS[p.L261F]FHPSSSLYCKRQNSGDSHLGGGPAAT	STFNHRGSF,SFHPSSSLY,GSFHPSSSL,STFNHRGSFH,GSFHPSSSLY,RGSFHPSSSL,ASTFNHRGSF	LUAD
SCN10A	c.3425G>A	p.R1142H	EGCIRHCPCCKLDTTKSPWDVGWQV[p.R1142H]HKTCYRIVEHSWFESFIIFMILLSSG	WQVHKTCYR,WQVHKTCYRI,VGWQVHKTCY,SPWDVGWQVH	MM
SCN10A	c.4709C>T	p.T1570M	IVVVLSIASLIFSAILKSLQSYFSP[p.T1570M]MLFRVIRLARIGRILRLIRAAKGIRT	SLQSYFSPM,LQSYFSPML,YFSPMLFRV,MLFRVIRLA,SYFSPMLFR,QSYFSPMLF,SPMLFRVIR,SLQSYFSPML,QSYFSPMLFR,MLFRVIRLAR,LQSYFSPMLF,SYFSPMLFRV,YFSPMLFRVI,KSLQSYFSPM,FSPMLFRVIR,SPMLFRVIRL	CRC
SCN2A	c.107G>A	p.R36K	PDSFRFFTRESLAAIEQRIAEEKAK[p.R36K]KPKQERKDEDDENGPKPNSDLEAGKS	RIAEEKAKK,KAKKPKQER,KAKKPKQERK	BRCA
SCN2A	c.464C>A	p.T155K	LFNMLIMCTILTNCVFMTMSNPPDW[p.T155K]KKNVEYTFTGIYTFESLIKILARGFC	TMSNPPDWK,MSNPPDWKK,WKKNVEYTF,MTMSNPPDWK,TMSNPPDWKK,DWKKNVEYTF	LUAD
SCN7A	c.4073G>A	p.R1358H	MTVGSYLVPPSLVQLILLSRIIHML[p.R1358H]HLGKGPKVFHNLMLPLMLSLPALLNI	IIHMLHLGK,MLHLGKGPK,LSRIIHMLH,SRIIHMLHL,HLGKGPKVF,MLHLGKGPKV,RIIHMLHLGK,HMLHLGKGPK,LSRIIHMLHL,LHLGKGPKVF	GBM
SCNN1G	c.1691G>A	p.R564H	MSCSVVCVIEIIEVFFIDFFSIIAR[p.R564H]HQWQKAKEWWAWKQAPPCPEAPR5PQ	IIARHQWQK,IARHQWQKA,DFFSIIARH,FSIIARHQW,HQWQKAKEW,IIARHQWQKA,SIIARHQWQK,FFSIIARHQW,IARHQWQKAK,HQWQKAKEWW	GBM
SCRIB	c.995G>T	p.G332V	SLGKLTKLTNLNVDRNHLEALPPEI[p.G332V]VGCVALSVLSLRDNRLAVLPPELAHT	IVGCVALSV,ALPPEIVGC,LEALPPEIV,PEIVGCVAL,LPPEIVGCV,ALPPEIVGCV,EIVGCVALSV,LPPEIVGCVA	TGCT
SCRT1	c.397T>G	p.S133A	VSEGYAADAFFITDGRSRRKASNAG[p.S133A]AAAAPSTASAAAPDGDAGGGGGAGGR	RRKASNAGA,KASNAGAAA,RKASNAGAA,KASNAGAAAA,RKASNAGAAA,AAAAPSTASA	ACC
SCUBE2	c.1024G>A	p.V342M	DGKTCKDIDECQTRNGGCDHFCKNI[p.V342M]MGSFDCGCKKGFKLLTDEKSCQDVDE	FCKNIMGSF,CDHFCKNIM,IMGSFDCGCK,HFCKNIMGSF	CRC
SDAD1	c.824delA	p.K275fs	YATGKKSSKNKKKLEKAMKVLKKQK[p.K275fs]RRKNQRCLTFQPFT*	KVLKKQKRR,VLKKQKRRK,KQKRRKNQR,RKNQRCLTF,QRCLTFQPF,KVLKKQKRRK,AMKVLKKQKR,NQRCLTFQPF,RRKNQRCLTF	STAD
SDHAP1	c.196C>T	p.H66Y	DYKVRIDEYDHSKPIQGQQKKPFEE[p.H66Y]YWRKHTLSYVDVSTGKVTVEYRPIID	YWRKHTLSY,QQKKPFEEY,EEYWRKHTL,EYWRKHTLSY,YWRKHTLSYV,GQQKKPFEEY,QQKKPFEEYW,FEEYWRKHTL	CESC
SDHAP2	c.110_111insTT	p.S37fs	VGRPPVPLHMVSTASGQTRCWTWLS[p.S37fs]LVRHVP*	CWTWLSLVR,TRCWTWLSL,WTWLSLVRHV,QTRCWTWLSL	CESC
SDHAP2	c.91C>T	p.R31C	LCPACTPVGRPPVPLHMVSTASGQT[p.R31C]CCWTWLSGQACALSIAESCRPGDKVP	SGQTCCWTW,GQTCCWTWL,TASGQTCCW	GBM,PRAD
SDHAP3	c.196G>A	p.A66T	AACASVHGANRLGANSLLDLVVFGQ[p.A66T]TCALSIEESCRPGDKVPPIKPNAGEE	VVFGQTCAL,FGQTCALSI,VFGQTCALSI,LVVFGQTCAL	GBM
SDK1	c.1524_1525insC	p.K508fs	RPVDTTVTDGMTAILRCEVSGAPKP[p.K508fs]RHHLEKRKPHSGQWLCPDS*	EVSGAPKPR,KRKPHSGQW,RKPHSGQWL,APKPRHHLEK,KPRHHLEKRK,KRKPHSGQWL	KIRC

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SDK1	c.3542C>T	p.T1181M	PSPYSPSSRVIQTLQAPPDVAPTSV[p.T1181M]MVRTASETSLRLRWVPLPDSQYNGNP	DVAPTSVMV,MVRTASETSL,DVAPTSVMVR,APTSVMVRTA	CRC
SDK1	c.6437A>G	p.Y2146C	ADASESEATDSDYEDALPKHSFVNH[p.Y2146C]CMSDPTYYNSWKRRAQGRAPAPHRYE	HCMSDPTYY,KHSFVNHCM,NHCMSDPTY,FVNHCMSDPT,VNHCMSDPTY	TGCT
SEC24D	c.150_151insC	p.A50fs	YGHYGDPSHTASPTGMMKPAGPLGA[p.A50fs]HRH*	MKPAGPLGAH	LUAD
SEC31B	c.2713C>T	p.P905S	GVRPASSQPQLLGGQRVQVPNPVGF[p.P905S]SGTWPLPGSPLPMACPGIMRPGSTSL	VGFSGTWPL,NPVGFSGTW	TGCT
SEC61A2	c.377G>T	p.G126V	EVGDTPKDRALFNGAQKLFGMIITI[p.G126V]VQAIVYVMTGMYGDPAEMGAGICLLI	ITIVQAIVY,MIITIVQAI,TIVQAIVYV,GMIITIVQA,IITIVQAIV,IVQAIVYVM,KLFGMIITIV,GMIITIVQAI,MIITIVQAIV,ITIVQAIVYV,IITIVQAIVY,TIVQAIVYVM	LUAD
SECISBP2	c.1824C>G	p.D608E	GMDELISTPSVEDKSEEPPGTELQR[p.D608E]ETEASHLAPNHTTFPKIHSRRFRDYC	LQRETEASH,RETEASHLA,TELQRETEA,LQRETEASHL,RETEASHLAP	KIRC
SELP	c.1285C>T	p.R429W	RAFQYDTNCSFRCAEGFMLRGADIV[p.R429W]WCDNLGQWTAPAPVCQALQCQDLPVP	VWCDNLGQW,MLRGADIVW,FMLRGADIVW,IVWCDNLGQW	UCEC
SELP	c.889G>A	p.A297T	NMTCLHSAKAFQHQSSCSFSCEEGF[p.A297T]TLVGPEVVQCTASGVWTAPAPVCKAV	FTLVGPEVV,FSCEEGFTL,FSCEEGFTLV,EGFTLVGPEV	TGCT
SEMA3A	c.241G>A	p.D81N	SYHTFLLDEERSRLYVGAKDHIFSF[p.D81N]NLVNIKDFQKIVWPVSYTRRDECKWA	FSFNLVNIK,IFSFNLVNI,KDHIFSFNL,HIFSFNLVNI,NLVNIKDFQK,SFNLVNIKDF,KDHIFSFNLV	CRC
SEMA4D	c.755G>A	p.R252Q	EDDRVYFFFTEVSVEYEFVFRVLIP[p.R252Q]QIARVCKGDQGGLRTLQKKWTSFLKA	VLIPQIARV,RVLIPQIAR,FVFRVLIPQI,RVLIPQIARV,VFRVLIPQIA	CRC
SEMG2	c.874C>T	p.R292C	QHQTKNLSQDQEHGRKAHKISYPSS[p.R292C]CTEERQLHHGEKSVQKDVSKGSISIQ	CTEERQLHH,HKISYPSSC	GBM
SENP7	c.2018C>A	p.S673Y	ELELSYPLSWVQAFPLFQNLSSKES[p.S673Y]YFIHYYCVSTCSFPAGVAVAEEMKLK	SYFIHYYCV,SSKESYFIH,KESYFIHYY,ESYFIHYYC,QNLSSKESY,NLSSKESYF,SKESYFIHY,NLSSKESYFI,SSKESYFIHY,FQNLSSKESY,SKESYFIHYY,ESYFIHYYCV,QNLSSKESYF,KESYFIHYYC	UCEC
SEPHS1	c.1112G>A	p.R371Q	GEGHQAWIIGIVEKGNRTARIIDKP[p.R371Q]QIIEVAPQVATQNVNPTPGATS*	QIIEVAPQV,RIIDKPQII,IIDKPQIIEV	CRC
SEPHS1	c.37G>A	p.E13K	MSTRESFNPESY[p.E13K]KLDKSFRLTRFTELKGTGCKVPQDVL	ESFNPESYK,SFNPESYKL,SYKLDKSFR,ESYKLDKSF,YKLDKSFRL,KLDKSFRLTR,SYKLDKSFRL,ESYKLDKSFR,ESFNPESYKL	UCEC
SERPINA12	c.631C>G	p.R211G	HGKINNLIENIDPGTVMLLANYIFF[p.R211G]GARWKHEFDPNVTKEEDFFLEKNSSV	LLANYIFFG,YIFFGARWK,NYIFFGARW,FGARWKHEF,ANYIFFGAR,LANYIFFGA,MLLANYIFFG,LLANYIFFGA,LANYIFFGAR,FFGARWKHEF,ANYIFFGARW	BLCA
SERPINA12	c.757G>T	p.D253Y	FFLEKNSSVKVPMMFRSGIYQVGYD[p.D253Y]YKLSCTILEIPYQKNITAIFILPDEG	YQVGYDYKL,GIYQVGYDY,YDYKLSCTI,GIYQVGYDYK,IYQVGYDYKL,SGIYQVGYDY,YDYKLSCTIL,YKLSCTILEI	LUAD
SERPINA3	c.474G>C	p.K158N	LQLSMGNAMFVKEQLSLLDRFTEDA[p.K158N]NRLYGSEAFATDFQDSAAAKKLINDY	FTEDANRLY,NRLYGSEAF,RFTEDANRLY,ANRLYGSEAF	CESC
SERPINA4	c.292C>T	p.R98C	HQQILETGEGSPSLKIAPANADFAF[p.R98C]CFYYLIASETPGKNIFFSPLSISAAY	NADFAFCFY,FAFCFYYLI,DFAFCFYYL,ADFAFCFYY,ANADFAFCF,NADFAFCFYY,FAFCFYYLIA,DFAFCFYYLI,ANADFAFCFY,ADFAFCFYYL	CESC
SERPINA9	c.1242G>T	p.M414I	TTKFIVRSKDGPSYFTVSFNRTFLM[p.M414I]IITNKATDGILFLGKVENPTKS*	FLMIITNKA,TFLMIITNK,SFNRTFLMI,FNRTFLMII,FLMIITNKAT,RTFLMIITNK,VSFNRTFLMI,SFNRTFLMII	LUAD
SERPINB12	c.503delA	p.Q168fs	PICQEYLDGVIQFYHTTIESVDFQK[p.Q168fs]TLKNPDKRLTSGLNVNPKVKSRNSSARTLLMLRLCWYW*	NSSARTLLM,SVDFQKTLK,KTLKNPDKR,TSGLNVNPK,SARTLLMLR,LMLRLCWYW,KVKSRNSSA,KSRNSSART,RNSSARTLL,LLMLRLCWY,NVNPKVKSR,KRLTSGLNV,SRNSSARTL,SSARTLLML,IESVDFQKT,LTSGLNVNPK,SSARTLLMLR,RTLLMLRLCW,LLMLRLCWYW,FQKTLKNPDK,SGLNVNPKVK,KVKSRNSSAR,KSRNSSARTL,RNSSARTLLM,SARTLLMLRL,TLLMLRLCWY,NPDKRLTSGL,IESVDFQKTL,SRNSSARTLL	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
SERPINB3	c.626C>G	p.S209C	GQWENKFKKENTKEEKFWPNKNTYK[p.S209C]CVQMMRQYNSFNFALLEDVQAKVLEI	KCVQMMRQY,TYKCVQMMR,NTYKCVQMM,NTYKCVQMMR,WPNKNTYKCV,NKNTYKCVQM,YKCVQMMRQY	KIRC
SERPINC1	c.134G>T	p.R45L	SLLLIGFWDCVTCHGSPVDICTAKP[p.R45L]LDIPMNPMCIYRSPEKKATEDEGSEQ	TAKPLDIPM,VDICTAKPL,CTAKPLDIPM,KPLDIPMNPM	LUAD
SERPINI1	c.243delA	p.L81fs	GMMELGAQGSTQKEIRHSMGYDSLK[p.L81fs]MVKNFLS*	SLKMVKNFL,SMGYDSLKM,SMGYDSLKMV,MGYDSLKMVK,SLKMVKNFLS,HSMGYDSLKM	STAD
SESTD1	c.918T>G	p.I306M	VMQVVNWLEGPGSEQLRAQWGIGDS[p.I306M]MRASQALQQKHEEIESQHSEWFAVYV	SMRASQALQ,DSMRASQAL,AQWGIGDSM,SMRASQALQQ,RAQWGIGDSM	KIRC
SETDB2	c.2145delA	p.R715fs	YGYEAGTVPEKEIFCQCGVNKCRKK[p.R715fs]YYKYVTNACL*	KYYKYVTNA,KCRKKYYKY,GVNKCRKKY,YKYVTNACL,KYYKYVTNAC,YYKYVTNACL,VNKCRKKYYK,KCRKKYYKYV,GVNKCRKKYY,KKYYKYVTNA	STAD
SEZ6L	c.620C>T	p.S207L	VPLWLDRKESAVPTTPAPLQISPFT[p.S207L]LQPYVAHTLPQRPEPGEPGPDMAQEA	TLQPYVAHT,LQPYVAHTL,ISPFTLQPY,LQISPFTLQ,SPFTLQPYV,TLQPYVAHTL,QISPFTLQPY,ISPFTLQPYV,APLQISPFTL,LQISPFTLQP,SPFTLQPYVA	CRC
SEZ6L2	c.221G>C	p.R74P	EALAELLHGALLRRGPEMGYLPGSD[p.R74P]PDPTLATPPAGQTLAVPSLPRATEPG	YLPGSDPDPT,LPGSDPDPTL	ACC
SF1	c.763C>T	p.R255W	IETPEDQNDLRKMQLRELARLNGTL[p.R255W]WEDDNRILRPWQSSETRSITNTTVCT	TLWEDDNRI,LARLNGTLW,TLWEDDNRIL	CESC
SF3B1	c.1868A>G	p.Y623C	SNLAKAAGLATMISTMRPDIDNMDE[p.Y623C]CVRNTTARAFAVVASALGIPSLLPFL	CVRNTTARA,CVRNTTARAF	CLL
SF3B1	c.1876A>T	p.N626Y	AKAAGLATMISTMRPDIDNMDEYVR[p.N626Y]YTTARAFAVVASALGIPSLLPFLKAV	NMDEYVRYT,YTTARAFAV,YVRYTTARA,RYTTARAFA,EYVRYTTAR,VRYTTARAF,DEYVRYTTA,NMDEYVRYTT,YTTARAFAVV,RYTTARAFAV,YVRYTTARAF,IDNMDEYVRY,DEYVRYTTAR	CLL
SF3B1	c.1996A>G	p.K666E	IPSLLPFLKAVCKSKKSWQARHTGI[p.K666E]EIVQQIAILMGCAILPHLRSLVEIIE	QARHTGIEI,EIVQQIAIL,IEIVQQIAI,WQARHTGIEI,EIVQQIAILM,IEIVQQIAIL	CLL
SF3B1	c.2098A>G	p.K700E	MGCAILPHLRSLVEIIEHGLVDEQQ[p.K700E]EVRTISALAIAALAEAATPYGIESFD	GLVDEQQEV,EVRTISALA,QEVRTISAL,DEQQEVRTI,EVRTISALAI,QQEVRTISAL,DEQQEVRTIS,QEVRTISALA	BRCA,CLL
SF3B1	c.2704G>A	p.E902K	GNLGAADIDHKLEEQLIDGILYAFQ[p.E902K]KQTTEDSVMLNGFGTVVNALGKRVKP	ILYAFQKQT,KQTTEDSVM,ILYAFQKQTT,FQKQTTEDSV,QKQTTEDSVM,KQTTEDSVML	BLCA
SF3B1	c.2870G>A	p.R957Q	ICGTVLWRLNNKSAKVRQQAADLIS[p.R957Q]QTAVVMKTCQEEKLMGHLGVVLYEYL	DLISQTAVV,ISQTAVVMK,LISQTAVVM,ADLISQTAV,LISQTAVVMK,QAADLISQTA,DLISQTAVVM,RQQAADLISQ	UCEC
SFI1	c.2462G>A	p.R821Q	THHLQCVRKRLLHRQSTQLLAQRLS[p.R821Q]QTCFRQWRQQLAARRQEQRATVRALW	LLAQRLSQT,SQTCFRQWR,AQRLSQTCF,LSQTCFRQW,LLAQRLSQTC,AQRLSQTCFR,LSQTCFRQWR,LAQRLSQTCF,RLSQTCFRQW	HNSC
SFPQ	c.1832G>A	p.R611Q	EEQMRRQREESYSRMGYMDPRERDM[p.R611Q]QMGGGGAMNMGDPYGSGGQKFPPLGG	MQMGGGGAM,DMQMGGGGAM,QMGGGGAMNM,MQMGGGGAMN	CRC
SFRP4	c.695G>A	p.R232Q	QRSGCNEVTTVVDVKEIFKSSSPIP[p.R232Q]QTQVPLITNSSCQCPHILPHQDVLIM	IPQTQVPLI,SSSPIPQTQV,SPIPQTQVPL	UCEC
SFSWAP	c.1850C>A	p.S617Y	PLEKNRVKLDDDSDDDEESKEGQES[p.S617Y]YSSAANTNPAVAPPCVVVEEKKPQLT	ESKEGQESY,GQESYSSAA,YSSAANTNPA,KEGQESYSSA,EESKEGQESY,QESYSSAANT	CRC
SGCG	c.659C>T	p.A220V	ESPTRSLSMDAPRGVHIQAHAGKIE[p.A220V]VLSQMDILFHSSDGMLVLDAETVCLP	EVLSQMDIL,VLSQMDILF,GKIEVLSQM,IEVLSQMDI,IQAHAGKIEV,QAHAGKIEVL,IEVLSQMDIL,EVLSQMDILF	CRC
SGCZ	c.123T>G	p.I41M	REQYILATQQNNLPRTENAQLYPVG[p.I41M]MYGWRKRCLYFFVLLLLVTMIVNLAM	LYPVGMYGW,MYGWRKRCL,AQLYPVGMY,GMYGWRKRCL,MYGWRKRCLY,NAQLYPVGMY,QLYPVGMYGW	CRC
SGIP1	c.1505G>T	p.R502L	GVGDVSRPFSPPIHSSSPPPIAPLA[p.R502L]LAESTSSISSTNSLSAATTPTVENEQ	ALAESTSSI,ALAESTSSIS,SPPPIAPLAL,LALAESTSSI	LUAD

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SGK1	c.1100_1102delAGA	p.K367del	AKDDFMEIKSHVFFSLINWDDLINK[p.K367del]ITPPFNPNVSGPNDLRHFDPEFTEEPVP	LINKITPPF,DLINKITPPF	UCEC
SGK3	c.183delA	p.L61fs	SEWFVFRRYAEFDKLYNTLKKQFPA[p.L61fs]WP*	TLKKQFPAW	STAD
SGOL2	c.1220delA	p.E407fs	KKSNKKTNEHGMKTFRKVKDSSSEK[p.E407fs]REKDQRDSLKIVQMSILGKRLKTGQKDLMSWMAKGVQKIPVLFSIMNSWLR*	LMSWMAKGV,WMAKGVQKI,SLKIVQMSI,IVQMSILGK,MSILGKRLK,SWMAKGVQK,FSIMNSWLR,GVQKIPVLF,KDLMSWMAK,GQKDLMSWM,REKDQRDSL,RDSLKIVQM,LKIVQMSIL,KGVQKIPVL,QKIPVLFSI,KIPVLFSIM,VLFSIMNSW,DLMSWMAKGV,VLFSIMNSWL,SLKIVQMSIL,KIVQMSILGK,QMSILGKRLK,MSWMAKGVQK,SWMAKGVQKI,KGVQKIPVLF,KVKDSSSEKR,REKDQRDSLK,LGKRLKTGQK,RLKTGQKDLM,MAKGVQKIPV,IVQMSILGKR,LFSIMNSWLR,VQMSILGKRL,KRLKTGQKDL,GQKDLMSWMA,AKGVQKIPVL,VQKIPVLFSI,QKIPVLFSIM	STAD
SGSM1	c.2452G>A	p.E818K	VLDAQRNTPTVLRPRDGSVDDRQSS[p.E818K]KATTSQDEAPREELAVQDSLESDLLA	SVDDRQSSK,RQSSKATTS,GSVDDRQSSK,RQSSKATTSQ	CESC
SGSM1	c.3351C>A	p.F1117L	IALALVEVYRDIILENNMDFTDIIK[p.F1117L]LFNEMAERHNTKQVLKLARDLVYKVQ	FTDIIKLFN,KLFNEMAER,DFTDIIKLF,DIIKLFNEM,MDFTDIIKL,NMDFTDIIKL,DIIKLFNEMA,MDFTDIIKLF	CRC
SH3KBP1	c.1688_1689insC	p.P563fs	ISQVSDNKASLPPKPGTMAAGGGGP[p.P563fs]SPSVLSGALPPVILFGNSWTQSQLPVSVRHGRKTKDGACGQQPGGRGGAKDTGPRAEEHHRDHEGPAETRD*	VLSGALPPV,TQSQLPVSV,GALPPVILF,PVSVRHGRK,SVRHGRKTK,LPVSVRHGR,SPSVLSGAL,SWTQSQLPV,SQLPVSVRH,SVLSGALPPV,VLSGALPPVI,ILFGNSWTQS,WTQSQLPVSV,VSVRHGRKTK,QLPVSVRHGR,NSWTQSQLPV,SGALPPVILF,FGNSWTQSQL,SQLPVSVRHG,PPVILFGNSW	KIRC
SH3KBP1	c.1720delC	p.L574fs	LPPKPGTMAAGGGGPAPLSSAAPSP[p.L574fs]CHPLWEQLDTEPTPRLCSARKENQRWSLRPAARRPWRS*	RWSLRPAAR,RPAARRPWR,CSARKENQR,WSLRPAARR,RKENQRWSL,NQRWSLRPA,QRWSLRPAA,WEQLDTEPT,APSPCHPLW,RWSLRPAARR,SLRPAARRPW,EQLDTEPTPR,SAAPSPCHPL,RPAARRPWRS,NQRWSLRPAA	STAD
SH3PXD2A	c.2276C>T	p.S759L	SSDLITLPATTPPCPTKKEWEGPAT[p.S759L]LYMTCSAYQKVQDSEISFPAGVEVQV	TLYMTCSAY,ATLYMTCSA,KEWEGPATL,WEGPATLYM,ATLYMTCSAY,LYMTCSAYQK,KEWEGPATLY,KKEWEGPATL,WEGPATLYMT	LUAD
SH3RF2	c.952C>T	p.R318C	RKVPGQFSITTALNTLNRMVHSPSG[p.R318C]CHMVEISTPVLISSSNPSVITQPMEK	HSPSGCHMV,VHSPSGCHM,MVHSPSGCHM,SPSGCHMVEI,RMVHSPSGCH,CHMVEISTPV	GBM
SH3TC2	c.265C>T	p.R89C	RCVNGPLQEAARRRLWALENEDQEV[p.R89C]CMLFKDLSARLVSIQSQRAQFLITFK	NEDQEVCML,CMLFKDLSAR,LENEDQEVCM,NEDQEVCMLF,QEVCMLFKDL	CRC
SHB	c.1378G>A	p.A460T	RNSQTSKHDYSLSLRSNQGFMHMKL[p.A460T]TKTKEKYVLGQNSPPFDSVPEVIHYY	FMHMKLTKT,GFMHMKLTK,KLTKTKEKY,KLTKTKEKYV,FMHMKLTKTK,QGFMHMKLTK,HMKLTKTKEK,LTKTKEKYVL,MKLTKTKEKY	GBM
SHROOM4	c.3468_3470delAGA	p.1156_1157EE>E	EEEEEEEEEEEEEEEEEEEAEEEEE[p.1156_1157EE>E]LPPQYFSSETSGSCALNPEEVLEQPQPL	EEAEEEEEL	PAAD
SI	c.3649G>T	p.V1217F	LDFYMFLGPTPEVATKQYHEVIGHP[p.V1217F]FMPAYWALGFQLCRYGYANTSEVREL	FMPAYWALG,PFMPAYWAL,IGHPFMPAY,HPFMPAYWA,YHEVIGHPF,HEVIGHPFM,FMPAYWALGF,QYHEVIGHPF,VIGHPFMPAY,EVIGHPFMPA,HPFMPAYWAL,YHEVIGHPFM,IGHPFMPAYW	LUAD
SI	c.5042T>A	p.I1681K	WFDYHTGKDIGVRGQFQTFNASYDT[p.I1681K]KNLHVRGGHILPCQEPAQNTFYSRQK	TFNASYDTK,QTFNASYDTK,ASYDTKNLHV	TGCT
SIGLEC1	c.954delC	p.P318fs	QAAWSDAGVYTCQAENGVGSLVSPP[p.P318fs]SASTSSWLRSR*	SASTSSWLR,STSSWLRSR,PPSASTSSW,ASTSSWLRSR,SPPSASTSSW	STAD
SIGLEC10	c.749C>T	p.T250M	SAQRTVRLRVAYAPRDLVISISRDN[p.T250M]MPALEPQPQGNVPYLEAQKGQFLRLL	ISRDNMPAL,MPALEPQPQ,SISRDNMPAL,LVISISRDNM,ISISRDNMPA,MPALEPQPQG	GBM
SIGLEC11	c.1088C>T	p.S363F	NRLGSQQQALDLSVQYPPENLRVMV[p.S363F]FQANRTVLENLGNGTSLPVLEGQSLR	MVFQANRTV,RVMVFQANR,VMVFQANRTV,RVMVFQANRT,MVFQANRTVL,FQANRTVLEN	CRC

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SIK1	c.2032delC	p.Q678fs	EVLEQQRLLQLQHHPAAAPGCSQAP[p.Q678fs]SRPLPRL*	QAPSRPLPR,APSRPLPRL,CSQAPSRPL,SQAPSRPLP,SQAPSRPLR	STAD
SIM1	c.637G>A	p.V213M	YLKIRQYSLDMSPFDGCYQNVGLVA[p.V213M]MGHSLPPSAVTEIKLHSNMFMFRASL	YQNVGLVAM,GLVAMGHSL,MGHSLPPSA,VAMGHSLPP,AMGHSLPPSA,CYQNVGLVAM,YQNVGLVAMG,MGHSLPPSAV	CESC
SIPA1L1	c.3188G>A	p.R1063Q	SETYRMPVMEYKMNEGVSYEFKFPF[p.R1063Q]QNNNKWQRNASKGPHSPQVPSQVQSP	KFPFQNNNK,FQNNNKWQR,FPFQNNNKW,YEFKFPFQN,KFPFQNNNKW,YEFKFPFQNN	CRC
SIPA1L1	c.3680C>A	p.S1227Y	PSWQRSEDSIADQMAYSYRGPQDFN[p.S1227Y]YFVLEQHEYTEPTCHLPAVSKVLPAF	RGPQDFNYF,YFVLEQHEY,YRGPQDFNY,YRGPQDFNYF,SYRGPQDFNY,NYFVLEQHEY,GPQDFNYFVL	CRC
SIPA1L3	c.2330G>C	p.G777A	RVHNPCTDNVCYSMAVTRSKDAPPF[p.G777A]APPIPSGTTFRKSDVFRDFLLAKVIN	RSKDAPPFA,DAPPFAPPI,RSKDAPPFAP,APPIPSGTTF,KDAPPFAPPI	KIRC
SIRPA	c.387_389delCGA	p.D131del	IRIGNITPADAGTYYCVKFRKGSPD[p.D131del]VEFKSGAGTELSVRAKPSAPVVSGPAAR	KGSPDVEFK,KFRKGSPDV,RKGSPDVEF,VKFRKGSPDV,FRKGSPDVEF	KIRC
SIRPA	c.697G>A	p.V233I	SIHSTAKVVLTREDVHSQVICEVAH[p.V233I]ITLQGDPLRGTANLSETIRVPPTLEV	QVICEVAHI,VICEVAHITL,SQVICEVAHI	PRAD
SIX1	c.571G>A	p.E191K	TQVSNWFKNRRQRDRAAEAKERENT[p.E191K]KNNNSSSNKQNQLSPLEGGKPLMSSS	KNNNSSSNK	UCEC
SIX3	c.79A>C	p.I27L	VFRSPLDLYSSHFLLPNFADSHHRS[p.I27L]LLLASSGGGNGAGGGGGAGGGSGGGN	FADSHHRSL,FADSHHRSLL	CLL
SKI	c.185C>G	p.A62G	AFSARWAQEAYKKESAKEAGAAAAVP[p.A62G]GPVPAATEPPPVLHLPAIQPPPPVLP	GAAAVPGPV,KEAGAAAVPG	KIRP
SKOR1	c.2648A>G	p.Y883C	EEMVQQLQIVRDTLCNELDQERKAR[p.Y883C]CAIQQKLKEAHDALHHFSCKMLTPRH	KARCAIQQK,RCAIQQKLK,QERKARCAI,KARCAIQQKL	LUAD
SLAMF1	c.829delA	p.S277fs	LIMVVILQLRRRGKTNHYQTTVEKK[p.S277fs]ALRSMPKSRNQVLFRRNLTPSQLRTLAPPYMLLPQSLSQSLSRKQIPSQSMLV*	TLAPPYMLL,SMPKSRNQV,KQIPSQSML,QIPSQSMLV,KSRNQVLFR,SLSQSLSRK,QSLSQSLSR,RTLAPPYML,PYMLLPQSL,KKALRSMPK,ALRSMPKSR,RSMPKSRNQ,RNLTPSQLR,QLRTLAPPY,TTVEKKALR,MPKSRNQVL,TPSQLRTLA,LPQSLSQSL,VEKKALRSM,NQVLFRRNL,RRNLTPSQL,SQLRTLAPP,LRTLAPPYM,SQSLSRKQI,RKQIPSQSM,LLPQSLSQSL,KQIPSQSMLV,SMPKSRNQVL,KSRNQVLFRR,QSLSQSLSRK,RTLAPPYMLL,KALRSMPKSR,RSMPKSRNQV,QLRTLAPPYM,SQLRTLAPPY,QTTVEKKALR,MPKSRNQVLF,PPYMLLPQSL,YQTTVEKKAL,FRRNLTPSQL,YMLLPQSLSQ,SRKQIPSQSM,RKQIPSQSML	BLCA
SLC10A4	c.843C>G	p.F281L	YKYSRVADYIVKVSLWSLLVTLVVL[p.F281L]LIMTGTMLGPELLASIPAAVYVIAIF	LLVTLVVLL,LLIMTGTML,VLLIMTGTM,SLLVTLVVLL,LLVTLVVLLI	CESC
SLC10A6	c.326delG	p.G109fs	YLLAISFSLKPVQAIAVLIMGCCPG[p.G109fs]APSLTFSPSGLMEIWISASV*	LIMGCCPGA,GLMEIWISA,SLTFSPSGL,FSPSGLMEI,LTFSPSGLM,MEIWISASV,CPGAPSLTF,APSLTFSPS,SPSGLMEIW,VLIMGCCPGA,GLMEIWISAS,LMEIWISASV,SLTFSPSGLM,TFSPSGLMEI,MGCCPGAPSL,SPSGLMEIWI	STAD
SLC10A7	c.782C>T	p.S261L	LILFIIFSIQLSFMLLTFIFSTRNN[p.S261L]LGFTPADTVAIIFCSTHKSLTLGIPM	FIFSTRNNL,STRNNLGFT,RNNLGFTPA,FSTRNNLGF,NLGFTPADTV,TFIFSTRNNL,IFSTRNNLGF	UCEC
SLC12A1	c.875C>T	p.S292L	ANAVAVAMYVVGFAETVVDLLKESD[p.S292L]LMMVDPTNDIRIIGSITVVILLGISV	LLKESDLMM,LLKESDLMMV,LMMVDPTNDI	CRC
SLC12A2	c.2483G>A	p.R828Q	ALLHLVHDFTKNVGLMICGHVHMGP[p.R828Q]QRQAMKEMSIDQAKYQRWLIKNKMKA	MGPQRQAMK,HMGPQRQAM,PQRQAMKEM,HMGPQRQAMK,HVHMGPQRQA,GPQRQAMKEM,VHMGPQRQAM	UCEC
SLC12A7	c.2056delC	p.H686fs	WGDGIRGLSLNAARYALLRVEHGPP[p.H686fs]TPRTGGPRCW*	LRVEHGPPT,RVEHGPPTPR	STAD

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SLC13A2	c.1478_1479insG	p.L493fs	IVLLLGGGYALAKGSERSGLSEWLG[p.L493fs]KQADPTAECASSSHCHHPLPPGGHLHRVH*	SGLSEWLGK,SSHCHHPLP,HPLPPGGHL,KQADPTAEC,SSSHCHHPL,SEWLGKQAD,GLSEWLGKQA,RSGLSEWLGK,KQADPTAECA,ASSSHCHHPL,SEWLGKQADP,LPPGGHLHRV	KIRC
SLC13A5	c.818A>C	p.Q273P	VNFASWFAFAFPNMLVMLLFAWLWL[p.Q273P]PFVYMRFNFKKSWGCGLESKKNEKAA	LLFAWLWLP,FAWLWLPFV,WLWLPFVYM,LFAWLWLPF,AWLWLPFVY,WLPFVYMRF,PFVYMRFNF,LWLPFVYMR,FAWLWLPFVY,LLFAWLWLPF,LFAWLWLPFV,AWLWLPFVYM,LWLPFVYMRF,PFVYMRFNFK,WLWLPFVYMR,LPFVYMRFNF	GBM
SLC16A14	c.1484G>A	p.R495Q	YDFSFYICGLLYMIGILFLLIQPCI[p.R495Q]QIIEQSRRKYMDGAHV*	LLIQPCIQI,CIQIIEQSR,FLLIQPCIQI,LLIQPCIQII,QIIEQSRRKY,CIQIIEQSRR	UCEC
SLC16A6	c.293_294insG	p.G98fs	LTFSAPLATVLSNRFGHRLVVMLGG[p.G98fs]ATCQHRDGGRLLLTRGFSYVRRHRHHLWSGILL*	LLTRGFSYV,RLVVMLGGA,LTRGFSYVR,YVRRHRHHL,RHRHHLWSG,LLLTRGFSY,GFSYVRRHR,CQHRDGGRL,GRLLLTRGF,RGFSYVRRH,RHHLWSGIL,HHLWSGILL,LLLTRGFSYV,RLLLTRGFSY,SYVRRHRHHL,LTRGFSYVR,RGFSYVRRHR,RHRHHLWSGI,MLGGATCQHR,ATCQHRDGGR,LLTRGFSYVR,VMLGGATCQH,CQHRDGGRLL,FSYVRRHRHH,YVRRHRHHLW,HRHHLWSGIL,RHHLWSGILL	STAD
SLC16A9	c.1407_1424delCTGCGTCCTGCTGGGAGG	p.CVLLGG470del	LGPPIVGWFYDWTQTYDIAFYFSGF[p.CVLLGG470del]FILLLAALPSWDTCNKQLPKPAPTTFLYKVASNV*	AFYFSGFFI,FYFSGFFIL,YFSGFFILL,IAFYFSGFF,IAFYFSGFFI,AFYFSGFFIL,FYFSGFFILL,YFSGFFILLL,DIAFYFSGFF	KIRC
SLC17A9	c.970G>A	p.V324I	HLINQGYRAITVRKLMQGMGLGLSS[p.V324I]IFALCLGHTSSFCESVVFASASIGLQ	GMGLGLSSI,GLSSIFALC,SIFALCLGH,MGLGLSSIF,LGLSSIFAL,LSSIFALCL,GLGLSSIFAL,GLSSIFALCL,GMGLGLSSIF,QGMGLGLSSI	GBM
SLC1A2	c.1044_1045insT	p.F348fs	LIIHGGIFLPLIYFVVTRKNPFSFF[p.F348fs]CWHFPSLDHCPGHRFQCWNFACHLSLPGRKSGD*	KNPFSFFCW,PFSFFCWHF,SFFCWHFPS,FFCWHFPSL,LDHCPGHRF,GHRFQCWNF,FQCWNFACH,WNFACHLSL,NPFSFFCWH,FPSLDHCPG,CPGHRFQCW,SFFCWHFPSL,FQCWNFACHL,CWNFACHLSL,FACHLSLPGR,FSFFCWHFPS,RKNPFSFFCW,NPFSFFCWHF,SLDHCPGHRF,FPSLDHCPGH	LUAD
SLC20A1	c.984_985delAG	p.P328fs	PLQAVVEERTVSFKLGDLEEAPERE[p.P328fs]ASQRGLERGNQHR*	LEEAPEREA,RGLERGNQHR	UCEC
SLC22A15	c.602C>T	p.S201L	NGGMSLVAFVLLNECVGTAYWALAG[p.S201L]LIGGLFFAVGIAQYALLGYFIRSWRT	ALAGLIGGL,GLIGGLFFA,LIGGLFFAV,TAYWALAGL,AYWALAGLI,LAGLIGGLF,AGLIGGLFF,GLIGGLFFAV,GTAYWALAGL,ALAGLIGGLF,TAYWALAGLI,LAGLIGGLFF	CRC
SLC22A9	c.1220G>A	p.R407Q	LQTLFGAVILLANCVAPWALKYMNR[p.R407Q]QASQMLLMFLLAICLLAIIFVPQEMQ	YMNRQASQM,ALKYMNRQA,KYMNRQASQ,RQASQMLLM,MNRQASQML,QASQMLLMF,LKYMNRQAS,YMNRQASQML,KYMNRQASQM,RQASQMLLMF,MNRQASQMLL,LKYMNRQASQ,NRQASQMLLM	GBM
SLC24A2	c.401C>T	p.A134V	SENSTDHAQGDYPKDIFSLEERRKG[p.A134V]VIILHVIGMIYMFIALAIVCDEFFVP	RKGVIILHV,VIILHVIGMI,SLEERRKGVI,RKGVIILHVI,EERRKGVIIL	CRC
SLC24A5	c.103C>A	p.R35S	ARRALLLGILWATAHLPLSGTSLPQ[p.R35S]SLPRATGNSTQCVISPSSEFPEGFFT	SLPQSLPRA,TSLPQSLPR,LPQSLPRAT,GTSLPQSLPR	LUAD
SLC25A17	c.84delT	p.F28fs	LSYESLVHAVAGAVGSVTAMTVFFP[p.F28fs]WIQLDFDFRLMRKENPKLHTWCSWRSLKKKDSWHHIEGGFQ*	AMTVFFPWI,IQLDFDFRL,RLMRKENPK,KLHTWCSWR,CSWRSLKKK,TWCSWRSLK,TAMTVFFPW,FFPWIQLDF,PWIQLDFDF,SWHHIEGGF,LMRKENPKL,HTWCSWRSL,WIQLDFDFR,DFDFRLMRK,TVFFPWIQL,KENPKLHTW,RSLKKKDSW,KKKDSWHHI,RLMRKENPKL,HTWCSWRSLK,TWCSWRSLKK,VTAMTVFFPW,TAMTVFFPWI,VFFPWIQLDF,LMRKENPKLH,MTVFFPWIQL,IQLDFDFRLM,RKENPKLHTW,LHTWCSWRSL,LKKKDSWHHI,FPWIQLDFDF,NPKLHTWCSW	STAD
SLC25A32	c.247C>G	p.Q83E	LRPKYNGILHCLTTIWKLDGLRGLY[p.Q83E]EGVTPNIWGAGLSWGLYFFFYNAIKS	GLYEGVTPN,GLRGLYEGV,LYEGVTPNI,YEGVTPNIW,GLYEGVTPNI,LYEGVTPNIW	BRCA
SLC25A40	c.287G>A	p.R96Q	EGGNKLWYKKPGNFQGTLDAFFKII[p.R96Q]QNEGIKSLWSGLPPTLVMAVPATVIY	IQNEGIKSL,KIIQNEGIK,FKIIQNEGI,IQNEGIKSLW	CRC
SLC25A45	c.316G>T	p.G106C	LLVLTATSHQERRAQPPSYMHIFLA[p.G106C]CCTGGFLQAYCLAPFDLIKVRLQNQT	FLACCTGGF,YMHIFLACC,SYMHIFLAC,YMHIFLACCT,FLACCTGGFL,SYMHIFLACC,IFLACCTGGF,CCTGGFLQAY	BRCA

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
SLC25A48	c.199G>A	p.A67T	TLSCIRVVYRRESMFGFFKGMSFPL[p.A67T]TSIAVYNSVVFGVFSNTQRFLSQHRC	GMSFPLTSI,TSIAVYNSV,MSFPLTSIA,FPLTSIAVY,MSFPLTSIAV,GMSFPLTSIA,LTSIAVYNSV,KGMSFPLTSI,SFPLTSIAVY,TSIAVYNSVV	DLBCL
SLC25A48	c.301C>A	p.R101S	VFGVFSNTQRFLSQHRCGEPEASPP[p.R101S]STLSDLLLASMVAGVVSVGLGGPVDL	SPPSTLSDL,EPEASPPSTL	LUAD
SLC25A5	c.235A>T	p.I79F	IIDCVVRIPKEQGVLSFWRGNLANV[p.I79F]FRYFPTQALNFAFKDKYKQIFLGGVD	NLANVFRYF,RGNLANVFR,VFRYFPTQA,GNLANVFRY,WRGNLANVF,FRYFPTQAL,NVFRYFPTQA,FWRGNLANVF,VFRYFPTQAL,RGNLANVFRY,GNLANVFRYF	CESC
SLC25A5	c.352G>A	p.A118T	DKYKQIFLGGVDKRTQFWLYFAGNL[p.A118T]TSGGAAGATSLCFVYPLDFARTRLAA	WLYFAGNLT,LTSGGAAGA,NLTSGGAAGA,WLYFAGNLTS	KIRC
SLC26A3	c.262G>A	p.V88I	WLPAYRLKEWLLSDIVSGISTGIVA[p.V88I]ILQGLAFALLVDIPPVYGLYASFFPA	GISTGIVAI,GIVAILQGL,AILQGLAFA,ILQGLAFAL,VAILQGLAF,ISTGIVAIL,AILQGLAFAL,ILQGLAFALL,GISTGIVAIL,GIVAILQGLA,IVAILQGLAF,SGISTGIVAI	GBM
SLC26A7	c.1886delT	p.I629fs	LAHCTASLIKAMTYYGNLDSEKPIF[p.I629fs]LNRYLLQ*	KPIFLNRYL,NLDSEKPIFL,SEKPIFLNRY,DSEKPIFLNR,KPIFLNRYLL	STAD
SLC27A3	c.1927delC	p.P643fs	VNVYGVTVPGHEGRAGMAALVLRPP[p.P643fs]TLWTLCSSTPTCLRTCHLMPGPDSSGSRSLWPPQRPSNSRKFGWQMRASTPAPCLTHCTFWTRL*	WQMRASTPA,ALVLRPPTL,CSSTPTCLR,LTHCTFWTR,GSRSLWPPQ,PQRPSNSRK,QMRASTPAP,RASTPAPCL,NSRKFGWQM,LVLRPPTLW,RKFGWQMRA,APCLTHCTF,VLRPPTLWTL,TLCSSTPTCL,GSRSLWPPQR,RSLWPPQRPS,NSRKFGWQMR,QMRASTPAPC,LTHCTFWTRL,CLTHCTFWTR,TPTCLRTCHL,GPDSSGSRSL,AALVLRPPTL,ALVLRPPTLW,PQRPSNSRKF,SNSRKFGWQM,RKFGWQMRAS,WQMRASTPAP,MRASTPAPCL,RPSNSRKFGW,APCLTHCTFW	STAD
SLC2A6	c.689C>A	p.A230D	LIMILLLSFMPNSPRFLLSRGRDEE[p.A230D]DLRALAWLRGTDVDVHWEFEQIQDNV	DLRALAWLR,EEDLRALAW,DEEDLRALAW,EEDLRALAWL	PRAD
SLC2A7	c.193G>A	p.A65T	YNLSVVNTPHKVFKSFYNETYFERH[p.A65T]TTFMDGKLMLLLWSCTVSMFPLGGLL	TYFERHTTF,ETYFERHTT,HTTFMDGKL,YFERHTTFM,TTFMDGKLM,TYFERHTTFM,ETYFERHTTF	CRC
SLC2A7	c.804C>A	p.H268Q	LRGHTDMEAELEDMRAEARAERAEG[p.H268Q]QLSVLHLCALRSLRWQLLSIIVLMAG	RAEGQLSVL,AERAEGQLS,AEGQLSVLH,QLSVLHLCAL,AERAEGQLSV,AEGQLSVLHL,GQLSVLHLCA	TGCT
SLC30A9	c.581G>A	p.R194H	LRSDVEAKSLEVWGSPEALAREKKL[p.R194H]HKEAEIEYRERLFRNQKILREYRDFL	LAREKKLHK,LHKEAEIEY,REKKLHKEA,ALAREKKLHK,KLHKEAEIEY	CRC
SLC32A1	c.1480G>A	p.V494I	CFLLPSLFHLRLLWRKLLWHQVFFD[p.V494I]IAIFVIGGICSVSGFVHSLEGLIEAY	VFFDIAIFV,LWHQVFFDI,FFDIAIFVI,IAIFVIGGI,QVFFDIAIF,HQVFFDIAI,LLWHQVFFDI,QVFFDIAIFV,VFFDIAIFVI,DIAIFVIGGI,HQVFFDIAIF,WHQVFFDIAI	STAD
SLC33A1	c.1625C>T	p.S542L	CVFIGFGWWFFLGPKFKKLQDEGSS[p.S542L]LWKCKRNN*	KLQDEGSSL,LQDEGSSLW,KKLQDEGSSL,KLQDEGSSLW	CRC
SLC35D3	c.1250G>C	p.*417S	VWRLVRGTRYMKKDYLIENEELPSP[p.*417S]SEGGACTYLCAYTYFIC*	PSEGGACTY,CTYLCAYTY,YLCAYTYFI,TYLCAYTYF,GACTYLCAY,SEGGACTYL,YLCAYTYFIC,CTYLCAYTYF,TYLCAYTYFI,GGACTYLCAY,ACTYLCAYTY,SPSEGGACTY	HNSC
SLC35F3	c.838G>A	p.A280T	CNKAFVFLLSWIVLRDRFMGVRIVA[p.A280T]TILAIAGIVMMTYADGFHSHSVIGIA	FMGVRIVAT,RIVATILAI,IVATILAIA,ATILAIAGI,GVRIVATIL,TILAIAGIV,MGVRIVATI,FMGVRIVATI,RIVATILAIA,ATILAIAGIV,RFMGVRIVAT,GVRIVATILA,MGVRIVATIL,VRIVATILAI,TILAIAGIVM	CRC
SLC35G2	c.184delA	p.K62fs	INEGYGNFMEENPKKGLLSEMKKKG[p.K62fs]ELSLEPWIPYLHQQKTQ*	LSLEPWIPY,SLEPWIPYL,SEMKKKGEL,MKKKGELSL,GELSLEPWI,IPYLHQQKT,LSLEPWIPYL,EMKKKGELSL,ELSLEPWIPY,KKGELSLEPW	CESC
SLC37A1	c.1582G>A	p.V528I	ACALLFLIRLIHKELSCPGSATGDQ[p.V528I]IPFKEQ*	ATGDQIPFK,SATGDQIPF,SATGDQIPFK,GSATGDQIPF,CPGSATGDQI	TGCT
SLC38A1	c.298G>A	p.G100R	MSVFNLSNAIMGSGILGLAFALANT[p.G100R]RILLFLVLLTSVTLLSIYSINLLLIC	ALANTRILL,RILLFLVLL,LAFALANTR,NTRILLFLV,LANTRILLF,FALANTRIL,TRILLFLVL,ALANTRILLF,NTRILLFLVL,GLAFALANTR,LAFALANTRI,FALANTRILL	TGCT
SLC38A10	c.3213_3215delCAT	p.1071_1072II>I	SDLRRRRRDLGPHAEGQLAPRDGVI[p.1071_1072II>I]GLNPLPDVQVNDLRGALDAQLRQAAGGA	APRDGVIGL,RDGVIGLNPL	PAAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
SLC39A12	c.1883G>C	p.C628S	ILMNFISSLTAFMGLYIGLSVSADP[p.C628S]SVQDWIFTVTAGMFLYLSLVEMLPEM	SVQDWIFTV,DPSVQDWIF,GLSVSADPSV	LUAD
SLC39A6	c.158G>T	p.R53L	AFPQTTEKISPNWESGINVDLAIST[p.R53L]LQYHLQQLFYRYGENNSLSVEGFRKL	TLQYHLQQL,AISTLQYHL,LQYHLQQLF,DLAISTLQY,LQYHLQQLFY,TLQYHLQQLF,INVDLAISTL,VDLAISTLQY,LAISTLQYHL,STLQYHLQQL	LUAD
SLC39A7	c.1144C>T	p.R382C	LHEVPHEVGDFAILVQSGCSKKQAM[p.R382C]CLQLLTAVGALAGTACALLTEGGAVG	KQAMCLQLL,AMCLQLLTA,KKQAMCLQL,AMCLQLLTAV,SKKQAMCLQL,KKQAMCLQLL,KQAMCLQLLT	CRC
SLC39A7	c.1367_1368insG	p.L456fs	SVLPELLREASPLQSLLEVLGLLGG[p.L456fs]SYHDGADCPP*	VLGLLGGSY,LLGGSYHDGA,EVLGLLGGSY,LEVLGLLGGS	CLL
SLC43A1	c.398C>T	p.P133L	LVGSACFTASCTLMALASRDVEALS[p.P133L]LLIFLALSLNGFGGICLTFTSLTLPN	ALSLLIFLA,LLIFLALSL,EALSLLIFL,RDVEALSLL,VEALSLLIF,LSLLIFLAL,ALSLLIFLAL,SLLIFLALSL,ASRDVEALSL,EALSLLIFLA,RDVEALSLLI,VEALSLLIFL	CRC
SLC43A3	c.647G>A	p.R216H	LLYEKGISLRASFIFISVCSTWHVA[p.R216H]HTFLLMPRGHIPYPLPPNYSYGLCPG	STWHVAHTF,TWHVAHTFL,HVAHTFLLM,WHVAHTFLL,STWHVAHTFL,VAHTFLLMPR,CSTWHVAHTF,TWHVAHTFLL,WHVAHTFLLM	CRC
SLC44A5	c.208G>T	p.V70F	KPADTPSEEEDFGDPRTYDPDFKGP[p.V70F]FANRSCTDVLCCMIFLLCIIGYIVLG	FANRSCTDV,DFKGPFANR,TYDPDFKGPF,FANRSCTDVL	KIRC
SLC44A5	c.554G>A	p.R185H	CPEKFLTYVEMQLLYTKDKSYWEDY[p.R185H]HQFCKTTAKPVKSLTQLLLDDDCPTA	HQFCKTTAK,SYWEDYHQF,YHQFCKTTA,KSYWEDYHQF,SYWEDYHQFC,HQFCKTTAKP,WEDYHQFCKT	CRC
SLC4A3	c.3183delG	p.L1061fs	SQKARRLLKGSGFHLDLLLIGSLGG[p.L1061fs]SVGCLGCPGSRLPRSAPSPMSMR*	LLIGSLGGS,LIGSLGGSV,SLGGSVGCL,RSAPSPMSM,SAPSPMSMR,LPRSAPSPM,LLIGSLGGSV,RLPRSAPSPM,RSAPSPMSMR,GSRLPRSAPS	STAD
SLC4A5	c.1597A>G	p.I533V	WFPSDFYDGFHIQSISAILFIYLGC[p.I533V]VTNAITFGGLLGDATDNYQGVMESFL	ILFIYLGCV,YLGCVTNAI,GCVTNAITF,AILFIYLGCV,FIYLGCVTNA,YLGCVTNAIT,ILFIYLGCVT,IYLGCVTNAI,LGCVTNAITF	LUAD
SLC4A8	c.687C>G	p.N229K	LNDSMRVKVREALLKKHHHQNEKKR[p.N229K]KNLIPIVRSFAEVGKKQSDPHLMDKH	KKRKNLIPI,KRKNLIPIV,KKRKNLIPIV,EKKRKNLIPI,HQNEKKRKNL,KNLIPIVRSF	KIRC
SLC52A1	c.1108_1110delGGC	p.G370del	LSLLGMLFGAYLMALAILSPCPPLV[p.G370del]TTAGVVLVVLSWVLCLCVFSYVKVAASS	VTTAGVVLV,LVTTAGVVL,LVTTAGVVLV,VTTAGVVLVV,CPPLVTTAGV	KIRC
SLC52A2	c.1197_1198insG	p.G399fs	LSWVLCLGVFSYVKVAASSLLHGGG[p.G399fs]PAGIAGSRRGHPGGLSARRCCYVPPDQHLSRVPQQKGLCRPL*	SLLHGGGPA,LSARRCCYV,HLSRVPQQK,CYVPPDQHL,GSRRGHPGG,RGHPGGLSA,GLSARRCCY,QQKGLCRPL,LLHGGGPAGI,GLSARRCCYV,GSRRGHPGGL,RGHPGGLSAR,SARRCCYVPP,VPPDQHLSRV	KIRC
SLC5A1	c.157G>T	p.G53W	DISIIVIYFVVVMAVGLWAMFSTNR[p.G53W]WTVGGFFLAGRSMVWWPIGASLFASN	WTVGGFFLA,WAMFSTNRW,MFSTNRWTV,RWTVGGFFL,AMFSTNRWT,TNRWTVGGF,NRWTVGGFF,AMFSTNRWTV,LWAMFSTNRW,RWTVGGFFLA,STNRWTVGGF,TNRWTVGGFF	LUAD
SLC5A7	c.1006G>T	p.G336C	KTTEEADMILPIVLQYLCPVYISFF[p.G336C]CLGAVSAAVMSSADSSILSASSMFAR	YISFFCLGA,CLGAVSAAV,ISFFCLGAV,VYISFFCLG,YISFFCLGAV,FCLGAVSAAV,VYISFFCLGA,CLGAVSAAVM,CPVYISFFCL	HNSC
SLC5A7	c.1325G>T	p.G442V	IFPQLLCVLFVKGTNTYGAVAGYVS[p.G442V]VLFLRITGGEPYLYLQPLIFYPGYYP	AVAGYVSVL,YVSVLFLRI,VAGYVSVLF,GYVSVLFLR,AGYVSVLFL,AGYVSVLFLR,AVAGYVSVLF,GYVSVLFLRI,YGAVAGYVSV,GAVAGYVSVL	LUAD
SLC6A10P	c.264A>C	p.K88N	WSFFTPLVCMGIFIFNVVYYKPLVY[p.K88N]NNTNVYPWWGEAMGWAFVLSSMLCMP	YYKPLVYNN,YYKPLVYNNT,KPLVYNNTNV	GBM,KIRC
SLC6A11	c.896G>T	p.W299L	TLPGASEGIKFYLYPDLSRLSDPQV[p.W299L]LVDAGTQIFFSYAICLGCLTALGSYN	RLSDPQVLV,VLVDAGTQI,SRLSDPQVL,LVDAGTQIF,LVDAGTQIFF,VLVDAGTQIF,LSRLSDPQVL	LUAD
SLC6A14	c.255_256insG	p.A85fs	FPYLTYSNGGGAFLIPYAIMLALAG[p.A85fs]FTFVLSGVFTGTIC*	LALAGFTFV,ALAGFTFVL,VLSGVFTGT,MLALAGFTF,FTFVLSGVF,AIMLALAGF,MLALAGFTFV,FVLSGVFTGT,VLSGVFTGTI,AIMLALAGFT,ALAGFTFVLS,AGFTFVLSGV,YAIMLALAGF,IMLALAGFTF,GFTFVLSGVF,FTFVLSGVFT,LALAGFTFVL	KIRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
SLC6A9	c.281G>A	p.R94K	LLPQLMAQHSLAMAQNGAVPSEATK[p.R94K]KDQNLKRGNWGNQIEFVLTSVGYAVG	AVPSEATKK,ATKKDQNLK,ATKKDQNLKR	CLL
SLC6A9	c.727C>T	p.R243W	AYCNNPWNTHDCAGVLDASNLTNGS[p.R243W]WPAALPSNLSHLLNHSLQRTSPSEEY	NLTNGSWPA,WPAALPSNL,ASNLTNGSW,NLTNGSWPAA,SWPAALPSNL,LTNGSWPAAL,DASNLTNGSW	BLCA
SLC7A10	c.471delC	p.P157fs	TSLAVISMTFSNYVLQPVFPNCIPP[p.P157fs]PQPPGCCPWPA*	FPNCIPPPQ	STAD
SLC7A2	c.964C>T	p.R322W	TLAGAATCFYAFVGFDCIATTGEEV[p.R322W]WNPQKAIPIGIVTSLLVCFMAYFGVS	EVWNPQKAI,EEVWNPQKA,IATTGEEVW,EEVWNPQKAI,GEEVWNPQKA	UCEC
SLC8A1	c.1292G>A	p.R431H	VSKIFFEQGTYQCLENCGTVALTII[p.R431H]HRGGDLTNTVFVDFRTEDGTANAGSD	GTVALTIIH,TVALTIIHR,GTVALTIIHR	CRC
SLC8A1	c.1297G>T	p.G433C	KIFFEQGTYQCLENCGTVALTIIRR[p.G433C]CGDLTNTVFVDFRTEDGTANAGSDYE	CGDLTNTVF,RCGDLTNTVF	LUAD
SLC9A2	c.2237delC	p.T746fs	SPQSYKMEWKNEVDVDSGRDMPSTP[p.T746fs]QHPTAEKRAPRRQAYYSSPFSLKTSLAQRGKTV*	SLAQRGKTV,KTSLAQRGK,RQAYYSSPF,AYYSSPFSL,RAPRRQAYY,YYSSPFSLK,SLKTSLAQR,KRAPRRQAY,PTAEKRAPR,MPSTPQHPT,SPFSLKTSL,AYYSSPFSLK,STPQHPTAEK,FSLKTSLAQR,RQAYYSSPFS,QAYYSSPFSL,KRAPRRQAYY,PTAEKRAPRR,MPSTPQHPTA,SPFSLKTSLA,RRQAYYSSPF,AEKRAPRRQA	STAD
SLC9A4	c.1892G>A	p.R631H	RTLSYNKYNLKPQTSEKQAKEILIR[p.R631H]HQNTLRESMRKGHSLPWGKPAGTKNI	ILIRHQNTL,LIRHQNTLR,HQNTLRESM,KEILIRHQN,ILIRHQNTLR,HQNTLRESMR,EILIRHQNTL,KQAKEILIRH,RHQNTLRESM,KEILIRHQNT	GBM
SLC9A5	c.1341G>C	p.L447F	TKVPAKDYFVATTIVVVFFTVIVQG[p.L447F]FTIKPLVKWLKVKRSEHHKPTLNQEL	VIVQGFTIK,FFTVIVQGF,FTIKPLVKW,GFTIKPLVK,FTVIVQGFT,TVIVQGFTI,VQGFTIKPL,FTIKPLVKWL,TVIVQGFTIK,QGFTIKPLVK,VFFTVIVQGF,GFTIKPLVKW,FTVIVQGFTI	BLCA
SLC9B1	c.1338_1339delGT	p.V446fs	FAGFSFKEKIFIALAWMPKATVQAV[p.V446fs]RSSGSRNSKSLRTPLGTICEGCDDSSIFSHLDHSSKWSSTYGHSGA*	HSSKWSSTY,SLRTPLGTI,RSSGSRNSK,FSHLDHSSK,GSRNSKSLR,SSKWSSTYG,NSKSLRTPL,SHLDHSSKW,SKWSSTYGH,AVRSSGSRNS,KSLRTPLGTI,IFSHLDHSSK,SSKWSSTYGH,MPKATVQAVR,RNSKSLRTPL,CEGCDDSSIF,FSHLDHSSKW	KIRC
SLCO2A1	c.1437G>C	p.M479I	IFHPVCGDNGIEYLSPCHAGCSNIN[p.M479I]ISSATSKQLIYLNCSCVTGGSASAKT	ISSATSKQL,NINISSATSK,ISSATSKQLI	CESC
SLIT1	c.4379G>T	p.R1460L	SGTKGAHCVCDPGFSGELCEQESEC[p.R1460L]LGDPVRDFHQVQRGYAICQTTRPLSW	ESECLGDPV,CLGDPVRDF,QESECLGDPV	LUAD
SLITRK1	c.134delA	p.K45fs	TGDVCKEKICSCNEIEGDLHVDCEK[p.K45fs]RASQVCSVSLPRLPSFTIYFCMAIPSLDFSLMSSLTFIMRLVCTWKTMACMKSFRGLFWGCSW*	FTIYFCMAI,SLMSSLTFI,LMSSLTFIM,SLTFIMRLV,IMRLVCTWK,TMACMKSFR,QVCSVSLPR,MSSLTFIMR,VSLPRLPSF,RLPSFTIYF,YFCMAIPSL,CMAIPSLDF,FSLMSSLTF,FIMRLVCTW,KTMACMKSF,CMKSFRGLF,RGLFWGCSW,TWKTMACMK,KSFRGLFWG,LPRLPSFTI,IPSLDFSLM,RLVCTWKTM,KRASQVCSV,ASQVCSVSL,SQVCSVSLP,LDFSLMSSL,CTWKTMACM,MKSFRGLFW,CEKRASQVC,LPSFTIYFC,SLPRLPSFTI,RLPSFTIYFC,SLDFSLMSSL,FSLMSSLTFI,SLMSSLTFIM,RLVCTWKTMA,LMSSLTFIMR,FIMRLVCTWK,CTWKTMACMK,KTMACMKSFR,SQVCSVSLPR,SFTIYFCMAI,IYFCMAIPSL,FCMAIPSLDF,DFSLMSSLTF,TFIMRLVCTW,CMKSFRGLFW,SSLTFIMRLV,MAIPSLDFSL,MSSLTFIMRL,RASQVCSVSL,LPRLPSFTIY,LPSFTIYFCM,MACMKSFRGL,SVSLPRLPSF,MRLVCTWKTM,WKTMACMKSF,ACMKSFRGLF,FRGLFWGCSW,CEKRASQVCS	STAD
SLITRK1	c.155G>A	p.R52H	KICSCNEIEGDLHVDCEKKGFTSLQ[p.R52H]HFTAPTSQFYHLFLHGNSLTRLFPNE	SLQHFTAPT,KGFTSLQHF,HFTAPTSQF,FTSLQHFTA,LQHFTAPTS,HFTAPTSQFY,KKGFTSLQHF,LQHFTAPTSQ,QHFTAPTSQF	CRC
SLITRK3	c.641G>T	p.R214L	PTNLFKAVSLTHLDLRGNRLKVLFY[p.R214L]LGMLDHIGRSLMELQLEENPWNCTCE	FYLGMLDHI,RLKVLFYLG,KVLFYLGML,LKVLFYLGM,LFYLGMLDHI,RLKVLFYLGM,YLGMLDHIGR,LKVLFYLGML	LUSC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
SLITRK3	c.893C>T	p.S298L	REIRKTELCPLLSDSEVEASLGIPH[p.S298L]LSSSKENAWPTKPSSMLSSVHFTASS	GIPHLSSSK,LSSSKENAW,LGIPHLSSSK,VEASLGIPHL,HLSSSKENAW	CRC
SLITRK5	c.1403G>T	p.R468M	NRISMIQDRAFGDLTNLRRLYLNGN[p.R468M]MIERLSPELFYGLQSLQYLFLQYNLI	RLYLNGNMI,YLNGNMIER,RRLYLNGNM,YLNGNMIERL,NMIERLSPEL,LYLNGNMIER,LRRLYLNGNM,RRLYLNGNMI,MIERLSPELF	LUAD
SLITRK5	c.203G>T	p.R68L	YYGEICDNACPCEEKDGILTVSCEN[p.R68L]LGIISLSEISPPRFPIYHLLLSGNLL	ILTVSCENL,TVSCENLGI,CENLGIISL,NLGIISLSEI,LTVSCENLGI,CENLGIISLS	LUAD
SLITRK6	c.2223C>A	p.N741K	HLQRSLLEQENHSPLTGSNMKYKTT[p.N741K]KQSTEFLSFQDASSLYRNILEKEREL	KQSTEFLSF,SNMKYKTTK,KYKTTKQST,TTKQSTEFL,KTTKQSTEF,GSNMKYKTTK,KTTKQSTEFL,MKYKTTKQST,YKTTKQSTEF,TKQSTEFLSF	LUAD
SMAD2	c.962G>A	p.R321Q	SLTVDGFTDPSNSERFCLGLLSNVN[p.R321Q]QNATVEMTRRHIGRGVRLYYIGGEVF	LLSNVNQNA,VNQNATVEM,GLLSNVNQNA,NVNQNATVEM	CRC
SMAD4	c.1082G>A	p.R361H	GETFKVPSSCPIVTVDGYVDPSGGD[p.R361H]HFCLGQLSNVHRTEAIERARLHIGKG	YVDPSGGDHF,DPSGGDHFCL	CRC
SMAP1	c.506delA	p.E169fs	QPLVSSPSLQAAVDKNKLEKEKEKK[p.E169fs]RKRKREKRSQKSRQNHLQLKSCRRKISNWSLKKVPALKKLRSPLWIF*	ALKKLRSPL,KISNWSLKK,SLKKVPALK,KLRSPLWIF,KKRKRKREK,RKREKRSQK,RSQKSRQNH,SQKSRQNHL,KSRQNHLQL,RRKISNWSL,RKISNWSLK,KVPALKKLR,HLQLKSCRR,WSLKKVPAL,RQNHLQLKS,KKVPALKKL,LKKLRSPLW,KKLRSPLWI,KISNWSLKKV,KSRQNHLQLK,SLKKVPALKK,WSLKKVPALK,KRKREKRSQK,RSQKSRQNHL,HLQLKSCRRK,RRKISNWSLK,CRRKISNWSL,NWSLKKVPAL,QKSRQNHLQL,RQNHLQLKSC,LQLKSCRRKI,ALKKLRSPLW,KKLRSPLWIF	UCS
SMARCA4	c.1142G>A	p.R381Q	QKPRGLDPVEILQEREYRLQARIAH[p.R381Q]QIQELENLPGSLAGDLRTKATIELKA	LQARIAHQI,RIAHQIQEL,HQIQELENL,RLQARIAHQI,ARIAHQIQEL	CRC
SMARCA4	c.2738C>T	p.P913L	NHHCKLTQVLNTHYVAPRRLLLTGT[p.P913L]LLQNKLPELWALLNFLLPTIFKSCST	RLLLTGTLL,LLQNKLPEL,LTGTLLQNK,RRLLLTGTL,TLLQNKLPEL,LLTGTLLQNK,RRLLLTGTLL	HNSC
SMARCA5	c.468_471delAGAA	p.T156fs	KQNLLSVGDYRHRRTEQEEDEELLT[p.T156fs]APKQPMFALDLKTLHRM*	APKQPMFAL,LLTAPKQPM,LTAPKQPMF,KQPMFALDL,LDLKTLHRM,KQPMFALDLK,LTAPKQPMFA,FALDLKTLHR,TAPKQPMFAL,LLTAPKQPMF,PMFALDLKTL,QEEDEELLTA	TGCT
SMC3	c.2908G>C	p.E970Q	ELGSLPQEAFEKYQTLSLKQLFRKL[p.E970Q]QQCNTELKKYSHVNKKALDQFVNFSE	KLQQCNTEL,KLQQCNTELK,QQCNTELKKY,RKLQQCNTEL	TGCT
SMCR8	c.523G>A	p.E175K	VRPFCMAYISADQHKIMQQFQELSA[p.E175K]KFSRASECLKTGNRKAFAGELEKKLK	ELSAKFSRA,QQFQELSAK,QFQELSAKF,AKFSRASEC,MQQFQELSAK,KFSRASECLK,QQFQELSAKF,AKFSRASECL,QELSAKFSRA	UCEC
SMG1	c.8087C>A	p.P2696H	LICNTTVERCQELYRKYEMQYAPQP[p.P2696H]HPTVCQFITATEMTLQRYAADINSRL	YAPQPHPTV,APQPHPTVC,QPHPTVCQF,MQYAPQPHP,QYAPQPHPTV,YEMQYAPQPH,MQYAPQPHPT,HPTVCQFITA,QPHPTVCQFI	TGCT
SMG7	c.2536_2537insA	p.E846fs	TQDPIKLFEPSLQPPVMQQQPLEKK[p.E846fs]NEAFSHGAI*	NEAFSHGAI,QPLEKKNEAF,KKNEAFSHGA	PRAD
SNAPC1	c.633delT	p.D211fs	QNMKHVISVDKSKPDKALSLIKDDF[p.D211fs]LTILRT*	LIKDDFLTI,IKDDFLTIL,SLIKDDFLTI,ALSLIKDDFL,LIKDDFLTIL	STAD
SNAPC2	c.875delC	p.T292fs	IPAGGSLGPAAEGDGAGSKAPEETP[p.T292fs]QPPRRPSTAN*	TPQPPRRPS,TPQPPRRPST	STAD
SND1	c.112C>G	p.Q38E	GPAVPTVQRGIIKMVLSGCAIIVRG[p.Q38E]EPRGGPPPERQINLSNIRAGNLARA	AIIVRGEPR,CAIIVRGEPR	CESC
SND1	c.2163delC	p.H721fs	VQDVETGTQLEKLMENMRNDIASHP[p.H721fs]L*	RNDIASHPL,MRNDIASHPL	STAD
SOAT1	c.190delT	p.F64fs	GRIDIKQLIAKKIKLTAEAEELKPF[p.F64fs]L*	AEAEELKPFL	STAD
SOLH	c.2141G>A	p.R714H	GFLMGASCGGGNMKVDDSAYESLGL[p.R714H]HPRHAYSILDVRDVQGTRLLRLRNPW	GLHPRHAYS,LGLHPRHAY,HPRHAYSIL,SAYESLGLH,YESLGLHPR,GLHPRHAYSI,SLGLHPRHAY,YESLGLHPRH	LIHC
SON	c.2723C>T	p.S908L	AQMLASGTMDAQMLASSTQDSAMLG[p.S908L]LKSPDPYRLAQDPYRLAQDPYRLGHD	GLKSPDPYR,LGLKSPDPY,TQDSAMLGL,LKSPDPYRL,GLKSPDPYRL,TQDSAMLGLK,MLGLKSPDPY,STQDSAMLGL	LUSC

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SON	c.4075_4098delGTCCTGGAGTCTTCGGCTGTGACC	p.VLESSAVT1359del	LAESILEPPAMAAPESSAMAVLESS[p.VLESSAVT1359del]TVTVLESSTVTVLEPSVVTVPEPPVVAEPDYVTIPVPVVSALEPSVPVL	AMAVLESST,MAVLESSTV,AMAVLESSTV,AVLESSTVTV	KIRC
SORBS1	c.1710C>A	p.F570L	VLTNEKMSRDISPEEIDLKNEPWYK[p.F570L]LFSELEFGKPPPKKIWDYTPGDCSIL	KNEPWYKLF,PWYKLFSEL,LKNEPWYKL,YKLFSELEF,KLFSELEFGK,WYKLFSELEF,EPWYKLFSEL,LKNEPWYKLF	CRC
SORBS1	c.3466G>A	p.V1156M	AERGAGERGPGGPKISKKSCLKPSD[p.V1156M]MVRCLSTEQRLSDLNTPEESRPGKPL	CLKPSDMVR,KPSDMVRCL,MVRCLSTEQR,KKSCLKPSDM	CRC
SORBS2	c.2596C>T	p.P866S	VFEALDSALKDICDQIKAEKKRGSL[p.P8665]SDNSILHRLISELLPDVPERNSSLRA	RGSLSDNSI,LSDNSILHRL,SLSDNSILHR,RGSLSDNSIL	PAAD
SORBS2	c.3472delG	p.E1158fs	DRIHSLSSNKPQRPVFTHENIQGGG[p.E1158fs]NRFRLCITILPGMKMSWSSEKVMSLMSWKSVMTAGLWGPQEEPNSLVLSPETTSRGCELRSLLL*	SSEKVMSLM,KMSWSSEKV,SLMSWKSVM,LMSWKSVMT,KVMSLMSWK,CITILPGMK,RFRLCITIL,ILPGMKMSW,MSLMSWKSV,MSWKSVMTA,TTSRGCELR,MTAGLWGPQ,ETTSRGCEL,GPQEEPNSL,MSWSSEKVM,NRFRLCITI,ITILPGMKM,WSSEKVMSL,EKVMSLMSW,WKSVMTAGL,KSVMTAGLW,QEEPNSLVL,SEKVMSLMS,VMSLMSWKSV,SLMSWKSVMT,LMSWKSVMTA,RLCITILPGM,GMKMSWSSEK,LVLSPETTSR,RFRLCITILP,MSLMSWKSVM,SWKSVMTAGL,NIQGGGNRFR,ETTSRGCELR,WSSEKVMSLM,KMSWSSEKVM,IQGGGNRFRL,NRFRLCITIL,MKMSWSSEKV,SEKVMSLMSW,MSWKSVMTAG,WKSVMTAGLW	STAD
SORCS2	c.958C>T	p.R320W	FWSVSGVDADPDLVHVEAQDLGGDF[p.R320W]WYVTCAIHNCSEKMLTAPFAGPIDHG	DLGGDFWYV,DFWYVTCAI,GDFWYVTCA,AQDLGGDFWY,GDFWYVTCAI,EAQDLGGDFW	CRC
SORL1	c.614G>T	p.R205L	ADAYAQYLWITFDFCNTLQGFSIPF[p.R205L]LAADLLLHSKASNLLLGFDRSHPNKQ	LQGFSIPFL,PFLAADLLL,IPFLAADLL,TLQGFSIPFL,FLAADLLLHS,LAADLLLHSK,FSIPFLAADL,IPFLAADLLL	LUAD
SOS1	c.697A>T	p.N233Y	FMAEIRQYIRELNLIIKVFREPFVS[p.N233Y]YSKLFSANDVENIFSRIVDIHELSVK	PFVSYSKLF,VFREPFVSY,VSYSKLFSA,EPFVSYSKL,REPFVSYSK,FVSYSKLFSA,KVFREPFVSY,VFREPFVSYS,REPFVSYSKL,EPFVSYSKLF	LUAD,UCEC
SOWAHA	c.371G>C	p.R124P	AAQPSKPTSTVLPRSASAPGAPPLV[p.R124P]PVPRPVEPPGDLGLPTEPQDTPGGPA	APGAPPLVPV	ACC
SOX17	c.1208G>T	p.S403I	PYQGHDSGVNLPDSHGAISSVVSDA[p.S403I]ISAVYYCNYPDV*	VSDAISAVY,ISAVYYCNY,VVSDAISAV,ISSVVSDAI,SDAISAVYY,VVSDAISAVY,VSDAISAVYY,SVVSDAISAV,AISSVVSDAI,AISAVYYCNY	UCEC
SOX6	c.2155C>T	p.R719W	HLEKYPNYKYKPRPKRTCIVDGKKL[p.R719W]WIGEYKQLMRSRRQEMRQFFTVGQQP	LWIGEYKQL,GKKLWIGEY,KLWIGEYKQL,LWIGEYKQLM,WIGEYKQLMR	CRC
SOX7	c.925delC	p.L309fs	RRIPHLPGHPYSPEYAPSPLHCSHP[p.L309fs]WAPWPLASPPASP*	SHPWAPWPL,SPLHCSHPW,HPWAPWPLA,HCSHPWAPW,WPLASPPAS,CSHPWAPWPL,APWPLASPPA,LHCSHPWAPW,HPWAPWPLAS	STAD
SOX9	c.223G>A	p.E75K	ENTFPKGEPDLKKESEEDKFPVCIR[p.E75K]KAVSQVLKGYDWTLVPMPVRVNGSSK	CIRKAVSQV,RKAVSQVLK,FPVCIRKAV,IRKAVSQVL,CIRKAVSQVL,IRKAVSQVLK,KAVSQVLKGY,FPVCIRKAVS	LUAD
SP4	c.17_19delAGG	p.E11del	MSDQKKEEEE[p.E11del]AAAAAAMATEGGKTSEPENNNKKPKTSG	KEEEEAAAA,KEEEEAAAAA	LUSC
SP4	c.19G>A	p.E7K	MSDQKK[p.E7K]KEEEEAAAAAAMATEGGKTSEPENNN	KEEEEAAAA,KEEEEAAAAA	TGCT
SPAG16	c.1315G>T	p.V439L	GDTTVKLWDLCKGDCILTFEGHSRA[p.V439L]LWSCTWHSCGNFVASSSLDKTSKIWD	ALWSCTWHS,HSRALWSCT,FEGHSRALW,SRALWSCTW,RALWSCTWH,ALWSCTWHSC,LTFEGHSRAL,TFEGHSRALW,HSRALWSCTW	LUAD
SPAG16	c.1462C>T	p.P488S	WDVNSERCRCTLYGHTDSVNSIEFF[p.P488S]SFSNTLLTSSADKTLSIWDARTGICE	EFFSFSNTL,NSIEFFSFS,VNSIEFFSF,IEFFSFSNT,FSFSNTLLT,SVNSIEFFSF,EFFSFSNTLL,IEFFSFSNTL,FSFSNTLLTS	SKCM
SPAG17	c.3790delC	p.Q1264fs	GQESTGQYVIDEEPTWDIMVRQSYP[p.Q1264fs]RG*	IMVRQSYPR,MVRQSYPRG,DIMVRQSYPR	STAD

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SPAM1	c.1037G>A	p.R346Q	LVYTFGETVALGASGIVIWGTLSIM[p.R346Q]QSMKSCLLLDNYMETILNPYIINVTL	IMQSMKSCL,MQSMKSCLL,TLSIMQSMK,GTLSIMQSM,QSMKSCLLL,IMQSMKSCLL,SIMQSMKSCL,MQSMKSCLLL,GTLSIMQSMK,WGTLSIMQSM	GBM
SPATA17	c.215G>A	p.R72K	QVRAYIRHLNRIVTIIQKWWRSFLG[p.R72K]KKQYQLTVQVAYYTMMMNLYNAMAVR	FLGKKQYQL,KWWRSFLGK,WWRSFLGKK,RSFLGKKQY,GKKQYQLTV,FLGKKQYQLT,SFLGKKQYQL,KWWRSFLGKK,WRSFLGKKQY,KKQYQLTVQV	CESC
SPATA22	c.449C>T	p.S150L	NDFKPQCKRTNLVANDGKNSCPVSS[p.S150L]VAQQQKQLRIPEPPNLSRNKETELLR	VSSVAQQQK,SVAQQQKQLR,GKNSCPVSSV	CRC
SPATA5L1	c.2055delT	p.C685fs	KVCTKTMPIGPDVSLENLAAETCFF[p.C685fs]LELILETSAQKLLCWLCKKMD*	LAAETCFFL,LILETSAQK,KLLCWLCKK,ETCFFLELI,AETCFFLEL,LETSAQKLL,LELILETSA,NLAAETCFFL,FLELILETSA,LILETSAQKL,KLLCWLCKKM,AQKLLCWLCK,ETCFFLELIL,AETCFFLELI	STAD
SPATA9	c.566G>T	p.C189F	AVLKKVKNIFQEEESIRQNREESEN[p.C189F]FRKAFSEPVLSEPMFAEGEIKAKPYR	FRKAFSEPV,EESENFRKA,NFRKAFSEPV,RQNREESENF,EESENFRKAF,FRKAFSEPVL,REESENFRKA	KIRC
SPEG	c.2831C>T	p.A944V	EAEGGLCRLRILAAERGDAGFYTCK[p.A944V]VVNEYGARQCEARLEVRAHPESRSLA	YTCKVVNEY,DAGFYTCKV,FYTCKVVNEY	CRC
SPEG	c.2975_2976insG	p.A992fs	AVLAPLQDVDVGAGEMALFECLVAG[p.A992fs]AH*	FECLVAGAH,ALFECLVAGA	KIRC
SPEN	c.2407_2408delGA	p.E803fs	RLERYTKNEKTDKERTFDPERVERE[p.E803fs]TLNTEGKSGKGQN*	TLNTEGKSGK	GBM
SPESP1	c.363C>G	p.F121L	EETTTFPTGGFTPEIGKKKHTESTP[p.F121L]LWSIKPNNVSIVLHAEEPYIENEEPE	KKHTESTPL,KHTESTPLW,TESTPLWSI,KKKHTESTPL,KKHTESTPLW	BLCA
SPG20	c.696delT	p.F232fs	QPPPLETLGLDADELILIPNGVQIF[p.F232fs]L*	IPNGVQIFL,LIPNGVQIFL	STAD
SPIN2B	c.448A>G	p.M150V	ANTIIGKAVEHMFEGEHGSKDEWRG[p.M150V]VVLAQAPIMKAWFYITYEKDPVLYMY	KDEWRGVVL,VVLAQAPIM,DEWRGVVLA,VVLAQAPIMK,SKDEWRGVVL,RGVVLAQAPI,DEWRGVVLAQ	TGCT
SPIN4	c.512A>G	p.Y171C	PVMDTWFYITYEKDPVLYMYTLLDD[p.Y171C]CKDGDLRIIPDSNYYFPTAEQEPGEV	YMYTLLDDC,YMYTLLDDCK	LUAD
SPINT1	c.947C>T	p.A316V	LREEECILACRGVQGGPLRGSSGAQ[p.A316V]VTFPQGPSMERRHPVCSGTCQPTQFR	VTFPQGPSM,GSSGAQVTF,RGSSGAQVTF,AQVTFPQGPS	GBM
SPOP	c.148G>A	p.E50K	TQIKVVKFSYMWTINNFSFCREEMG[p.E50K]KVIKSSTFSSGANDKLKWCLRVNPKG	KVIKSSTFS,GKVIKSSTF,FSFCREEMGK,MGKVIKSSTF	UCEC
SPOP	c.304T>G	p.F102V	DEESKDYLSLYLLLVSCPKSEVRAK[p.F102V]VKFSILNAKGEETKAMESQRAYRFVQ	KSEVRAKVK,RAKVKFSIL,KVKFSILNA,SEVRAKVKF,KVKFSILNAK,RAKVKFSILN,EVRAKVKFSI,KSEVRAKVKF,VRAKVKFSIL,AKVKFSILNA,CPKSEVRAKV	PRAD
SPOP	c.305T>G	p.F102C	DEESKDYLSLYLLLVSCPKSEVRAK[p.F102C]CKFSILNAKGEETKAMESQRAYRFVQ	KSEVRAKCK,RAKCKFSIL,KCKFSILNA,SEVRAKCKF,RAKCKFSILN,KCKFSILNAK,EVRAKCKFSI,KSEVRAKCKF,VRAKCKFSIL	PRAD
SPOP	c.391T>G	p.W131G	ILNAKGEETKAMESQRAYRFVQGKD[p.W131G]GGFKKFIRRDFLLDEANGLLPDDKLT	QGKDGGFKK,GGFKKFIRR,GKDGGFKKF,RFVQGKDGGF	PRAD
SPOP	c.397T>A	p.F133I	NAKGEETKAMESQRAYRFVQGKDWG[p.F133I]IKKFIRRDFLLDEANGLLPDDKLTLF	FVQGKDWGI,DWGIKKFIR,WGIKKFIRR,GKDWGIKKF,RFVQGKDWGI,DWGIKKFIRR	PRAD
SPOP	c.397T>G	p.F133V	NAKGEETKAMESQRAYRFVQGKDWG[p.F133V]VKKFIRRDFLLDEANGLLPDDKLTLF	FVQGKDWGV,DWGVKKFIR,GKDWGVKKF,DWGVKKFIRR	PRAD
SPOP	c.398T>G	p.F133C	NAKGEETKAMESQRAYRFVQGKDWG[p.F133C]CKKFIRRDFLLDEANGLLPDDKLTLF	DWGCKKFIR,GKDWGCKKF,DWGCKKFIRR	PRAD
SPOP	c.399C>G	p.F133L	NAKGEETKAMESQRAYRFVQGKDWG[p.F133L]LKKFIRRDFLLDEANGLLPDDKLTLF	FVQGKDWGL,DWGLKKFIR,GKDWGLKKF,LKKFIRRDF,FVQGKDWGLK,RFVQGKDWGL,DWGLKKFIRR	PRAD

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SPTA1	c.5195A>C	p.K1732T	EKLKEAYALFQFFQDLDDEESWIEE[p.K1732T]TLIRVSSQDYGRDLQGVQNLLKKHKR	WIEETLIRV,EESWIEETL,SWIEETLIRV,TLIRVSSQDY,ESWIEETLIR,DEESWIEETL,EESWIEETLI	STAD
SPTA1	c.6032C>T	p.A2011V	PEITDLKDKLISAQHNQSKAIEERY[p.A2011V]VALLKRWEQLLEASAVHRQKLLEKQL	RYVALLKRW,AIEERYVAL,KAIEERYVA,IEERYVALL,AIEERYVALL,KAIEERYVAL	GBM
SPTA1	c.6727G>T	p.D2243Y	DLGDNLEDALILDIKYSTIGLAQQW[p.D2243Y]YQLYQLGLRMQHNLEQQIQAKDIKGV	LAQQWYQLY,GLAQQWYQL,QQWYQLYQL,WYQLYQLGL,AQQWYQLYQ,STIGLAQQWY,AQQWYQLYQL,QWYQLYQLGL,GLAQQWYQLY,WYQLYQLGLR,YQLYQLGLRM	LUAD
SPTA1	c.7099G>T	p.G2367C	FLIDKESENIKSSDEIENAFQALAE[p.G2367C]CKSYITKEDMKQALTPEQVSFCATHM	ALAECKSYI,QALAECKSY,ALAECKSYIT,NAFQALAECK,FQALAECKSY,CKSYITKEDM	LUAD
SPTB	c.256C>T	p.R86C	KWVNSHLARVSCRITDLYKDLRDGR[p.R86C]LLIKLLEVLSGEMLPKPTKGKMRIHC	RLLIKLLEV,LLIKLLEVL,RDGRLLIKL,RLLIKLLEVL,DLRDGRLLIK	CRC
SPTB	c.5591C>T	p.T1864I	AFERELHLLGVQVQQFQDVATRLQT[p.T1864I]VYAGEKAEAIQNKEQEVSAAWQALLD	ATRLQTVYA,VATRLQTVY,DVATRLQTV,RLQTVYAGEK,VYAGEKAEAI,ATRLQTVYAG,TVYAGEKAEA,DVATRLQTVY,LQTVYAGEKA	KIRC
SPTBN4	c.5978C>T	p.A1993V	ADKPRDVSSVEVLMNYHQGLKTELE[p.A1993V]VRVPELTTCQELGRSLLLNKSAMADE	ELEVRVPEL,TELEVRVPE,GLKTELEVRV,HQGLKTELEV,TELEVRVPEL,LEVRVPELTT	CRC
SPTLC3	c.290G>A	p.R97K	IGTLFGYLRDFLRNWGIEKCNAAVE[p.R97K]KKEQKDFVPLYQDFENFYTRNLYMRI	KKEQKDFVPL	SKCM
SPTY2D1	c.1454delC	p.P485fs	GSSRGPGRPVSSPHELRRPVSGLGP[p.P485fs]RGGLSVALGDP*	GPRGGLSVA,GLGPRGGLSV,GPRGGLSVAL	STAD
SRCAP	c.5625_5626insC	p.Q1875fs	RSGPPSPPSTATSFGGPRPRRQPPP[p.Q1875fs]TTSFPFLSGLPGGKAEAAAV*	GLPGGKAEA,RQPPPTTSF,TSFPFLSGL,RPRRQPPPT,FPFLSGLPG,FLSGLPGGKA,GLPGGKAEAA,TTSFPFLSGL,RPRRQPPPTT,QPPPTTSFPF,RRQPPPTTSF,FPFLSGLPGG	KIRP
SRCAP	c.5626_5627insC	p.P1876fs	RSGPPSPPSTATSFGGPRPRRQPPP[p.P1876fs]TTSFPFLSGLPGGKAEAAAV*	GLPGGKAEA,RQPPPTTSF,TSFPFLSGL,RPRRQPPPT,FPFLSGLPG,FLSGLPGGKA,GLPGGKAEAA,TTSFPFLSGL,RPRRQPPPTT,QPPPTTSFPF,RRQPPPTTSF,FPFLSGLPGG	STAD
SRCIN1	c.2595delC	p.P865fs	LSQSPKKVTAETDFNKSVDFEMPPP[p.P865fs]APR*	FEMPPPAPR,VDFEMPPPA,DFEMPPPAPR	STAD
SREBF2	c.2289delC	p.H763fs	LSRAQSLCGPEHSAVPDSLRWLCHP[p.H763fs]WARSFSWSGAGL*	RWLCHPWAR,RSFSWSGAG,HPWARSFSW,SLRWLCHPW,LCHPWARSF,SLRWLCHPWA,CHPWARSFSW,RWLCHPWARS,WARSFSWSGA,RSFSWSGAGL,HPWARSFSWS,WLCHPWARSF,DSLRWLCHPW	STAD
SRGAP1	c.182C>T	p.T61M	EQQTEMRVQLLQDLQDFFRKKAEIE[p.T61M]MEYSRNLEKLAERFMAKTRSTKDHQQ	MEYSRNLEK,KKAEIEMEY,IEMEYSRNL,RKKAEIEMEY,MEYSRNLEKL	MM
SRPRB	c.40G>A	p.G14S	MASADSRRVADGG[p.G14S]SAGGTFQPYLDTLRQELQQTDPTLLS	SAGGTFQPY,GSAGGTFQPY,ADGGSAGGTF	BLCA
SRRM2	c.6769G>T	p.A2257S	IPAASAAAMNLASARTPAIPTAVNL[p.A2257S]SDSRTPAAAAAMNLASPRTAVAPSAV	NLSDSRTPA,NLSDSRTPAA	TGCT
SRSF11	c.51_52insG	p.G17fs	MSNTTVVPSTAGPGPSGG[p.G17fs]ARWRRWWWRRRRRHRGNPGD*	RWRRWWWRR,RWWWRRRRR,GARWRRWWWR,RWRRWWWRRR,RWWWRRRRRH,WWWRRRRRHR	PRAD
SSPO	c.12593delC	p.S4198fs	PRGQQSRFRSSTSGSWAPECREEQS[p.S4198fs]RASPALSPRAHPCACRALAPAPWGTAGCRGSASGAPAPRRV*	ALAPAPWGT,ALSPRAHPC,RASPALSPR,SASGAPAPR,QSRASPALS,RAHPCACRA,RGSASGAPA,SPALSPRAH,SPRAHPCAC,APAPWGTAG,EQSRASPAL,CRALAPAPW,EEQSRASPA,ALAPAPWGTA,ALSPRAHPCA,GSASGAPAPR,RASPALSPRA,RAHPCACRAL,REEQSRASPA,EEQSRASPAL,ACRALAPAPW	PRAD
ST18	c.2334C>A	p.H778Q	KTLKSLMAANSQELKCPTPGCDGSG[p.H778Q]QVTGNYASHRSLSGCPRARKGGVKMT	GSGQVTGNY,GQVTGNYAS,QVTGNYASHR,GQVTGNYASH	LUAD
ST6GALNAC1	c.1061G>A	p.S354N	ELNYSLVQKVVTRFPPVPQQQLLLA[p.S354N]NLPAGSLRCITCAVVGNGGILNNSHM	LLANLPAGS,QQQLLLANL,LANLPAGSL,LLANLPAGSL,NLPAGSLRCI,LANLPAGSLR,QQLLLANLPA	TGCT

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
STAB1	c.3358_3359insC	p.P1120fs	ASVDVADLLATNGVLHILSQVLLPP[p.P1120fs]PRGCARWAGVAAAAGLGACLQPLPGIAAAPWVGAPD*	GLGACLQPL,RGCARWAGV,CARWAGVAA,RWAGVAAAA,IAAAPWVGA,QPLPGIAAA,ARWAGVAAA,LQPLPGIAA,LPGIAAAPW,GIAAAPWVGA,RGCARWAGVA,CARWAGVAAA,LLPPPRGCAR,ARWAGVAAAA,AAAAGLGACL,AGLGACLQPL,LQPLPGIAAA,LPPPRGCARW,LPGIAAAPWV	STAD
STAC3	c.349G>T	p.G117W	FKDHFFKKPKFCDVCARMIVLNNKF[p.G117W]WLRCKNCKTNIHEHCQSYVEMQRCFG	VLNNKFWLR,WLRCKNCKT,IVLNNKFWLR,RMIVLNNKFW,KFWLRCKNCK,MIVLNNKFWL	LUAD
STAMBPL1	c.427T>C	p.Y143H	TDELKNDLLKKYNVEYQEYLQSKNK[p.Y143H]HKAEILKKLEHQRLIEAERKRIAQMR	KHKAEILKK,YLQSKNKHKA,KNKHKAEILK,SKNKHKAEIL	TGCT
STARD8	c.1985G>C	p.G662A	RRNKTPDYRGQHVFGVPPLIHVQRT[p.G662A]AQPLPQSIQQAMRYLRSQCLDQVGIF	HVQRTAQPL,RTAQPLPQSI,IHVQRTAQPL	TGCT
STAT2	c.1466_1467insC	p.P489fs	AWASVLWFNLLSPNLQNQQFFSNPP[p.P489fs]NGPLELAGPCSQLAVLLLCWPRPQLRPAEHAEKQAVRAEL*	LLCWPRPQL,AVLLLCWPR,FSNPPNGPL,ELAGPCSQL,NPPNGPLEL,WPRPQLRPA,RPQLRPAEH,QQFFSNPPN,AEHAEKQAV,LLLCWPRPQL,QLRPAEHAEK,SQLAVLLLCW,LAVLLLCWPR,LLCWPRPQLR,ELAGPCSQLA,WPRPQLRPAE,RPQLRPAEHA,RPAEHAEKQA,QQFFSNPPNG,FFSNPPNGPL,LELAGPCSQL,AEKQAVRAEL	STAD
STAT3	c.1982A>T	p.D661V	SVEPYTKQQLNNMSFAEIIMGYKIM[p.D661V]VATNILVSPLVYLYPDIPKEEAFGKY	IIMGYKIMV,IMGYKIMVA,IMVATNILV,KIMVATNIL,YKIMVATNI,IIMGYKIMVA,KIMVATNILV,IMGYKIMVAT,GYKIMVATNI,EIIMGYKIMV,YKIMVATNIL,IMVATNILVS,VATNILVSPL	HNSC
STAT5B	c.1101_1102insC	p.P367fs	KTQTKFAATVRLLVGGKLNVHMNPP[p.P367fs]PGEGHHHQ*	HMNPPPGEGH	STAD
STAT6	c.1061_1062insC	p.P354fs	QVLKTQTKFQAGVRFLLGLRFLGAP[p.P354fs]SQASAGQGRHGDREAGAGAECASGSWGWSRKHWRNHQQHCALGEQHSWELLLCPVQEPASQEDQAV*	LLCPVQEPA,ASGSWGWSR,SGSWGWSRK,SWGWSRKHW,RFLGAPSQA,WSRKHWRNH,WGWSRKHWR,REAGAGAEC,RNHQQHCAL,CALGEQHSW,GEQHSWELL,EQHSWELLL,WELLLCPVQ,FLGAPSQASA,ALGEQHSWEL,HSWELLLCPV,LLLCPVQEPA,CASGSWGWSR,ASGSWGWSRK,HWRNHQQHCA,SWGWSRKHWR,LRFLGAPSQA,SQASAGQGRH,REAGAGAECA,AGAECASGSW,AECASGSWGW,GSWGWSRKHW,RKHWRNHQQH,WRNHQQHCAL,QQHCALGEQH,GEQHSWELLL	KIRC
STAT6	c.1402G>C	p.D468H	LGPGKLPIQLQALSLPLVVIVHGNQ[p.D468H]HNNAKATILWDNAFSEMDRVPFVVAE	HGNQHNNAK,NQHNNAKAT,NQHNNAKATI	DLBCL
STK11	c.837delC	p.G279fs	EGDNIYKLFENIGKGSYAIPGDCGP[p.G279fs]RSLTC*	YAIPGDCGPR,IPGDCGPRSL	LUSC
STK11IP	c.464C>A	p.A155E	PLHCLHGLRGIYSQLETLICSRSLQ[p.A155E]ELEELLSACGGDFCSALPWLALLSAN	SLQELEELL,QELEELLSA,LICSRSLQEL,RSLQELEELL,LQELEELLSA,QELEELLSAC	KIRC
STK19	c.265G>A	p.D89N	RGARPGGGDAGGTPGETVRHCSAPE[p.D89N]NPIFRFSSLHSYPFPGTIKSRDMSWK	SAPENPIFR,NPIFRFSSL,CSAPENPIF,CSAPENPIFR,SAPENPIFRF,RHCSAPENPI,HCSAPENPIF,NPIFRFSSLH	SKCM
STK19	c.52_53insG	p.R18fs	MQKWFSAFDDAIIQRQWR[p.R18fs]GKPLPGRGRCELHEGG*	IIQRQWRGK,LPGRGRCEL,QRQWRGKPL,RQWRGKPLP,AIIQRQWRGK,QWRGKPLPGR,RGKPLPGRGR,IQRQWRGKPL,RQWRGKPLPG	PRAD
STOML3	c.256G>T	p.D86Y	VVFRLGRIQADKAKGPGLILVLPCI[p.D86Y]YVFVKVDLRTVTCNIPPQEILTRDSV	ILVLPCIYV,VLPCIYVFV,YVFVKVDLR,LVLPCIYVF,IYVFVKVDL,LILVLPCIY,LILVLPCIYV,LVLPCIYVFV,VLPCIYVFVK,ILVLPCIYVF,GLILVLPCIY,IYVFVKVDLR,LPCIYVFVKV	LUAD
STON1-GTF2A1L	c.1352A>G	p.N451S	KVTKEGKFVESAVITQIYCLCFVNG[p.N451S]SLECFLTLNDLELPKRDESYYEKDSE	CLCFVNGSL,FVNGSLECF,GSLECFLTL,FVNGSLECFL,CFVNGSLECF	TGCT
STRA6	c.203A>G	p.Q68R	QPAGNQTSPGATEDYSYGSWYIDEP[p.Q68R]RGGEELQPEGEVPSCHTSIPPGLYHA	GSWYIDEPR	BRCA

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
STRADA	c.997delC	p.R333fs	EELTMSPSRSVANSGLSDSLTTSTP[p.R333fs]GPPTVTRPPTPTTEPSPPTSTTLWSSAFSATRMPGPVPAPS*	TLWSSAFSA,WSSAFSATR,VTRPPTPTT,ATRMPGPVP,TTLWSSAFS,STTLWSSAF,SSAFSATRM,TRMPGPVPA,MPGPVPAPS,SPPTSTTLW,TLWSSAFSAT,FSATRMPGPV,TTLWSSAFSA,ATRMPGPVPA,STPGPPTVTR,LWSSAFSATR,TTSTPGPPTV,EPSPPTSTTL,TSTTLWSSAF,WSSAFSATRM	STAD
STRN3	c.654G>T	p.K218N	LDVRSQRVRSLLGLSNSEPNGSVET[p.K218N]NNLEQILNGGESPKQKGQEIKRSSGD	ETNNLEQIL,VETNNLEQI,VETNNLEQIL	UCEC
STT3B	c.1747G>T	p.D583Y	TSNAYSSPSVVLASYNHDGTRNILD[p.D583Y]YFREAYFWLRQNTDEHARVMSWWDYG	ILDYFREAY,NILDYFREA,DYFREAYFW,YFREAYFWL,GTRNILDYF,LDYFREAYF,GTRNILDYFR,DYFREAYFWL,YFREAYFWLR,NILDYFREAY,ILDYFREAYF	CRC
STX2	c.320G>T	p.R107L	KKTANKIRAKLKAIEQSFDQDESGN[p.R107L]LTSVDLRIRRTQHSVLSRKFVEAMAE	DESGNLTSV,LTSVDLRIRR	LUAD
STX2	c.756delA	p.K252fs	MINNIERNVMNATDYVEHAKEETKK[p.K252fs]LSNIRARQEGKSG*	NIRARQEGK,ETKKLSNIR	STAD
STXBP6	c.274G>A	p.D92N	QFEGSTSFVRRSQWMLEQLRQVNGI[p.D92N]NPNGDSAEFDLLFENAFDQWVASTAS	RQVNGINPN,NPNGDSAEF,RQVNGINPNG	UCEC
SULT1C4	c.254G>A	p.R85Q	WTQEIVELIQNEGDVEKSKRAPTHQ[p.R85Q]QFPFLEMKIPSLGSGLEQAHAMPSPR	QQFPFLEMK,QFPFLEMKI,APTHQQFPF,HQQFPFLEM,KRAPTHQQF,HQQFPFLEMK,RAPTHQQFPF,KSKRAPTHQQ,APTHQQFPFL,SKRAPTHQQF,THQQFPFLEM,QQFPFLEMKI	CRC
SULT1E1	c.230G>A	p.R77Q	WVSEIVYMIYKEGDVEKCKEDVIFN[p.R77Q]QIPFLECRKENLMNGVKQLDEMNSPR	VIFNQIPFL,DVIFNQIPF,KEDVIFNQI,DVIFNQIPFL	UCEC
SUMF2	c.329G>A	p.G110E	IFPVTNKDFRDFVREKKYRTEAEMF[p.G110E]EWSFVFEDFVSDELRNKATQPMKSVL	EMFEWSFVF,EWSFVFEDF,AEMFEWSFV,FEWSFVFED,EAEMFEWSF,TEAEMFEWS,AEMFEWSFVF,EAEMFEWSFV,TEAEMFEWSF,FEWSFVFEDF	LUAD
SUN3	c.1016C>A	p.P339Q	TFELQHAVSEYLLCVKLNIFSNWGH[p.P339Q]QKYTCLYRFRVHGTPGKHI*	FSNWGHQKY,IFSNWGHQK,HQKYTCLYR,GHQKYTCLY,WGHQKYTCL,QKYTCLYRF,NIFSNWGHQK,HQKYTCLYRF,IFSNWGHQKY,WGHQKYTCLY	LUAD
SUN3	c.370C>A	p.L124I	LRMPKEQLELLKKESQNLENNFRQI[p.L124I]IFLIEQIDVLKALLRDMKDGMDNNHN	QIIFLIEQI,NFRQIIFLI,LENNFRQII,RQIIFLIEQ,RQIIFLIEQI,IFLIEQIDVL,LENNFRQIIF	UCEC
SUN3	c.382G>A	p.E128K	KEQLELLKKESQNLENNFRQILFLI[p.E128K]KQIDVLKALLRDMKDGMDNNHNWNTH	FLIKQIDVL,KQIDVLKAL,LIKQIDVLK,ILFLIKQIDV,KQIDVLKALL,RQILFLIKQI,FLIKQIDVLK,NFRQILFLIK,IKQIDVLKAL	CRC
SUPT6H	c.2869G>A	p.A957T	SSDEDILCLKFHPLQEHVVKEELLN[p.A957T]TLYCEFINRVNEVGVDVNRAIAHPYS	TLYCEFINR,LLNTLYCEF,VKEELLNTL,KEELLNTLY,LLNTLYCEFI,TLYCEFINRV,NTLYCEFINR,ELLNTLYCEF,VKEELLNTLY	CRC
SUSD1	c.1027C>T	p.R343C	SRRINPKISYVISIKGQRLDPMESV[p.R343C]CEETVNLTTDSRTPEVCLALYPGTNY	MESVCEETV,CEETVNLTT	UCEC
SUSD5	c.1538C>T	p.T513M	YELTSSTLEILTVNTVKQTPNHIPS[p.T513M]MIMATTQPPVETTVPEIQDSFPYLLS	TPNHIPSMI,SMIMATTQP,MIMATTQPP,IPSMIMATT,MIMATTQPPV,KQTPNHIPSM,QTPNHIPSMI,TPNHIPSMIM,SMIMATTQPP	GBM
SV2A	c.412delG	p.E138fs	MADGAPLAGVRGGLSDGEGPPGGRG[p.E138fs]RHNDGKNEKNWPNSMKPSYGSVATAASSGHCILCLVWR*	SMKPSYGSV,KPSYGSVAT,WPNSMKPSY,NEKNWPNSM,MKPSYGSVA,AASSGHCIL,SMKPSYGSVA,GGRGRHNDGK,NWPNSMKPSY,NSMKPSYGSV,KPSYGSVATA,KNEKNWPNSM,MKPSYGSVAT,TAASSGHCIL,SGHCILCLVW	STAD
SV2C	c.179C>A	p.P60Q	DRAQDEYTQRSYSRFQDEEDDDDYY[p.P60Q]QAGETYNGEANDDEGSSEATEGHDED	YYQAGETYNG,DDYYQAGETY	LUAD
SVIL	c.278T>C	p.M93T	EKQTRSKYCTETSGVHGDSPYGSGT[p.M93T]TDTHSLESKAERIARYKAERRRQLAE	TTDTHSLESK	KIRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
SVIL	c.5586delG	p.G1862fs	EERGAQVQVLQGKEPPCFLQCFQGG[p.G1862fs]WWCTRGGGKRKKKMCKVSGGCTACVERCPWKGICWKWPVTVAA*	KGICWKWPV,PWKGICWKW,CTRGGGKRK,RGGGKRKKK,CWKWPVTVA,FQGGWWCTR,LQCFQGGWW,CKVSGGCTA,WKWPVTVAA,VERCPWKGI,KVSGGCTACV,GICWKWPVTV,TACVERCPWK,CFLQCFQGGW,GWWCTRGGGK,CTRGGGKRKK,GGKRKKKMCK,CWKWPVTVAA,CFQGGWWCTR,CPWKGICWKW	STAD
SYCP2	c.1422A>T	p.K474N	KPSKYIKNSDKGNRNNSQLEKTTPS[p.K474N]NRKMSEASMIVSGADRYTMRSPVLFS	KTTPSNRKM,NRKMSEASM,TPSNRKMSEA,SQLEKTTPSN,SNRKMSEASM	HNSC
SYMPK	c.1007C>G	p.A336G	HPASLEFQAQITTLLVDLGTPQAEI[p.A336G]GRNMPSSKDTRKRPRDDSDSTLKKMK	IGRNMPSSK,PQAEIGRNM,AEIGRNMPS,TPQAEIGRNM,AEIGRNMPSS	TGCT
SYN2	c.99_101delAGC	p.A34del	LSDSSFIANLPNGYMTDLQRPEPQQ[p.A34del]PTPPPPGPGAASAAAPPTASPGPERTPP	LQRPEPQQPT	BLCA,KIRP,PRAD
SYNDIG1	c.403G>T	p.D135Y	CCETTFIEDRSPTKDSLEYPDGKFI[p.D135Y]YLSADDIKIHTLSYDVEEEEEFQELE	YLSADDIKI,FIYLSADDI,YPDGKFIYL,FIYLSADDIK,EYPDGKFIYL,KFIYLSADDI,IYLSADDIKI,LEYPDGKFIY	LUAD
SYNE2	c.9309G>T	p.K3103N	ESRRLNAQILSQRIEKAKCLCDEII[p.K3103N]NKLNENKTFDDSFKEKEILQIKLNAE	CLCDEIINK,IINKLNENK,NKLNENKTF,CLCDEIINKL	CRC
SYNGR4	c.506G>A	p.R169Q	QAAIAFTFFSILVWIFQAYLAFQDL[p.R169Q]QNDAPVPYKRFLDEGGMVLTTLPLPS	LQNDAPVPY,FQDLQNDAPV,LQNDAPVPYK,DLQNDAPVPY	CRC
SYNJ1	c.2041A>T	p.I681F	KTISRDNKYVLLASEQLVGVCLFVF[p.I681F]FRPQHAPFIRDVAVDTVKTGMGGATG	FVFFRPQHA,GVCLFVFFR,VGVCLFVFF,FFRPQHAPF,VFFRPQHAPF,FFRPQHAPFI,VGVCLFVFFR	CLL
SYNJ2	c.2495A>C	p.K832T	WRKKHPFDKTAGELNLLDSDLDVDT[p.K832T]TVRHTWSPGALQYYGRAELQASDHRP	TVRHTWSPG,TVRHTWSPGA	KIRC
SYNJ2	c.3331_3332insC	p.P1111fs	HRSPSRSLSVPNRPRPPQPPQRPPP[p.P1111fs]SNRFNGEKVGFRCVHLLRHPWTVFNFADGKTSTRSTSATSQGSDWNK*	HLLRHPWTV,TVFNFADGK,TSQGSDWNK,RFNGEKVGF,RHPWTVFNF,KVGFRCVHL,GFRCVHLLR,KTSTRSTSA,STRSTSATS,LLRHPWTVF,CVHLLRHPW,HPWTVFNFA,GEKVGFRCV,VGFRCVHLLR,WTVFNFADGK,ATSQGSDWNK,HLLRHPWTVF,LRHPWTVFNF,KVGFRCVHLL,GFRCVHLLRH,KTSTRSTSAT,STRSTSATSQ,RFNGEKVGFR,NFADGKTSTR,PQRPPPSNRF,NRFNGEKVGF,RCVHLLRHPW	STAD
SYNM	c.1547G>A	p.R516Q	RTVILGKKTEVKATREQERNRPETI[p.R516Q]QTKPEEKMFDSKEKASEERNLRWEEL	TIQTKPEEK,IQTKPEEKM,RNRPETIQTK,IQTKPEEKMF	UCEC
SYNPO	c.1856_1857insC	p.G619fs	SSHLKGQAVPASKTGILEESMARRG[p.G619fs]QPQIHVYFRGEAQGDPESRLAGSGTDSG*	GQPQIHVYF,MARRGQPQI,RGQPQIHVY,QPQIHVYFR,AQGDPESRL,SMARRGQPQI,RGQPQIHVYF,MARRGQPQIH,RRGQPQIHVY	KIRC
SYT4	c.1delA	p.M1fs	[p.M1fs]WLRSPPAGKNLMKSPQWWGSSVHLAWSSQSLSLHGSAVRENHPSLTRLLHTSLCMCLRELIFTLKT*	HLAWSSQSL,SLSLHGSAV,CLRELIFTL,LLHTSLCMC,SLCMCLREL,WLRSPPAGK,HTSLCMCLR,QWWGSSVHL,AVRENHPSL,LTRLLHTSL,LSLHGSAVR,SPPAGKNLM,SPQWWGSSV,RLLHTSLCM,KNLMKSPQW,PQWWGSSVH,WGSSVHLAW,AWSSQSLSL,CMCLRELIF,RELIFTLKT,SLTRLLHTSL,LLHTSLCMCL,SLCMCLRELI,CLRELIFTLK,WWGSSVHLAW,KSPQWWGSSV,AVRENHPSLT,SLSLHGSAVR,HPSLTRLLHT,LAWSSQSLSL,GKNLMKSPQW,PQWWGSSVHL,VHLAWSSQSL,SQSLSLHGSA,SAVRENHPSL,RENHPSLTRL,TRLLHTSLCM,LCMCLRELIF,SPQWWGSSVH	STAD
SYT7	c.1046C>T	p.T349M	TMKRNLNPIFNESFAFDIPTEKLRE[p.T349M]MTIIITVMDKDKLSRNDVIGKIYLSW	KLREMTIII,IPTEKLREM,REMTIIITV,EMTIIITVM,MTIIITVMDK,KLREMTIIIT,REMTIIITVM	CRC
SYT8	c.1117C>T	p.R373W	GARASGQPLQHWADMLAHARRPIAQ[p.R373W]WHPLRPAREVDRMLALQPRLRLRLPL	QWHPLRPAR,PIAQWHPLR,RPIAQWHPL,HARRPIAQW,AQWHPLRPA,HARRPIAQWH,RPIAQWHPLR,AHARRPIAQW,RRPIAQWHPL	ACC
SYTL2	c.1320C>G	p.I440M	FPINGLHSHSEVLTARPQSMENSPT[p.I440M]MNEPKDKSSELTRLESVLPRSPADEL	QSMENSPTM,PQSMENSPTM	BLCA

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TAB3	c.632G>C	p.R211T	HIPRYSTNPITVTVSQNLPSGQTVP[p.R211T]TALQILPQIPSNLYGSPGSIYIRQTS	QTVPTALQI,LPSGQTVPT,TALQILPQI,GQTVPTALQI,LPSGQTVPTA	BLCA
TADA2B	c.199G>A	p.E67K	IGHHRRYHGYQLVDGGRFTLWGPEA[p.E67K]KGGWTSREEQLLLDAIEQFGFGNWED	FTLWGPEAK,EAKGGWTSR,RFTLWGPEAK	CESC
TAF1	c.2527C>T	p.R843W	SKDRPRRIRMEDIKKAFPSHSESSI[p.R843W]WKRLKLCADFKRTGMDSNWWVLKSDF	IWKRLKLCA,HSESSIWKR,SESSIWKRL,FPSHSESSIW,WKRLKLCADF	UCEC
TAF1A	c.514_515CG>AT	p.R172M	HGMLKDAKRNLSEAETWRHGENTSS[p.R172M]MEILINLIQAYKGLLQYYTWSEKKMEL	SSMEILINL,SMEILINLI,NTSSMEILI,RHGENTSSM,GENTSSMEI,MEILINLIQ,SSMEILINLI,WRHGENTSSM,GENTSSMEIL,MEILINLIQA	SKCM
TAF1B	c.874C>T	p.R292C	GIESWPDYEDIYKKTVEVGTFLDLP[p.R292C]CFPDITEDCYLHPNILCMKYLMEVNL	GTFLDLPCF,LDLPCFPDI,FLDLPCFPDI,VGTFLDLPCF	BLCA
TAF1L	c.2553delA	p.K851fs	QVFIYRLFWKSKDRPRRIRMEDIKK[p.K851fs]PFLPIQKAASGRG*	DIKKPFLPI,RMEDIKKPF,MEDIKKPFL,KPFLPIQKAA,IRMEDIKKPF,RMEDIKKPFL	STAD
TAF5	c.388T>G	p.S130A	RQSKLREAEEALRREAGLLEEAVAG[p.S130A]AGAPGEVDSAGAEVTSALLSRVTASA	LLEEAVAGA,EEAVAGAGA,GLLEEAVAGA,LEEAVAGAGA	ACC
TANK	c.1139C>T	p.S380L	LDSPGKAIRGPQQPIWKPFPNQDSD[p.S380L]LVVLSGTDSELHIPRVCEFCQAVFPP	NQDSDLVVL,FPNQDSDLV,KPFPNQDSDL,FPNQDSDLVV	CRC
TAOK2	c.2696_2697insG	p.Q899fs	QRVEEELLALQTGRSERIRSLLERQ[p.Q899fs]GP*	RIRSLLERQG	KIRC
TARBP1	c.2344C>G	p.L782V	VLTELINLHLKVGWKRGNPIWRVIS[p.L782V]VLKNASIQHLQEMDSGQEPTVGSQIQ	RVISVLKNA,IWRVISVLK,NPIWRVISV,VLKNASIQHL,PIWRVISVLK,NPIWRVISVL	LUSC
TARS2	c.595G>A	p.E199K	RGSELPVLERICQELTAAARPFRRL[p.E199K]KASRDQLRQLFKDNPFKLHLIEEKVT	AARPFRRLK,RLKASRDQL,RPFRRLKAS,AAARPFRRLK,AARPFRRLKA,RPFRRLKASR,RLKASRDQLR,RRLKASRDQL	LUAD
TARSL2	c.1097G>A	p.G366D	KGPHVRHTGKIKTIKIFKNSSTYWE[p.G366D]DNPEMETLQRIYGISFPDNKMMRDWE	TYWEDNPEM,STYWEDNPEM,WEDNPEMETL	GBM
TAS1R2	c.808C>T	p.R270C	PNQNMTSEERQRLVTIVDKLQQSTA[p.R270C]CVVVVFSPDLTLYHFFNEVLRQNFTG	KLQQSTACV,LQQSTACVV,STACVVVVF,QSTACVVVV,QQSTACVVV,KLQQSTACVV,QQSTACVVVV,STACVVVVFS,LQQSTACVVV,QSTACVVVVF	CRC
TAS1R3	c.1573G>A	p.E525K	SRQCQEGQVRRVKGFHSCCYDCVDC[p.E525K]KAGSYRQNPDDIACTFCGQDEWSPER	CVDCKAGSY,CVDCKAGSYR	BLCA
TAS2R1	c.549C>A	p.F183L	KFFSQNATIQKEDTLAIQIFSFVAE[p.F183L]LSVPLLIFLFAVLLLIFSLGRHTRQM	QIFSFVAEL,FVAELSVPL,FSFVAELSV,ELSVPLLIF,AELSVPLLI,IQIFSFVAEL,FVAELSVPLL,IFSFVAELSV,SFVAELSVPL,LSVPLLIFLF,ELSVPLLIFL,FSFVAELSVP,AELSVPLLIF	CRC
TAS2R16	c.531G>T	p.Q177H	IQLLTMEHLPRNSTVTDKLENFHQY[p.Q177H]HFQAHTVALVIPFILFLASTIFLMAS	QYHFQAHTV,HFQAHTVAL,LENFHQYHF,FHQYHFQAH,HQYHFQAHT,YHFQAHTVA,HQYHFQAHTV,KLENFHQYHF,YHFQAHTVAL	LUAD
TAS2R16	c.691G>A	p.V231I	QIQHHSTGHCNPSMKARFTALRSLA[p.V231I]ILFIVFTSYFLTILITIIGTLFDKRC	RSLAILFIV,FTALRSLAI,ILFIVFTSY,SLAILFIVF,ALRSLAILF,TALRSLAIL,ALRSLAILFI,FTALRSLAIL,SLAILFIVFT,RFTALRSLAI,TALRSLAILF,RSLAILFIVF,ILFIVFTSYF,AILFIVFTSY	MM
TAS2R30	c.707_708insT	p.L236fs	HGKGSQDPSTKVHIKALQTVTSFLL[p.L236fs]VMCHLLSVHDHISL*	FLLVMCHLL,LVMCHLLSV,HLLSVHDHI,SFLLVMCHL,QTVTSFLLV,TVTSFLLVM,VMCHLLSVH,LSVHDHISL,LLVMCHLLSV,LLSVHDHISL,SFLLVMCHLL,QTVTSFLLVM,LVMCHLLSVH,LQTVTSFLLV,TSFLLVMCHL	KICH
TAS2R38	c.932T>C	p.I311T	MAACPSGHAAILISGNAKLRRAVMT[p.I311T]TLLWAQSSLKVRADHKADSRTLC*	AVMTTLLWA,TLLWAQSSL,RAVMTTLLW,KLRRAVMTT,LRRAVMTTL,RRAVMTTLL,KLRRAVMTTL,TLLWAQSSLK,RRAVMTTLLW,RAVMTTLLWA,TTLLWAQSSL,LRRAVMTTLL	KIRC
TAS2R41	c.763G>A	p.A255T	TRALKSLISFLILYALSFLSLIIDA[p.A255T]TKFISMQNDFYWPWQIAVYLCISVHP	FLSLIIDAT,LIIDATKFI,LSLIIDATK,SLIIDATKF,IDATKFISM,SLIIDATKFI,LSLIIDATKF,IIDATKFISM,TKFISMQNDF	GBM
TAS2R8	c.294G>C	p.W98C	PDVYTKNKQQIVIFTFWTFANYLNM[p.W98C]CITTCLNVFYFLKIASSSHPLFLWLK	YLNMCITTC,FANYLNMCI,LNMCITTCL,CITTCLNVF,YLNMCITTCL,NMCITTCLNV,TFANYLNMCI,CITTCLNVFY,MCITTCLNVF	TGCT

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
TAS2R9	c.487G>C	p.E163Q	FLISLIISVPKNDDMWYHLFKVSHE[p.E163Q]QNITWKFKVSKIPGTFKQLTLNLGVM	HEQNITWKF,FKVSHEQNI,VSHEQNITW,VSHEQNITWK,KVSHEQNITW,SHEQNITWKF	BLCA
TAT	c.1100G>A	p.R367H	TLSFLKSNADLCYGALAAIPGLRPV[p.R367H]HPSGAMYLMVGIEMEHFPEFENDVEF	GLRPVHPSG,PVHPSGAMY,RPVHPSGAM,HPSGAMYLM,GLRPVHPSGA,RPVHPSGAMY,HPSGAMYLMV,AAIPGLRPVH,LRPVHPSGAM	GBM
TBC1D1	c.212C>T	p.S71F	EVRRLSRQSTRKEPVTKQVRLCVSP[p.S71F]FGLRCEPEPGRSQQWDPLIYSSIFEC	RLCVSPFGL,QVRLCVSPF,RLCVSPFGLR,KQVRLCVSPF,QVRLCVSPFG,VRLCVSPFGL	BLCA
TBC1D1	c.830A>G	p.H277R	DGGLRSSGFFSSFEESDIENHLISG[p.H277R]RNIVQPTDIEENRTMLFTIGQSEVYL	HLISGRNIV,DIENHLISGR	KIRC
TBC1D12	c.1823T>A	p.F608Y	PDVGYVQGMSFIAAVLILNLEEADA[p.F608Y]YIAFANLLNKPCQLAFFRVDHSMMLK	NLEEADAYI,AYIAFANLL,EADAYIAFA,DAYIAFANL,EEADAYIAF,LNLEEADAY,LEEADAYIA,YIAFANLLNK,ILNLEEADAY,DAYIAFANLL,LEEADAYIAF,EEADAYIAFA,ADAYIAFANL	KIRC
TBC1D2B	c.2759G>A	p.R920Q	ILDARKLISISFGDLNPFPLRQIRN[p.R920Q]QRAYHLEKVRLELTELEAIREDFLRE	QIRNQRAYH,NQRAYHLEK,RQIRNQRAY,IRNQRAYHL,RQIRNQRAYH,QIRNQRAYHL,RNQRAYHLEK,LRQIRNQRAY,NQRAYHLEKV	BLCA,KIRP,PRAD
TBC1D9	c.3697C>A	p.P1233T	DWAITFEQFLASLLTEPALVKYFDK[p.P1233T]TVCMMARITSAKNIRMMGKPLTSASD	ALVKYFDKT,KTVCMMARI,KYFDKTVCM,YFDKTVCMM,ALVKYFDKTV,KYFDKTVCMM,VKYFDKTVCM	PRAD
TBCD	c.1426C>T	p.R476C	DEKRGACSVGTNVRDAACYVCWAFA[p.R476C]CAYEPQELKPFVTAISSALVIAAVFD	YVCWAFACA,CAYEPQELK,VCWAFACAY,YVCWAFACAY,FACAYEPQEL	LUSC
TBL1XR1	c.377delA	p.N126fs	DKLAQQQAAAAAAAAAAASQQGSAK[p.N126fs]MEKTQQMGRRMEHIL*	QMGRRMEHI,KTQQMGRRM,MGRRMEHIL,ASQQGSAKM,AKMEKTQQM,QQMGRRMEH,QQMGRRMEHI,SQQGSAKMEK,AASQQGSAKM,TQQMGRRMEH	STAD
TBX3	c.559C>T	p.H187Y	RYKFHNSRWMVAGKADPEMPKRMYI[p.H187Y]YPDSPATGEQWMSKVVTFHKLKLTNN	YIYPDSPAT,EMPKRMYIY,MYIYPDSPA,RMYIYPDSP,RMYIYPDSPA,PEMPKRMYIY	BRCA
TBX4	c.1109delC	p.S370fs	LDLPCKRSYLEAPSSVGEDHYFRSP[p.S370fs]LPTTSKC*	RSPLPTTSK,GEDHYFRSPL	STAD
TCEB3C	c.922G>A	p.E308K	DLLSAFEAMTSQANPEALSAPALQE[p.E308K]KAAFPGRRVNAKMPVYSGSRPACQLQ	LSAPALQEK,KAAFPGRRV,LQEKAAFPG,ALSAPALQEK,APALQEKAAF	SKCM
TCF7	c.419A>C	p.H140P	GMYKETVYSAFNLLMHYPPPSGAGQ[p.H140P]PPQPQPPLHKANQPPHGVPQLSLYEH	QPPQPQPPL,GQPPQPQPPL	KIRC
TCHP	c.515delA	p.E172fs	KLREMELDLHQKHVVNSWEMQKEEK[p.E172fs]NSKKPPQSKRTNGMKMNMKGPEGRR*	MQKEEKNSK,NSKKPPQSK,QSKRTNGMK,RTNGMKMNM,KMNMKGPEG,MNMKGPEGR,NMKGPEGRR,SKRTNGMKM,RTNGMKMNMK,MQKEEKNSKK,KNSKKPPQSK,KMNMKGPEGR,NSKKPPQSKR,MNMKGPEGRR,KRTNGMKMNM,MKMNMKGPEG	STAD
TCOF1	c.4084_4086delAAG	p.K1366del	GWESRKRKLSGDQPAARTPRSKKKK[p.K1366del]LGAGEGGEASVSPEKTSTTSKGKAKRDK	RSKKKKLGA,TPRSKKKKL,RSKKKKLGAG	PRAD
TCOF1	c.791A>G	p.K264R	APAPGKVGDVTPQVKGGALPPAKRA[p.K264R]RKPEEESESSEEGSESEEEAPAGTRS	ALPPAKRARK	LUAD
TCTE1	c.380G>T	p.S127I	PEHQQKVLNHLSPDLPLAVTANLID[p.S127I]IENYWLRCCMHRWPVCHVAHHGGSWK	NLIDIENYWL,IENYWLRCCM,TANLIDIENY	LUAD
TCTEX1D2	c.221C>T	p.S74L	HAVLKEELANAEYSPEEMPQLTKHL[p.S74L]LENIKDKLKEMGFDRYKMVVQVVIGE	MPQLTKHLL,QLTKHLLENI,LTKHLLENIK	CESC
TDO2	c.591G>C	p.Q197H	RVPYNRRHYRDNFKGEENELLLKSE[p.Q197H]HEKTLLELVEAWLERTPGLEPHGFNF	LLLKSEHEK,LKSEHEKTL,NELLLKSEH,HEKTLLELV,LKSEHEKTLL,SEHEKTLLEL	LUAD
TDRD10	c.828G>T	p.W276C	CLAEYHLGDYGHAWNRCWVLDRVDT[p.W276C]CAVVMFIDFGQLATIPVQSLRSLDSD	DTCAVVMFI,RVDTCAVVM,CAVVMFIDF,VLDRVDTCAV,RVDTCAVVMF	KIRC

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TDRD10	c.965C>T	p.S322L	SLDSDDFWTIPPLTQPFMLEKDILS[p.S322L]LYEVVHRILKGKITGALNSAVTAPAS	MLEKDILSL,SLYEVVHRI,LYEVVHRIL,LEKDILSLY,DILSLYEVV,KDILSLYEV,MLEKDILSLY,FMLEKDILSL,SLYEVVHRIL,ILSLYEVVHR,KDILSLYEVV	CRC
TEAD2	c.894_895insC	p.P298fs	DVRQIYDKFPEKKGGLRELYDRGPP[p.P298fs]PCLLPGQVLGGPELGPKW*	GQVLGGPEL,VLGGPELGPK,RELYDRGPPP	STAD
TECTB	c.85C>A	p.L29I	KAFVLLAIFAEASAKSCAPNKADVI[p.L29I]IVFCYPKTIITKIPECPYGWEVHQLA	VIIVFCYPK,APNKADVII,NKADVIIVF,IVFCYPKTI,KADVIIVFCY,DVIIVFCYPK,APNKADVIIV,IVFCYPKTII	CRC
TEDDM1	c.498G>A	p.M166I	LLVLTAELWAPNMCHLQLMETFLIL[p.M166I]IMGSWLMQAGFILYRPVSGYPWQDDD	LMETFLILI,ILIMGSWLM,IMGSWLMQA,METFLILIM,FLILIMGSW,QLMETFLILI,FLILIMGSWL,LIMGSWLMQA,TFLILIMGSW,ETFLILIMGS,LMETFLILIM,LILIMGSWLM	CESC
TEKT5	c.1202G>A	p.R401H	LLERSIMAKEGPLKVAQTRLECRTR[p.R401H]HPNMELCRDIPQLKLVNEVFTIDDTL	RTRHPNMEL,RTRHPNMELC,LECRTRHPNM,HPNMELCRDI	CRC
TET1	c.4415C>G	p.T1472S	AAVREIMENRYGQKGNAIRIEIVVY[p.T1472S]SGKEGKSSHGCPIAKWVLRRSSDEEK	VVYSGKEGK,RIEIVVYSGK,IVVYSGKEGK	TGCT
TEX15	c.4954G>C	p.E1652Q	ASSLQILQEETKVCLNILPLFVEAF[p.E1652Q]QRKQECSVEQILISRELLVDQNLWNN	FQRKQECSV	CESC
TFE3	c.1444_1445insG	p.G482fs	SLKPEQLDIEEEGRPGAATFHVGGG[p.G482fs]TCPECSPSAAPCTALRCPSGPALSQRPPGGPGRPLPPGAGGHSDGGGGGGGGRTVGGCPVPTAGCLRSPALFSVPCCLQGQQPPQQLQHGRGVLIRPHPSPGTFPPRKGGPVRMRPRLFPHPPMRLPCPGILGEEEM*	ALFSVPCCL,ALRCPSGPA,RMRPRLFPH,RLFPHPPMR,SAAPCTALR,LFPHPPMRL,LIRPHPSPG,PPGGPGRPL,CPVPTAGCL,SPALFSVPC,RPHPSPGTF,FPPRKGGPV,GPVRMRPRL,RPRLFPHPP,LRCPSGPAL,SQRPPGGPG,GCLRSPALF,LRSPALFSV,QQLQHGRGV,LQHGRGVLI,MRLPCPGIL,HPSPGTFPP,CLRSPALFSV,RLFPHPPMRL,ALRCPSGPAL,SQRPPGGPGR,KGGPVRMRPR,RMRPRLFPHP,RPRLFPHPPM,HPSPGTFPPR,SPSAAPCTAL,RPPGGPGRPL,PPRKGGPVRM,GPVRMRPRLF,FPHPPMRLPC,AGCLRSPALF,LQGQQPPQQL,GQQPPQQLQH,QQLQHGRGVL,IRPHPSPGTF,CPGILGEEEM	STAD
TFG	c.1145C>T	p.A382V	YQPRPGFTSLPGSTMTPPPSGPNPY[p.A382V]VRNRPPFGQGYTQPGPGYR*	PYVRNRPPF,YVRNRPPFG,NPYVRNRPPF	CLL
TFPI2	c.616C>T	p.R206C	RTCDAFTYTGCGGNDNNFVSREDCK[p.R206C]CACAKALKKKKKMPKLRFASRIRKIR	CACAKALKK,KCACAKALK,CKCACAKAL,REDCKCACA,CACAKALKKK,KCACAKALKK	GBM
TFPI2	c.664C>T	p.R222C	NFVSREDCKRACAKALKKKKKMPKL[p.R222C]CFASRIRKIRKKQF*	LCFASRIRK,CFASRIRKI,MPKLCFASR,KLCFASRIR,KKKMPKLCF,KKMPKLCFA,KLCFASRIRK,KKKMPKLCFA,KMPKLCFASR,CFASRIRKIR,MPKLCFASRI,KKKKMPKLCF,KKMPKLCFAS	BLCA
TFPT	c.755C>G	p.S252C	EALDSSWVSRGPDKLLPYPTLASPA[p.S252C]CD*	YPTLASPAC	BRCA
TGFBR1	c.722C>T	p.S241L	FGEVWRGKWRGEEVAVKIFSSREER[p.S241L]LWFREAEIYQTVMLRHENILGFIAAD	RLWFREAEI,LWFREAEIY,SSREERLWF,EERLWFREA,FSSREERLW,SSREERLWFR,IFSSREERLW,KIFSSREERL,RLWFREAEIY,FSSREERLWF,REERLWFREA	CRC
TGM6	c.1073delC	p.T358fs	WNESWFARQDLGPSYNGWQVLDATP[p.T358fs]RRRVKVCSGAAQPQSPPSARVMCTWLTMAPSCLRRSTPTTSPGCGTRMRAGSVYTQTRRRLGDASAPRRWAVTPAWTSLTSTSIRKGPGKRGRCTARR*	RVMCTWLTM,VMCTWLTMA,WLTMAPSCL,LTMAPSCLR,TMAPSCLRR,SVYTQTRRR,SLTSTSIRK,RLGDASAPR,TSLTSTSIR,TSIRKGPGK,RVKVCSGAA,SARVMCTWL,GTRMRAGSV,RMRAGSVYT,QTRRRLGDA,ASAPRRWAV,SIRKGPGKR,QVLDATPRR,TTSPGCGTR,WTSLTSTSI,APSCLRRST,AVTPAWTSL,TPRRRVKVC,AQPQSPPSA,TRMRAGSVY,RRWAVTPAW,TPAWTSLTS,RVMCTWLTMA,LTMAPSCLRR,TSLTSTSIRK,STSIRKGPGK,TWLTMAPSCL,RVKVCSGAAQ,SARVMCTWLT,GTRMRAGSVY,RMRAGSVYTQ,RAGSVYTQTR,SVYTQTRRRL,QVLDATPRRR,WLTMAPSCLR,WTSLTSTSIR,TSIRKGPGKR,DASAPRRWAV,WAVTPAWTSL,RLGDASAPRR,QPQSPPSARV,APRRWAVTPA,TPAWTSLTST,RRVKVCSGAA,PQSPPSARVM,ARVMCTWLTM,AWTSLTSTSI,PPSARVMCTW	STAD
THADA	c.5822C>T	p.S1941L	RLLAFLEGKEGEDTLVLSVWDSYAE[p.S1941L]LRQLTLPRTEAAC*	SVWDSYAEL,ELRQLTLPR,YAELRQLTL,SVWDSYAELR,SYAELRQLTL,LSVWDSYAEL	UCEC

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THAP5	c.860C>A	p.S287Y	EELNTNKESVIAIFVPAENSKPSVN[p.S287Y]YFISAQKETTEMEDTDIEDSLYKDVD	VNYFISAQK,NSKPSVNYF,SVNYFISAQK,NSKPSVNYFI,KPSVNYFISA,AENSKPSVNY	CRC
THEM4	c.50T>G	p.L17R	MLRSCAARLRTLGALC[p.L17R]RPPVGRRLPGSEPRPELRSFSSEEVI	ALCRPPVGR,TLGALCRPPV,RLRTLGALCR,RPPVGRRLPG	ACC
THRAP3	c.1652A>G	p.K551R	YKAVQEKSSSPPPRKTSESRDKLGA[p.K551R]RGDFPTGKSSFSITREAQVNVRMDSF	ESRDKLGAR,GARGDFPTGK	KIRC
THSD7B	c.268C>T	p.R90C	VCDWHSDLFQWEVSDWHHCVLVPYA[p.R90C]CGEVKPRTAECVTAQHGLQHRMVRCI	LVPYACGEV,VLVPYACGEV	GBM
THSD7B	c.269G>A	p.R90H	VCDWHSDLFQWEVSDWHHCVLVPYA[p.R90H]HGEVKPRTAECVTAQHGLQHRMVRCI	LVPYAHGEV,YAHGEVKPR,VLVPYAHGEV	CRC
THSD7B	c.376G>A	p.E126K	VTAQHGLQHRMVRCIQKLNRTVVAN[p.E126K]KICEHFALQPPTEQACLIPCPRDCVV	LNRTVVANK,VANKICEHF,NKICEHFAL,KLNRTVVANK,VVANKICEHF	SKCM
TIAM1	c.739_740GG>AT	p.G247M	QLSTCQRANSLGDLYAQKNSGVTAN[p.G247M]MGPGSKFAGYCRNLVSDIPNLANHKMP	TANMGPGSK,KNSGVTANM,ANMGPGSKF,VTANMGPGSK,MGPGSKFAGY,QKNSGVTANM,TANMGPGSKF	TGCT
TIFAB	c.129C>A	p.D43E	GPSAFANVPPRLQHDTSPLLLGRGQ[p.D43E]EAHLQLQLPRLSRRHLSLEPYLEKGS	LLLGRGQEA,RGQEAHLQL,QEAHLQLQL,LLGRGQEAHL,EAHLQLQLPR,GQEAHLQLQL	LUAD
TIGD4	c.935C>T	p.S312F	VESFPAHPEVKNLKSIELAFFPSCL[p.S312F]FSKCIAMKQGVIKSLKIKYRHCLIKK	CLFSKCIAM,LFSKCIAMK,LAFFPSCLF,FPSCLFSKC,AFFPSCLFSK,CLFSKCIAMK,ELAFFPSCLF,SCLFSKCIAM,FPSCLFSKCI	LUAD
TIMD4	c.455_457delCAA	p.T152del	VRLNLQRASTTTHRTATTTTRRTTT[p.T152del]SPTTTRQMTTTPAALPTTVVTTPDLTTG	RTTTSPTTTR,TTRRTTTSPT	PRAD
TIMM44	c.249delA	p.K83fs	GFLSGLLDNVKQELAKNKEMKESIK[p.K83fs]NSVTRPEG*	ESIKNSVTR,KESIKNSVT,EMKESIKNSV,KEMKESIKNS	STAD
TIMP3	c.596_597insC	p.A199fs	YQSKHYACIRQKGGYCSWYRGWAPP[p.A199fs]G*	SWYRGWAPPG	STAD
TINAG	c.1207G>A	p.E403K	MQVREDFFHYKTGIYRHVTSTNKES[p.E403K]KKYRKLQTHAVKLTGWGTLRGAQGQK	VTSTNKESK,STNKESKKY,KKYRKLQTH,VTSTNKESKK,STNKESKKYR,HVTSTNKESK,KKYRKLQTHA	MM
TLL1	c.158C>A	p.P53Q	CAGLDYDYTFDGNEEDKTETIDYKD[p.P53Q]QCKAAVFWGDIALDDEDLNIFQIDRT	KDQCKAAVF,YKDQCKAAVF	LUAD
TLL1	c.458C>T	p.T153M	VKGKVPLQFSGQNEKNRVPRAATSR[p.T153M]MERIWPGGVIPYVIGGNFTGSQRAMF	RAATSRMER,VPRAATSRM,MERIWPGGV,RMERIWPGGV,RVPRAATSRM,RAATSRMERI,MERIWPGGVI	CRC
TLL2	c.2615C>T	p.S872L	LGRFCGSKKPDPTVASGSSMFLRFY[p.S872L]LDASVQRKGFQAVHSTECGGRLKAEV	FLRFYLDAS,SSMFLRFYL,FYLDASVQR,LRFYLDASV,SMFLRFYLDA,FLRFYLDASV,RFYLDASVQR	CRC
TLN2	c.623C>T	p.S208L	REQGVDENETLLLRRKFFYSDQNVD[p.S208L]LRDPVQLNLLYVQARDDILNGSHPVS	FFYSDQNVDL	UCEC
TLR2	c.980A>T	p.D327V	RVIDPGKVETLTIRRLHIPRFYLFY[p.D327V]VLSTLYSLTERVKRITVENSKVFLVP	YLFYVLSTL,YVLSTLYSL,VLSTLYSLT,FYLFYVLST,LFYVLSTLY,IPRFYLFYV,HIPRFYLFYV,YLFYVLSTLY,FYLFYVLSTL,FYVLSTLYSL,RFYLFYVLST,IPRFYLFYVL	CLL
TLR4	c.1492T>G	p.L498V	LEVLKMAGNSFQENFLPDIFTELRN[p.L498V]VTFLDLSQCQLEQLSPTAFNSLSSLQ	DIFTELRNV,FTELRNVTF,TELRNVTFL,LRNVTFLDL,IFTELRNVTF,ELRNVTFLDL	STAD
TM6SF1	c.44C>G	p.S15W	MSASAATGVFVLSL[p.S15W]WAIPVTYVFNHLAAQHDSWTIVGVAA	VLSLWAIPV,VFVLSLWAI,WAIPVTYVF,SLWAIPVTY,GVFVLSLWAI,FVLSLWAIPV,VLSLWAIPVT,SLWAIPVTYV,LWAIPVTYVF,LSLWAIPVTY	BLCA
TM9SF2	c.272G>A	p.R91H	RLDSVESVLPYEYTAFDFCQASEGK[p.R91H]HPSENLGQVLFGERIEPSPYKFTFNK	HPSENLGQV,HPSENLGQVL,SEGKHPSENL	CRC

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TMC5	c.826C>T	p.R276C	DYGSSETPKMTRGVLSRTSSIQPSF[p.R276C]CHRSDDPVGSLWGENDYPEGIEMASM	SIQPSFCHR,SSIQPSFCHR,RTSSIQPSFC	SKCM
TMCC3	c.329G>A	p.R110H	EQTSRDGNVAEYLKLVNNADKQQAG[p.R110H]HIKQVFEKKNQKSAHSIAQLQKKLEQ	QQAGHIKQV,HIKQVFEKK,QAGHIKQVF,AGHIKQVFEK,QQAGHIKQVF,KQQAGHIKQV	CRC
TMCO2	c.43_44delTC	p.S15fs	MSTSSSSSWDNLLESLS[p.S15fs]QHSMELDTSKFFGRD*	SLSQHSMEL,HSMELDTSK,MELDTSKFF,LESLSQHSM,SQHSMELDT,SMELDTSKF,ELDTSKFFGR,ESLSQHSMEL,HSMELDTSKF,LLESLSQHSM,SQHSMELDTS,SMELDTSKFF,MELDTSKFFG	BLCA
TMEM102	c.328G>C	p.A110P	AELLLLRGGIREGSLDLGHAPLGPY[p.A110P]PRGPHYDAGFTLLVPMFSLDGTELQL	HAPLGPYPR,YPRGPHYDA,GPYPRGPHY,LGPYPRGPHY,YPRGPHYDAG	KIRC
TMEM121	c.879_881delGCC	p.P299del	FPPPALSLELQPPPPQRNSVPPPPP[p.P299del]LHGPPGRPHMSSPTRDPLDT*	NSVPPPPPL,RNSVPPPPPL	PRAD
TMEM131	c.3955G>C	p.E1319Q	AHSPLEQHPQPPLPPPVPQPQEPQP[p.E1319Q]QRLSPAPLAHPSHPERASSARHSSED	PQRLSPAPL,QPQEPQPQRL,EPQPQRLSPA,QPQRLSPAPL	CESC
TMEM132A	c.1441C>T	p.R481C	EACDAVFVAGKESRGARGVRVDFWW[p.R481C]CRLRASLRLTVWAPLLPLRIELTDTT	RVDFWWCRLR,FWWCRLRASL,GVRVDFWWCR,WWCRLRASLR,WCRLRASLRL,VRVDFWWCRL	CRC
TMEM132D	c.1732C>T	p.R578W	GDSEEEEDDERRGRGCTLQYQHAMV[p.R578W]WVLTQFVAEAAGPGGHLAHLLGSDWQ	YQHAMVWVL,MVWVLTQFV,AMVWVLTQF,LQYQHAMVW,QYQHAMVWV,LQYQHAMVWV,YQHAMVWVLT,AMVWVLTQFV,MVWVLTQFVA,WVLTQFVAEA,QYQHAMVWVL,HAMVWVLTQF,TLQYQHAMVW	CRC
TMEM132D	c.618delC	p.P206fs	SCRLQGDLGLCVAELELLSSWFSPP[p.P206fs]RWLPGGGSPWTSRRGPPWSSTTPCTQGVREGTASGKTRGEAMGSGQATVTSMSPGPPCRGSGASSFIRHTGNPP*	AMGSGQATV,STTPCTQGV,LSSWFSPPR,SMSPGPPCR,GSGASSFIR,SWFSPPRWL,TSRRGPPWS,GVREGTASG,KTRGEAMGS,RGSGASSFI,SGKTRGEAM,SSWFSPPRW,WLPGGGSPW,WTSRRGPPW,SGQATVTSM,CRGSGASSF,GEAMGSGQA,WLPGGGSPWT,LLSSWFSPPR,GVREGTASGK,TSMSPGPPCR,RWLPGGGSPW,KTRGEAMGSG,RGSGASSFIR,STTPCTQGVR,SSTTPCTQGV,EAMGSGQATV,SPWTSRRGPP,LSSWFSPPRW,SSWFSPPRWL,ASGKTRGEAM,GEAMGSGQAT,GSGQATVTSM	STAD
TMEM147	c.275C>T	p.A92V	FIGEFMKASVDVADLIGLNLVMSRN[p.A92V]VGKGEYKIMVAALGWATAELIMSRCI	LVMSRNVGK,SRNVGKGEY,GLNLVMSRNV,MSRNVGKGEY	GBM
TMEM156	c.241C>T	p.R81C	SFVTFLQPVRETQIIMRIFLNPSNF[p.R81C]CNFTRTCQDITGEFKMCSSCLVCESK	PSNFCNFTR,FLNPSNFCNF,NPSNFCNFTR	GBM
TMEM161B	c.425T>C	p.L142P	VYLVTEVYYNFMKPTQEMNISLVWC[p.L142P]PLVLSFAIKVLFSLTTHYFKVEDGGE	ISLVWCPLV,SLVWCPLVL,VWCPLVLSF,NISLVWCPL,CPLVLSFAI,NISLVWCPLV,ISLVWCPLVL,LVWCPLVLSF,MNISLVWCPL	KIRC
TMEM161B	c.944G>A	p.R315Q	KDYIMNPPLGKESIPLMTEATFDTL[p.R315Q]QLWLIIILCALRLAMMRSHLQAYLNL	TLQLWLIIL,LQLWLIIILL,EATFDTLQL,ATFDTLQLW,TLQLWLIIILL,QLWLIIILLCA,ATFDTLQLWL,TFDTLQLWLI,TEATFDTLQL,EATFDTLQLW	UCEC
TMEM19	c.993delT	p.G331fs	LDNNAVNLFSSVLIALLLPTAAWGF[p.G331fs]GPGGELYFISTG*	GFGPGGELY,WGFGPGGEL,GELYFISTG,GFGPGGELYF,WGFGPGGELY	BLCA
TMEM230	c.419A>G	p.D140G	LFLIGAFLIIIGSLLLSGYISKGGA[p.D140G]GRAVPVLIIGILVFLPGFYHLRIAYY	ISKGGAGRA,AGRAVPVLI,YISKGGAGR,SKGGAGRAV,YISKGGAGRA,AGRAVPVLII	KIRC
TMEM247	c.382C>G	p.Q128E	EMELEKVRMEFELTRLKYLHEKNQR[p.Q128E]ERQHEVVMEQLQQ	NQRERQHEV,YLHEKNQRER,NQRERQHEVV	ACC
TMEM41A	c.467delT	p.F156fs	VVSYFPDKVALLQRKVEENRNSLFF[p.F156fs]SYCF*	NSLFFSYCF,NRNSLFFSY,RNSLFFSYCF,ENRNSLFFSY	STAD
TMEM41B	c.690delT	p.F230fs	RITPFLPNWFINITSPVINVPLKVF[p.F230fs]LLVLF*	NVPLKVFLL,LKVFLLVLF,VPLKVFLLV,NVPLKVFLLV,VPLKVFLLVL	STAD
TMEM47	c.259G>A	p.G87S	ASLDIWHCESTLSSDWQIATLALLL[p.G87S]SGAAIILIAFLVGLISICVGSRRRFY	TLALLLSGA,ALLLSGAAI,LLLSGAAII,LLSGAAIIL,ALLLSGAAII,LLLSGAAIIL,LLSGAAIILI,TLALLLSGAA,SGAAIILIAF,LALLLSGAAI	KIRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
TMEM55A	c.566G>A	p.R189Q	MELRFNTLAKCPHCKKISSVGSALP[p.R189Q]QRRCCAYITIGMICIFIGVGLTVGTP	SVGSALPQR,LPQRRCCAY,SSVGSALPQR,ALPQRRCCAY,LPQRRCCAYI	CRC
TMEM60	c.231delA	p.K77fs	LIVKMAGRCKSGFDPRHGSHNIKKK[p.K77fs]PGTSLQCYLN*	IKKKPGTSL,NIKKKPGTSL,KKPGTSLQCY	KIRP
TMEM71	c.188G>A	p.R63Q	DSLDGYHSFECGSIDPLTGSHYTCR[p.R63Q]QSPRLLTNGYYIWTEDSFLCDKDGNI	HYTCRQSPR,RQSPRLLTN,SHYTCRQSPR,QSPRLLTNGY,RQSPRLLTNG	BRCA
TMEM74	c.374G>A	p.R125Q	CNCCSQELETSFTYVDKNINLEQRN[p.R125Q]QSSPSAKGHNHPGELGWENPNEWSQE	RNQSSPSAK,EQRNQSSPSA	CRC
TMEM79	c.481_482insC	p.P161fs	ERQPQEDLIVRCEAGEGECRTFMPP[p.P161fs]PGHPPRPH*	RTFMPPPGH,MPPPGHPPR,RTFMPPPGHP,FMPPPGHPPR,GECRTFMPPP	STAD
TMPRSS11A	c.863C>T	p.S288L	IHEKYRSAAREYDIAVVQVSSRVTF[p.S288L]LDDIRQICLPEASASFQPNLTVHITG	QVSSRVTFL,FLDDIRQICL,VQVSSRVTFL,SSRVTFLDDI	CRC
TMPRSS11E	c.775G>T	p.G259C	FTTYKNPARWTASFGVTIKPSKMKR[p.G259C]CLRRIIVHEKYKHPSHDYDISLAELS	KMKRCLRRI,PSKMKRCLR,KPSKMKRCL,MKRCLRRII,CLRRIIVHEK,KMKRCLRRII,SKMKRCLRRI,MKRCLRRIIV	LUAD
TMPRSS11F	c.821G>A	p.R274Q	CFWKNKDPTQWIATFGATITPPAVK[p.R274Q]QNVRKIILHENYHRETNENDIALVQL	KQNVRKIIL,TPPAVKQNV,KQNVRKIILH,ITPPAVKQNV,VKQNVRKIIL	LUSC
TMPRSS3	c.47G>A	p.R16Q	MGENDPPAVEAPFSF[p.R16Q]QSLFGLDDLKISPVAPDADAVAAQIL	FSFQSLFGL,EAPFSFQSL,APFSFQSLF,VEAPFSFQS,QSLFGLDDLK,VEAPFSFQSL,FQSLFGLDDL	UCEC
TMPRSS6	c.904G>A	p.V302I	ITSVYGCSRQEPVVEVLASGAIMAV[p.V302I]IWKKGLHSYYDPFVLSVQPVVFQACE	AIMAVIWKK,GAIMAVIWK,IWKKGLHSY,SGAIMAVIW,IMAVIWKKGL,SGAIMAVIWK,GAIMAVIWKK,VIWKKGLHSY,IWKKGLHSYY,LASGAIMAVI,ASGAIMAVIW	GBM
TMTC2	c.1226C>G	p.T409R	RTQLPSTENIVVLSLSLLIIPFVPA[p.T409R]RNLFFYVGFVIAERVLYIPSMGFCLL	LIIPFVPAR,PFVPARNLF,FVPARNLFF,RNLFFYVGF,PARNLFFYV,VPARNLFFY,IPFVPARNL,FVPARNLFFY,PFVPARNLFF,RNLFFYVGFV,LLIIPFVPAR,VPARNLFFYV,IPFVPARNLF,ARNLFFYVGF	HNSC
TMTC4	c.1831C>T	p.R611C	EAAEQSYRTAIKHRRKYPDCYYNLG[p.R611C]CLYADLNRHVDALNAWRNATVLKPEH	CYYNLGCLY,CLYADLNRHV	STAD
TMX3	c.451C>T	p.R151C	AHRVSGALIRPLPSQQMFEHMQKRH[p.R151C]CVFFVYVGGESPLKEKYIDAASELIV	HMQKRHCVF,MQKRHCVFF,KRHCVFFVY,EHMQKRHCV,MQKRHCVFFV,HMQKRHCVFF,KRHCVFFVYV,QKRHCVFFVY,EHMQKRHCVF,FEHMQKRHCV	LUAD
TNF	c.139C>T	p.L47F	GGPQGSRRCLFLSLFSFLIVAGATT[p.L47F]FFCLLHFGVIGPQREEFPRDLSLISP	ATTFFCLLH,IVAGATTFF,TTFFCLLHF,LIVAGATTF,TFFCLLHFGV,FLIVAGATTF,ATTFFCLLHF,FFCLLHFGVI,LIVAGATTFF	DLBCL
TNFSF9	c.694G>A	p.A232T	SAGQRLGVHLHTEARARHAWQLTQG[p.A232T]TTVLGLFRVTPEIPAGLPSPRSE*	WQLTQGTTV,QLTQGTTVL,GTTVLGLFR,TTVLGLFRV,TQGTTVLGL,TQGTTVLGLF,WQLTQGTTVL	GBM
TNIP2	c.217C>G	p.R73G	LRARLAALEGDAAPSLVDALLEQVA[p.R73G]GFREQLRRQEGGAAEAQMRQEIERLT	ALLEQVAGF,QVAGFREQL,ALLEQVAGFR,QVAGFREQLR,EQVAGFREQL,DALLEQVAGF	ACC
TNIP2	c.415G>A	p.A139T	QPQHEREKEVVLLRRSMAEGERARA[p.A139T]TSDVLCRSLANETHQLRRTLTATAHM	RARATSDVL,AEGERARAT,RARATSDVLC,GERARATSDV	CRC
TNK2	c.1894_1895insC	p.P632fs	PTRALPRPLHPTPVVDWDARPLPPP[p.P632fs]ARL*	RPLPPPARL,DARPLPPPAR	STAD
TNKS2	c.1856_1857insA	p.T619fs	HEAAAKGKYEICKLLLQHGADPTKK[p.T619fs]KQGWKYSFGSC*	PTKKKQGWK,KKQGWKYSF,PTKKKQGWKY,KKKQGWKYSF	CESC,CLL
TNR	c.2074C>A	p.L692I	SAVMNSQQSVPATMNARTELDSPRD[p.L692I]IMVTASSETSISLIWTKASGPIDHYR	IMVTASSET,SPRDIMVTA,TELDSPRDI,DSPRDIMVTA,SPRDIMVTAS,TELDSPRDIM,IMVTASSETS	LUAD
TNS1	c.547C>T	p.P183S	GQPSQRRYVHYFSGLLSGSIKMNNK[p.P183S]SLFLHHVIMHGIPNFESKGGCRPFLR	KMNNKSLFL,KSLFLHHVI,SIKMNNKSL,SLFLHHVIM,IKMNNKSLF,KMNNKSLFLH,SIKMNNKSLF,KSLFLHHVIM,IKMNNKSLFL,NKSLFLHHVI,SLFLHHVIMH	TGCT
TNXB	c.2116_2117delGT	p.V706fs	EEPPASACPGGCGPRELCRAGQCVC[p.V706fs]RGLPRP*	RAGQCVCRGL	ACC

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TOP2A	c.2207G>T	p.R736L	NERSIPSMVDGLKPGQRKVLFTCFK[p.R736L]LNDKREVKVAQLAGSVAEMSSYHHGE	KVLFTCFKL,KLNDKREVK,FTCFKLNDK,KLNDKREVKV,FTCFKLNDKR,RKVLFTCFKL	LUAD
TOP2A	c.3595A>G	p.K1199E	FIEELEAVEAKEKQDEQVGLPGKGG[p.K1199E]EAKGKKTQMAEVLPSPRGQRVIPRIT	KGGEAKGKK,GEAKGKKTQM	THCA
TOP2B	c.1967G>A	p.R656H	IKYYKGLGTSTAKEAKEYFADMERH[p.R656H]HILFRYAGPEDDAAITLAFSKKKIDD	DMERHHILF,MERHHILFR,RHHILFRYA,ADMERHHIL,FADMERHHI,YFADMERHHI,MERHHILFRY,DMERHHILFR,FADMERHHIL,ADMERHHILF	CRC
TOPBP1	c.4141delA	p.I1381fs	ILDVLTGINVQQRRLALAAMRWRKK[p.I1381fs]SSKDKNLALLREHLVGGRLFYMWISLEKQASNAFFSQEEQRCYLVILYLYLKRPHIFFLT*	FSQEEQRCY,LVGGRLFYM,RLFYMWISL,YLVILYLYL,YLYLKRPHI,NLALLREHL,HLVGGRLFY,LVILYLYLK,FYMWISLEK,VILYLYLKR,VGGRLFYMW,CYLVILYLY,LYLKRPHIF,YLKRPHIFF,KSSKDKNLA,SSKDKNLAL,GGRLFYMWI,AFFSQEEQR,AMRWRKKSS,EQRCYLVIL,LKRPHIFFL,LEKQASNAF,REHLVGGRL,EKQASNAFF,KQASNAFFS,SQEEQRCYL,RCYLVILYL,EEQRCYLVI,QEEQRCYLV,NLALLREHLV,HLVGGRLFYM,YMWISLEKQA,YLKRPHIFFL,AMRWRKKSSK,LFYMWISLEK,YLVILYLYLK,LVGGRLFYMW,CYLVILYLYL,LYLYLKRPHI,YLYLKRPHIF,LYLKRPHIFF,RWRKKSSKDK,SSKDKNLALL,EQRCYLVILY,RCYLVILYLY,LLREHLVGGR,NAFFSQEEQR,LVILYLYLKR,SLEKQASNAF,LEKQASNAFF,KSSKDKNLAL,KNLALLREHL,REHLVGGRLF,GRLFYMWISL,KQASNAFFSQ,ILYLYLKRPH,EEQRCYLVIL,QEEQRCYLVI	STAD
TOR1AIP2	c.436G>A	p.G146R	PSDKVGRADAHLGSSSVALPKEASD[p.G146R]RTGASQEPPTTDSQEAQSPGHSSAGQ	KEASDRTGA	TGCT
TOR3A	c.37T>C	p.F13L	MLRGPWRQLWLF[p.F13L]LLLLLPGAPEPRGASRPWEGTDEPGS	RQLWLFLLL,QLWLFLLLL,FLLLLLPGA,PWRQLWLFL,LWLFLLLLL,RQLWLFLLLL,QLWLFLLLLL,PWRQLWLFLL,GPWRQLWLFL	ACC
TOX	c.1061C>T	p.S354L	RASLVSKSYSEPVDVKTSQPPQLIN[p.S354L]LKPSVFHGPSQAHSALYLSSHYHQQP	QLINLKPSV,LINLKPSVF,SQPPQLINL,SQPPQLINLK,QLINLKPSVF	CRC
TP53	c.1010G>T	p.R337L	TSSSPQPKKKPLDGEYFTLQIRGRE[p.R337L]LFEMFRELNEALELKDAQAGKEPGGS	ELFEMFREL,LQIRGRELF,RGRELFEMF,TLQIRGREL,IRGRELFEM,RGRELFEMFR,TLQIRGRELF,IRGRELFEMF,RELFEMFREL	LUAD,LUSC
TP53	c.173delC	p.P58fs	SPLPSQAMDDLMLSPDDIEQWFTED[p.P58fs]QVQMKLPECQRLLPPWPLHQQLLHRRPLHQPPPGPCHLLSLPRKPTRAATVSVWASCILGQPSL*	KLPECQRLL,SLPRKPTRA,RLLPPWPLH,LSLPRKPTR,PTRAATVSV,RAATVSVWA,QMKLPECQR,TVSVWASCI,LPRKPTRAA,QQLLHRRPL,MKLPECQRL,QRLLPPWPL,TRAATVSVW,VSVWASCIL,WPLHQQLLH,TEDQVQMKL,SLPRKPTRAA,CQRLLPPWPL,LLSLPRKPTR,ATVSVWASCI,TVSVWASCIL,LPPWPLHQQL,LPRKPTRAAT,KPTRAATVSV,HQQLLHRRPL,QWFTEDQVQM,MKLPECQRLL,QQLLHRRPLH,HQPPPGPCHL,ASCILGQPSL,IEQWFTEDQV	HNSC
TP53	c.216delC	p.P72fs	DDIEQWFTEDPGPDEAPRMPEAAPP[p.P72fs]WPLHQQLLHRRPLHQPPPGPCHLLSLPRKPTRAATVSVWASCILGQPSL*	SLPRKPTRA,RMPEAAPPW,LSLPRKPTR,PTRAATVSV,RAATVSVWA,TVSVWASCI,LPRKPTRAA,QQLLHRRPL,TRAATVSVW,VSVWASCIL,WPLHQQLLH,PEAAPPWPL,SLPRKPTRAA,LLSLPRKPTR,ATVSVWASCI,TVSVWASCIL,MPEAAPPWPL,APPWPLHQQL,LPRKPTRAAT,KPTRAATVSV,HQQLLHRRPL,QQLLHRRPLH,HQPPPGPCHL,ASCILGQPSL	LUAD
TP53	c.313G>T	p.G105C	PTPAAPAPAPSWPLSSSVPSQKTYQ[p.G105C]CSYGFRLGFLHSGTAKSVTCTYSPAL	YQCSYGFRL,KTYQCSYGF,CSYGFRLGF,SQKTYQCSY,TYQCSYGFR,KTYQCSYGFR,TYQCSYGFRL,PSQKTYQCSY,QKTYQCSYGF,YQCSYGFRLG,CSYGFRLGFL	LUAD
TP53	c.323delG	p.G108fs	AAPAPAPSWPLSSSVPSQKTYQGSY[p.G108fs]VSVWASCILGQPSL*	YVSVWASCI,TYQGSYVSV,YQGSYVSVW,SYVSVWASC,KTYQGSYVS,VSVWASCIL,KTYQGSYVSV,YQGSYVSVW,SQKTYQGSYV,YVSVWASCIL,TYQGSYVSVW,SYVSVWASCI,ASCILGQPSL	BRCA
TP53	c.328delC	p.R110fs	PAPAPSWPLSSSVPSQKTYQGSYGF[p.R110fs]VWASCILGQPSL*	TYQGSYGFV,YQGSYGFVW,SYGFVWASC,YGFVWASCI,KTYQGSYGFV,YQGSYGFVWA,TYQGSYGFVW,SYGFVWASCI,YGFVWASCIL,ASCILGQPSL	BRCA

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
TP53	c.329G>T	p.R110L	PAPAPSWPLSSSVPSQKTYQGSYGF[p.R110L]LLGFLHSGTAKSVTCTYSPALNKMFC	YQGSYGFLL,FLLGFLHSG,TYQGSYGFL,SYGFLLGFL,GSYGFLLGF,FLLGFLHSGT,KTYQGSYGFL,LLGFLHSGTA,TYQGSYGFLL,YQGSYGFLLG,QGSYGFLLGF	HNSC,LUAD
TP53	c.396G>C	p.K132N	YGFRLGFLHSGTAKSVTCTYSPALN[p.K132N]NMFCQLAKTCPVQLWVDSTPPPGTRV	ALNNMFCQL,NMFCQLAKT,TYSPALNNM,YSPALNNMF,ALNNMFCQLA,TYSPALNNMF,CTYSPALNNM	BLCA,BRCA
TP53	c.396G>T	p.K132N	YGFRLGFLHSGTAKSVTCTYSPALN[p.K132N]NMFCQLAKTCPVQLWVDSTPPPGTRV	ALNNMFCQL,NMFCQLAKT,TYSPALNNM,YSPALNNMF,ALNNMFCQLA,TYSPALNNMF,CTYSPALNNM	OV
TP53	c.421T>G	p.C141G	SGTAKSVTCTYSPALNKMFCQLAKT[p.C141G]GPVQLWVDSTPPPGTRVRAMAIYKQS	CQLAKTGPV,KTGPVQLWV,AKTGPVQLW,QLAKTGPVQL,KMFCQLAKTG,LAKTGPVQLW	PRAD
TP53	c.422G>A	p.C141Y	SGTAKSVTCTYSPALNKMFCQLAKT[p.C141Y]YPVQLWVDSTPPPGTRVRAMAIYKQS	CQLAKTYPV,KTYPVQLWV,MFCQLAKTY,LAKTYPVQL,AKTYPVQLW,QLAKTYPVQL,KMFCQLAKTY,LAKTYPVQLW,YPVQLWVDST	BRCA
TP53	c.427G>A	p.V143M	TAKSVTCTYSPALNKMFCQLAKTCP[p.V143M]MQLWVDSTPPPGTRVRAMAIYKQSQH	KTCPMQLWV,CQLAKTCPM,AKTCPMQLW,MQLWVDSTP,QLAKTCPMQL,FCQLAKTCPM,LAKTCPMQLW,MQLWVDSTPP,CPMQLWVDST	HNSC
TP53	c.451C>A	p.P151T	YSPALNKMFCQLAKTCPVQLWVDST[p.P151T]TPPGTRVRAMAIYKQSQHMTEVVRRC	STTPPGTRV,VQLWVDSTT,STTPPGTRVR,TPPGTRVRAM,VQLWVDSTTP	HNSC
TP53	c.455delC	p.P152fs	SPALNKMFCQLAKTCPVQLWVDSTP[p.P152fs]RPAPASAPWPSTSSHST*	QLWVDSTPR,TPRPAPASA,RPAPASAPW,APWPSTSSH,WPSTSSHST,STPRPAPASA,TPRPAPASAP,APASAPWPST	STAD
TP53	c.461G>T	p.G154V	ALNKMFCQLAKTCPVQLWVDSTPPP[p.G154V]VTRVRAMAIYKQSQHMTEVVRRCPHH	WVDSTPPPV,VTRVRAMAI,DSTPPPVTR,STPPPVTRV,PPVTRVRAM,VTRVRAMAIY,DSTPPPVTRV,LWVDSTPPPV	LUAD
TP53	c.464C>A	p.T155N	LNKMFCQLAKTCPVQLWVDSTPPPG[p.T155N]NRVRAMAIYKQSQHMTEVVRRCPHHE	STPPPGNRV,PPGNRVRAM,GNRVRAMAI,NRVRAMAIY,GNRVRAMAIY,DSTPPPGNRV	GBM
TP53	c.469G>T	p.V157F	KMFCQLAKTCPVQLWVDSTPPPGTR[p.V157F]FRAMAIYKQSQHMTEVVRRCPHHERC	RFRAMAIYK,GTRFRAMAI,TRFRAMAIY,PPGTRFRAM,TRFRAMAIYK,GTRFRAMAIY,RFRAMAIYKQ,STPPPGTRFR	HNSC,LIHC,LUAD,LUSC,OV
TP53	c.473G>A	p.R158H	MFCQLAKTCPVQLWVDSTPPPGTRV[p.R158H]HAMAIYKQSQHMTEVVRRCPHHERCS	RVHAMAIYK,GTRVHAMAI,PPGTRVHAM,TRVHAMAIY,GTRVHAMAIY	GBM,LIHC
TP53	c.473G>T	p.R158L	MFCQLAKTCPVQLWVDSTPPPGTRV[p.R158L]LAMAIYKQSQHMTEVVRRCPHHERCS	RVLAMAIYK,GTRVLAMAI,TPPPGTRVL,PPGTRVLAM,TRVLAMAIY,GTRVLAMAIY	LUAD,LUSC
TP53	c.475G>C	p.A159P	FCQLAKTCPVQLWVDSTPPPGTRVR[p.A159P]PMAIYKQSQHMTEVVRRCPHHERCSD	RVRPMAIYK,GTRVRPMAI,PPGTRVRPM,TRVRPMAIY,GTRVRPMAIY,RVRPMAIYKQ	LUAD
TP53	c.476C>T	p.A159V	FCQLAKTCPVQLWVDSTPPPGTRVR[p.A159V]VMAIYKQSQHMTEVVRRCPHHERCSD	RVRVMAIYK,GTRVRVMAI,RVMAIYKQS,TRVRVMAIY,GTRVRVMAIY,RVRVMAIYKQ,VMAIYKQSQH	BLCA,OV
TP53	c.488A>G	p.Y163C	AKTCPVQLWVDSTPPPGTRVRAMAI[p.Y163C]CKQSQHMTEVVRRCPHHERCSDSDGL	RVRAMAICK,AICKQSQHM,GTRVRAMAIC,RVRAMAICKQ,MAICKQSQHM	BRCA,HNSC,LUAD,LUSC,OV
TP53	c.517G>A	p.V173M	DSTPPPGTRVRAMAIYKQSQHMTEV[p.V173M]MRRCPHHERCSDSDGLAPPQHLIRVE	MRRCPHHER,QSQHMTEVM,VMRRCPHHER,KQSQHMTEVM	BRCA,HNSC
TP53	c.517G>T	p.V173L	DSTPPPGTRVRAMAIYKQSQHMTEV[p.V173L]LRRCPHHERCSDSDGLAPPQHLIRVE	VLRRCPHHER,QSQHMTEVLR,KQSQHMTEVL	BRCA,HNSC
TP53	c.523C>G	p.R175G	TPPPGTRVRAMAIYKQSQHMTEVVR[p.R175G]GCPHHERCSDSDGLAPPQHLIRVEGN	TEVVRGCPH,VVRGCPHHER	LUSC
TP53	c.523C>T	p.R175C	TPPPGTRVRAMAIYKQSQHMTEVVR[p.R175C]CCPHHERCSDSDGLAPPQHLIRVEGN	TEVVRCCPH,VVRCCPHHER	CRC

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TP53	c.524G>A	p.R175H	TPPPGTRVRAMAIYKQSQHMTEVVR[p.R175H]HCPHHERCSDSDGLAPPQHLIRVEGN	TEVVRHCPH,VVRHCPHHER,SQHMTEVVRH	BLCA,BRCA,CLL,CRC,GBM,HNSC,LUAD,OV,PAAD,PRAD,STAD,UCS
TP53	c.527G>A	p.C176Y	PPPGTRVRAMAIYKQSQHMTEVVRR[p.C176Y]YPHHERCSDSDGLAPPQHLIRVEGNL	HMTEVVRRY,TEVVRRYPH,VVRRYPHHER,QHMTEVVRRY	OV
TP53	c.527G>T	p.C176F	PPPGTRVRAMAIYKQSQHMTEVVRR[p.C176F]FPHHERCSDSDGLAPPQHLIRVEGNL	HMTEVVRRF,TEVVRRFPH,VVRRFPHHER,QHMTEVVRRF	BRCA,LUAD,STAD
TP53	c.535C>T	p.H179Y	GTRVRAMAIYKQSQHMTEVVRRCPH[p.H179Y]YERCSDSDGLAPPQHLIRVEGNLRVE	VVRRCPHYE,EVVRRCPHY,VVRRCPHYER,TEVVRRCPHY,YERCSDSDGL	HNSC
TP53	c.536A>G	p.H179R	GTRVRAMAIYKQSQHMTEVVRRCPH[p.H179R]RERCSDSDGLAPPQHLIRVEGNLRVE	EVVRRCPHR,VVRRCPHRER,RERCSDSDGL	BRCA,GBM,HNSC,OV,UCS
TP53	c.536A>T	p.H179L	GTRVRAMAIYKQSQHMTEVVRRCPH[p.H179L]LERCSDSDGLAPPQHLIRVEGNLRVE	EVVRRCPHL,VVRRCPHLER,TEVVRRCPHL,LERCSDSDGL	LUSC
TP53	c.572_574delCTC	p.P191del	SQHMTEVVRRCPHHERCSDSDGLAP[p.P191del]QHLIRVEGNLRVEYLDDRNTFRHSVVVP	GLAPQHLIR,GLAPQHLIRV	OV
TP53	c.577C>T	p.H193Y	HMTEVVRRCPHHERCSDSDGLAPPQ[p.H193Y]YLIRVEGNLRVEYLDDRNTFRHSVVV	GLAPPQYLI,YLIRVEGNL,DSDGLAPPQY,GLAPPQYLIR,QYLIRVEGNL,YLIRVEGNLR	BRCA
TP53	c.578A>G	p.H193R	HMTEVVRRCPHHERCSDSDGLAPPQ[p.H193R]RLIRVEGNLRVEYLDDRNTFRHSVVV	GLAPPQRLI,RLIRVEGNL,RLIRVEGNLR	BRCA,LIHC,OV,UCS
TP53	c.578A>T	p.H193L	HMTEVVRRCPHHERCSDSDGLAPPQ[p.H193L]LLIRVEGNLRVEYLDDRNTFRHSVVV	GLAPPQLLI,LLIRVEGNL,GLAPPQLLIR,LLIRVEGNLR	BRCA,HNSC,LUSC
TP53	c.581T>G	p.L194R	MTEVVRRCPHHERCSDSDGLAPPQH[p.L194R]RIRVEGNLRVEYLDDRNTFRHSVVVP	GLAPPQHRI,RIRVEGNLR,APPQHRIRV,RIRVEGNLRV	BRCA,OV
TP53	c.584T>C	p.I195T	TEVVRRCPHHERCSDSDGLAPPQHL[p.I195T]TRVEGNLRVEYLDDRNTFRHSVVVPY	GLAPPQHLT,LTRVEGNLR,GLAPPQHLTR,LTRVEGNLRV,HLTRVEGNLR	BRCA,OV
TP53	c.587G>C	p.R196P	EVVRRCPHHERCSDSDGLAPPQHLI[p.R196P]PVEGNLRVEYLDDRNTFRHSVVVPYE	HLIPVEGNL,APPQHLIPV,IPVEGNLRV,HLIPVEGNLR,LAPPQHLIPV	HNSC
TP53	c.596G>T	p.G199V	RRCPHHERCSDSDGLAPPQHLIRVE[p.G199V]VNLRVEYLDDRNTFRHSVVVPYEPPE	HLIRVEVNL,LIRVEVNLR,EVNLRVEYL,VEVNLRVEY,LIRVEVNLRV,RVEVNLRVEY,HLIRVEVNLR,VEVNLRVEYL	BRCA
TP53	c.614A>G	p.Y205C	ERCSDSDGLAPPQHLIRVEGNLRVE[p.Y205C]CLDDRNTFRHSVVVPYEPPEVGSDCT	CLDDRNTFR,ECLDDRNTFR,VECLDDRNTF,VEGNLRVECL	OV
TP53	c.626_627delGA	p.R209fs	DSDGLAPPQHLIRVEGNLRVEYLDD[p.R209fs]KHFST*	YLDDKHFST,VEYLDDKHF,RVEYLDDKHF	BRCA
TP53	c.641A>G	p.H214R	APPQHLIRVEGNLRVEYLDDRNTFR[p.H214R]RSVVVPYEPPEVGSDCTTIHYNYMCN	NTFRRSVVV,FRRSVVVPY,TFRRSVVVPY,YLDDRNTFRR	LUSC
TP53	c.644G>T	p.S215I	PPQHLIRVEGNLRVEYLDDRNTFRH[p.S215I]IVVVPYEPPEVGSDCTTIHYNYMCNS	NTFRHIVVV,RNTFRHIVV,FRHIVVVPY,TFRHIVVVPY	LUAD
TP53	c.645T>G	p.S215R	PPQHLIRVEGNLRVEYLDDRNTFRH[p.S215R]RVVVPYEPPEVGSDCTTIHYNYMCNS	NTFRHRVVV,RHRVVVPYE,FRHRVVVPY,TFRHRVVVPY	OV

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
TP53	c.646G>A	p.V216M	PQHLIRVEGNLRVEYLDDRNTFRHS[p.V216M]MVVPYEPPEVGSDCTTIHYNYMCNSS	NTFRHSMVV,DRNTFRHSM,FRHSMVVPY,MVVPYEPPEV,TFRHSMVVPY	BRCA,GBM,OV
TP53	c.659A>C	p.Y220S	IRVEGNLRVEYLDDRNTFRHSVVVP[p.Y220S]SEPPEVGSDCTTIHYNYMCNSSCMGG	VVPSEPPEV,VVVPSEPPEV	BRCA
TP53	c.659A>G	p.Y220C	IRVEGNLRVEYLDDRNTFRHSVVVP[p.Y220C]CEPPEVGSDCTTIHYNYMCNSSCMGG	VVPCEPPEV,VVVPCEPPEV	BRCA,GBM,HNSC,LUSC,OV,UCEC
TP53	c.701A>G	p.Y234C	RNTFRHSVVVPYEPPEVGSDCTTIH[p.Y234C]CNYMCNSSCMGGMNRRPILTIITLED	CTTIHCNYM,TTIHCNYMC,CNYMCNSSCM	BRCA,GBM,LUSC,OV
TP53	c.706T>G	p.Y236D	TFRHSVVVPYEPPEVGSDCTTIHYN[p.Y236D]DMCNSSCMGGMNRRPILTIITLEDSS	NDMCNSSCM	HNSC
TP53	c.707A>G	p.Y236C	TFRHSVVVPYEPPEVGSDCTTIHYN[p.Y236C]CMCNSSCMGGMNRRPILTIITLEDSS	YNCMCNSSCM	HNSC,OV
TP53	c.711G>A	p.M237I	FRHSVVVPYEPPEVGSDCTTIHYNY[p.M237I]ICNSSCMGGMNRRPILTIITLEDSSG	CTTIHYNYI,YNYICNSSCM	HNSC
TP53	c.711G>C	p.M237I	FRHSVVVPYEPPEVGSDCTTIHYNY[p.M237I]ICNSSCMGGMNRRPILTIITLEDSSG	CTTIHYNYI,YNYICNSSCM	LUAD
TP53	c.713G>A	p.C238Y	RHSVVVPYEPPEVGSDCTTIHYNYM[p.C238Y]YNSSCMGGMNRRPILTIITLEDSSGN	TTIHYNYMY,YMYNSSCMG,YNYMYNSSC,CTTIHYNYMY,YMYNSSCMGG,YNYMYNSSCM,IHYNYMYNSS,MYNSSCMGGM	BRCA,GBM
TP53	c.713G>T	p.C238F	RHSVVVPYEPPEVGSDCTTIHYNYM[p.C238F]FNSSCMGGMNRRPILTIITLEDSSGN	YMFNSSCMG,TTIHYNYMF,NYMFNSSCM,YNYMFNSSC,YMFNSSCMGG,CTTIHYNYMF,YNYMFNSSCM,IHYNYMFNSS,MFNSSCMGGM	BRCA,GBM,HNSC
TP53	c.722C>A	p.S241Y	VVVPYEPPEVGSDCTTIHYNYMCNS[p.S241Y]YCMGGMNRRPILTIITLEDSSGNLLG	NYMCNSYCM,HYNYMCNSY,SYCMGGMNR,NSYCMGGMNR,IHYNYMCNSY,SYCMGGMNRR,YNYMCNSYCM,MCNSYCMGGM	UCS
TP53	c.722C>T	p.S241F	VVVPYEPPEVGSDCTTIHYNYMCNS[p.S241F]FCMGGMNRRPILTIITLEDSSGNLLG	HYNYMCNSF,NYMCNSFCM,SFCMGGMNR,YMCNSFCMG,NSFCMGGMNR,IHYNYMCNSF,SFCMGGMNRR,YNYMCNSFCM	OV
TP53	c.723delC	p.S241fs	VVPYEPPEVGSDCTTIHYNYMCNSS[p.S241fs]AWAA*	YMCNSSAWA,NYMCNSSAW,YNYMCNSSA,YMCNSSAWAA,HYNYMCNSSA,YNYMCNSSAW	BRCA
TP53	c.725G>T	p.C242F	VVPYEPPEVGSDCTTIHYNYMCNSS[p.C242F]FMGGMNRRPILTIITLEDSSGNLLGR	SSFMGGMNR,YNYMCNSSF,NYMCNSSFM,SFMGGMNRR,YMCNSSFMG,FMGGMNRRPI,SSFMGGMNRR,HYNYMCNSSF,NSSFMGGMNR,YNYMCNSSFM,YMCNSSFMGG,MCNSSFMGGM	CLL,HNSC,LUSC
TP53	c.730G>T	p.G244C	PYEPPEVGSDCTTIHYNYMCNSSCM[p.G244C]CGMNRRPILTIITLEDSSGNLLGRNS	YMCNSSCMC,SSCMCGMNR,CGMNRRPIL,SSCMCGMNRR,NSSCMCGMNR,MCNSSCMCGM,CMCGMNRRPI	OV
TP53	c.731G>A	p.G244D	PYEPPEVGSDCTTIHYNYMCNSSCM[p.G244D]DGMNRRPILTIITLEDSSGNLLGRNS	SSCMDGMNR,DGMNRRPIL,NSSCMDGMNR,CMDGMNRRPI	CRC
TP53	c.733G>A	p.G245S	YEPPEVGSDCTTIHYNYMCNSSCMG[p.G245S]SMNRRPILTIITLEDSSGNLLGRNSF	SSCMGSMNR,GSMNRRPIL,MGSMNRRPI,CNSSCMGSM,SMNRRPILTI,SSCMGSMNRR,NSSCMGSMNR,MGSMNRRPIL,MCNSSCMGSM,CMGSMNRRPI	CRC,GBM,HNSC,OV,PRAD
TP53	c.734G>A	p.G245D	YEPPEVGSDCTTIHYNYMCNSSCMG[p.G245D]DMNRRPILTIITLEDSSGNLLGRNSF	SSCMGDMNR,NSSCMGDMNR,CMGDMNRRPI	OV
TP53	c.734G>T	p.G245V	YEPPEVGSDCTTIHYNYMCNSSCMG[p.G245V]VMNRRPILTIITLEDSSGNLLGRNSF	SSCMGVMNR,GVMNRRPIL,SCMGVMNRR,MGVMNRRPI,CNSSCMGVM,YMCNSSCMGV,VMNRRPILTI,SSCMGVMNRR,NSSCMGVMNR,MGVMNRRPIL,MCNSSCMGVM,CMGVMNRRPI	HNSC,LUSC,OV

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TP53	c.742C>T	p.R248W	PEVGSDCTTIHYNYMCNSSCMGGMN[p.R248W]WRPILTIITLEDSSGNLLGRNSFEVR	NWRPILTII,SSCMGGMNW,MGGMNWRPI,MNWRPILTI,CMGGMNWRPI,GMNWRPILTI,SSCMGGMNWR,MNWRPILTII,NSSCMGGMNW	BLCA,BRCA,CLL,CRC,GBM,HNSC,OV,PAAD,UCEC
TP53	c.743G>A	p.R248Q	PEVGSDCTTIHYNYMCNSSCMGGMN[p.R248Q]QRPILTIITLEDSSGNLLGRNSFEVR	MNQRPILTI,NQRPILTII,CMGGMNQRPI,GMNQRPILTI,SSCMGGMNQR,NQRPILTIIT	BLCA,BRCA,CLL,GBM,HNSC,OV,PRAD,STAD,UCEC,UCS
TP53	c.743G>C	p.R248P	PEVGSDCTTIHYNYMCNSSCMGGMN[p.R248P]PRPILTIITLEDSSGNLLGRNSFEVR	SCMGGMNPR,NPRPILTII,GMNPRPILTI,CMGGMNPRPI,SSCMGGMNPR,NPRPILTIIT	LUAD
TP53	c.745A>G	p.R249G	EVGSDCTTIHYNYMCNSSCMGGMNR[p.R249G]GPILTIITLEDSSGNLLGRNSFEVRV	GPILTIITL,MNRGPILTI,GMNRGPILTI,CMGGMNRGPI,MNRGPILTII	LUAD
TP53	c.746G>T	p.R249M	EVGSDCTTIHYNYMCNSSCMGGMNR[p.R249M]MPILTIITLEDSSGNLLGRNSFEVRV	MNRMPILTI,MPILTIITL,MGGMNRMPI,SCMGGMNRM,NRMPILTII,CMGGMNRMPI,GMNRMPILTI,RMPILTIITL,MNRMPILTII,SSCMGGMNRM,MPILTIITLE	LUAD
TP53	c.747G>T	p.R249S	EVGSDCTTIHYNYMCNSSCMGGMNR[p.R249S]SPILTIITLEDSSGNLLGRNSFEVRV	MNRSPILTI,SPILTIITL,MGGMNRSPI,GMNRSPILTI,CMGGMNRSPI,RSPILTIITL,MNRSPILTII	HNSC,LIHC,LUAD
TP53	c.749C>T	p.P250L	VGSDCTTIHYNYMCNSSCMGGMNRR[p.P250L]LILTIITLEDSSGNLLGRNSFEVRVC	RLILTIITL,GMNRRLILT,MNRRLILTI,GGMNRRLIL,GMNRRLILTI,MNRRLILTII,RRLILTIITL	OV
TP53	c.763A>T	p.I255F	TTIHYNYMCNSSCMGGMNRRPILTI[p.I255F]FTLEDSSGNLLGRNSFEVRVCACPGR	RPILTIFTL,NRRPILTIF,FTLEDSSGNL,MNRRPILTIF,RRPILTIFTL	LUAD
TP53	c.775G>T	p.D259Y	YNYMCNSSCMGGMNRRPILTIITLE[p.D259Y]YSSGNLLGRNSFEVRVCACPGRDRRT	ILTIITLEY,LEYSSGNLL,PILTIITLEY,EYSSGNLLGR,LEYSSGNLLG	OV
TP53	c.785G>T	p.G262V	MCNSSCMGGMNRRPILTIITLEDSS[p.G262V]VNLLGRNSFEVRVCACPGRDRRTEEE	IITLEDSSV,DSSVNLLGR,LEDSSVNLL,VNLLGRNSF,TIITLEDSSV,TLEDSSVNLL,SVNLLGRNSF	HNSC
TP53	c.796G>A	p.G266R	SCMGGMNRRPILTIITLEDSSGNLL[p.G266R]RRNSFEVRVCACPGRDRRTEEENLRK	LLRRNSFEV,DSSGNLLRR,GNLLRRNSF,NLLRRNSFEV,LLRRNSFEVR,SGNLLRRNSF	OV
TP53	c.797G>A	p.G266E	SCMGGMNRRPILTIITLEDSSGNLL[p.G266E]ERNSFEVRVCACPGRDRRTEEENLRK	LLERNSFEV,DSSGNLLER,GNLLERNSF,NLLERNSFEV,SGNLLERNSF,LERNSFEVRV	BRCA,HNSC
TP53	c.797G>T	p.G266V	SCMGGMNRRPILTIITLEDSSGNLL[p.G266V]VRNSFEVRVCACPGRDRRTEEENLRK	LLVRNSFEV,LVRNSFEVR,GNLLVRNSF,NLLVRNSFEV,LVRNSFEVRV,SGNLLVRNSF,LEDSSGNLLV	OV
TP53	c.800G>C	p.R267P	CMGGMNRRPILTIITLEDSSGNLLG[p.R267P]PNSFEVRVCACPGRDRRTEEENLRKK	LLGPNSFEV,GNLLGPNSF,NLLGPNSFEV,SGNLLGPNSF	LUSC
TP53	c.811G>A	p.E271K	MNRRPILTIITLEDSSGNLLGRNSF[p.E271K]KVRVCACPGRDRRTEEENLRKKGEPH	LLGRNSFKV,NLLGRNSFK,LGRNSFKVR,KVRVCACPG,NSFKVRVCA,SFKVRVCAC,NLLGRNSFKV,GNLLGRNSFK,KVRVCACPGR	BLCA,LUSC
TP53	c.814G>A	p.V272M	NRRPILTIITLEDSSGNLLGRNSFE[p.V272M]MRVCACPGRDRRTEEENLRKKGEPHH	LLGRNSFEM,LGRNSFEMR,NSFEMRVCA,FEMRVCACP,NLLGRNSFEM,EMRVCACPGR,FEMRVCACPG	BRCA,OV
TP53	c.817C>T	p.R273C	RRPILTIITLEDSSGNLLGRNSFEV[p.R273C]CVCACPGRDRRTEEENLRKKGEPHHE	NSFEVCVCA,EVCVCACPGR,FEVCVCACPG	BLCA,BRCA,CRC,HNSC,OV,STAD,UCEC

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TP53	c.818G>A	p.R273H	RRPILTIITLEDSSGNLLGRNSFEV[p.R273H]HVCACPGRDRRTEEENLRKKGEPHHE	NSFEVHVCA,LGRNSFEVH,EVHVCACPGR,HVCACPGRDR,FEVHVCACPG	BRCA,CLL,CRC,GBM,HNSC,LUAD,OV,STAD,UCEC,UCS
TP53	c.818G>T	p.R273L	RRPILTIITLEDSSGNLLGRNSFEV[p.R273L]LVCACPGRDRRTEEENLRKKGEPHHE	NSFEVLVCA,LGRNSFEVL,LLGRNSFEVL,EVLVCACPGR,FEVLVCACPG	LUAD,LUSC,OV
TP53	c.820G>T	p.V274F	RPILTIITLEDSSGNLLGRNSFEVR[p.V274F]FCACPGRDRRTEEENLRKKGEPHHEL	NSFEVRFCA,GRNSFEVRF,EVRFCACPGR,LGRNSFEVRF,FEVRFCACPG	LUAD
TP53	c.824G>A	p.C275Y	PILTIITLEDSSGNLLGRNSFEVRV[p.C275Y]YACPGRDRRTEEENLRKKGEPHHELP	RNSFEVRVY,YACPGRDRR,NSFEVRVYA,RVYACPGRDR,EVRVYACPGR,GRNSFEVRVY,FEVRVYACPG	OV
TP53	c.824G>T	p.C275F	PILTIITLEDSSGNLLGRNSFEVRV[p.C275F]FACPGRDRRTEEENLRKKGEPHHELP	FACPGRDRR,NSFEVRVFA,RNSFEVRVF,FEVRVFACP,RVFACPGRDR,EVRVFACPGR,VFACPGRDRR,GRNSFEVRVF,FEVRVFACPG	HNSC,LUAD
TP53	c.830G>T	p.C277F	LTIITLEDSSGNLLGRNSFEVRVCA[p.C277F]FPGRDRRTEEENLRKKGEPHHELPPG	CAFPGRDRR,SFEVRVCAF,EVRVCAFPGR,NSFEVRVCAF,FEVRVCAFPG	LUAD
TP53	c.832C>T	p.P278S	TIITLEDSSGNLLGRNSFEVRVCAC[p.P278S]SGRDRRTEEENLRKKGEPHHELPPGS	CACSGRDRR,FEVRVCACS,EVRVCACSGR,FEVRVCACSG	HNSC
TP53	c.841G>A	p.D281N	TLEDSSGNLLGRNSFEVRVCACPGR[p.D281N]NRRTEEENLRKKGEPHHELPPGSTKR	CACPGRNRR,RVCACPGRNR	LUAD
TP53	c.844C>T	p.R282W	LEDSSGNLLGRNSFEVRVCACPGRD[p.R282W]WRTEEENLRKKGEPHHELPPGSTKRA	CACPGRDWR,RDWRTEEENL	BRCA,CRC,GBM,HNSC,OV,STAD
TP53	c.853G>A	p.E285K	SSGNLLGRNSFEVRVCACPGRDRRT[p.E285K]KEENLRKKGEPHHELPPGSTKRALPN	RTKEENLRK,RTKEENLRKK	BLCA,CESC,HNSC,LUAD
TP53	c.856G>A	p.E286K	SGNLLGRNSFEVRVCACPGRDRRTE[p.E286K]KENLRKKGEPHHELPPGSTKRALPNN	RTEKENLRK,RTEKENLRKK	BRCA,STAD
TP53	c.945_946delTC	p.S315fs	KGEPHHELPPGSTKRALPNNTSSSP[p.S315fs]AKEETTGWRIFHPSDPWA*	KEETTGWRI,RIFHPSDPW,EETTGWRIF,RIFHPSDPWA,LPNNTSSSPA,KEETTGWRIF,WRIFHPSDPW,EETTGWRIFH,SPAKEETTGW	OV
TP53RK	c.520delC	p.L174fs	VLARMHDEDLIHGDLTTSNMLLKPP[p.L174fs]WNS*	SNMLLKPPW	STAD
TPO	c.1193G>C	p.S398T	AACAPEPGIPGETRGPCFLAGDGRA[p.S398T]TEVPSLTALHTLWLREHNRLAAALKA	FLAGDGRAT,GRATEVPSL,TEVPSLTAL,TEVPSLTALH	ACC
TPO	c.1672G>A	p.E558K	GGLDPLIRGLLARPAKLQVQDQLMN[p.E558K]KELTERLFVLSNSSTLDLASINLQRG	QVQDQLMNK,KELTERLFV,LMNKELTERL,QLMNKELTER,VQDQLMNKEL,MNKELTERLF,KELTERLFVL	LUAD
TPO	c.2476G>A	p.A826T	ADGAHPPCHASARCRNTKGGFQCLC[p.A826T]TDPYELGDDGRTCVDSGRLPRVTWIS	CLCTDPYEL,FQCLCTDPY,GFQCLCTDPY	CRC
TPPP	c.89G>A	p.R30K	AKPAKAANRTPPKSPGDPSKDRAAK[p.R30K]KLSLESEGAGEGAAASPELSALEEAF	KLSLESEGA,PSKDRAAKK,DRAAKKLSL	KIRP
TPR	c.6464C>T	p.S2155L	EDRTVPSTPTLVVPHRTDGFAEAIH[p.S2155L]LPQVAGVPRFRFGPPEDMPQTSSSHS	AEAIHLPQV,FAEAIHLPQV,AIHLPQVAGV,HLPQVAGVPR,LPQVAGVPRF,AEAIHLPQVA	CRC
TPRX1	c.598T>C	p.S200P	NPGPIPGPNPGPIPGPISGPIPGPI[p.S200P]PVPIPGPIPGPISGPISGPNPGPIPG	GPIPGPIPV,IPGPIPVPI,IPVPIPGPI	TGCT

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TPTE	c.1268C>T	p.S423L	AQVKHLYNWNLPPRRILFIKHFIIY[p.S423L]LIPRYVRDLKIQIEMEKKVVFSTISL	FIKHFIIYL,IIYLIPRYV,FIIYLIPRY,HFIIYLIPR,IYLIPRYVR,IKHFIIYLI,FIKHFIIYLI,FIIYLIPRYV,YLIPRYVRDL,IIYLIPRYVR,LIPRYVRDLK,LFIKHFIIYL,KHFIIYLIPR,HFIIYLIPRY	CRC,UCEC
TPTE	c.1623G>A	p.M541I	DNLHKQKARRIYPSDFAVEILFGEK[p.M541I]ITSSDVVAGSD*	VEILFGEKI,GEKITSSDV,GEKITSSDVV,VEILFGEKIT	LUSC
TPTE2	c.773G>A	p.R258Q	FPSSGRQSFYRNPIEEVVRFLDKKH[p.R258Q]QNHYRVYNLCSERAYDPKHFHNRVSR	KHQNHYRVY,QNHYRVYNL,KKHQNHYRV,FLDKKHQNHY,HQNHYRVYNL,KKHQNHYRVY	CRC
TRAF3	c.26C>T	p.S9F	MESSKKMD[p.S9F]FPGALQTNPPLKLHTDRSAGTPVFVP	MESSKKMDF,KKMDFPGAL,SSKKMDFPGA,SKKMDFPGAL	CESC
TRAF7	c.32G>A	p.R11H	MSSGKSARYN[p.R11H]HFSGGPSNLPTPDVTTGTRMETTFGP	KSARYNHFS,SARYNHFSG,GKSARYNHF,KSARYNHFSG,SARYNHFSGG,SGKSARYNHF,NHFSGGPSNL	DLBCL
TRAK1	c.1879G>A	p.D627N	DPRPGVVTKGFRTLDVDLDEVYCLN[p.D627N]NFEEDDTGDHISLPRLATSTPVQHPE	DEVYCLNNF	CRC
TRAM1	c.121G>C	p.E41Q	HEFVLQNHADIVSCVAMVFLLGLMF[p.E41Q]QITAKASIIFVTLQYNVTLPATEEQA	FLLGLMFQI,LMFQITAKA,FQITAKASI,GLMFQITAK,FLLGLMFQIT,GLMFQITAKA,FQITAKASII,LGLMFQITAK,VFLLGLMFQI,MFQITAKASI,LMFQITAKAS,QITAKASIIF	BLCA
TRAM1L1	c.1033delA	p.R345fs	LQRWVEDSNIQASCMKKKRSRSSKK[p.R345fs]EQKTEWEWKLQIE*	SKKEQKTEW,TEWEWKLQI,KEQKTEWEW,RSRSSKKEQK	STAD
TRANK1	c.2536G>A	p.E846K	YNISRRLSKLRVLPWSIHELYGDEI[p.E846K]KDFTQAELALLMKCINDPNSMFLTGD	LYGDEIKDF,IKDFTQAEL,DEIKDFTQA,EIKDFTQAEL,KDFTQAELAL,DEIKDFTQAE	UCEC
TRAPPC10	c.399_400insA	p.K133fs	WQNVLKAHSSVDWLIVIVENDAKKK[p.K133fs]KQNQHPSPNLYCGQNKK*	NLYCGQNKK,NQHPSPNLY,KQNQHPSPN,KQNQHPSPNL,QNQHPSPNLY	GBM
TRAPPC11	c.1703G>A	p.R568Q	MNESPDPEPDCDILAVKTAQKLWAD[p.R568Q]QISLAGSNIFTIGVQDFVPFVQCKAK	KLWADQISL,AQKLWADQI,KLWADQISLA,QISLAGSNIF,QKLWADQISL,DQISLAGSNI	CRC
TRDN	c.2190A>C	p.*730Y	PFTPADRPGESSGQANSPGQKQQGQ[p.*730Y]YTHMYDPYKCFKILKM*	YTHMYDPYK,MYDPYKCFK,QQGQYTHMY,KQQGQYTHM,HMYDPYKCF,QKQQGQYTH,GQYTHMYDP,YKCFKILKM,DPYKCFKIL,HMYDPYKCFK,MYDPYKCFKI,KQQGQYTHMY,GQYTHMYDPY,GQKQQGQYTH,QKQQGQYTHM,THMYDPYKCF,SPGQKQQGQY	KIRC
TRIM23	c.1187G>A	p.R396Q	QQQFTEVADHIQLDASIPVTFTKDN[p.R396Q]QVHIGPKMEIRVVTLGLDGAGKTTIL	FTKDNQVHI,NQVHIGPKM,KDNQVHIGPK	CRC
TRIM23	c.866G>A	p.R289Q	IVEDGIGMAHTEHVPGTAENARSCI[p.R289Q]QAYFYDLHETLCRQEEMALSVVDAHV	RSCIQAYFY,CIQAYFYDL,NARSCIQAY,ARSCIQAYF,IQAYFYDLH,ARSCIQAYFY,ENARSCIQAY,NARSCIQAYF,AENARSCIQA	CRC
TRIM4	c.1193G>T	p.R398L	NVFTSGKHYWEVESRDSLEVAVGVC[p.R398L]LEDVMGITDRSKMSPDVGIWAIYWSA	LEVAVGVCL	LUAD
TRIM42	c.379C>A	p.Q127K	TFHKGRLRSIHTSSKTALRTGSSDT[p.Q127K]KVDEVKSIPANSHLVNHLNCPMCSRL	ALRTGSSDTK	LUAD
TRIM48	c.278C>A	p.A93D	CFECIKTIQQRNLKTNIRLKKMASL[p.A93D]DRKASLWLFLSSEEQMCGIHRETKKM	RLKKMASLD,KMASLDRKA,RLKKMASLDR,MASLDRKASL,KKMASLDRKA,ASLDRKASLW,LDRKASLWLF	LUAD
TRIM61	c.294G>C	p.K98N	SLTEIAKQLQIRSKKRKRQEEKHVC[p.K98N]NKHNQVLTFFCQKDLELLCPRCSLST	NKHNQVLTF,RQEEKHVCNK,CNKHNQVLTF,NKHNQVLTFF	CESC
TRIM7	c.994C>A	p.L332I	MKNKVWNVSLKTFVLKGMLKKFKED[p.L332I]IRGELEKEEKVELTLDPDTANPRLIL	MLKKFKEDI,KFKEDIRGEL,MLKKFKEDIR	LUSC
TRIM9	c.1009C>A	p.R337S	FEACLVAQCDALIDALNRRKAQLLA[p.R337S]SVNKEHEHKLKVVRDQISHCTVKLRQ	AQLLASVNK,SVNKEHEHK,RKAQLLASV,KAQLLASVNK,ASVNKEHEHK,RRKAQLLASV	LUAD
TRIML1	c.1197C>A	p.H399Q	DLFSLIGLKIGDDYSLWVSSPLKGQ[p.H399Q]QVREPVCKVGVFLDYESGHIAFYNGT	LKGQQVREPV	LUAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
TRIO	c.1981C>T	p.R661W	QTGECDPEEIYQAAHQLEDRIQDFV[p.R661W]WRVEQRKILLDMSVSFHTHVKELWTW	RIQDFVWRV,FVWRVEQRK,DFVWRVEQR,WRVEQRKIL,DFVWRVEQRK,WRVEQRKILL	CRC
TRIOBP	c.3899A>G	p.H1300R	DLPPPRRLAQRQPGPQAQCSSGGRT[p.H1300R]RSPGRAEVERLFGQERRKSEAAGAFQ	GGRTRSPGR,RTRSPGRAE,GGRTRSPGRA,RTRSPGRAEV	ACC
TRIP11	c.1622delA	p.K541fs	DQLSKQQNEGDSIISKLKQDLNDEK[p.K541fs]REFINLKMIKWTLLKS*	KMIKWTLLK,EFINLKMIK,NLKMIKWTL,LKMIKWTLL,KREFINLKM,REFINLKMI,DEKREFINL,NLKMIKWTLL,EKREFINLKM,KMIKWTLLKS	STAD
TRIP12	c.5324T>C	p.L1775P	KLMAKAIMDFRLVDLPLGLPFYKWM[p.L1775P]PRQETSLTSHDLFDIDPVVARSVYHL	WMPRQETSL,KWMPRQETS,LPFYKWMPR,MPRQETSLT,YKWMPRQET,KWMPRQETSL,GLPFYKWMPR,MPRQETSLTS,YKWMPRQETS	MM
TRMT61A	c.731G>T	p.S244I	ALAARGFSELSTLEVLPQVYNVRTV[p.S244I]ILPPPDLGTGTDGPAGSDTSPFRSGT	VYNVRTVIL,QVYNVRTVI,PQVYNVRTVI,QVYNVRTVIL	TGCT
TRPA1	c.162G>T	p.K54N	TEDFKESLKVVFEGSAYGLQNFNKQ[p.K54N]NKLKRCDDMDTFFLHYAAAEGQIELM	NFNKQNKLKR,LQNFNKQNKL	CRC
TRPA1	c.2017delA	p.T673fs	DKSCRDYYIEYNFKYLQCPLEFTKK[p.T673fs]HLHRMLYMNRLQPSTQWYKITA*	YMNRLQPST,RLQPSTQWY,LQPSTQWYK,LHRMLYMNR,STQWYKITA,KKHLHRMLY,EFTKKHLHR,FTKKHLHRM,LEFTKKHLH,KHLHRMLYM,HRMLYMNRL,QPSTQWYKI,MLYMNRLQPS,HLHRMLYMNR,RLQPSTQWYK,LQPSTQWYKI,KKHLHRMLYM,FTKKHLHRML,TKKHLHRMLY,RMLYMNRLQP,YMNRLQPSTQ,MNRLQPSTQW,CPLEFTKKHL	STAD
TRPC5	c.1469C>T	p.S490L	PREEWEMWHPTLIAEALFAISNILS[p.S490L]LLRLISLFTANSHLGPLQISLGRMLL	FAISNILSL,AISNILSLL,ISNILSLLR,SLLRLISLF,LSLLRLISL,FAISNILSLL,ILSLLRLISL,LLRLISLFTA,AISNILSLLR,LFAISNILSL,LSLLRLISLF,ISNILSLLRL	CRC,UCEC
TRPM3	c.1285C>T	p.R429W	TRTQAQHLFIILMECMKKKELITVF[p.R429W]WMGSEGHQDIDLAILTALLKGANASA	KELITVFWM,WMGSEGHQDI,KKKELITVFW,KKELITVFWM,KELITVFWMG	UCEC
TRPM3	c.892G>T	p.G298W	QTMSNPMSKLTVLNSMHSHFILADN[p.G298W]WTTGKYGAEVKLRRQLEKHISLQKIN	FILADNWTT,LADNWTTGK,ADNWTTGKY,SHFILADNW,LADNWTTGKY,ILADNWTTGK,WTTGKYGAEV,HSHFILADNW	LUAD
TRPM6	c.2984G>A	p.R995H	IAKMTANMFYIVIIMAIVLLSFGVA[p.R995H]HKAILSPKEPPSWSLARDIVFEPYWM	LLSFGVAHK,SFGVAHKAI,AHKAILSPK,LSFGVAHKA,VLLSFGVAH,LLSFGVAHKA,VLLSFGVAHK,VAHKAILSPK,LSFGVAHKAI	CRC
TRPM7	c.2528G>A	p.R843Q	VRILDSNEGKNEMEIQMKSKKLPIT[p.R843Q]QKFYAFYHAPIVKFWFNTLAYLGFLM	ITQKFYAFY,KSKKLPITQ,KLPITQKFY,KKLPITQKF,TQKFYAFYH,QKFYAFYHA,LPITQKFYA,KLPITQKFYA,KSKKLPITQK,ITQKFYAFYH,TQKFYAFYHA,KKLPITQKFY,PITQKFYAFY,LPITQKFYAF,SKKLPITQKF,QKFYAFYHAP	CRC
TRPM7	c.5584C>T	p.R1862C	PQDEPSDLNLQPGNSTKESESTNSV[p.R1862C]CLML*	SESTNSVCL,KESESTNSVC,SESTNSVCLM	CRC
TRPM8	c.2295_2296insC	p.H765fs	VFYIAFLLLFAYVLLMDFHSVPHPP[p.H765fs]RAGPVLAGLCPLL*	VLAGLCPLL,HSVPHPPRA,HPPRAGPVL,RAGPVLAGL,DFHSVPHPPR,VPHPPRAGPV,GPVLAGLCPL	STAD
TRPS1	c.3373C>T	p.R1125W	IEKYQYPLFGLPFVHNDFQSEADWL[p.R1125W]WFWSKYKLSVPGNPHYLSHVPGLPNP	WLWFWSKYK,FQSEADWLW,SEADWLWFW,LWFWSKYKL,WLWFWSKYKL,EADWLWFWSK,DFQSEADWLW,FQSEADWLWF,WFWSKYKLSV,DWLWFWSKYK,ADWLWFWSKY,SEADWLWFWS	CRC
TRPV2	c.1865_1867delTGC	p.L627del	KFTIGMGELAFQEQLHFRGMVLLLL[p.L627del]AYVLLTYILLLNMLIALMSETVNSVATD	MVLLLLAYV,VLLLLAYVL,RGMVLLLLA,GMVLLLLAY,GMVLLLLAYV,MVLLLLAYVL,VLLLLAYVLL,RGMVLLLLAY	CLL
TRPV3	c.653C>A	p.A218E	FAEENDILGRFINAEYTEEAYEGQT[p.A218E]ELNIAIERRQGDIAALLIAAGADVNA	GQTELNIAI,ELNIAIERR,EAYEGQTEL,YEGQTELNI,AYEGQTELNI,QTELNIAIER,EEAYEGQTEL,YEGQTELNIA	KIRP
TRPV5	c.1475G>A	p.R492H	YFTRGFQMLGPFTIMIQKMIFGDLM[p.R492H]HFCWLMAVVILGFASAFYIIFQTEDP	LMHFCWLMA,MHFCWLMAV,KMIFGDLMH,MIFGDLMHF,DLMHFCWLM,GDLMHFCWL,MIFGDLMHFC,LMHFCWLMAV,KMIFGDLMHF,IFGDLMHFCW,HFCWLMAVVI,MHFCWLMAVV,GDLMHFCWLM	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
TRRAP	c.10543C>T	p.R3515W	THYYIKIARFMPRVEIVQKHNTAAR[p.R3515W]WLYIRGHNGKIYPYLVMNDACLTESR	TAARWLYIR,AARWLYIRG,HNTAARWLY,NTAARWLYI,QKHNTAARW,KHNTAARWL,WLYIRGHNGK,NTAARWLYIR,AARWLYIRGH,RWLYIRGHNG,KHNTAARWLY,VQKHNTAARW,QKHNTAARWL	CRC
TRRAP	c.2917G>T	p.A973S	DCLKSANTEPYYRRQAWEVIKCFLV[p.A973S]SMMSLEDNKHALYQLLAHPNFTEKTI	SMMSLEDNK,CFLVSMMSL,VIKCFLVSM,IKCFLVSMM,VSMMSLEDNK,EVIKCFLVSM,KCFLVSMMSL,SMMSLEDNKH,WEVIKCFLVS	KICH
TSC1	c.1132G>T	p.G378C	CGMTTPPTSPGNVPPDLSHPYSKVF[p.G378C]CTTAGGKGTPLGTPATSPPPAPLCHS	KVFCTTAGG,YSKVFCTTA,SKVFCTTAG,KVFCTTAGGK,HPYSKVFCTT	LUAD
TSC22D2	c.1255G>A	p.A419T	AQPSSTGAAASPATAATLPVGTGQN[p.A419T]TSSVGAQLMGASSQPSEAMAPRTGPA	NTSSVGAQL,GQNTSSVGA,NTSSVGAQLM	ACC
TSG101	c.794A>G	p.K265R	WRMKEEMDRAQAELNALKRTEEDLK[p.K265R]RGHQKLEEMVTRLDQEVAEVDKNIEL	DLKRGHQKL,RGHQKLEEM	THCA
TSG101	c.826C>A	p.R276S	AELNALKRTEEDLKKGHQKLEEMVT[p.R276S]SLDQEVAEVDKNIELLKKKDEELSSA	KLEEMVTSL,SLDQEVAEV,MVTSLDQEV,EMVTSLDQEV,TSLDQEVAEV,QKLEEMVTSL	LUAD
TSHZ1	c.1503G>C	p.K501N	EDSLEKFEPSTLYPYLREEDLDDSP[p.K501N]NGGLDILKSLENTVSTAISKAQNGAP	SPNGGLDIL	LUAD
TSHZ1	c.2642G>T	p.R881M	QAQFASSLRETTEGKYIMSDLGPQE[p.R881M]MVHISKFTGLSMTTISHWLANVKYQL	MSDLGPQEM,QEMVHISKF,MSDLGPQEMV,IMSDLGPQEM,MVHISKFTGL,PQEMVHISKF,QEMVHISKFT	CRC
TSHZ2	c.664G>A	p.A222T	LYRQSSKMCGTVFTGASRFRCRQCS[p.A222T]TAYDTLVELTVHMNETGHYQDDNRKK	RFRCRQCST,RCRQCSTAY,CSTAYDTLV,TAYDTLVEL,RQCSTAYDT,STAYDTLVEL,RFRCRQCSTA,FRCRQCSTAY,RQCSTAYDTL	GBM
TSHZ3	c.2030G>T	p.G677V	EPIKMEASSDGGFRSQENSPSPPRD[p.G677V]VCKDGSPLAEPVENGKELVKPLASSL	RDVCKDGSPL	LUAD
TSKS	c.1537G>A	p.E513K	CPSCQRLHKKILELERQALAKHVRA[p.E513K]KALSSTLRLAQDEALRAKNLLLTDKM	ALAKHVRAK,LAKHVRAKA,HVRAKALSS,RAKALSSTL,KALSSTLRL,AKHVRAKAL,ALAKHVRAKA,QALAKHVRAK,HVRAKALSST,RAKALSSTLR,KALSSTLRLA,LAKHVRAKAL,VRAKALSSTL,AKALSSTLRL	BLCA
TSPAN4	c.274C>G	p.L92V	IGFVGCLGAIKENKCLLLTFFLLLL[p.L92V]VVFLLEATIAILFFAYTDKIDRYAQQ	LTFFLLLLV,FLLLLVVFL,LLLLVVFLL,LLVVFLLEA,FFLLLLVVF,LLTFFLLLLV,LTFFLLLLVV,FLLLLVVFLL,LLLVVFLLEA,TFFLLLVVF,FFLLLLVVFL	PRAD,TGCT
TSSK1B	c.901G>A	p.E301K	ARGSPSVAINKEGESSRGTEPLWTP[p.E301K]KPGSDKKSATKLEPEGEAQPQAQPET	GTEPLWTPK,RGTEPLWTPK	UCEC
TTBK2	c.249T>G	p.C83W	KQVLKMEVAVLKKLQGKDHVCRFIG[p.C83W]WGRNDRFNYVVMQLQGRNLADLRRSQ	WGRNDRFNY,VCRFIGWGR,FIGWGRNDR,IGWGRNDRF,HVCRFIGWGR,GWGRNDRFNY,RFIGWGRNDR,FIGWGRNDRF	KIRP
TTC21A	c.809C>A	p.S270Y	ESNIDACQILTVHELAREGNMTTVS[p.S270Y]YLKTQKATNHVRNLIKALETREPENP	NMTTVSYLK,TVSYLKTQK,EGNMTTVSY,GNMTTVSYL,GNMTTVSYLK,TTVSYLKTQK,REGNMTTVSY	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
TTF1	c.1007delA	p.K336fs	RPAVGLHGETAGIPAPAYKNKSKKK[p.K336fs]RKSPITRNLRQWPCLRASRVHTLKDHRWAVRLGLWKAVQLLKGSRNPTVQRRSLRKGSLRLSKGHECLVMIFQCPVRTLRAHSLIQ*	TLKDHRWAV,GLWKAVQLL,LVMIFQCPV,SLRKGSLRL,RLSKGHECL,RASRVHTLK,TVQRRSLRK,WAVRLGLWK,LWKAVQLLK,RSLRKGSLR,RWAVRLGLW,IFQCPVRTL,RTLRAHSLI,KNKSKKKRK,KKRKSPITR,KSPITRNLR,RNLRQWPCL,CLRASRVHT,RVHTLKDHR,HTLKDHRWA,AVRLGLWKA,GSRNPTVQR,NLRQWPCLR,QWPCLRASR,PTVQRRSLR,VMIFQCPVR,FQCPVRTLR,WPCLRASRV,NPTVQRRSL,SKKKRKSPI,LRASRVHTL,RKSPITRNL,RQWPCLRAS,HRWAVRLGL,SKGHECLVM,GHECLVMIF,VRTLRAHSL,CPVRTLRAH,KDHRWAVRL,RLSKGHECLV,CLVMIFQCPV,MIFQCPVRTL,CLRASRVHTL,LLKGSRNPTV,GLWKAVQLLK,RWAVRLGLWK,LVMIFQCPVR,KSKKKRKSPI,KKKRKSPITR,KRKSPITRNL,ITRNLRQWPC,RNLRQWPCLR,RQWPCLRASR,HTLKDHRWAV,TLKDHRWAVR,AVRLGLWKAV,GSRNPTVQRR,RSLRKGSLRL,SLRKGSLRLS,RTLRAHSLIQ,IFQCPVRTLR,LSKGHECLVM,RVHTLKDHRW,HRWAVRLGLW,LRLSKGHECL,KGHECLVMIF,FQCPVRTLRA,SPITRNLRQW	STAD
TTF1	c.1589A>G	p.Q530R	IKDRATSTIKRMYRDDLERFKEFKA[p.Q530R]RGVAIKFGKFSVKENKQLEKNVEDFL	RGVAIKFGK,RFKEFKARG,KARGVAIKF,EFKARGVAI,KEFKARGVA,RFKEFKARGV,EFKARGVAIK,KARGVAIKFG,KEFKARGVAI,FKARGVAIKF,RGVAIKFGKF	TGCT
TTF2	c.2281C>A	p.R761S	LDEAHNVKNPRVQTSIAVCKLQACA[p.R761S]SWAVTGTPIQNNLLDMYSLLKFLRCS	KLQACASWA,LQACASWAV,CKLQACASW,SWAVTGTPI,KLQACASWAV,LQACASWAVT,ASWAVTGTPI	LUAD
TTI1	c.2120G>A	p.R707H	CGYDSLQHLINQNSDYLVNGISLNL[p.R707H]HHLALHPHTPKVLEVMLRNSDANLLP	SLNLHHLAL,GISLNLHHL,LHHLALHPH,GISLNLHHLA,ISLNLHHLAL	STAD
TTLL11	c.367_368insAGGCCA	p.122_123insKA	SELAARWEAEAVAAAKAAAKAEAEA[p.122_123insKA]KATAETVAEQVRVDAGAAGEPECKAGEEQPK	AAKAEAEAK,EAKATAETV,AEAEAKATA,AKATAETVA,AEAKATAET,AAAKAEAEAK,AEAKATAETV	ACC
TTLL7	c.2252G>A	p.R751H	LIKLDSVKQRKVLDIVKTSIRTVLP[p.R751H]HIWKVPDVEEVNLYRIFNRVFNRLLW	TVLPHIWKV,SIRTVLPHI,RTVLPHIWK,TSIRTVLPH,KTSIRTVLPH,RTVLPHIWKV,TSIRTVLPHI,SIRTVLPHIW,LPHIWKVPDV	UCEC
TUBA1C	c.436C>T	p.L146F	EDGVVGLNYSCGNLGRRVNGELQLG[p.L146F]FLAIIN*	LQLGFLAII,ELQLGFLAI,VNGELQLGF,GELQLGFLA,RVNGELQLGF,GELQLGFLAI	ACC,TGCT
TUBA3C	c.526_527insC	p.Q176fs	SLLMERLSVDYGKKSKLEFAIYPAP[p.Q176fs]PGLHGRGGALQLHPDHPHDPGTF*	AIYPAPPGL,GLHGRGGAL,HGRGGALQL,LQLHPDHPH,FAIYPAPPGL,AIYPAPPGLH,LEFAIYPAPP,LHGRGGALQL	LUAD
TUBA3D	c.728G>A	p.R243Q	DIERPTYTNLNRLIGQIVSSITASL[p.R243Q]QFDGALNVDLTEFQTNLVPYPRIHFP	LQFDGALNV,SSITASLQF,ASLQFDGAL,SLQFDGALNV,ITASLQFDGA,VSSITASLQF,LQFDGALNVD	CRC
TUBBP5	c.304G>A	p.V102M	TYHGDSHLQLERINVHHHEASGGRY[p.V102M]MPRAVLVDLEPGTMDSVRSGPFGQVL	ASGGRYMPR,RYMPRAVLV,GGRYMPRAV,MPRAVLVDL,HEASGGRYM,GRYMPRAVL,YMPRAVLVDL,EASGGRYMPR,HHEASGGRYM	GBM
TUBBP5	c.356G>A	p.R119H	HEASGGRYVPRAVLVDLEPGTMDSV[p.R119H]HSGPFGQVLRPDNFIFGELRARTGVR	MDSVHSGPF,HSGPFGQVL,SVHSGPFGQV,HSGPFGQVLR,TMDSVHSGPF,VHSGPFGQVL	UCS
TUBD1	c.599C>T	p.A200V	YGTGEVIVQNYNSILTLSHLYRSSD[p.A200V]VLLLHENDAIHKICAKLMNIKQISFS	HLYRSSDVL,RSSDVLLLH,LYRSSDVLL,YRSSDVLLL,HLYRSSDVLL,VLLLHENDAI,LYRSSDVLLL,SHLYRSSDVL	BRCA
TUFT1	c.1018G>A	p.A340T	KSQQRKVRQMIEQLQNSKAVIQSKD[p.A340T]TTIQELKEKIAYLEAENLEMHDRMEH	TTIQELKEK,SKDTTIQEL,AVIQSKDTTI	CRC
TUFT1	c.303G>C	p.L101F	HSAGHSLASELVESHDGHEEIIKVY[p.L101F]FKGRSGDKMIHEKNINQLKSEVQYIQ	IIKVYFKGR,KVYFKGRSG,YFKGRSGDK,FKGRSGDKM,HEEIIKVYF,VYFKGRSGDK,EIIKVYFKGR	CESC
TWISTNB	c.918T>A	p.H306Q	KKKHQEVQDQDPVFQGSDSSGYQSD[p.H306Q]QKKKKKKRKHSEEAEFTPPLKCSPKR	SSGYQSDQK	CLL
TXNDC15	c.1028G>A	p.R343Q	LIKSVDWLLVFSLFFLISFIMYATI[p.R343Q]QTESIRWLIPGQEQEHVE*	FIMYATIQT,IQTESIRWL,QTESIRWLI,YATIQTESI,IMYATIQTE,IQTESIRWLI,IMYATIQTES,MYATIQTESI	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
TXNL1	c.700C>T	p.R234C	AERSEPTQALELTEDDIKEDGIVPL[p.R234C]CYVKFQNVNSVTIFVQSNQGEEETTR	GIVPLCYVK,IVPLCYVKF,DGIVPLCYV,KEDGIVPLCY,GIVPLCYVKF	UCEC
TYRP1	c.1054_1057delACAA	p.T352fs	PEPQDVAQCLEVGLFDTPPFYSNST[p.T352fs]VSETQWKVTVTPRESMTLLFEVFTIWLIYS*	TVSETQWKV,ESMTLLFEV,TLLFEVFTI,STVSETQWK,SMTLLFEVF,EVFTIWLIY,QWKVTVTPR,MTLLFEVFT,TPRESMTLL,SETQWKVTV,TQWKVTVTP,LLFEVFTIW,FEVFTIWLI,MTLLFEVFTI,LLFEVFTIWL,STVSETQWKV,TQWKVTVTPR,ESMTLLFEVF,TLLFEVFTIW,LFEVFTIWLI,KVTVTPRESM,EVFTIWLIYS,TPRESMTLLF,RESMTLLFEV,FEVFTIWLIY,SETQWKVTVT,TPPFYSNSTV	GBM
U2AF1	c.101C>A	p.S34Y	FGTEKDKVNCSFYFKIGACRHGDRC[p.S34Y]YRLHNKPTFSQTIALLNIYRNPQNSS	YRLHNKPTF,CYRLHNKPTF,GDRCYRLHNK,GACRHGDRCY	LAML
U2AF1	c.101C>T	p.S34F	FGTEKDKVNCSFYFKIGACRHGDRC[p.S34F]FRLHNKPTFSQTIALLNIYRNPQNSS	FRLHNKPTF,CFRLHNKPTF,ACRHGDRCFR,GDRCFRLHNK,GACRHGDRCF	CESC,LAML,LUAD,UCS
UBC	c.2051delG	p.G684fs	EDGRTLSDYNIQKESTLHLVLRLRG[p.G684fs]VSKFPLLRFQQISLHFPFNKVVAF	SLHFPFNKV,HLVLRLRGV,LLRFQQISL,VLRLRGVSK,GVSKFPLLR,ISLHFPFNK,RFQQISLHF,QQISLHFPF,RLRGVSKFP,RGVSKFPLL,FPLLRFQQI,FPFNKVVAF,LRLRGVSKF,LRGVSKFPL,VSKFPLLRF,LHFPFNKVV,RLRGVSKFPL,SLHFPFNKVV,LVLRLRGVSK,QISLHFPFNK,KFPLLRFQQI,FQQISLHFPF,HFPFNKVVAF,RGVSKFPLLR,ISLHFPFNKV,VLRLRGVSKF,GVSKFPLLRF,LRFQQISLHF,LHFPFNKVVA,FPLLRFQQIS	STAD
UBC	c.572T>C	p.I191T	TLEVEPSDTIENVKAKIQDKEGIPP[p.I191T]TSRGSSLQASSWKMAVLFLTTTSRRS	TSRGSSLQA,PPTSRGSSL,IPPTSRGSSL,IQDKEGIPPT	PRAD
UBE2J2	c.577G>T	p.G193W	KQKQKAQDELSSRPQTLPLPDVVPD[p.G193W]WETHLVQNGIQLLNGHAPGAVPNLAG	VPDWETHLV,VVPDWETHLV,DVVPDWETHL,WETHLVQNGI,LPLPDVVPDW	LUAD
UBE2M	c.392G>A	p.G131D	LEGNVCLNILREDWKPVLTINSIIY[p.G131D]DLQYLFLEPNPEDPLNKEAAEVLQNN	NSIIYDLQY,SIIYDLQYL,TINSIIYDL,IIYDLQYLF,IYDLQYLFL,IIYDLQYLFL,SIIYDLQYLF,INSIIYDLQY,LTINSIIYDL,NSIIYDLQYL	TGCT
UBE2NL	c.257G>T	p.R86I	EEYPMAAPKVRFMTKIYHPNVDKLE[p.R86I]IISLDILKDKWSPALQIRTVLLSIQA	EIISLDILK,HPNVDKLEI,LEIISLDIL,HPNVDKLEII	CRC
UBE2O	c.3354_3355insG	p.R1118fs	YENSRCYNEMALIRVVQSMTQLVRR[p.R1118fs]APRGL*	SMTQLVRRA,TQLVRRAPR,LVRRAPRGL,MTQLVRRAPR	KIRC
UBIAD1	c.289G>A	p.A97T	AYRSHGVLDPRLLVGCAVAVLAVHG[p.A97T]TGNLVNTYYDFSKGIDHKKSDDRTLV	GTGNLVNTY,AVHGTGNLV,TGNLVNTYY,GTGNLVNTYY,VLAVHGTGNL,HGTGNLVNTY,LAVHGTGNLV	CRC
UBOX5	c.1250C>T	p.S417L	LPTTSEHTAKKMKATNEPSLTHMDC[p.S417L]LTGPLSHEQKLSQSLEIALASTLGSM	HMDCLTGPL,LTGPLSHEQK,THMDCLTGPL	BLCA
UBQLN2	c.1568delC	p.A523fs	PIGPIVPFTPIGPIGPIGPTGPAAP[p.A523fs]LAPPALVAPRGLLCPALHLVKPRVLHQNLDPTSSSFSKWCRPWLEQMLHSCRIQKSDFSNNWNSSTQWGS*	GLLCPALHL,LLCPALHLV,ALHLVKPRV,ALVAPRGLL,VLHQNLDPT,MLHSCRIQK,SSSFSKWCR,SFSKWCRPW,APRGLLCPA,KPRVLHQNL,EQMLHSCRI,NLDPTSSSF,WCRPWLEQM,QKSDFSNNW,NNWNSSTQW,APLAPPALV,GLLCPALHLV,LLCPALHLVK,QMLHSCRIQK,TSSSFSKWCR,SFSKWCRPWL,KWCRPWLEQM,LAPPALVAPR,GPAAPLAPPA,APLAPPALVA,APRGLLCPAL,IQKSDFSNNW,RGLLCPALHL,HQNLDPTSSS,QNLDPTSSSF,SSFSKWCRPW,LEQMLHSCRI,HSCRIQKSDF,SNNWNSSTQW,DPTSSSFSKW	STAD
UBR1	c.4939G>T	p.G1647W	KHPVLCLFCGAILCSQNICCQEIVN[p.G1647W]WEEVGACIFHALHCGAGVCIFLKIRE	WEEVGACIF,QEIVNWEEV,WEEVGACIFH	LUAD
UBR4	c.8406delC	p.P2802fs	TAENVNNGNPSPLEALLAGAEGFPP[p.P2802fs]CWTSHLMQMTRPWLN*	LMQMTRPWL,TSHLMQMTR,CWTSHLMQM,FPPCWTSHL,HLMQMTRPW,AEGFPPCWT,HLMQMTRPWL,WTSHLMQMTR,GFPPCWTSHL,FPPCWTSHLM,SHLMQMTRPW,AEGFPPCWTS	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
UBR5	c.6360delA	p.K2120fs	EVLPTKMSYAANLKNVMNMQNRQKK[p.K2120fs]KGKNSPCCQKKLRVQNQGHLLMILLHN*	KNSPCCQKK,KLRVQNQGH,RVQNQGHLL,VQNQGHLLM,LRVQNQGHL,NQGHLLMIL,MQNRQKKKGK,KGKNSPCCQK,KLRVQNQGHL,RVQNQGHLLM,LRVQNQGHLL,VQNQGHLLMI,NQGHLLMILL	KICH
UBR5	c.7551G>T	p.R2517S	LDDTDDGDDNAPLFYQPGKRGFYTP[p.R2517S]SPGKNTEARLNCFRNIGRILGLCLLQ	GFYTPSPGK,RGFYTPSPG,RGFYTPSPGK,SPGKNTEARL	TGCT
UBXN7	c.827C>T	p.A276V	LDQVTGFLGEHGQLDGLSSSPPKKC[p.A276V]VRSESLIDASEDSQLEAAIRASLQET	KKCVRSESL	CLL
UGP2	c.784G>C	p.D262H	ASFYNSGLLDTFIGEGKEYIFVSNI[p.D262H]HNLGATVDLYILNHLMNPPNGKRCEF	NIHNLGATV,IFVSNIHNL,YIFVSNIHNL,FVSNIHNLGA,HNLGATVDLY,KEYIFVSNIH	BLCA
UGT1A1	c.10A>G	p.T4A	MAR[p.T4A]AGWTSPIPLCVSLLLTCGFAEAGKLL	ARAGWTSPI,AGWTSPIPL,MARAGWTSPI,RAGWTSPIPL	KIRP
UGT2A1	c.290delA	p.N97fs	EIYRVPFGKERIEGVIKDFVLTWLE[p.N97fs]IDHLLQPFGDSIRRWPK*	LLQPFGDSI,DFVLTWLEI,TWLEIDHLL,LEIDHLLQP,VLTWLEIDHL,HLLQPFGDSI,LEIDHLLQPF,KDFVLTWLEI,QPFGDSIRRW	CRC
UGT2B11	c.1340G>T	p.R447I	STDLLNALKTVINDPLYKENIMKLS[p.R447I]IIQHDQPVKPLDRAVFWIEFVMPHKG	KENIMKLSI,IMKLSIIQH,YKENIMKLSI,KENIMKLSII	TGCT
UGT2B28	c.866C>A	p.P289H	FQFPHPFLPNIDFVGGLHCKPAKPL[p.P289H]HKEMEEFVQSSGENGVVVFSLGSVIS	HCKPAKPLHK,KPAKPLHKEM	GBM
UGT2B7	c.642G>A	p.M214I	FPPSYVPVVMSELTDQMTFMERVKN[p.M214I]IIYVLYFDFWFEIFDMKKWDQFYSEV	RVKNIIYVL,TFMERVKNI,KNIIYVLYF,IIYVLYFDF,VKNIIYVLY,MERVKNIIY,FMERVKNII,FMERVKNIIY,RVKNIIYVLY,TFMERVKNII,NIIYVLYFDF,IIYVLYFDFW,MTFMERVKNI,MERVKNIIYV,VKNIIYVLYF	LUAD
UGT8	c.304G>A	p.E102K	FNSTTSDAFLQSKMRNIFSGRLTAI[p.E102K]KLFDILDHYTKNCDLMVGNHALIQGL	KLFDILDHY,FSGRLTAIK,SGRLTAIKL,TAIKLFDIL,GRLTAIKLF,RLTAIKLFDI,KLFDILDHYT,IFSGRLTAIK,SGRLTAIKLF,IKLFDILDHY	CRC,UCEC
UHRF1BP1	c.3990delC	p.I1330fs	EIPVVVPMQIELLNSSITLKDDIPP[p.I1330fs]SIQHLQAPSPSLWPWNMLC*	HLQAPSPSL,SLWPWNMLC,IQHLQAPSP,LQAPSPSLW,APSPSLWPW,SPSLWPWNM,TLKDDIPPSI,SPSLWPWNML,IQHLQAPSPS,QHLQAPSPSL,HLQAPSPSLW,IPPSIQHLQA	STAD
UMODL1	c.1677G>A	p.M559I	CQCRTTRDATPSRAGRACEGDLVSP[p.M559I]IGGGLSAATGVTVPGLGTGTAALGLE	LVSPIGGGL,SPIGGGLSA,CEGDLVSPI,SPIGGGLSAA	TGCT
UNC93A	c.1334_1335TC>CG	p.V445A	LTMVAYGLVECVESKNPIRPHAPGQ[p.V445A]ANQAEDEEIQTKM*	RPHAPGQAN	TGCT
UNC93B1	c.1492G>A	p.V498M	YHWWQAVAIFTVYLGSSLHMKAKLA[p.V498M]MLLVTLVAAAVSYLRMEQKLRRGVAP	KLAMLLVTL,LAMLLVTLV,AMLLVTLVA,MLLVTLVAA,HMKAKLAML,KAKLAMLLV,LHMKAKLAM,MKAKLAMLL,AKLAMLLVT,KLAMLLVTLV,AMLLVTLVAA,MLLVTLVAAA,HMKAKLAMLL,KAKLAMLLVT,SLHMKAKLAM,LHMKAKLAML,MKAKLAMLLV,AKLAMLLVTL,LAMLLVTLVA	CESC
UPK2	c.145delC	p.P49fs	DFNISSLSGLLSPALTESLLVALPP[p.P49fs]VTSQEAMPH*	SLLVALPPV,ALPPVTSQEA,ESLLVALPPV,LPPVTSQEAM	STAD
UPK3A	c.816_817insC	p.G272fs	QITQEAVPKSLGASESSYTSVNRGP[p.G272fs]ATGQG*	YTSVNRGPA	KIRC
UQCRFS1	c.16T>G	p.S6A	MLSVA[p.S6A]ARSGPFAPVLSATSRGVAGALRPLVQ	SVAARSGPF,ARSGPFAPV,SVAARSGPFA,AARSGPFAPV,LSVAARSGPF,ARSGPFAPVL	ACC
UQCRFS1	c.247A>G	p.I83V	QAVRRPLVASVGLNVPASVCYSHTD[p.I83V]VKVPDFSEYRRLEVLDSTKSSRESSE	VKVPDFSEY,SVCYSHTDVK,DVKVPDFSEY,SHTDVKVPDF	KIRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
URGCP	c.1916_1917insG	p.G639fs	HFLREMGQFYEAESCLVEAGRLPAG[p.G639fs]PEAFCPLPRLGLGAAADRAASGANRWEHAEHARPLGHRAPEGAARPTGETVKAGGSVNRRGARHGQVHTPQHHVWAAVCHREELRSSRGLHAAHHSG*	HVWAAVCHR,RLPAGPEAF,HARPLGHRA,AARPTGETV,RSSRGLHAA,SSRGLHAAH,AVCHREELR,EAFCPLPRL,ETVKAGGSV,QVHTPQHHV,HTPQHHVWA,LPRLGLGAA,RPLGHRAPE,APEGAARPT,TPQHHVWAA,RAASGANRW,AEHARPLGH,RGARHGQVH,GQVHTPQHH,EELRSSRGL,GQVHTPQHHV,AGRLPAGPEA,AARPTGETVK,TVKAGGSVNR,RSSRGLHAAH,SSRGLHAAHH,HTPQHHVWAA,LPRLGLGAAA,RPLGHRAPEG,TPQHHVWAAV,ELRSSRGLHA,GRLPAGPEAF,WEHAEHARPL,QVHTPQHHVW,WAAVCHREEL,REELRSSRGL,LRSSRGLHAA,PEAFCPLPRL,GETVKAGGSV,CPLPRLGLGA	KICH
URI1	c.39_40insC	p.S13fs	MEAPTVETPPDPSPP[p.S13fs]FGPGPCPGSVARPGCGAAARGAGKGGH*	GAAARGAGK,VARPGCGAA,SVARPGCGA,TPPDPSPPF,VARPGCGAAA,CGAAARGAGK,SVARPGCGAA	HNSC
USF1	c.155G>A	p.R52Q	DPTSVAIASIQSAATFPDPNVKYVF[p.R52Q]QTENGGQVMYRVIQVSEGQLDGQTEG	FQTENGGQV,QTENGGQVMY,FQTENGGQVM	UCEC
USH2A	c.11156G>A	p.R3719H	NSTTVELYWSLPEKPNGLVSQYQLS[p.R3719H]HNGNLLFLGGSEEQNFTDKNLEPNSR	YQLSHNGNL,QLSHNGNLL,LSHNGNLLF,SQYQLSHNG,SHNGNLLFL,YQLSHNGNLL,QYQLSHNGNL,QLSHNGNLLF,SQYQLSHNGN,LSHNGNLLFL	GBM
USH2A	c.7107C>A	p.F2369L	KAHVRWEAPFRPNGLLTHSVLFTGI[p.F2369L]LYVDPVGNNYTLLNVTKVMYSGEETN	VLFTGILYV,SVLFTGILY,TGILYVDPV,HSVLFTGIL,HSVLFTGILY,SVLFTGILYV,FTGILYVDPV,LYVDPVGNNY	CRC
USP11	c.856G>A	p.A286T	VLDAALETGQLIIMETRKKDGTWPS[p.A286T]TQLHVMNNNMSEEDEDFKGQPGICGL	GTWPSTQLH,TWPSTQLHV,WPSTQLHVM,TWPSTQLHVM,TQLHVMNNNM	CRC
USP15	c.2344delA	p.K782fs	KKRYFDENAAEDFEKHESVEYKPPK[p.K782fs]NPL*	VEYKPPKNPL	STAD
USP16	c.1364G>A	p.R455Q	DIPSGTSKHLQKKAKKQAKKQAKNQ[p.R455Q]QRQQKIQGKVLHLNDICTIDHPEDSE	QAKNQQRQQK,QQRQQKIQGK,AKNQQRQQKI	UCEC
USP25	c.2618G>A	p.R873H	FKAIKLEYARLVKLAQEDTPPETDY[p.R873H]HLHHVVVYFIQNQAPKKIIEKTLLEQ	ETDYHLHHV,HLHHVVVYF,YHLHHVVVY,TDYHLHHVV,ETDYHLHHVV,HLHHVVVYFI,YHLHHVVVYF,DTPPETDYHL,TDYHLHHVVV	UCEC
USP25	c.3356G>A	p.R1119Q	EPPKLPSYSTHELCERFARIMLSLS[p.R1119Q]QTPADGR*	MLSLSQTPA,RIMLSLSQT,IMLSLSQTP,IMLSLSQTPA	CRC
USP26	c.2582G>A	p.R861Q	TLKSGHYICDAYDFEKQIWFTYDDM[p.R861Q]QVLGIQEAQMQEDRRCTGYIFFYMHN	FTYDDMQVL,MQVLGIQEA,TYDDMQVLGI,MQVLGIQEAQ	CRC
USP29	c.243C>A	p.F81L	NIRSVVLRHCKKRQSHLRLTLKNNV[p.F81L]LLFIDKLSYRDAKQLNMFLDIIHQNK	LLFIDKLSY,TLKNNVLLF,RLTLKNNVL,LKNNVLLFI,TLKNNVLLFI,LLFIDKLSYR,LTLKNNVLLF,KNNVLLFIDK,VLLFIDKLSY,LRLTLKNNVL,RLTLKNNVLL	CRC
USP31	c.1171G>A	p.D391N	LTEMYYDGFHRSFCDTDDLETVHES[p.D391N]NCIFAFETPEIFRPEGILSQRGIHLN	ETVHESNCI,TVHESNCIF,HESNCIFAF,TVHESNCIFA,ESNCIFAFET,VHESNCIFAF	CRC
USP33	c.107G>A	p.R36Q	LTLKVLPHFESLGKQEKIPNKMSAF[p.R36Q]QNHCPHLDSVGEITKEDLIQKSLGTC	KMSAFQNHC,SAFQNHCPH,MSAFQNHCPH,SAFQNHCPHL	UCEC
USP4	c.775C>G	p.L259V	STAPSRNFTTSPKSSASPYSSVSAS[p.L259V]VIANGDSTSTCGMHSSGVSRGGSGFS	YSSVSASVI,PYSSVSASVI,SPYSSVSASV,YSSVSASVIA	CESC
USP40	c.2552C>T	p.S851L	DSYTLKEAELKMGSSLGLCLGKAPS[p.S851L]LSQLFLFFAMGSDVQPGTEMEIVVEE	KAPSLSQLF,PSLSQLFLF,SLSQLFLFF,APSLSQLFL,GKAPSLSQL,SLSQLFLFFA,PSLSQLFLFF,KAPSLSQLFL,LGKAPSLSQL,GKAPSLSQLF,APSLSQLFLF,LSQLFLFFAM	CRC
USP42	c.2336G>C	p.R779P	SPAAESLEEPDAAAGLSSTKKAPPP[p.R779P]PDPGTPATKEGAWEAMAVAPEEPPPS	STKKAPPPP,STKKAPPPPD	ACC
USP46	c.410A>G	p.Q137R	LFDNYMQQDAHEFLNYLLNTIADIL[p.Q137R]REEKKQEKQNGKLKNGNMNEPAENNK	TIADILREEK,ILREEKKQEK,LLNTIADILR	TGCT

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
UTP14A	c.442G>A	p.V148I	EEIERIHREVAFNKTAQVLSKWDPV[p.V148I]ILKNRQAEQLVFPLEKEEPAIAPIEH	VLSKWDPVI,VLSKWDPVIL,ILKNRQAEQL,LSKWDPVILK	CRC
UTP3	c.226_228delGAG	p.E81del	SRAALAKGWNEVQSGDEEDGEEEEE[p.E81del]VLALDMDDEDDEDGGNAGEEEEEENADD	GEEEEEVLAL	PRAD
UTS2R	c.866C>A	p.A289E	VLLFWACFLPFWLWQLLAQYHQAPL[p.A289E]EPRTARIVNYLTTCLTYGNSCANPFL	LEPRTARIV,APLEPRTARI,AQYHQAPLEP,HQAPLEPRTA,EPRTARIVNY	KIRP
UXS1	c.298G>C	p.V100L	QKYPPVKFLSEKDRKRILITGGAGF[p.V100L]LGSHLTDKLMMDGHEVTVVDNFFTGR	LITGGAGFL,ILITGGAGFL,FLGSHLTDKL	OV
VARS	c.151_152CC>AG	p.P51S	EAGEGPGWGGAHPRICLQPPPTSRT[p.P51S]SFPPPRLPALEQGPGGLWVWGATAVAQ	TSRTSFPPP,RTSFPPPRL,TSRTSFPPPR,SFPPPRLPAL,TSFPPPRLPA,QPPPTSRTSF	ACC
VASH1	c.7delG	p.G3fs	MPGG[p.G3fs]RRWLGVAAAVPLQRPLRPPPPLGSGVWRPAKEPQPREMRSQKRKGKRTCETEASPSLSTGVGYLWMRPPGKGCGNTWPRSTPMERRWRNGSVGPQTCPRSPYRVCLRSSRLHLSLSAWKLCSATSESCSTITQGHSSLKLRRADL*	SLSTGVGYL,HLSLSAWKL,LSAWKLCSA,ATSESCSTI,YLWMRPPGK,ITQGHSSLK,VAAAVPLQR,GSGVWRPAK,SVGPQTCPR,QTCPRSPYR,RWLGVAAAV,GGRRWLGVA,AVPLQRPLR,RSQKRKGKR,RWRNGSVGP,RSPYRVCLR,RVCLRSSRL,CLRSSRLHL,RSSRLHLSL,SSRLHLSLS,TGVGYLWMR,NTWPRSTPM,RPLRPPPPL,CPRSPYRVC,ERRWRNGSV,SLKLRRADL,RLHLSLSAW,GRRWLGVAA,RRWLGVAAA,LGVAAAVPL,AAVPLQRPL,LQRPLRPPP,AKEPQPREM,CETEASPSL,LSTGVGYLW,RSTPMERRW,RRWRNGSVG,PQTCPRSPY,SRLHLSLSA,TQGHSSLKL,TEASPSLST,WLGVAAAVPL,SLSAWKLCSA,RLHLSLSAWK,TITQGHSSLK,GVAAAVPLQR,STGVGYLWMR,GSVGPQTCPR,GGRRWLGVAA,LGSGVWRPAK,EMRSQKRKGK,KGKRTCETEA,GYLWMRPPGK,RSTPMERRWR,RWRNGSVGPQ,RVCLRSSRLH,CLRSSRLHLS,RSSRLHLSLS,SSRLHLSLSA,TWPRSTPMER,EASPSLSTGV,QTCPRSPYRV,STITQGHSSL,MPGGRRWLGV,RPPPPLGSGV,CPRSPYRVCL,MERRWRNGSV,SPSLSTGVGY,RRWLGVAAAV,AAAVPLQRPL,LQRPLRPPPP,SLSTGVGYLW,LSTGVGYLWM,GNTWPRSTPM,GPQTCPRSPY,YRVCLRSSRL,LRSSRLHLSL,SRLHLSLSAW,LHLSLSAWKL,SATSESCSTI	STAD
VAV3	c.2053G>A	p.E685K	CVPKPVDYSCQPWYAGAMERLQAET[p.E685K]KLINRVNSTYLVRHRTKESGEYAISI	RLQAETKLI,KLINRVNST,AETKLINRV,KLINRVNSTY,AMERLQAETK,MERLQAETKL	CRC
VCAN	c.3374G>A	p.R1125H	HSVSYPPGAVTEHKVKTDEVVTLTP[p.R1125H]HIGPKVSLSPGPEQKYETEGSSTTGF	TLTPHIGPK,EVVTLTPHI,LTPHIGPKV,DEVVTLTPH,TLTPHIGPKV,VTLTPHIGPK,TPHIGPKVSL,DEVVTLTPHI	CRC
VCAN	c.3923C>G	p.S1308C	SSPPATQPTRPPTVEDKEAFGPQAL[p.S1308C]CTPQPPASTKFHPDINVYIIEVRENK	ALCTPQPPA,CTPQPPASTK,KEAFGPQALC	CESC
VEZF1	c.1063_1064insACA	p.355_356insN	ETSNQKQQQQQQQQQQQQQQQQ QH[p.355_356insN]NVTSWPGKQVETLRLWEEAVKARKKEAA	HNVTSWPGK,QQQQQHNVT,QQQQHNVTS,QQQHNVTSW,NVTSWPGKQV,QQQQQQQHNV,QQQQQQHNVT,QQQQHNVTSW,QQHNVTSWPG	STAD
VHL	c.115G>A	p.G39S	GAEEAGVEEYGPEEDGGEESGAEES[p.G39S]SPEESGPEELGAEEEMEAGRPRPVLR	SPEESGPEEL	KIRC
VHL	c.134C>T	p.P45L	VEEYGPEEDGGEESGAEESGPEESG[p.P45L]LEELGAEEEMEAGRPRPVLRSVNSRE	PEESGLEEL,LEELGAEEEM,EESGPEESGL	KIRC
VHL	c.194C>T	p.S65L	PEESGPEELGAEEEMEAGRPRPVLR[p.S65L]LVNSREPSQVIFCNRSPRVVLPVWLN	RPRPVLRLV,PVLRLVNSR,LVNSREPSQV,AGRPRPVLRL,RPRPVLRLVN	KIRC
VHL	c.221T>A	p.V74D	GAEEEMEAGRPRPVLRSVNSREPSQ[p.V74D]DIFCNRSPRVVLPVWLNFDGEPQPYP	PSQDIFCNR,DIFCNRSPR,SREPSQDIF,DIFCNRSPRV,NSREPSQDIF	KIRC

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VHL	c.232A>G	p.N78D	EMEAGRPRPVLRSVNSREPSQVIFC[p.N78D]DRSPRVVLPVWLNFDGEPQPYPTLPP	VIFCDRSPR,VIFCDRSPRV,QVIFCDRSPR	KIRC
VHL	c.236G>C	p.R79P	MEAGRPRPVLRSVNSREPSQVIFCN[p.R79P]PSPRVVLPVWLNFDGEPQPYPTLPPG	VIFCNPSPR,SQVIFCNPS,VIFCNPSPRV,QVIFCNPSPR,NPSPRVVLPV,SQVIFCNPSP,FCNPSPRVVL	KIRC
VHL	c.245G>C	p.R82P	GRPRPVLRSVNSREPSQVIFCNRSP[p.R82P]PVVLPVWLNFDGEPQPYPTLPPGTGR	RSPPVVLPV,SPPVVLPVW,VIFCNRSPPV,RSPPVVLPVW	KIRC
VHL	c.263G>T	p.W88L	LRSVNSREPSQVIFCNRSPRVVLPV[p.W88L]LLNFDGEPQPYPTLPPGTGRRIHSYR	VVLPVLLNF,SPRVVLPVL,RVVLPVLLNF,SPRVVLPVLL,RSPRVVLPVL	KIRC
VHL	c.266T>A	p.L89H	RSVNSREPSQVIFCNRSPRVVLPVW[p.L89H]HNFDGEPQPYPTLPPGTGRRIHSYRG	VVLPVWHNF,RVVLPVWHNF,HNFDGEPQPY	KIRC
VHL	c.266T>C	p.L89P	RSVNSREPSQVIFCNRSPRVVLPVW[p.L89P]PNFDGEPQPYPTLPPGTGRRIHSYRG	VVLPVWPNF,WPNFDGEPQ,RVVLPVWPNF	KIRC
VHL	c.320G>C	p.R107P	RVVLPVWLNFDGEPQPYPTLPPGTG[p.R107P]PRIHSYRGHLWLFRDAGTHDGLLVNQ	GTGPRIHSY,TLPPGTGPR,TGPRIHSYR,LPPGTGPRI,TLPPGTGPRI,GTGPRIHSYR	KIRC
VHL	c.332G>A	p.S111N	PVWLNFDGEPQPYPTLPPGTGRRIH[p.S111N]NYRGHLWLFRDAGTHDGLLVNQTELF	NYRGHLWLF,TGRRIHNYR,RIHNYRGHL,GTGRRIHNY,IHNYRGHLW,HNYRGHLWL,GTGRRIHNYR,HNYRGHLWLF,RIHNYRGHLW,NYRGHLWLFR,RRIHNYRGHL,IHNYRGHLWL	KIRC
VHL	c.333C>A	p.S111R	PVWLNFDGEPQPYPTLPPGTGRRIH[p.S111R]RYRGHLWLFRDAGTHDGLLVNQTELF	RYRGHLWLF,TGRRIHRYR,RIHRYRGHL,GTGRRIHRY,IHRYRGHLW,HRYRGHLWL,GTGRRIHRYR,HRYRGHLWLF,RIHRYRGHLW,RYRGHLWLFR,RRIHRYRGHL,IHRYRGHLWL	KIRC
VHL	c.343C>A	p.H115N	NFDGEPQPYPTLPPGTGRRIHSYRG[p.H115N]NLWLFRDAGTHDGLLVNQTELFVPSL	SYRGNLWLF,RIHSYRGNL,HSYRGNLWL,IHSYRGNLW,HSYRGNLWLF,RIHSYRGNLW,SYRGNLWLFR,RRIHSYRGNL,IHSYRGNLWL	KIRC
VHL	c.347delT	p.L116fs	DGEPQPYPTLPPGTGRRIHSYRGHL[p.L116fs]GSSEMQGHTMGFWLTKLNYLCHLSMLTDSLFLPISHCQCIL*	LTDSLFLPI,TMGFWLTKL,YLCHLSMLT,SMLTDSLFL,HLSMLTDSL,SLFLPISHC,FLPISHCQC,HTMGFWLTK,FWLTKLNYL,NYLCHLSML,RGHLGSSEM,GFWLTKLNY,EMQGHTMGF,LSMLTDSLF,LNYLCHLSM,SSEMQGHTM,SEMQGHTMG,MQGHTMGFW,TKLNYLCHL,LPISHCQCI,KLNYLCHLSM,MLTDSLFLPI,FLPISHCQCI,HTMGFWLTKL,GFWLTKLNYL,RIHSYRGHLG,LTKLNYLCHL,MGFWLTKLNY,LPISHCQCIL,SEMQGHTMGF,HLSMLTDSLF,HSYRGHLGSS,YRGHLGSSEM,GSSEMQGHTM,MQGHTMGFWL,LNYLCHLSML,CHLSMLTDSL,LSMLTDSLFL	KIRC
VHL	c.361G>T	p.D121Y	QPYPTLPPGTGRRIHSYRGHLWLFR[p.D121Y]YAGTHDGLLVNQTELFVPSLNVDGQP	RYAGTHDGL,RGHLWLFRY,WLFRYAGTH,RYAGTHDGLL,RGHLWLFRYA,YRGHLWLFRY,FRYAGTHDGL	KIRC
VHL	c.367delG	p.G123fs	PTLPPGTGRRIHSYRGHLWLFRDAG[p.G123fs]HTMGFWLTKLNYLCHLSMLTDSLFLPISHCQCIL*	LTDSLFLPI,TMGFWLTKL,YLCHLSMLT,SMLTDSLFL,WLFRDAGHT,HLSMLTDSL,SLFLPISHC,FLPISHCQC,HTMGFWLTK,FWLTKLNYL,NYLCHLSML,GFWLTKLNY,LSMLTDSLF,LFRDAGHTM,LNYLCHLSM,RDAGHTMGF,TKLNYLCHL,LPISHCQCI,WLFRDAGHTM,KLNYLCHLSM,MLTDSLFLPI,FLPISHCQCI,HTMGFWLTKL,GFWLTKLNYL,LTKLNYLCHL,MGFWLTKLNY,LPISHCQCIL,HLSMLTDSLF,FRDAGHTMGF,RDAGHTMGFW,LNYLCHLSML,CHLSMLTDSL,LSMLTDSLFL	KIRC
VHL	c.383T>A	p.L128H	PGTGRRIHSYRGHLWLFRDAGTHDG[p.L128H]HLVNQTELFVPSLNVDGQPIFANITL	HLVNQTELF,GHLVNQTEL,HLVNQTELFV,GHLVNQTELF	KIRC
VHL	c.405A>T	p.L135F	HSYRGHLWLFRDAGTHDGLLVNQTE[p.L135F]FFVPSLNVDGQPIFANITLPVYTLKE	LVNQTEFFV,EFFVPSLNV,GLLVNQTEF,LLVNQTEFF,NQTEFFVPS,LLVNQTEFFV,NQTEFFVPSL,GLLVNQTEFF,TEFFVPSLNV	KIRC
VHL	c.452T>C	p.I151T	DGLLVNQTELFVPSLNVDGQPIFAN[p.I151T]TTLPVYTLKERCLQVVRSLVKPENYR	FANTTLPVY,TTLPVYTLK,IFANTTLPV,NTTLPVYTL,QPIFANTTL,PIFANTTLPV,NTTLPVYTLK,IFANTTLPVY,GQPIFANTTL	KIRC

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VHL	c.458T>C	p.L153P	LLVNQTELFVPSLNVDGQPIFANIT[p.L153P]PPVYTLKERCLQVVRSLVKPENYRRL	IFANITPPV,ITPPVYTLK,FANITPPVY,NITPPVYTL,PIFANITPPV,NITPPVYTLK,IFANITPPVY,ANITPPVYTL	KIRC
VHL	c.472C>G	p.L158V	TELFVPSLNVDGQPIFANITLPVYT[p.L158V]VKERCLQVVRSLVKPENYRRLDIVRS	NITLPVYTV,ITLPVYTVK,TVKERCLQV,YTVKERCLQV,NITLPVYTVK,TVKERCLQVV	KIRC
VHL	c.473T>C	p.L158P	TELFVPSLNVDGQPIFANITLPVYT[p.L158P]PKERCLQVVRSLVKPENYRRLDIVRS	ITLPVYTPK,TPKERCLQV,NITLPVYTPK,YTPKERCLQV,TPKERCLQVV	KIRC
VHL	c.492delG	p.Q164fs	LNVDGQPIFANITLPVYTLKERCLQ[p.Q164fs]LSGA*	TLKERCLQL,KERCLQLSGA	KIRC
VHL	c.506T>C	p.L169P	GQPIFANITLPVYTLKERCLQVVRS[p.L169P]PVKPENYRRLDIVRSLYEDLEDHPNV	CLQVVRSPV,LQVVRSPVK,RSPVKPENY,PVKPENYRR,CLQVVRSPVK,VRSPVKPENY	KIRC
VHL	c.551T>C	p.L184P	KERCLQVVRSLVKPENYRRLDIVRS[p.L184P]PYEDLEDHPNVQKDLERLTQERIAHQ	RLDIVRSPY,SPYEDLEDH,RRLDIVRSPY	KIRC
VHL	c.563T>C	p.L188P	LQVVRSLVKPENYRRLDIVRSLYED[p.L188P]PEDHPNVQKDLERLTQERIAHQRMGD	YEDPEDHPNV	KIRC
VLDLR	c.692G>A	p.R231H	IPISWVCDDDADCSDQSDESLEQCG[p.R231H]HQPVIHTKCPASEIQCGSGECIHKKW	LEQCGHQPV,EQCGHQPVI,SLEQCGHQPV,CGHQPVIHTK,LEQCGHQPVI	BRCA
VMP1	c.1105G>C	p.E369Q	AQRQKLHHKSEMGTPQGENWLSWMF[p.E369Q]QKLVVVMVCYFILSIINSMAQSYAKR	WLSWMFQKL,WMFQKLVVV,FQKLVVVMV,NWLSWMFQK,SWMFQKLVV,MFQKLVVVM,WLSWMFQKLV,WMFQKLVVVM,NWLSWMFQKL,SWMFQKLVVV,MFQKLVVVMV,ENWLSWMFQK,LSWMFQKLVV,QKLVVVMVCY	LUAD
VPRBP	c.2405G>A	p.R802Q	ARLQKADVVAQSRISFPEKELLLLI[p.R802Q]QNHLISKGLGETATVLTKEADLPMTA	LLLLIQNHL,LLLIQNHLI,LIQNHLISK,KELLLLIQN,LLLLIQNHLI,IQNHLISKGL,LLIQNHLISK	UCEC
VPRBP	c.2817delA	p.K939fs	CNGRKIRVLRQKSDHGAYSQSPAIK[p.K939fs]NSWTDIFLPHLRWTV*	WTDIFLPHL,FLPHLRWTV,AIKNSWTDI,SWTDIFLPH,IKNSWTDIF,WTDIFLPHLR,SWTDIFLPHL,IFLPHLRWTV,AIKNSWTDIF,SQSPAIKNSW,IKNSWTDIFL	STAD
VPS13A	c.8647delT	p.F2883fs	ILGLDVLGNPFGLIREFSEGVEAFF[p.F2883fs]MNLTREPSRVLKSLWKEWH*	NLTREPSRV,LTREPSRVL,EAFFMNLTR,MNLTREPSR,EPSRVLKSL,SEGVEAFFM,FMNLTREPS,VLKSLWKEW,VEAFFMNLT,FSEGVEAFFM,LTREPSRVLK,RVLKSLWKEW,PSRVLKSLWK,FMNLTREPSR,EGVEAFFMNL,REPSRVLKSL,EPSRVLKSLW	STAD
VPS13B	c.2075G>A	p.R692Q	IMGEKNSSNFMNTTNFQSLRPLPSI[p.R692Q]QILVDKINLEHSVPMYAEQLVHVVSS	RPLPSIQIL,SLRPLPSIQI,RPLPSIQILV,IQILVDKINL	UCEC
VPS13B	c.7723G>T	p.G2575W	AQADCKLLECRNVTMQSVVKPFSIF[p.G2575W]WQMAVSSDVVEKLLDCTVIVDSVFVN	FSIFWQMAV,WQMAVSSDV,KPFSIFWQM,WQMAVSSDVV,FSIFWQMAVS,VKPFSIFWQM,KPFSIFWQMA	LUAD
VPS13C	c.4075G>T	p.D1359Y	SWYHKVPVVEIKGHLDSMNVSLNQE[p.D1359Y]YLNLLFRILTENLCEGTEDLDKVKPR	SLNQEYLNL,YLNLLFRIL,EYLNLLFRI,MNVSLNQEY,NVSLNQEYL,NQEYLNLLF,SLNQEYLNLL,YLNLLFRILT,EYLNLLFRIL,SMNVSLNQEY,MNVSLNQEYL,LNQEYLNLLF,QEYLNLLFRI	CRC
VWA2	c.950G>A	p.G317D	RTTCPGPCDSQPCQNGGTCVPEGLD[p.G317D]DYQCLCPLAFGGEANCALKLSLECRV	DDYQCLCPL,DYQCLCPLAF	TGCT
VWA3A	c.2863G>A	p.V955I	LEKVLRRYVQRLQWLLSGSRRLFGT[p.V955I]ILESKVCILLDTSGSMGPYLQQVKTE	RLFGTILES,ILESKVCIL,GSRRLFGTI,SRRLFGTIL,ILESKVCILL,RLFGTILESK,GSRRLFGTIL	BRCA
VWA3B	c.1670G>T	p.R557L	QFIQEQLKYKSKFNFVKFDGQAVAW[p.R557L]LEQLAEVNEDNLEQAQSWIRDIKIGS	QAVAWLEQL,VAWLEQLAEV,GQAVAWLEQL	LUAD
VWA7	c.2375T>G	p.V792G	FSLTSNLSRAHLELNESAWGRLWLE[p.V792G]GPDSAAPDSVVMVTVTAGGREANPVP	RLWLEGPDSA	TGCT

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VWF	c.5160A>T	p.K1720N	LLDGSSSFPASYFDEMKSFAKAFIS[p.K1720N]NANIGPRLTQVSVLQYGSITTIDVPW	FAKAFISNA,ISNANIGPR,KAFISNANI,KSFAKAFISN,SFAKAFISNA,FISNANIGPR,AKAFISNANI,ISNANIGPRL	BRCA
WAPAL	c.1564delA	p.R522fs	GFDDLSESEDDEDDDCQVERKTSKK[p.R522fs]ELKQLHHPPCSLPQKAMIIPRTVSLVLTMQRTCLVCLKV*	MIIPRTVSL,IIPRTVSLV,LTMQRTCLV,QLHHPPCSL,SLPQKAMII,MQRTCLVCL,VSLVLTMQR,KAMIIPRTV,RTVSLVLTM,IPRTVSLVL,KQLHHPPCSL,AMIIPRTVSL,MIIPRTVSLV,VLTMQRTCLV,MQRTCLVCLK,TVSLVLTMQR,VERKTSKKEL,TMQRTCLVCL,KELKQLHHPP	STAD
WASF3	c.913_914insC	p.P305fs	EHEYRPPSASARHMALNRPQQPPPP[p.P305fs]ASPSGPRGVPGLCTDGSSRLRDAPSADN*	SSRLRDAPS,RPQQPPPPA,GLCTDGSSRL,SSRLRDAPSA,RPQQPPPPAS,SPSGPRGVPG	STAD
WASH3P	c.523G>A	p.G175S	APREVVDPSGGRATLLESIRQAGGI[p.G175S]SKAKLRSMKERKLEKKQQKEQEQVRA	RQAGGISKA,ISKAKLRSM,SIRQAGGISK,RQAGGISKAK,ISKAKLRSMK	GBM,KIRC,PRAD,SKCM
WASH3P	c.559C>G	p.L187V	ATLLESIRQAGGIGKAKLRSMKERK[p.L187V]VEKKQQKEQEQVRATSQGGHLMSDLF	SMKERKVEK,RSMKERKVEK,SMKERKVEKK,KLRSMKERKV	PRAD,TGCT
WBP1	c.412_413insC	p.P138fs	LRFLSTFKPPAYEDVVHRPGTPPPP[p.P138fs]LYCGPRPPLDCFQ*	LYCGPRPPL,RPGTPPPPL,GPRPPLDCF	STAD
WBSCR17	c.682C>T	p.R228C	LEEYVHKRYPGLVKVVRNQKREGLI[p.R228C]CARIEGWKVATGQVTGFFDAHVEFTA	REGLICARI,LICARIEGWK	CRC
WDFY3	c.5525delT	p.L1842fs	FIFGVPASSGTVVSSIHNVCTEAVF[p.L1842fs]YYWECSAAC*	CTEAVFYYW,YYWECSAAC,EAVFYYWEC,FYYWECSAA,AVFYYWECSA,HNVCTEAVFY,TEAVFYYWEC	STAD
WDR17	c.832C>T	p.P278S	SESLSCITTFNLPSAAASVQCLAWV[p.P278S]SSAPGMFITGDSQVGVLRIWNVSRTT	AWVSSAPGM,WVSSAPGMF,WVSSAPGMFI,AWVSSAPGMF,LAWVSSAPGM,VQCLAWVSSA	CESC
WDR3	c.2521G>A	p.E841K	KSSELEESLLVLPFSYVPDILKLFN[p.E841K]KFIQLGSDVELICRCLFFLLRIHFGQ	KLFNKFIQL,LKLFNKFIQL	CRC
WDR34	c.178T>G	p.W60G	PGPLQDETLGVASVPSQWRAVQGIR[p.W60G]GETKSCQTASIATASASAQARNHVDA	GETKSCQTA,AVQGIRGETK	ACC
WDR5	c.642delC	p.N214fs	DGLCRIWDTASGQCLKTLIDDDNPP[p.N214fs]CLL*	TLIDDDNPPC	STAD
WDR59	c.2509C>A	p.R837S	EHLSSPWGESSPEELRFGSLTYSDP[p.R837S]SERERDQHDKNKRLLDPANTQQFDDF	LTYSDPSER	LUAD
WDR59	c.479delA	p.N160fs	IKDTRKPTVALSAVAGASQVKWNKK[p.N160fs]MLTALPPAMTAMCGYGIRGNPVQQWNI*	KMLTALPPA,MLTALPPAM,ALPPAMTAM,KWNKKMLTA,PAMTAMCGY,TAMCGYGIR,MTAMCGYGI,WNKKMLTAL,SQVKWNKKM,KKMLTALPP,KMLTALPPAM,AMTAMCGYGI,MLTALPPAMT,ALPPAMTAMC,MTAMCGYGIR,KWNKKMLTAL,LTALPPAMTA,TALPPAMTAM,SQVKWNKKML,VKWNKKMLTA,KKMLTALPPA,PPAMTAMCGY	STAD
WDR60	c.1235delA	p.Q412fs	DGDDDESSNEPESREKLEELPLAQK[p.Q412fs]RKYKKFKELLMQKMKGLASYL*	LLMQKMKGL,KMKGLASYL,KYKKFKELL,LAQKRKYKK,KFKELLMQK,QKMKGLASY,RKYKKFKEL,MQKMKGLAS,AQKRKYKKF,YKKFKELLM,FKELLMQKM,LPLAQKRKY,LLMQKMKGLA,KYKKFKELLM,AQKRKYKKFK,KFKELLMQKM,MQKMKGLASY,LAQKRKYKKF,RKYKKFKELL,QKMKGLASYL	STAD
WDR7	c.784delG	p.G262fs	RVFDAGDYSLLCSGPSENGQTWTGG[p.G262fs]TLSHQIKSSFGQKMGKVIFTNYLPVAFQLVIHSAVMWGRQLKI*	FTNYLPVAF,VIFTNYLPV,YLPVAFQLV,FQLVIHSAV,VMWGRQLKI,QIKSSFGQK,SSFGQKMGK,AVMWGRQLK,NYLPVAFQL,MGKVIFTNY,LPVAFQLVI,LSHQIKSSF,QLVIHSAVM,GQTWTGGTL,HQIKSSFGQ,IKSSFGQKM,GQKMGKVIF,GKVIFTNYL,LVIHSAVMW,SAVMWGRQL,KVIFTNYLPV,VIFTNYLPVA,YLPVAFQLVI,HQIKSSFGQK,KSSFGQKMGK,KMGKVIFTNY,VIHSAVMWGR,SAVMWGRQLK,IFTNYLPVAF,NYLPVAFQLV,MGKVIFTNYL,AVMWGRQLKI,WTGGTLSHQI,SSFGQKMGKV,TLSHQIKSSF,FQLVIHSAVM,FGQKMGKVIF,VAFQLVIHSA,HSAVMWGRQL,LPVAFQLVIH	STAD

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WDR73	c.944_961delATGGAACACGGAGCCAAG	p.DGTRSQ315del	CLAISGFDGTVQVYDATSWDGTRSQ[p.DGTRSQ315del]VEPLFTHRGHIFLDGNGMDPAPLVTTHTWHPCRPRTLLSATND	TSWDGTRSQV	KIRC
WDR75	c.860C>A	p.P287Q	SLLSGGRESVLVEWRDATEKNKEFL[p.P287Q]QRLGATIEHISVSPAGDLFCTSHSDN	FLQRLGATI,KEFLQRLGA,EFLQRLGATI,KEFLQRLGAT,LQRLGATIEH	LUAD
WDR78	c.330T>A	p.N110K	NQSRMAVSKTVLIPPELKTVEKPNP[p.N110K]KIKTTQVFDINGTDVTPRPLYHPDPL	KTVEKPNPK,KIKTTQVFD,NPKIKTTQV,PKIKTTQVF,KIKTTQVFDI,NPKIKTTQVF	CLL
WDR88	c.298G>T	p.G100W	KHQVPEKLIWGDQDPLSKIPFKILS[p.G100W]WHEHAVSTCHFCVDDTKLLSGSYDCT	KILSWHEHA,ILSWHEHAV,KIPFKILSW,FKILSWHEH,KILSWHEHAV,SKIPFKILSW,FKILSWHEHA	LUAD
WDTC1	c.861_862insG	p.M287fs	RLRVLVATYVTFSPNGTELLVNMGG[p.M287fs]GTGLFV*	NMGGGTGLF,VNMGGGTGL,NMGGGTGLFV,VNMGGGTGLF	STAD
WHSC1L1	c.1254_1255insA	p.K418fs	YIDKQPEEALSQAKKSVASKTEVKK[p.K418fs]NPTTKICAEYSARTDQCRGGGLLTLKY*	PTTKICAEY,KICAEYSAR,RGGGLLTLK,GGGLLTLKY,CRGGGLLTL,TTKICAEYSA,RGGGLLTLKY,EYSARTDQCR,NPTTKICAEY,AEYSARTDQC	STAD
WNK4	c.1816delG	p.G606fs	CETDGYLSSSGFLDASDPALQPPGG[p.G606fs]CHPAWLSPISACPRLLPYPFHVLALEVTFPPGTAMPQMQLQALAMWEKGWDK*	RLLPYPFHV,LLPYPFHVL,AMPQMQLQA,AMWEKGWDK,SACPRLLPY,LQALAMWEK,PYPFHVLAL,HVLALEVTF,MQLQALAMW,EVTFPPGTA,SPISACPRL,CPRLLPYPF,MPQMQLQAL,VTFPPGTAM,QMQLQALAM,HPAWLSPIS,LPYPFHVLA,LEVTFPPGT,ISACPRLLPY,RLLPYPFHVL,LLPYPFHVLA,AMPQMQLQAL,QLQALAMWEK,LAMWEKGWDK,WLSPISACPR,YPFHVLALEV,EVTFPPGTAM,HPAWLSPISA,SPISACPRLL,LPYPFHVLAL,FPPGTAMPQM,MPQMQLQALA,LQPPGGCHPA,FHVLALEVTF,LEVTFPPGTA,PQMQLQALAM,QMQLQALAMW,QPPGGCHPAW,QALAMWEKGW	STAD
WNT1	c.500delG	p.W167fs	SEGSIESCTCDYRRRGPGGPDWHWG[p.W167fs]AAATTLTSAASSAGSSWTPGRRGGTCASS*	TLTSAASSA,GPDWHWGAA,WHWGAAATT,HWGAAATTL,AASSAGSSW,SAGSSWTPGR,TTLTSAASSA,GPDWHWGAAA,SAASSAGSSW,WHWGAAATTL,AAATTLTSAA	STAD
WNT11	c.1031G>A	p.C344Y	NPYTDRVVERCHCKYHWCCYVTCRR[p.C344Y]YERTVERYVCK*	CCYVTCRRY,RYERTVERY,YVTCRRYER,YERTVERYV,RRYERTVERY,CYVTCRRYER,YERTVERYVC	OV
WNT16	c.494delG	p.W165fs	GNMTECSCDTTLQNGGSASEGWHWG[p.W165fs]AAPMMSSMACGSAESS*	MMSSMACGS,SMACGSAES,MSSMACGSA,APMMSSMAC,GAAPMMSSM,SEGWHWGAA,GWHWGAAPM,WHWGAAPMM,MMSSMACGSA,SASEGWHWGA,EGWHWGAAPM,WGAAPMMSSM,GWHWGAAPMM,SMACGSAESS	STAD
WNT5B	c.979A>G	p.K327E	RLCNKTSEGMDGCELMCCGRGYNQF[p.K327E]ESVQVERCHCKFHWCCFVRCKKCTEI	RGYNQFESV,QFESVQVER,NQFESVQVE,NQFESVQVER	TGCT
WT1	c.1142_1143insCGGTC	p.S381fs	HTHGVFRGIQDVRRVPGVAPTLVRS[p.S381fs]GRHLRPVRNAPSCVLTQAAIRDILSCPTYRCTAGSTLVRNHTSVTSRTVNEGFLVQTSSKDTKGDIQV*	TLVRNHTSV,CTAGSTLVR,LVRSGRHLR,RSGRHLRPV,SGRHLRPVR,LVRNHTSVT,RNHTSVTSR,HTSVTSRTV,GFLVQTSSK,RDILSCPTY,CVLTQAAIR,DILSCPTYR,RPVRNAPSC,TLVRSGRHL,VRNAPSCVL,TQAAIRDIL,YRCTAGSTL,TSRTVNEGF,LVQTSSKDTK,TYRCTAGSTL,RSGRHLRPVR,HLRPVRNAPS,STLVRNHTSV,TSRTVNEGFL,TLVRSGRHLR,RPVRNAPSCV,APSCVLTQAA,IRDILSCPTY,VTSRTVNEGF	LAML
WWP2	c.1373G>C	p.G458A	EDPRTQGMIQEPALPPGWEMKYTSE[p.G458A]AVRYFVDHNTRTTTFKDPRPGFESGT	EMKYTSEAV,KYTSEAVRY,YTSEAVRYF,TSEAVRYFV,WEMKYTSEA,YTSEAVRYFV,KYTSEAVRYF,MKYTSEAVRY,EMKYTSEAVR,WEMKYTSEAV,SEAVRYFVDH	KIRC
XAB2	c.2344G>A	p.E782K	SDLAPGQSGMDDMKLLEQRAEQLAA[p.E782K]KAERDQPLRAQSKILFVRSDASREEL	EQLAAKAER,AKAERDQPL,EQRAEQLAAK	BLCA
XDH	c.1228C>T	p.P410S	MDHTFFPGYRKTLLSPEEILLSIEI[p.P410S]SYSREGEYFSAFKQASRREDDIAKVT	ISYSREGEY,LSIEISYSR,SYSREGEYF,ILLSIEISY,IEISYSREG,ISYSREGEYF,LLSIEISYSR,EILLSIEISY,EEILLSIEIS	TGCT
XIRP2	c.7315G>A	p.D2439N	GKTGVLPPPTLPKPKLPKHIKDNKN[p.D2439N]NFSPKVELATSLSDMECKITTSKDQK	KDNKNNFSPK,KHIKDNKNNF	SKCM
XIRP2	c.9023T>A	p.V3008E	IPGWLISEDKREYAVHIAMENNLEK[p.V3008E]EKEEITHIKTQAEDMLVSYENIIQTA	KEKEEITHI	CLL

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XKR6	c.803G>A	p.R268Q	SVIHLLQMGQVWRYIRTMYLGIQSQ[p.R268Q]QRKEHQRRFYWAMMYEYADVNMLRLL	MYLGIQSQQR,QQRKEHQRRF	CRC
XPO1	c.1711G>A	p.E571K	QYPRFLRAHWKFLKTVVNKLFEFMH[p.E571K]KTHDGVQDMACDTFIKIAQKCRRHFV	KLFEFMHKT,FMHKTHDGV,KTHDGVQDM,KLFEFMHKTH,VNKLFEFMHK,KTHDGVQDMA,EFMHKTHDGV,FMHKTHDGVQ,HKTHDGVQDM	BRCA,CLL
XPOT	c.1621C>T	p.R541W	EPQHIPCVLMAFLDHRGLRHSSAKV[p.R541W]WSRTAYLFSRFVKSLNKQMNPFIEDI	KVWSRTAYL,HSSAKVWSR,VWSRTAYLF,SAKVWSRTA,WSRTAYLFS,AKVWSRTAY,LRHSSAKVW,KVWSRTAYLF,SAKVWSRTAY,WSRTAYLFSR,GLRHSSAKVW,AKVWSRTAYL	CRC
XYLB	c.260C>T	p.S87F	TSPVLMWVQALDIILEKMKASGFDF[p.S87F]FQVLALSGAGQQHGSIYWKAGAQQAL	FQVLALSGA,MKASGFDFF,SGFDFFQVL,FDFFQVLAL,KASGFDFFQV,KMKASGFDFF,FQVLALSGAG	BLCA
XYLT2	c.1578delC	p.Y526fs	RKFESTVNQEVLEILDFHLYGSYPP[p.Y526fs]ARQPSRPTGRTPTTRLMAPVGSVMSCSLLTQPSPASACTMPPLLHPQWAPHSAGLSPGACRPACTCISMTTISRATW*	HLYGSYPPA,RLMAPVGSV,SLLTQPSPA,LMAPVGSVM,CISMTTISR,RTPTTRLMA,TTRLMAPVG,ASACTMPPL,ISMTTISRA,LYGSYPPAR,PTTRLMAPV,HSAGLSPGA,RPTGRTPTT,HPQWAPHSA,SPGACRPAC,RPACTCISM,LLHPQWAPH,GSVMSCSLL,MTTISRATW,MPPLLHPQW,RLMAPVGSVM,LLTQPSPASA,GLSPGACRPA,HLYGSYPPAR,TMPPLLHPQW,TGRTPTTRLM,ASACTMPPLL,SYPPARQPSR,TCISMTTISR,TPTTRLMAPV,QPSPASACTM,HPQWAPHSAG,APHSAGLSPG,RPACTCISMT,FHLYGSYPPA,PQWAPHSAGL,SMTTISRATW,MPPLLHPQWA	STAD
YBX1	c.749C>T	p.P250L	GAGEQGRPVRQNMYRGYRPRFRRGP[p.P250L]LRQRQPREDGNEEDKENQGDETQGQQ	RFRRGPLRQ,RPRFRRGPL,RPRFRRGPLR,RFRRGPLRQR	KIRP
YBX2	c.677delC	p.P226fs	SAGTGPGSKGERAEDSGQRPRRWCP[p.P226fs]HPSSTDGGLCEAPGLPTSSSL*	RWCPHPSST,HPSSTDGGL,CEAPGLPTS,GQRPRRWCPH,RPRRWCPHPS,APGLPTSSSL,RRWCPHPSST,CEAPGLPTSS	STAD
YIF1A	c.391delC	p.R131fs	LGLLVFPYTHQNWEVQYSRDAPLPP[p.R131fs]GKTSTPLTSISPRWPSLLTCSWLGWHWAFRKGSPRRCWACVQAQRWCGW*	KTSTPLTSI,SISPRWPSL,LGWHWAFRK,WLGWHWAFR,ISPRWPSLL,SWLGWHWAF,AFRKGSPRR,KGSPRRCWA,TPLTSISPR,WAFRKGSPR,CWACVQAQR,PPGKTSTPL,SPRWPSLLT,SPRRCWACV,LLTCSWLGW,RKGSPRRCW,VQAQRWCGW,WPSLLTCSW,WACVQAQRW,SISPRWPSLL,WLGWHWAFRK,STPLTSISPR,SWLGWHWAFR,RWPSLLTCSW,SLLTCSWLGW,CSWLGWHWAF,CWACVQAQRW,TSISPRWPSL,HWAFRKGSPR,WAFRKGSPRR,APLPPGKTST,LPPGKTSTPL,SPRWPSLLTC,WPSLLTCSWL,GKTSTPLTSI,TPLTSISPRW	STAD
YLPM1	c.3533delA	p.E1178fs	RGLGRSDFGRDRGPFRPEPGDGGEK[p.E1178fs]CIHITGMSLLGLHGTMEKSEGMKSFH*	LGLHGTMEK,TMEKSEGMK,CIHITGMSL,IHITGMSLL,SLLGLHGTM,EKSEGMKSF,CIHITGMSLL,HITGMSLLGL,GMSLLGLHGT,LLGLHGTMEK,GTMEKSEGMK,MEKSEGMKSF,MSLLGLHGTM,GEKCIHITGM,KCIHITGMSL	STAD
YTHDC2	c.1900G>A	p.E634K	IMHLLYNICHSCDAGAVLIFLPGYD[p.E634K]KIVGLRDRILFDDKRFADSTHRYQVF	FLPGYDKIV,LIFLPGYDK,IFLPGYDKI,VLIFLPGYDK,LPGYDKIVGL	CRC
YTHDC2	c.553G>A	p.E185K	NREMSKTSGRLNNGIPQIPVKRGES[p.E185K]KFDSFRQSLPVFEKQEEIVKIIKENK	RGESKFDSF,IPVKRGESKF,KRGESKFDSF,SKFDSFRQSL	UCEC
ZAR1	c.126G>C	p.Q42H	CPPCSYRYPYPAATKGKGAAGGSWQ[p.Q42H]HRGRGCLPASSPCSAGAASLSFPGCG	WQHRGRGCL,WQHRGRGCLP	ACC
ZBBX	c.1787G>T	p.R596I	TKSSLLLQEIACRSKPITKQYQGLE[p.R596I]IFFIFDTNERLNLLPSHRLECNNSST	YQGLEIFFI,KQYQGLEIF,QYQGLEIFF,QGLEIFFIF,TKQYQGLEI,LEIFFIFDT,KQYQGLEIFF,QYQGLEIFFI,YQGLEIFFIF,ITKQYQGLEI,IFFIFDTNER,TKQYQGLEIF	CRC
ZBBX	c.453_455delAGA	p.E151del	KPKINGKVCGQCENKAALLVCLECG[p.E151del]DYCSGCFAKVHQKGALKLHRTTLLQAKS	LVCLECGDY,LLVCLECGDY	STAD
ZBED4	c.1154C>T	p.S385L	PSLLPPEGELSSVSSSPVKPVRESP[p.S385L]LASSSPDRLTEDLQSHLNPGDGLMED	RESPLASSS,RESPLASSSP	CESC

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ZBTB20	c.2075delC	p.P692fs	CKKKFSHKTLLERHVALHSASNGTP[p.P692fs]LQAHPQVPALAPQAWWPARRGPLTSAPSAQQSLTKSSSSTTT*	APQAWWPAR,HSASNGTPL,LAPQAWWPA,TPLQAHPQV,WPARRGPLT,WWPARRGPL,LQAHPQVPA,QAHPQVPAL,VPALAPQAW,LQAHPQVPAL,ALAPQAWWPA,AWWPARRGPL,LAPQAWWPAR,APQAWWPARR,WPARRGPLTS,LHSASNGTPL,TSAPSAQQSL,AQQSLTKSSS,VPALAPQAWW	STAD
ZBTB24	c.1819C>A	p.L607I	QNMTADQAANLTLLTQQPEQLQNLI[p.L607I]ISAQQEQTEHIQSLNMIESQMGPSQT	QLQNLIISA,LQNLIISAQ,EQLQNLIISA,QPEQLQNLII	CRC
ZBTB40	c.786_787insA	p.L262fs	QLNFLLENEGVFSDALMVTQDVLKK[p.L262fs]TRNVFRN*	VLKKTRNVF,VLKKTRNVFR,VTQDVLKKTR	STAD
ZBTB7C	c.1025_1026insG	p.G342fs	ELPPPPPPPFPNDFFKDMFPDLPGG[p.G342fs]ASGTHQGGERLRCLSQLPECHPPGRPLPTLAPGRRAQAEAQGLSAVPHLPQSHHGGREAAAAHEDPYRGEAIHVHHLRGPLHQAGQAENPHAEAHRGAALPVHPLQRQVRAQLRPQEPHAHPHGRAALPVRVLLQELHAL*	VLLQELHAL,HLRGPLHQA,RLRCLSQLP,HVHHLRGPL,QLRPQEPHA,HAHPHGRAA,HGRAALPVR,AALPVRVLL,RVLLQELHA,AAAAHEDPY,EAIHVHHLR,HPPGRPLPT,RPLPTLAPG,HAEAHRGAA,HPLQRQVRA,LQRQVRAQL,RAALPVRVL,SQLPECHPP,RAQAEAQGL,AEAQGLSAV,AQGLSAVPH,SHHGGREAA,GEAIHVHHL,AENPHAEAH,AEAHRGAAL,AHRGAALPV,GAALPVHPL,RQVRAQLRP,AQLRPQEPH,FPDLPGGAS,DPYRGEAIH,DMFPDLPGGA,TLAPGRRAQA,AQAEAQGLSA,GQAENPHAEA,AAAAHEDPYR,AALPVHPLQR,RLRCLSQLPE,HVHHLRGPLH,LQRQVRAQLR,HAHPHGRAAL,HGRAALPVRV,RAALPVRVLL,RVLLQELHAL,HLPQSHHGGR,EAHRGAALPV,HPPGRPLPTL,APGRRAQAEA,HAEAHRGAAL,LPVHPLQRQV,RPQEPHAHPH,HPHGRAALPV,LPVRVLLQEL,EAAAAHEDPY,HQGGERLRCL,GERLRCLSQL,SQLPECHPPG,RRAQAEAQGL,AQGLSAVPHL,HEDPYRGEAI,IHVHHLRGPL,HQAGQAENPH,AHRGAALPVH,RGAALPVHPL,RQVRAQLRPQ,AQLRPQEPHA,GRAALPVRVL,FPDLPGGASG,AEAQGLSAVP,DPYRGEAIHV	STAD
ZBTB7C	c.460delG	p.D154fs	ILNAARMLEIQCIVNVCLEIMEPGG[p.D154fs]TGGRRMTRRTMTTTKMMMMRRTKRRRRKRRRMTMMTRRTLLTKKTCLTPRTSAATKALPRQTISQRRPIQTPPGTSLTPSRLAVLAIWG*	TMMTRRTLL,SLTPSRLAV,CLTPRTSAA,KMMMMRRTK,MMMMRRTKR,MMMRRTKRR,MTRRTLLTK,GTGGRRMTR,TTTKMMMMR,TTKMMMMRR,SAATKALPR,RMTRRTMTT,MTRRTMTTT,TRRTMTTTK,RTMTTTKMM,MMRRTKRRR,RTKRRRRKR,RRRMTMMTR,MTMMTRRTL,RTSAATKAL,MTTTKMMMM,QTISQRRPI,RRKRRRMTM,TLLTKKTCL,IQTPPGTSL,RRTMTTTKM,TMTTTKMMM,RKRRRMTMM,TKALPRQTI,SQRRPIQTP,SRLAVLAIW,TMMTRRTLLT,CLTPRTSAAT,SLTPSRLAVL,MTRRTMTTTK,KMMMMRRTKR,MMMMRRTKRR,MMMRRTKRRR,MMTRRTLLTK,MTRRTLLTKK,MTTTKMMMMR,TTTKMMMMRR,LTPRTSAATK,TSAATKALPR,RTMTTTKMMM,MMRRTKRRRR,MRRTKRRRRK,RTKRRRRKRR,RRRKRRRMTM,KRRRMTMMTR,RRRMTMMTRR,RMTMMTRRTL,MTMMTRRTLL,RTLLTKKTCL,LTKKTCLTPR,KTCLTPRTSA,ATKALPRQTI,RQTISQRRPI,TPRTSAATKA,TPSRLAVLAI,RRKRRRMTMM,RMTRRTMTTT,TRRTMTTTKM,RRTMTTTKMM,TMTTTKMMMM,SQRRPIQTPP,IQTPPGTSLT	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ZBTB7C	c.469delG	p.E157fs	AARMLEIQCIVNVCLEIMEPGGDGG[p.E157fs]RRMTRRTMTTTKMMMMRRTKRRRRKRRRMTMMTRRTLLTKKTCLTPRTSAATKALPRQTISQRRPIQTPPGTSLTPSRLAVLAIWG*	TMMTRRTLL,SLTPSRLAV,CLTPRTSAA,KMMMMRRTK,MMMMRRTKR,MMMRRTKRR,MTRRTLLTK,TTTKMMMMR,TTKMMMMRR,SAATKALPR,RMTRRTMTT,MTRRTMTTT,TRRTMTTTK,RTMTTTKMM,MMRRTKRRR,RTKRRRRKR,RRRMTMMTR,MTMMTRRTL,RTSAATKAL,MTTTKMMMM,QTISQRRPI,RRKRRRMTM,TLLTKKTCL,IQTPPGTSL,RRTMTTTKM,TMTTTKMMM,RKRRRMTMM,TKALPRQTI,SQRRPIQTP,SRLAVLAIW,TMMTRRTLLT,CLTPRTSAAT,SLTPSRLAVL,MTRRTMTTTK,KMMMMRRTKR,MMMMRRTKRR,MMMRRTKRRR,MMTRRTLLTK,MTRRTLLTKK,MTTTKMMMMR,TTTKMMMMRR,LTPRTSAATK,TSAATKALPR,RTMTTTKMMM,MMRRTKRRRR,MRRTKRRRRK,RTKRRRRKRR,RRRKRRRMTM,KRRRMTMMTR,RRRMTMMTRR,RMTMMTRRTL,MTMMTRRTLL,RTLLTKKTCL,LTKKTCLTPR,KTCLTPRTSA,ATKALPRQTI,RQTISQRRPI,TPRTSAATKA,TPSRLAVLAI,RRKRRRMTMM,RMTRRTMTTT,TRRTMTTTKM,RRTMTTTKMM,TMTTTKMMMM,SQRRPIQTPP,IQTPPGTSLT	STAD
ZC3H12D	c.1213C>T	p.P405S	SAGGRVPGPLSLPSPESQFSPGDLP[p.P405S]SPPGLQLQPRGEHRPRDLHGDLLSPR	LPSPPGLQL,SQFSPGDLPS	ACC
ZC3H13	c.3018delA	p.K1006fs	NIETTSEDGQVFSPKKGQKKKSIEK[p.K1006fs]NVKNPKVILIFLMKKQPSKVRRKEAHGLPL*	LMKKQPSKV,KVILIFLMK,VILIFLMKK,FLMKKQPSK,KNPKVILIF,KQPSKVRRK,KVRRKEAHG,RKEAHGLPL,FLMKKQPSKV,KVILIFLMKK,SIEKNVKNPK,IFLMKKQPSK,LMKKQPSKVR,KVRRKEAHGL,RRKEAHGLPL,QPSKVRRKEA,VKNPKVILIF,NPKVILIFLM,IEKNVKNPKV	STAD
ZC3H18	c.2102_2103insC	p.T701fs	PVPEPTKPGDPREARRKERPARTPP[p.T701fs]QEADAKRQRQWQW*	AKRQRQWQW,RTPPQEADAK,RPARTPPQEA	STAD
ZC3H18	c.2473delC	p.P825fs	PKSAKPPAGGKSSQQPSTPQQAPPG[p.P825fs]SPSRAHLWPTRRSS*	RAHLWPTRR,QQAPPGSPS,PSRAHLWPTR,RAHLWPTRRS,SPSRAHLWPT	STAD
ZC3H4	c.2392G>A	p.E798K	IQQKQQEEEERARRLAESSKQDREN[p.E798K]KEGDTGNWYSSDEDEGGSSVTSILKT	SSKQDRENK,KEGDTGNWY	BLCA
ZC3H7A	c.1724G>C	p.C575S	NGKINLTVFKLLQEHLGEFIFLCEK[p.C575S]SFDHKPRMISKRNKDNSTACSHPVTK	KSFDHKPRM,FIFLCEKSF,EFIFLCEKSF,KSFDHKPRMI,GEFIFLCEKS	TGCT
ZCCHC6	c.2811A>T	p.K937N	GKHVERALLVELNKISLKEENVCEE[p.K937N]NNSPVDQSDFFYEFSKLIFTKGKSPT	NVCEENNSPV	KIRC
ZCRB1	c.228A>T	p.L76F	KGVAFILFLDKDSAQNCTRAINNKQ[p.L76F]FFGRVIKASIAIDNGRAAEFIRRRNY	KQFFGRVIK,RAINNKQFF,INNKQFFGR,NKQFFGRVI,AINNKQFFGR,FFGRVIKASI,RAINNKQFFG,KQFFGRVIKA,CTRAINNKQF	CLL
ZCWPW2	c.430G>A	p.D144N	DRFKGKYVTYDPDGNVEEYHIEFLG[p.D144N]NPHSRSWIKATFVGHYSITLKPEKCK	EFLGNPHSR,LGNPHSRSW,IEFLGNPHS,YHIEFLGNPH,FLGNPHSRSW	CRC
ZDHHC11	c.750C>G	p.H250Q	PVQVQTLIVVIIGMLVLLLDFLGLV[p.H250Q]QLGQLLIFHIYLKAKKMTTFEYLINN	GLVQLGQLL,VQLGQLLIF,LDFLGLVQL,LLDFLGLVQL,FLGLVQLGQL,QLGQLLIFHI,GLVQLGQLLI,LVQLGQLLIF	TGCT
ZDHHC4	c.899G>A	p.R300H	LFVLYLAATNQTTNEWYRGDWAWCQ[p.R300H]HCPLVAWPPSAEPQVHRNIHSHGLRS	WAWCQHCPL,CQHCPLVAW,WAWCQHCPLV	GBM
ZDHHC5	c.1947_1949delAGA	p.E651del	PTAPYLGRSMSYSSQKAQPGVSETE[p.E651del]VALQPLLTPKDEVQLKTTYSKSNGQPKS	ETEVALQPL,TEVALQPLL,AQPGVSETEV,ETEVALQPLL,SETEVALQPL,TEVALQPLLT	STAD
ZDHHC7	c.948delC	p.P316fs	LKSEKPTWERRLRWEGMKSVFGGPP[p.P316fs]HSSG*	KSVFGGPPH,MKSVFGGPPH	STAD
ZEB2	c.3280G>A	p.E1094K	SYSQHMNHRYSYCKREAEEREAAER[p.E1094K]KAREKGHLEPTELLMNRAYLQSITPQ	KAREKGHLE,KAREKGHLEP	CESC

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ZEB2	c.467G>A	p.R156H	NNGTVKNANCTSDFEEYFAKRKLEE[p.R156H]HDGHAVSIEEYLQRSDTAIIYPEAPE	LEEHDGHAV,EEHDGHAVS,KLEEHDGHAV,EEHDGHAVSI	CRC
ZFAND2B	c.446T>C	p.I149T	IKHRHPLDHDCSGEGHPTSRAGLAA[p.I149T]TSRAQAVASTSTVPSPSQTMPSCTSP	TSRAGLAAT,RAGLAATSR,ATSRAQAVA,GLAATSRAQA,TSRAQAVAST,LAATSRAQAV	KIRC
ZFC3H1	c.1155delA	p.K385fs	KKLGEDEEELSELQLRLLALQSASK[p.K385fs]NGNKKNSR*	QSASKNGNK,LQSASKNGNK	STAD
ZFHX3	c.2287delG	p.E763fs	KGNLSIHMQSDKHLNNMQNLQNGGG[p.E763fs]SRSSATLPGRRRRRWLRRRRQPISVAPAGPPRRPNQKPNPPGGARCVIMRPTWPGTSAFT*	RQPISVAPA,RSSATLPGR,SSATLPGRR,SVAPAGPPR,ATLPGRRRR,RRRRRWLRR,RRRRQPISV,IMRPTWPGT,TLPGRRRRR,WLRRRRQPI,RPNQKPNPP,RPTWPGTSA,LQNGGGSRS,RRRQPISVA,RCVIMRPTW,PTWPGTSAF,QPISVAPAG,RSSATLPGRR,ISVAPAGPPR,SVAPAGPPRR,RWLRRRRQPI,GSRSSATLPG,ATLPGRRRRR,RRRRRWLRRR,RRRRQPISVA,AGPPRRPNQK,IMRPTWPGTS,LPGRRRRRWL,RPNQKPNPPG,RPTWPGTSAF,WLRRRRQPIS,LRRRRQPISV,LQNGGGSRSS,RRQPISVAPA	STAD
ZFHX3	c.2330_2332delTGG	p.V777del	NNMQNLQNGGGEQVFSHTAGAAAAA[p.V777del]AAAAAAANISSSCGAPSPTKPKTKPTWR	HTAGAAAAAA	PAAD
ZFHX3	c.5677_5678delAG	p.R1893fs	LQPSQHPEKKNKLVIKEKEKESQRE[p.R1893fs]GQRRGGRGQHRSEGNTARCLEGQREERVGTRGWF*	TARCLEGQR,SEGNTARCL,EERVGTRGW,NTARCLEGQR,GQRRGGRGQH,GQHRSEGNTA,REERVGTRGW,EERVGTRGWF	STAD,UCEC
ZFHX4	c.1224_1225insG	p.L408fs	ASTSSSAEQPLGITQMPKAEVNLGG[p.L408fs]AV*	AEVNLGGAV	STAD
ZFHX4	c.2433G>T	p.L811F	MTSEKHMHNMMLLQQNMKQIQHNLH[p.L811F]FGLAPAEAELYQYYLAQNIGLTGMKL	IQHNLHFGL,NLHFGLAPA,KQIQHNLHF,MKQIQHNLHF,KQIQHNLHFG,IQHNLHFGLA,LHFGLAPAEA	LUAD
ZFHX4	c.4988C>A	p.T1663N	IAANVNSPGQGMLDSMSLAAVNSKD[p.T1663N]NHLDAKELNKKQTPDLISAQPAHHPP	NSKDNHLDAK	LUAD
ZFHX4	c.7533C>A	p.H2511Q	LPPQLLQYQCDQCTVAFPTLELWQE[p.H2511Q]QQHMHFLAAQNQFLHSPFLERPMDMP	QQHMHFLAA,ELWQEQQHM,WQEQQHMHF,QEQQHMHFL,LWQEQQHMHF,LELWQEQQHM,WQEQQHMHFL,EQQHMHFLAA,QQHMHFLAAQ,QEQQHMHFLA	LUAD
ZFP14	c.1156C>T	p.R386C	SIHTGEKPYECKECGKTFRLRQQLV[p.R386C]CHQRIHTREKPYECMECWKTFSSYSQ	RLRQQLVCH,QQLVCHQRI,RQQLVCHQRI,LVCHQRIHTR,QQLVCHQRIH	CRC
ZFP14	c.50A>T	p.Q17L	MAHGSVTFRDVAIDFS[p.Q17L]LEEWEFLDPAQRDLYRDVMWENYSNF	DFSLEEWEF,RDVAIDFSL,VAIDFSLEEW,IDFSLEEWEF,LEEWEFLDPA	LUAD
ZFP2	c.449G>T	p.R150I	TGEKPYKCNVCGKHFIERSSLTVHQ[p.R150I]IIHTGEKPYKCNECGKAFSQSMNLTV	RSSLTVHQI,SSLTVHQII,RSSLTVHQII	CRC
ZFP3	c.818G>T	p.R273I	TGEKPYECNECGKTFRVSSQLIQHQ[p.R273I]IIHTEERYHECNECGKAFKHSSGLIR	QIIHTEERY,HQIIHTEER,IQHQIIHTE,HQIIHTEERY	CRC
ZFP36L2	c.718G>A	p.D240N	IHNADERRPAPSGGASGDLRAFGTR[p.D240N]NALHLGFPREPRPKLHHSLSFSGFPS	RAFGTRNAL,GTRNALHLG,NALHLGFPR,TRNALHLGF,RAFGTRNALH,GTRNALHLGF,RNALHLGFPR,LRAFGTRNAL	LUSC
ZFP42	c.679G>A	p.V227I	RAALRKHLLIHGPRDHVCAECGKAF[p.V227I]IESSKLKRHFLVHTGEKPFRCTFEGC	AFIESSKLK,KAFIESSKL,KAFIESSKLK,CGKAFIESSK,AFIESSKLKR,GKAFIESSKL,IESSKLKRHF,AECGKAFIES	GBM
ZFP42	c.791C>T	p.T264M	HTGEKPFRCTFEGCGKRFSLDFNLR[p.T264M]MHVRIHTGEKRFVCPFQGCNRRFIQS	RMHVRIHTG,DFNLRMHVR,FSLDFNLRM,SLDFNLRMHV,RFSLDFNLRM,RMHVRIHTGE,NLRMHVRIHT	GBM
ZFP90	c.1772_1773insA	p.R591fs	IQHERTHTGEKPYECNECGRAFRKK[p.R591fs]NQPA*	AFRKKNQPA,RAFRKKNQPA	PRAD

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ZFPM1	c.1330_1331delGA	p.E444fs	GLAPTPSPGLDRKALAEATNGEARA[p.E444fs]ASGPEWRQQRAPGGPQEHQGGGGGGAGGGPHPGPRRAWAPGPVADAVAAQPRPGQGQGRAVQPHAGLQPGARRAGPGRGPVPSAVRVRARRGAPRLGDPGQDVRAGAQPAAAGRGRGRRRRADRALPRGPQGRYVLRVRDHLQQRQQLLRAQAPLLFRPPCARGRACRAQAQGAPRPGPRAPRPARRTRRAALVPGPRSARGGGWGRGHARGRRGRPGQRGQPEPG*	QLLRAQAPL,RLGDPGQDV,LLRAQAPLL,ALVPGPRSA,RAQAPLLFR,LLFRPPCAR,RAQAQGAPR,RAALVPGPR,RAWAPGPVA,QGRAVQPHA,GARRAGPGR,RAGPGRGPV,SAVRVRARR,AVRVRARRG,RVRARRGAP,RARRGAPRL,RAGAQPAAA,AGRGRGRRR,RGRGRRRRA,RGRRRRADR,RALPRGPQG,QGRYVLRVR,RVRDHLQQR,CARGRACRA,RGRACRAQA,RTRRAALVP,SARGGGWGR,RGHARGRRG,RGRRGRPGQ,SGPEWRQQR,HAGLQPGAR,LVPGPRSAR,HPGPRRAWA,GPRRAWAPG,APGPVADAV,RPGQGQGRA,RAVQPHAGL,VPSAVRVRA,RRRRADRAL,RPPCARGRA,APRPGPRAP,RPARRTRRA,ARRTRRAAL,RPGQRGQPE,HLQQRQQLL,ARAASGPEW,RRAWAPGPV,GQGRAVQPH,RQQLLRAQA,LRAQAPLLF,GPVADAVAA,LPRGPQGRY,QLLRAQAPLL,RVRARRGAPR,RSARGGGWGR,RYVLRVRDHL,AVRVRARRGA,RARRGAPRLG,AGRGRGRRRR,RGRRRRADRA,RRRADRALPR,RALPRGPQGR,RVRDHLQQRQ,LLRAQAPLLF,LFRPPCARGR,RGRACRAQAQ,RAPRPARRTR,RTRRAALVPG,RGHARGRRGR,RGRRGRPGQR,ALPRGPQGRY,HAGLQPGARR,HLQQRQQLLR,WAPGPVADAV,GPHPGPRRAW,RPGQGQGRAV,LPRGPQGRYV,RPPCARGRAC,RPGPRAPRPA,RPARRTRRAA,PARRTRRAAL,GPRSARGGGW,QQLLRAQAPL,RQQRAPGGPQ,RRAWAPGPVA,GQGRAVQPHA,RRAGPGRGPV,VRARRGAPRL,RDHLQQRQQL,LQQRQQLLRA,RQQLLRAQAP,AQAPLLFRPP,AQAQGAPRPG	ACC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ZFPM1	c.1335delT	p.P445fs	APTPSPGLDRKALAEATNGEARAEP[p.P445fs]WPRMEAAASPRRPPGASRWRRWRSRRRPPSWAPESLGPRPRRGRRRRAAPPRPGSRPSCPAPRRAPARCPASWAWPGPCSFRSTCSGPTRRPPPRRSWPRCPSWCTAGCSRARARAPAARRPGSSPGPPRALRASSARSPSATSTTTTCTSASTVQAAVRPRTRLPRAGPRRPPARPARPPASPPNPTRRARPRAPERARRGLGARPRPRTARAAGAARAARARVAPWTTRRTTPAARCARPATSASAATRPTPCTSGTTAPRATTRRRADRPRPRDPLGRPRPRPPLPPRLCARADAASSTSCTRPAPRPPRRPATPPRPSRRGPEAEAEAAPASPLRARPAPRPTAPST*	RMEAAASPR,RVAPWTTRR,STCSGPTRR,RALRASSAR,TVQAAVRPR,ATSASAATR,CTSGTTAPR,TTAPRATTR,TSCTRPAPR,WAWPGPCSF,RSWPRCPSW,ASRWRRWRS,RWRRWRSRR,RWRSRRRPP,RSRRRPPSW,RPRRGRRRR,RGRRRRAAP,RRRRAAPPR,RSTCSGPTR,PTRRPPPRR,RARARAPAA,RARAPAARR,ALRASSARS,RASSARSPS,ASSARSPSA,AVRPRTRLP,RPRTRLPRA,RTRLPRAGP,RLPRAGPRR,RAGPRRPPA,PARPARPPA,PTRRARPRA,RARPRAPER,RARRGLGAR,GARPRPRTA,RPRPRTARA,RTARAAGAA,TARAAGAAR,AAGAARAAR,AARAARARV,AARARVAPW,RARVAPWTT,TTRRTTPAA,RTTPAARCA,AARCARPAT,ATRPTPCTS,ATTRRRADR,RPRPPLPPR,CTRPAPRPP,RPAPRPPRR,PLRARPAPR,RARPAPRPT,EARAEPWPR,GASRWRRWR,ESLGPRPRR,SWCTAGCSR,CTAGCSRAR,QAAVRPRTR,TTPAARCAR,EAAPASPLR,TTCTSASTV,CTSASTVQA,SASTVQAAV,WTTRRTTPA,EPWPRMEAA,WPRMEAAAS,SPRRPPGAS,CPAPRRAPA,APARCPASW,APAARRPGS,RPARPPASP,APERARRGL,RPRTARAAG,RAAGAARAA,APWTTRRTT,RPATSASAA,RPTPCTSGT,RPRPRPPLP,APRPPRRPA,RPATPPRPS,RPSRRGPEA,RPAPRPTAP,APRPTAPST,ARAEPWPRM,RRAPARCPA,ARCPASWAW,AAVRPRTRL,AEAAPASPL,CPASWAWPG,AEAEAAPAS,AEPWPRMEA,LPPRLCARA,STVQAAVRPR,RTARAAGAAR,RTTPAARCAR,GTTAPRATTR,TTAPRATTRR,STSCTRPAPR,SWAWPGPCSF,RMEAAASPRR,AASPRRPPGA,ASRWRRWRSR,RWRRWRSRRR,RWRSRRRPPS,RSRRRPPSWA,RGRRRRAAPP,RAAPPRPGSR,GSRPSCPAPR,SFRSTCSGPT,RSTCSGPTRR,SGPTRRPPPR,RSWPRCPSWC,CSRARARAPA,RARARAPAAR,RARAPAARRP,AARRPGSSPG,RALRASSARS,RASSARSPSA,AVRPRTRLPR,RTRLPRAGPR,RAGPRRPPAR,RARPRAPERA,RPRAPERARR,RARRGLGARP,RGLGARPRPR,GARPRPRTAR,TARAAGAARA,RAAGAARAAR,AARAARARVA,AARARVAPWT,RARVAPWTTR,TTRRTTPAAR,AARCARPATS,CARPATSASA,ATRPTPCTSG,RATTRRRADR,TTRRRADRPR,RRRADRPRPR,RPRPRDPLGR,RPRDPLGRPR,LGRPRPRPPL,RPRPPLPPRL,CTRPAPRPPR,RARPAPRPTA,SWAPESLGPR,CPAPRRAPAR,WAWPGPCSFR,RPPPRRSWPR,TAGCSRARAR,SASTVQAAVR,DAASSTSCTR,SPLRARPAPR,CTAGCSRARA,TTTCTSASTV,CTSASTVQAA,TSASTVQAAV,WTTRRTTPAA,CTSGTTAPRA,EAEAAPASPL,EAAPASPLRA,WPRMEAAASP,RPPSWAPESL,RPRRGRRRRA,RPGSRPSCPA,RPSCPAPRRA,APARCPASWA,WPRCPSWCTA,APAARRPGSS,PPRALRASSA,RPRTRLPRAG,LPRAGPRRPP,GPRRPPARPA,RPARPPASPP,RPRPRTARAA,RPRTARAAGA,APWTTRRTTP,TPAARCARPA,RPATSASAAT,RPTPCTSGTT,APRATTRRRA,RPRPRPPLPP,RPPLPPRLCA,APRPPRRPAT,RPAPRPTAPS,WRSRRRPPSW,RAPARCPASW,RRSWPRCPSW,ARAAGAARAA,RAARARVAPW,EPWPRMEAAA,AEPWPRMEAA,AEAEAAPASP,PEAEAEAAPA	ACC
ZFR2	c.319T>A	p.Y107N	TTMATYQDSYSYGQSAAARSYEDRP[p.Y107N]NFQSAALQSGRMTAADSGQPGTQEAC	RSYEDRPNF,RPNFQSAAL,ARSYEDRPNF,YEDRPNFQSA	KIRC
ZFYVE1	c.797G>A	p.R266Q	GATVNLSQRTRLLLKVLAISDLVIY[p.R266Q]QTHADRLHNDLFKFLGDASEAYLKHF	IYQTHADRL,VIYQTHADR,YQTHADRLH,AISDLVIYQT,LVIYQTHADR,VIYQTHADRL	UCEC
ZFYVE9	c.3441G>C	p.M1147I	VVQGLVVDMEVRKTSIKIPSNRYNE[p.M1147I]IMKAMNKSNEHVLAGGACFNEKADSH	SNRYNEIMK,IPSNRYNEI,RYNEIMKAM,IPSNRYNEIM,NRYNEIMKAM	CESC
ZHX3	c.747C>A	p.N249K	EVREGDHSFINGAVPVSQASASSAK[p.N249K]KPHAANGPLIGTVPVLPAGIAQFLSL	QASASSAKK,ASSAKKPHA,KPHAANGPL,SQASASSAKK,KPHAANGPLI,KKPHAANGPL	STAD

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ZIC1	c.335C>A	p.A112E	GSYSSAAFNSTRDFLFRNRGFGDAA[p.A112E]EAASAQHSLFAASAGGFGGPHGHTDA	EAASAQHSL,AEAASAQHS,EAASAQHSLF,RGFGDAAEAA,AEAASAQHSL	LUAD
ZIC4	c.914C>T	p.S305L	GEKPFRCEFEGCERRFANSSDRKKH[p.S305L]LHVHTSDKPYTCKVRGCDKCYTHPSS	HLHVHTSDK,KKHLHVHTS,KHLHVHTSDK,LHVHTSDKPY	CRC
ZIM3	c.1054G>A	p.D352N	RIHTGEKPYKCSICEKAFSQKSNVI[p.D352N]NHEKIHTGKRAYECDLCGNTFIQKKN	KSNVINHEK,SQKSNVINH,KSNVINHEKI,INHEKIHTGK	CRC
ZIM3	c.1150delA	p.I384fs	GKRAYECDLCGNTFIQKKNLIQHKK[p.I384fs]SILGKSPMNVTDVEKPSFRSQTFIAIRKLIAERGPIDVVNVEKPSSGN*	ILGKSPMNV,FIAIRKLIA,KLIAERGPI,SQTFIAIRK,RSQTFIAIR,TFIAIRKLI,QHKKSILGK,KSILGKSPM,SFRSQTFIA,AIRKLIAER,KPSFRSQTF,NLIQHKKSI,LIQHKKSIL,FRSQTFIAI,AERGPIDVV,SILGKSPMNV,LIAERGPIDV,IQHKKSILGK,RSQTFIAIRK,SFRSQTFIAI,IAIRKLIAER,QTFIAIRKLI,KPSFRSQTFI,NLIQHKKSIL,KKSILGKSPM,SQTFIAIRKL,RKLIAERGPI,NVTDVEKPSF	STAD
ZKSCAN1	c.1621_1622delAG	p.R541fs	KCTKCGKAFTRSSTLTLHHRIHARE[p.R541fs]SL*	HRIHARESL,HHRIHARESL	UCEC
ZKSCAN3	c.598_599AA>GC	p.K200A	VGSQPLQDRVLQVPVLAHGGCCRED[p.K200A]AVVASRLTPESQGLLKVEDVALTLTPE	REDAVVASRL	TGCT
ZKSCAN4	c.956G>A	p.R319Q	IPTHAEAGEQEGRLQRKQKNAIGSR[p.R319Q]QHYCHECGKSFAQSSGLTKHRRIHTG	NAIGSRQHY,RQHYCHECG,RQHYCHECGK,KNAIGSRQHY	CRC
ZKSCAN5	c.39delC	p.D13fs	MIMTESREVIDLDP[p.D13fs]QLRLPRSRKTFS*	QLRLPRSRK,EVIDLDPQL,RLPRSRKTF,EVIDLDPQLR,DLDPQLRLPR,REVIDLDPQL,LRLPRSRKTF	STAD
ZMIZ1	c.3144delC	p.D1048fs	MPEPSLDLLPELTNPDELLSYLDPP[p.D1048fs]TCRAIVTMTSCLYLRTTEGHPVGAIPPHSASYPTYPTHFSTWEPVPSDRPAPEPRAVGRGALPRCSPLRTEG*	IVTMTSCLY,YLDPPTCRA,AIVTMTSCL,TMTSCLYLR,AVGRGALPR,SYPTYPTHF,TYPTHFSTW,VTMTSCLYL,AIPPHSASY,SYLDPPTCR,SASYPTYPT,RPAPEPRAV,EPRAVGRGA,GALPRCSPL,RAIVTMTSC,ASYPTYPTH,THFSTWEPV,HPVGAIPPH,YPTYPTHFS,EPVPSDRPA,TEGHPVGAI,YLDPPTCRAI,YLRTTEGHPV,VTMTSCLYLR,LSYLDPPTCR,AIVTMTSCLY,STWEPVPSDR,RAVGRGALPR,ASYPTYPTHF,PTYPTHFSTW,RAIVTMTSCL,RTTEGHPVGA,RGALPRCSPL,GALPRCSPLR,GAIPPHSASY,HSASYPTYPT,YPTYPTHFST,RPAPEPRAVG,EPRAVGRGAL,PPHSASYPTY,WEPVPSDRPA	PRAD
ZMIZ2	c.457_501delGTGGCTGCTGCGGCAGCCACTGCCACCGCCACAGCCACAGCCACC	p.VAAAAATATATATATT153del	LGLPSHAARPSTDFTQAAAAAAVAA[p.VAAAAATATATATAT153del]LQEKQSQELSQYGAMGAGQSFNSQFLQHGGPRGPSVPAGMNPTGIGGVMGPSGLSPLAMNPTRAAGMTPL	AAAAAVAAL,AAVAALQEK,AAAVAALQEK,AAAAAAVAAL	PAAD
ZMYM4	c.1033delA	p.K345fs	SSGMNKMLPSVPATAVRVSCSGCKK[p.K345fs]SSRRGKLLIRGKGLLSYSAPHCASLDIQFHLPAHRLLSPRKLVQVAQKTF*	LLIRGKGLL,YSAPHCASL,KSSRRGKLL,SSRRGKLLI,RGKLLIRGK,RGKGLLSYS,AHRLLSPRK,RLLSPRKLV,IRGKGLLSY,CSGCKKSSR,IQFHLPAHR,PAHRLLSPR,APHCASLDI,LPAHRLLSP,SPRKLVQVA,LVQVAQKTF,GLLSYSAPH,HCASLDIQF,ASLDIQFHL,LDIQFHLPA,FHLPAHRLL,SLDIQFHLPA,IQFHLPAHRL,LLSPRKLVQV,LLSYSAPHCA,SYSAPHCASL,GCKKSSRRGK,KSSRRGKLLI,SSRRGKLLIR,RGKGLLSYSA,PAHRLLSPRK,LIRGKGLLSY,DIQFHLPAHR,LPAHRLLSPR,KLVQVAQKTF,KKSSRRGKLL,LDIQFHLPAH	STAD
ZMYM4	c.1100C>T	p.T367I	SGCKKILQKGQTAYQRKGSTQLFCS[p.T367I]ILCLTGYTVPPARPPPPLTKKTCSSC	CSILCLTGY,QLFCSILCL,ILCLTGYTV,GSTQLFCSI,TQLFCSILCL,QLFCSILCLT,SILCLTGYTV,KGSTQLFCSI,GSTQLFCSIL,FCSILCLTGY	TGCT
ZMYM4	c.4337G>A	p.R1446Q	TYLRFFPPLQKQESEPDKLTVGKRK[p.R1446Q]QNEDDEVPVGVEMAENTDNPLRCPVR	KQNEDDEVPV	CRC
ZNF117	c.554G>T	p.R185I	TGEKPYKCKECGKAFNQTSHLIRHK[p.R185I]IIHTEEKPYKCEECGKAFNQSSTLTT	QTSHLIRHKI	CRC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ZNF124	c.1015delA	p.T339fs	GEKPYECQKCGKAFSRASTLWKHKK[p.T339fs]LILEKSPINVKKCKGFNHYSFCQKHEQSHT*	KLILEKSPI,ILEKSPINV,KHKKLILEK,KGFNHYSFC,FNHYSFCQK,KKCKGFNHY,LWKHKKLIL,CKGFNHYSF,LILEKSPINV,ILEKSPINVK,GFNHYSFCQK,KSPINVKKCK,TLWKHKKLIL,KKLILEKSPI,VKKCKGFNHY,KCKGFNHYSF	STAD
ZNF154	c.1223C>A	p.T408N	RPYECSECGKSFTQNSGLIKHRRVH[p.T408N]NGEKPYECTECGKSFSHNSSLIKHQR	HRRVHNGEK,KHRRVHNGEK,RRVHNGEKPY	LUAD
ZNF16	c.1354C>T	p.R452W	HTGEKPYKCSDCGKAFSQSSSLIQH[p.R452W]WRIHTGEKPHVCNVCGKAFSYSSVLR	QSSSLIQHW,QSSSLIQHWR,SQSSSLIQHW	CESC
ZNF167	c.2048G>T	p.R683I	TGEKPYECNECGKVFSYSSSLMVHQ[p.R683I]ITHTGEKPYKCNDCGKAFSDSSQLIV	LMVHQITHT,SLMVHQITH,SLMVHQITHT,YSSSLMVHQI	CRC
ZNF174	c.1057C>A	p.P353T	CDDCGKSFTWNSELKRHKRVHTGER[p.P353T]TYTCGECGNCFGRQSTLKLHQRIHTG	RVHTGERTY,RVHTGERTYT,KRVHTGERTY	TGCT
ZNF180	c.1202G>T	p.R401I	TGEKPYECSECGKSFSRSSHLVSHQ[p.R401I]ITHTGEKPYRCNQCGKSFSQSYVLVV	HLVSHQITH,HLVSHQITHT,ITHTGEKPYR,RSSHLVSHQI	CRC
ZNF180	c.1706G>T	p.R569I	TGEKPYECSECGKSFNRSSHLVMHQ[p.R569I]IIHTGEKPYECNQCGKSFSQSYVLVV	SHLVMHQII,RSSHLVMHQI,SSHLVMHQII	UCEC
ZNF180	c.1874G>T	p.R625I	TGEKPYECSQCGKSFRQSSCLTQHQ[p.R625I]ITHTGEKPFECNQCGKTFSLSARLIV	ITHTGEKPF,TQHQITHTG,QITHTGEKPF	UCEC
ZNF19	c.1046G>T	p.R349I	TGEKPYSCKVCGQAFNFHTKLTRHQ[p.R349I]IIHSEEKPFDCVDCGKAFSAQEQLKR	HTKLTRHQI,HQIIHSEEK,TKLTRHQII,IIHSEEKPF,HTKLTRHQII,RHQIIHSEEK,QIIHSEEKPF	CRC
ZNF195	c.176G>A	p.R59Q	LENYRNLFSVGLTVCKPGLITCLEQ[p.R59Q]QKEPWNVKRQEAADGHPEMGFHHATQ	QQKEPWNVK,QQKEPWNVKR,LEQQKEPWNV	UCEC
ZNF205	c.1150C>T	p.R384C	TGEKPYTCPACRKSFSHHSTLIQHQ[p.R384C]CIHTGEKPYVCDRCAKRFTRRSDLVT	HQCIHTGEK,IQHQCIHTG,CIHTGEKPYV,QCIHTGEKPY	CRC
ZNF223	c.67G>T	p.G23W	MTMSKEAVTFKDVAVVFTEEEL[p.G23W]WLLDLAQRKLYRDVMLENFRNLLSVG	FTEEELWLL,EELWLLDLA,EEELWLLDL,VVFTEEELW,WLLDLAQRKL,VFTEEELWLL,ELWLLDLAQR,TEEELWLLDL,EELWLLDLAQ,EEELWLLDLA	LUAD
ZNF23	c.366delT	p.F122fs	NIKKEKSNTIDGTVKDETSPVEECF[p.F122fs]LVKVQTHISVIPSLESSPLGVQDWGNPSALIQNS*	FLVKVQTHI,KVQTHISVI,SLESSPLGV,IPSLESSPL,VKVQTHISV,THISVIPSL,VQDWGNPSA,QDWGNPSAL,VEECFLVKV,SPVEECFLV,VQDWGNPSAL,VIPSLESSPL,CFLVKVQTHI,LVKVQTHISV,QTHISVIPSL,ETSPVEECFL,TSPVEECFLV,VKVQTHISVI	STAD
ZNF236	c.4229C>T	p.T1410M	NITLQIDPSILQQTLQQGNLLAQQL[p.T1410M]MGEPGLAPQNSSLQTSDSTVPASVVI	QLMGEPGLA,AQQLMGEPG,QQLMGEPGL,LMGEPGLAP,AQQLMGEPGL	STAD
ZNF236	c.4439C>T	p.S1480L	GPLSEQDSVLTTNSSGTQDLTQVMT[p.S1480L]LQGLVSPSGGPHEITLTINNSSLSQV	TQVMTLQGL,QVMTLQGLV,TQVMTLQGLV,MTLQGLVSPS,TQDLTQVMTL	CRC
ZNF248	c.1703G>T	p.R568I	TGEKPYECNACGKTFSQRSVLTKHQ[p.R568I]IIHTRVKALSTS*	HQIIHTRVK,SVLTKHQII,IIHTRVKAL,RSVLTKHQI,LTKHQIIHTR,KHQIIHTRVK,RSVLTKHQII,HQIIHTRVKA	CRC
ZNF254	c.537G>T	p.K179N	FQCDKYLKVFYKFLNSNRPKIRHTE[p.K179N]NKSFKCKKRVKLFCMLSHKTQHKSIY	KIRHTENKS,RHTENKSFK,IRHTENKSF,HTENKSFKCK,RPKIRHTENK,KIRHTENKSF	UCEC
ZNF257	c.1175G>T	p.R392I	TKEKPYKCEECGKAFNRSSHLTKHK[p.R392I]IIHTREKAYKCDEYCKAFNWSSALTT	IIHTREKAY,IIHTREKAYK,KIIHTREKAY,RSSHLTKHKI	UCEC
ZNF259	c.521G>T	p.R174I	LITRAISGLEQDQPARRANKDATAE[p.R174I]IIDEFIVKLKELKQVASPFTLIIDDP	IIDEFIVKL,ATAEIIDEF,AEIIDEFIV,ATAEIIDEFI,IIDEFIVKLK,EIIDEFIVKL,RANKDATAEI	CRC
ZNF263	c.1529G>T	p.R510I	TGEKPYKCPECGEIFAHSSNLLRHQ[p.R510I]IIHTGERPYKCPECGKSFSRSSHLVI	SNLLRHQII	UCEC

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ZNF266	c.1031G>A	p.R344Q	TAKDPFECKICGKSFRNSSCLSDHF[p.R344Q]QIHTGIKPYKCKDCGKAFTQNSDLTK	HFQIHTGIK,FQIHTGIKP,CLSDHFQIHT,QIHTGIKPYK,FQIHTGIKPY	CRC
ZNF266	c.1535G>A	p.R512Q	TGEKPYKCKQCGKSFSYSNSFQLHE[p.R512Q]QTHTGEKPYECKECGKAFSSSSSFRN	FQLHEQTHT,EQTHTGEKPY,FQLHEQTHTG	CRC
ZNF268	c.2700_2702delCTT	p.F901del	NSQLIVHQRTHSGEKPYGCNECGKT[p.F901del]SQKSILSAHQRTHTGEKPCKCTECGKAF	KTSQKSILS,KTSQKSILSA	BRCA
ZNF273	c.957T>A	p.N319K	DCGKVFSVFSVLTKHKIIHTGTKPY[p.N319K]KCEECGKGFSIFSTLTKHKIIHTGEK	IIHTGTKPYK	KIRC
ZNF280B	c.1087G>A	p.E363K	SWENHTTCQHCHRQFPTPFQLQCHI[p.E363K]KNVHTAQEPSTVCKICELSFETDQVL	QLQCHIKNV,LQCHIKNVH,CHIKNVHTA,FQLQCHIKNV	CRC
ZNF280B	c.1198G>A	p.E400K	CKICELSFETDQVLLQHMKDHHKPG[p.E400K]KMPYVCQVCHYRSSVFADVETHFRTC	HHKPGKMPY,GKMPYVCQV,HMKDHHKPGK,MKDHHKPGKM,GKMPYVCQVC	GBM
ZNF283	c.1175G>A	p.R392Q	KIHTGKKPYECKICGKAFCWGYQLT[p.R392Q]QHQIFHTGEKPYECKECGKAFNCGSS	GYQLTQHQI,YQLTQHQIF,TQHQIFHTG,GYQLTQHQIF,WGYQLTQHQI,YQLTQHQIFH	CRC
ZNF32	c.185C>T	p.S62L	EATGSSSWDIQNSFRREKLEQKSPD[p.S62L]LKTLQEDSPGVRQRVYECQECGKSFR	KLEQKSPDLK	CRC
ZNF322	c.318G>T	p.K106N	VQSSDLTSHQRIHNYEKPYKCSKCE[p.K106N]NSFWHHLVLSGHQRTHAGKKFYTCDI	ENSFWHHLV,NSFWHHLVL,KCSKCENSF,CENSFWHHL,YKCSKCENSF,CENSFWHHLV	LUAD
ZNF333	c.1661G>A	p.R554Q	TGEKLYECATCGQVLSRLSTLKSHM[p.R554Q]QTHTGEKPYVCQECGRAFSEPSSLRK	HMQTHTGEK,KSHMQTHTG,SHMQTHTGEK,MQTHTGEKPY,QTHTGEKPYV	UCEC
ZNF334	c.1278delA	p.K426fs	ECKECGKTFFCQSALTAHQRIHTGE[p.K426fs]NPMNVVNVRKPSFVNLPSMCIEEVIQERSPMNAVNVENFYVRNQPSLHIR*	AVNVENFYV,FVNLPSMCI,FYVRNQPSL,RIHTGENPM,HTGENPMNV,EVIQERSPM,NAVNVENFY,VVNVRKPSF,VRKPSFVNL,PSFVNLPSM,QERSPMNAV,MNAVNVENF,VRNQPSLHI,LPSMCIEEV,NLPSMCIEEV,VVNVRKPSFV,AVNVENFYVR,SFVNLPSMCI,NVRKPSFVNL,YVRNQPSLHI,MNAVNVENFY,HTGENPMNVV,NAVNVENFYV,KPSFVNLPSM,NFYVRNQPSL,QRIHTGENPM,GENPMNVVNV,NVVNVRKPSF,EEVIQERSPM,IQERSPMNAV,PMNAVNVENF,LPSMCIEEVI	STAD
ZNF354B	c.1205G>T	p.R402I	TGEKPFKCSECGRAFSQSASLIQHE[p.R402I]IIHTGEKPYRCNECGKGFTSISRLNR	SASLIQHEI,IQHEIIHTG,SLIQHEIIHT,QSASLIQHEI	UCEC
ZNF354B	c.1825G>A	p.D609N	GKLFSQRSSLTNHYKIHIEEDSLKA[p.D609N]NLHV*	EEDSLKANL,IEEDSLKANL	UCEC
ZNF358	c.389delC	p.T130fs	DPNSDTLSPGDPKVDPISSGLTATP[p.T130fs]RSWPPAPRCSPPPPARPGPSPARIAGEPSAAAPG*	RIAGEPSAA,SSGLTATPR,ATPRSWPPA,RPGPSPARI,GLTATPRSW,ARIAGEPSA,RIAGEPSAAA,ISSGLTATPR,PARPGPSPAR,TPRSWPPAPR,APRCSPPPPA,RPGPSPARIA,SGLTATPRSW,ARIAGEPSAA	STAD
ZNF382	c.558T>A	p.H186Q	FGDSTGWEKSLLNTKHEKIHPAVNL[p.H186Q]QKQTERVLSGKQELIQHQKVQAPEQP	NLQKQTERV,LQKQTERVL,KIHPAVNLQK	CLL
ZNF385D	c.677C>G	p.T226S	KRLLYCSLCKVAVNSASQLEAHNSG[p.T226S]SKHKTMLEARNGSGTIKAFPRAGVKG	SKHKTMLEA,GSKHKTMLEA,SQLEAHNSGS,LEAHNSGSKH	LUAD
ZNF43	c.752delA	p.N251fs	GEKPYTCEECGKVFNWSSRLTTHKK[p.N251fs]IILDTNSTNVKNVAKLLTSPQSLLPIR*	ILDTNSTNV,KLLTSPQSL,LLTSPQSLL,IILDTNSTNV,KLLTSPQSLL,ILDTNSTNVK,SSRLTTHKKI,DTNSTNVKNV,LTSPQSLLPI,RLTTHKKIIL,AKLLTSPQSL	STAD
ZNF43	c.838C>T	p.R280C	YKLYKCEECGKAFNKSSILTTHKII[p.R280C]CTGEKFYKCKECAKAFNQSSNLTEHK	IICTGEKFY,KIICTGEKF,IICTGEKFYK,CTGEKFYKCK,THKIICTGEK,KIICTGEKFY,HKIICTGEKF	UCEC
ZNF434	c.916C>T	p.R306C	QNSQIYRAMAEGLWEQGFLRTPEQC[p.R306C]CTKFKSLQLSYRKVRRGRVPEPCIFY	RTPEQCCTK,CTKFKSLQL,TPEQCCTKF,RTPEQCCTKF	CRC

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ZNF439	c.785G>T	p.R262I	TGEKPYECKQCGKSFSYSATHRIHE[p.R262I]ITHIGEKPYECQECGKAFHSPRSCHR	ITHIGEKPY,HRIHEITHI,YSATHRIHEI	CRC
ZNF442	c.926G>A	p.R309Q	ERTHTGEKPYKCKRCGRAFSVSSSL[p.R309Q]QIHERTHTGEKPYECKQCGKAFHHLG	SSSLQIHER,FSVSSSLQI,VSSSLQIHER,RAFSVSSSLQ,FSVSSSLQIH	UCEC
ZNF443	c.902G>T	p.R301I	TGEKPYKCKQCSKAFPDSSSCLIHE[p.R301I]ITHTGEKPYTCKQCGKAFSVSGSLQR	CLIHEITHT,SSSCLIHEI,DSSSCLIHEI,EITHTGEKPY	CRC
ZNF445	c.2044C>A	p.L682M	ECREGFRQSPDCSQPQGAPAVEKTF[p.L682M]MCQQCGKTFTRKKTLVDHQRIHTGEK	TFMCQQCGK,KTFMCQQCG,APAVEKTFM,MCQQCGKTF,KTFMCQQCGK,FMCQQCGKTF	CRC
ZNF454	c.1127G>T	p.R376I	TGEKPFECNECGKAFRVNSSLTEHQ[p.R376I]IIHTGEKPYKCNECGKAFRDNSSFAR	SSLTEHQII,TEHQIIHTG,SLTEHQIIHT	UCEC
ZNF454	c.569G>T	p.S190I	SDQSQGFQPSKNAFECSECGKVFSK[p.S190I]ISTLNKHQKIHNEKNANQKIHIKEKR	KVFSKISTL,FSKISTLNK,ISTLNKHQK,VFSKISTLNK,KISTLNKHQK,GKVFSKISTL,SECGKVFSKI	LUAD
ZNF462	c.1948T>A	p.S650T	FCDNLPKFEGQPSSLPLENETDSHP[p.S650T]TSSNTVKKSQTSILGLSSKNNFVAKA	PTSSNTVKK,DSHPTSSNTV,LENETDSHPT	KIRC
ZNF470	c.1922G>T	p.R641I	TGEKPYECNVCGKAFSHRKSLTLHQ[p.R641I]IIHTGEKPYECKECSKAFSQVAHLTL	KSLTLHQII,RKSLTLHQI,KSLTLHQIIH,RKSLTLHQII	CRC
ZNF471	c.845G>T	p.R282I	TGEKLFECKECRKAFKQSEHLIQHQ[p.R282I]IIHTGEKPYKCKECRKAFRQPAHLAQ	SEHLIQHQI,SEHLIQHQII	CRC
ZNF48	c.704G>A	p.R235H	HQRTHTGEKPYKCGICGKGFGDSSA[p.R235H]HIKHQRTHRGEQPPRPVVPRRQPSRA	SSAHIKHQR,HIKHQRTHR,KGFGDSSAH,AHIKHQRTH,DSSAHIKHQR,KGFGDSSAHI	LUSC
ZNF48	c.739delC	p.P247fs	ICGKGFGDSSARIKHQRTHRGEQPP[p.P247fs]DQWCPDGSHLGQPRQLPRDRRPRTSHISALIAARGLCSAAAS*	RTSHISALI,HISALIAAR,RPRTSHISA,AARGLCSAA,LPRDRRPRT,SHISALIAA,LIAARGLCSA,RQLPRDRRPR,RTSHISALIA,TSHISALIAA,AARGLCSAAA,HLGQPRQLPR,SHISALIAAR,LPRDRRPRTS,RPRTSHISAL,DQWCPDGSHL,IAARGLCSAA	STAD
ZNF484	c.412C>T	p.R138C	SILEELWKDDEHTRKCGENQNKPLS[p.R138C]CVVFINKKTLANDSIFEYKDIGEIVH	NQNKPLSCV,LSCVVFINK,NKPLSCVVF,KPLSCVVFI,NQNKPLSCVV,PLSCVVFINK,LSCVVFINKK,QNKPLSCVVF	CRC
ZNF485	c.1121G>T	p.R374I	SGNKPYQCRDCGKAFTKSSTLTGHQ[p.R374I]IIHTGEKPYHCKKCGKAFRHSSGLVE	KSSTLTGHQI	UCEC
ZNF488	c.617G>A	p.R206Q	PAGESADALGELSGLLNTTDLACWG[p.R206Q]QLSTPKLLVGDLWNLQALPQNAPLCS	QLSTPKLLV,GQLSTPKLL,CWGQLSTPKL,GQLSTPKLLV	UCEC
ZNF491	c.1028G>A	p.R343Q	ERTHTGEKPDGCKQCGKAFRSAKYI[p.R343Q]QIHGRTHTGEKPYECKQCGKAFHCVS	SAKYIQIHG,RSAKYIQIH,FRSAKYIQI,IQIHGRTHT,AFRSAKYIQI,SAKYIQIHGR,IQIHGRTHTG	CRC
ZNF492	c.1175C>A	p.P392H	CEVCSKAFSRFSHLTTHKRIHTGEK[p.P392H]HYKCEECGKAFNLSSQLTTHKIIHTG	RIHTGEKHY,RIHTGEKHYK,KRIHTGEKHY	LUAD
ZNF514	c.242T>G	p.V81G	PGEEGTTNSFLKARPRDLMTFEDVA[p.V81G]GEFSQWEWGQLNPAQKDLYREVMLEN	MTFEDVAGE,MTFEDVAGEF,VAGEFSQWEW	KIRP
ZNF519	c.1291C>T	p.H431Y	CKECGKAFNRASHLTQHQRIHTGEK[p.H431Y]YFKCKECGKAFNRGSHLTRHQRIHTG	YFKCKECGK,QRIHTGEKY,RIHTGEKYF,RIHTGEKYFK,HTGEKYFKCK,KYFKCKECGK,HQRIHTGEKY,QRIHTGEKYF	KIRC
ZNF521	c.1918G>T	p.G640C	TSLKMMQAVGGAPARPTGEYICNQC[p.G640C]CAKYTSLDSFQTHLKTHLDTVLPKLT	ICNQCCAKY,GEYICNQCC,YICNQCCAKY,CAKYTSLDSF,NQCCAKYTSL,GEYICNQCCA	LUAD
ZNF521	c.809C>A	p.P270H	TQKCSQCEEGFDFPEDLQKHIAECH[p.P270H]HECSPNEDRAALQCVYCHELFVEETS	LQKHIAECHH	LUAD

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ZNF528	c.836G>A	p.R279Q	SNLSQHQRIHTGEKPYKCHECDKVF[p.R279Q]QSSSKLAQHQRIHTGEKPYKCHECDK	KVFQSSSKL,FQSSSKLAQ,KVFQSSSKLA,FQSSSKLAQH,HECDKVFQSS	CRC
ZNF534	c.1749T>A	p.N583K	TGEKPYSCNECGKVFSRNSHLARHR[p.N583K]KIHTGEKPHSCNECGKVFSRNSHLAR	RKIHTGEKPH	GBM
ZNF536	c.1987G>T	p.G663W	RVFRTYHQVVVHSRVHKRDRKGEED[p.G663W]WLHVGLDERRGSGSDQESQSVSRSTT	EEDWLHVGL,DWLHVGLDER,GEEDWLHVGL	LUAD
ZNF536	c.556G>T	p.G186C	PYCDHRAAQKGNLKIHLRTHKLGNL[p.G186C]CKGRGRVREENRLLHELEERAILRDK	RTHKLGNLC,RTHKLGNLCK,NLCKGRGRVR	LUAD
ZNF559	c.850G>A	p.E284K	PSSSHLRECVRIYGGERPYTHKEYV[p.E284K]KTFSHSTALFVHMQTQDGEKFYECKA	KTFSHSTAL,THKEYVKTF,KEYVKTFSH,VKTFSHSTA,YVKTFSHSTA,KTFSHSTALF,YTHKEYVKTF,RPYTHKEYVK,VKTFSHSTAL,KEYVKTFSHS	UCEC
ZNF563	c.622delT	p.W208fs	NLRRHMVVQGGNRPYKCKLCGKAFF[p.W208fs]GPVYYVCMKELTLERNRMNVSSVLKPFLFTVPIEDMRECTLGRNRMNVSSVLKPCLIPVPI*	AFFGPVYYV,VLKPFLFTV,KAFFGPVYY,CMKELTLER,FFGPVYYVC,VYYVCMKEL,SSVLKPFLF,CGKAFFGPV,GKAFFGPVY,FTVPIEDMR,KPFLFTVPI,NVSSVLKPF,KAFFGPVYYV,SVLKPFLFTV,FLFTVPIEDM,FFGPVYYVCM,YYVCMKELTL,VSSVLKPFLF,CGKAFFGPVY,GKAFFGPVYY,NVSSVLKPFL,MNVSSVLKPF,KELTLERNRM,LKPFLFTVPI	GBM
ZNF563	c.78G>T	p.K26N	MDAVAFEDVAVNFTQEEWALLGPSQ[p.K26N]NNLYRYVMQETIRNLDCIRMIWEEQN	PSQNNLYRY,LLGPSQNNL,SQNNLYRYV,LGPSQNNLY,QNNLYRYVM,ALLGPSQNNL,LLGPSQNNLY,SQNNLYRYVM,GPSQNNLYRY	CRC
ZNF573	c.1049G>T	p.R350I	TGKKPYECKECGKGYTTASYFLLHQ[p.R350I]IIHKGGKPYECKECKKTFTLYRNLTR	FLLHQIIHK,SYFLLHQII,HQIIHKGGK,IIHKGGKPY,ASYFLLHQI,QIIHKGGKPY,TASYFLLHQI,ASYFLLHQII	CRC
ZNF578	c.931G>A	p.G311S	PYKCNECGKSFSYKSSLTCHRRCHT[p.G311S]SEKPYKCNECGKSFSYKSSLTCHHRC	CHRRCHTSEK	CLL
ZNF583	c.1031G>T	p.R344I	TGERPFECIECGKAFSNGSFLAQHQ[p.R344I]IIHTGEKPYVCNVCGKAFSHRGYLIV	SFLAQHQII,GSFLAQHQI,FLAQHQIIH,FLAQHQIIHT,GSFLAQHQII	CRC
ZNF585A	c.1473G>T	p.E491D	YMCNKCGKAFTNRSNLITHQKTHTG[p.E491D]DKSYICSKCGKAFTQRSDLITHQRIH	HQKTHTGDK,KTHTGDKSY,KTHTGDKSYI,QKTHTGDKSY	CRC
ZNF585A	c.1912G>A	p.E638K	KSFTSKSQLLVHQPVHTGEKPYVCA[p.E638K]KCGKAFSGRSNLSKHQKTHTGEKPYI	VCAKCGKAF,KPYVCAKCGK,YVCAKCGKAF,GEKPYVCAKC	CRC
ZNF592	c.1498C>A	p.P500T	PGSQTGKKQQSTALQASTLAPANLL[p.P500T]TKAVHLANLNLVPHSVAASVTAKSSV	LLTKAVHLA,NLLTKAVHL,TKAVHLANL,NLLTKAVHLA,TLAPANLLTK,LTKAVHLANL,APANLLTKAV	TGCT
ZNF592	c.970A>C	p.K324Q	VTKEDQPGHTKDLSGPTKESSKGSP[p.K324Q]QMPKSPKSPRSPLEATRKSIKPSDSP	SSKGSPQMPK,QMPKSPKSPR,KESSKGSPQM	TGCT
ZNF594	c.860G>T	p.R287I	TGEKPYECYDCGQMFSQSSHLVPHQ[p.R287I]IIHTGEKPLKCNECEKAFRQHSHLTE	HLVPHQIIH,IIHTGEKPLK,SSHLVPHQII	UCEC
ZNF598	c.74A>G	p.E25G	MAAAGGAEGRRADMEAEAAAAPER[p.E25G]GGGSCVLCCGDLEATALGRCDHPVCY	AEAAAAPERG	ACC,KIRP
ZNF608	c.1393delG	p.A465fs	SAAAAPGSEASFTESRGLQNKNRGG[p.A465fs]PMGKGGGAASMPADEGHPQIVLLRISKPALPPPTKGKTSLQWSWT*	QIVLLRISK,KNRGGPMGK,LLRISKPAL,KPALPPPTK,GPMGKGGGA,PPTKGKTSL,GKGGGAASM,TKGKTSLQW,GKTSLQWSW,DEGHPQIVL,MPADEGHPQ,HPQIVLLRI,VLLRISKPAL,ISKPALPPPT,EGHPQIVLLR,MPADEGHPQI,GPMGKGGGAA,MGKGGGAASM,LQNKNRGGPM,KGKTSLQWSW,DEGHPQIVLL	STAD
ZNF611	c.1169G>T	p.R390I	TGEKPYKCEECDKVFSRKSTIETHK[p.R390I]IIHTGEKPYRCKVCDTAFTWHSQLAR	RKSTIETHKI	UCEC

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ZNF625	c.704G>A	p.R235Q	TGEKPYECSECGKAFHSSTCLHAHK[p.R235Q]KTHTGEKPYECKQCGKAFVSFNSVRY	STCLHAHKK,SSTCLHAHKK,AHKKTHTGEK	CRC
ZNF626	c.1418A>G	p.K473R	TGEKFYKCEECGKAFKCSSNLTTHK[p.K473R]RIHTGERPYKCEECGKAFNQSSILTT	CSSNLTTHKR	LUSC
ZNF638	c.1198G>A	p.D400N	SQADIPIRSPFGIVKASWLPKFSHA[p.D400N]NAQKMKRLPTPSMMNDYYAASPRIFP	KFSHANAQK,HANAQKMKR,FSHANAQKM,WLPKFSHANA,FSHANAQKMK,KFSHANAQKM	LIHC
ZNF644	c.61G>T	p.G21W	MRSFLQQDVNKTKSRLNVLN[p.G21W]WLANNMDDLKINTDITGAKEELLDDN	RLNVLNWLA,WLANNMDDL,VLNWLANNM,KSRLNVLNW,SRLNVLNWL,WLANNMDDLK,KSRLNVLNWL,NVLNWLANNM,TKSRLNVLNW	LUAD
ZNF645	c.460C>T	p.R154C	SLQAHIKRRHKRARKQVTSASLEKV[p.R154C]CPHIAPPQTEISDIPKRLQDRDHLSY	SLEKVCPHI,LEKVCPHIA	UCEC
ZNF649	c.593G>T	p.R198I	NIEKAHECTDCGKAFLKKSQLTEHK[p.R198I]IIHTGKKPHVCSLCGKAFYKKYRLTE	SQLTEHKII,IIHTGKKPHV,KKSQLTEHKI,SQLTEHKIIH	UCEC
ZNF652	c.981G>T	p.K327N	VSCNKSFKKLWSLHEHIKIVHGYAE[p.K327N]NKFSCEICEKKFYTMAHVRKHMVAHT	IVHGYAENK,AENKFSCEI,KIVHGYAENK,IVHGYAENKF,AENKFSCEIC	CRC
ZNF674	c.1214G>T	p.R405I	TKENIYECSKCGKSFRGKSHLSVHQ[p.R405I]IIHTGEKPYECSICGKTFSGKSHLSV	SHLSVHQII,KSHLSVHQI,KSHLSVHQII,GKSHLSVHQI	UCEC
ZNF675	c.659G>T	p.R220I	TKVNFCKCEECEKAVNQSSKLTKHK[p.R220I]IIYTCEKLYKCQECDRTFNQFSNLTE	KLTKHKIIY,IIYTCEKLY,SSKLTKHKI,IIYTCEKLYK,SSKLTKHKII,KHKIIYTCEK,KIIYTCEKLY,SKLTKHKIIY,HKIIYTCEKL	UCEC
ZNF676	c.127C>A	p.P43T	PDLIIFLEQGKEPWNMKRHEMVEEP[p.P43T]TVICSHFSQEFWPEQGIEDSFQKMIL	HEMVEEPTV,EPTVICSHF,HEMVEEPTVI,EEPTVICSHF	LUSC
ZNF677	c.1352G>T	p.R451I	PGEKPHKCNVCGRAFIQSSSLVEHQ[p.R451I]IIHTGEKPYKCNKCDKAFIKRSHLWG	SSLVEHQII,VEHQIIHTG,SLVEHQIIHT	CRC
ZNF677	c.392G>C	p.R131T	FDSLWDYDVKNYKGMPLTCNKNLTH[p.R131T]TKDQQHNKSSIHFSLKQSVSIRDSAH	HTKDQQHNK,CNKNLTHTK	CESC
ZNF680	c.1501C>T	p.R501W	TLANHKRIHAREKPYKCEECGKAFN[p.R501W]WSSHLTRHKKIHTGEKLYKPEKCDNN	FNWSSHLTR,WSSHLTRHKK,AFNWSSHLTR,FNWSSHLTRH	TGCT
ZNF687	c.2573T>G	p.F858C	DTVFTHKPLLSSHFDQHLLPQRVSV[p.F858C]CKCPSCPLLFAQKRTMLEHLKNTHQS	LLPQRVSVC,CKCPSCPLLF	KIRC
ZNF699	c.122G>T	p.R41I	QDSVVFEDVAVDFTQEEWALLDLAQ[p.R41I]INLYRDVMLENFQNLASLGYPLHTPH	LLDLAQINL,DLAQINLYR,LDLAQINLY,AQINLYRDV,QINLYRDVM,WALLDLAQI,LLDLAQINLY,ALLDLAQINL,AQINLYRDVM	CRC
ZNF7	c.1010G>T	p.R337I	TGEKPYRCEECGKAFGQSSSLIHHQ[p.R337I]IIHTGERPYGCRECGKAFSQQSQLVR	SSSLIHHQI,SSLIHHQII,SLIHHQIIHT,QSSSLIHHQI	CRC
ZNF70	c.731G>T	p.R244I	TGKRPYECRECGKDFSRSSSLRKHE[p.R244I]IIHTGERPYQCKECGKSFNQSSGLSQ	SLRKHEIIH,RSSSLRKHEI,EIIHTGERPY	CRC
ZNF700	c.1946C>G	p.S649C	NLRKHGRTHTGEKPYECKQCGKAFR[p.S649C]CASNLQMHERTHTGEKPYECKECEKA	KAFRCASNL,FRCASNLQM,CASNLQMHER,AFRCASNLQM,GKAFRCASNL	CLL
ZNF700	c.1954A>C	p.N652H	KHGRTHTGEKPYECKQCGKAFRSAS[p.N652H]HLQMHERTHTGEKPYECKECEKAFCK	ASHLQMHER,AFRSASHLQ,RSASHLQMH,FRSASHLQM,SASHLQMHER,AFRSASHLQM	CLL
ZNF700	c.1961A>G	p.Q654R	GRTHTGEKPYECKQCGKAFRSASNL[p.Q654R]RMHERTHTGEKPYECKECEKAFCKFS	ASNLRMHER,AFRSASNLR,FRSASNLRM,KAFRSASNLR,SASNLRMHER,AFRSASNLRM	CLL
ZNF705A	c.892G>A	p.D298N	GNKIIHTGEKPHACLLCGKAFSLSS[p.D298N]NLR*	AFSLSSNLR,KAFSLSSNLR	CLL

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ZNF706	c.23T>A	p.I8N	MARGQQK[p.I8N]NQSQQKNAKKQAGQKKKQGHDQKAAA	QQKNQSQQK,KNQSQQKNAK	BLCA
ZNF709	c.1403G>T	p.R468I	TGEKPYECKQCGKAFSCSSSFRMHE[p.R468I]IIHTGEKPYECKQCGKAFSFSSSFRM	RMHEIIHTG,SFRMHEIIH,SSFRMHEII,SFRMHEIIHT,CSSSFRMHEI,SSFRMHEIIH	UCEC
ZNF711	c.1231G>T	p.V411L	ICKKHFTGRSSLIVHQIVHTGEKPY[p.V411L]LCGECGKAFSQSAYLIEHQRIHTGEK	YLCGECGKA,LCGECGKAF,YLCGECGKAF,GEKPYLCGEC	LUAD
ZNF711	c.2211delA	p.L737fs	SVHTKDQPLKCKRCKRGFRQQNELK[p.L737fs]N!*	RQQNELKNI	STAD
ZNF716	c.788A>T	p.H263L	EKPYRCEECGKAFSWSASLTKHKRI[p.H263L]LTGEKPYTCEERGKVFSRSTLTNYKR	LTKHKRILT,SLTKHKRIL,KHKRILTGEK	LUAD
ZNF717	c.1781A>T	p.N594I	GKSFHCKSFLTIHQRTHAGKKPYEC[p.N594I]IECEKTFINKLNLGIHKRTHTGERPY	YECIECEKTF	MM
ZNF717	c.2530T>A	p.C844S	CRKTFSQKSKLFVHHRTHTGEKPFR[p.C844S]SNECRKTFSQKSGLSIHQRTHTGEKP	RSNECRKTF,KPFRSNECRK,RSNECRKTFS,FRSNECRKTF	MM
ZNF717	c.945G>C	p.W315C	KPSISKSDLMLQCKMPTEEKPYACN[p.W315C]CCEKLFSYKSSLIIHQRIHTGEKPYG	KPYACNCCEK,YACNCCEKLF	MM
ZNF750	c.287_288delCT	p.S96fs	LDPKQTNQPDATAKPASSKSVANGL[p.S96fs]CLRLEASAQLCQGRHQGKPGAASPGNPQVPGTEASPPQGITLQEPSSGSRPRCPACSGRRSSAFCICSSRRAQTQGARQRRGARDTGFTQPHCQGRVFPHQVGLPHSWLPLESRLTFPSTRVST*	RVFPHQVGL,GLPHSWLPL,RLTFPSTRV,SVANGLCLR,SAFCICSSR,HSWLPLESR,SWLPLESRL,GSRPRCPAC,SGRRSSAFC,GARQRRGAR,AFCICSSRR,QTQGARQRR,FTQPHCQGR,RPRCPACSG,QPHCQGRVF,FPHQVGLPH,LPLESRLTF,CSGRRSSAF,KSVANGLCL,LRLEASAQL,HQGKPGAAS,RRGARDTGF,HQVGLPHSW,TEASPPQGI,LESRLTFPS,SVANGLCLRL,GLCLRLEASA,CLRLEASAQL,FTQPHCQGRV,KSVANGLCLR,SSAFCICSSR,SAFCICSSRR,WLPLESRLTF,SSGSRPRCPA,GSRPRCPACS,RPRCPACSGR,SGRRSSAFCI,SSRRAQTQGA,RAQTQGARQR,RVFPHQVGLP,EASAQLCQGR,TLQEPSSGSR,ESRLTFPSTR,EASPPQGITL,SKSVANGLCL,HQGKPGAASP,ACSGRRSSAF,RQRRGARDTG,QRRGARDTGF,TQPHCQGRVF,GRVFPHQVGL,HQVGLPHSWL,VGLPHSWLPL,HSWLPLESRL,LESRLTFPST	HNSC
ZNF765	c.761C>T	p.S254L	LLRKHQLIHLGEKQYKCDICGKVFN[p.S254L]LKRYVARHRRCHTGEKPYKCNECGKT	KVFNLKRYV,FNLKRYVAR,GKVFNLKRY,KVFNLKRYVA,CGKVFNLKRY,DICGKVFNLK,VFNLKRYVAR,NLKRYVARHR	UCEC
ZNF774	c.1268G>A	p.R423Q	TGERPYKCGECGKSFNQSSHFITHQ[p.R423Q]QIHLGDRPYRCPECGKTFNQRSHFLT	FITHQQIHL,QIHLGDRPY,SHFITHQQI,SSHFITHQQI,QQIHLGDRPY,QIHLGDRPYR,SHFITHQQIH	CRC
ZNF780A	c.1397G>A	p.R466Q	SNEKPFVCRECEMAFRYHCQLIEHS[p.R466Q]QIHTGDKPFECQDCGKAFNRGSSLVQ	HSQIHTGDK,QIHTGDKPF,CQLIEHSQI,QLIEHSQIH,QLIEHSQIHT,SQIHTGDKPF,CQLIEHSQIH	UCEC
ZNF782	c.1450G>T	p.G484W	FNYKSILIVHQRTHTGEKPFECNEC[p.G484W]WKSFSHMSGLRNHRRTHTGERPYKCD	NECWKSFSH,KPFECNECW,CWKSFSHMSG,FECNECWKSF,NECWKSFSHM,WKSFSHMSGL	LUAD
ZNF782	c.434G>T	p.C145F	KPHNRDINIFRARMMPCKCDIAGSA[p.C145F]FQGLSLMAPHCQYSKEKAHERNVCDK	SAFQGLSLM,KCDIAGSAF,IAGSAFQGL,GSAFQGLSL,FQGLSLMAP,DIAGSAFQGL,CKCDIAGSAF,AGSAFQGLSL,GSAFQGLSLM,SAFQGLSLMA,FQGLSLMAPH	TGCT
ZNF782	c.740A>C	p.K247T	KAFLEKAALVTSNSTHPKGKSYNFN[p.K247T]TFGENKYDKSTFIIPQNMNPEKSHYE	KGKSYNFNT,KSYNFNTFG,GKSYNFNTF,FNTFGENKY,NTFGENKYDK,KGKSYNFNTF	CRC
ZNF799	c.121T>G	p.W41G	IRVDAGHKPHEYQEYGEKRNTRKQF[p.W41G]GKTFSYCHSFQTHKISHTGHKPYDCK	KQFGKTFSY,RNTRKQFGK,TRKQFGKTF,KRNTRKQFGK,RKQFGKTFSY,KQFGKTFSYC,GKTFSYCHSF	BLCA
ZNF799	c.127A>G	p.T43A	VDAGHKPHEYQEYGEKRNTRKQFWK[p.T43A]AFSYCHSFQTHKISHTGHKPYDCKEC	KQFWKAFSY,KAFSYCHSF,NTRKQFWKA,TRKQFWKAF,KAFSYCHSFQ,RKQFWKAFSY,NTRKQFWKAF,WKAFSYCHSF,KQFWKAFSYC	BLCA

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ZNF799	c.1357T>C	p.C453R	KAYRISSSLRRHETTHTGEKPYKCK[p.C453R]RGKAFIDFYSFQNHKTTHAGEKPYEC	KPYKCKRGK,KCKRGKAFI,RGKAFIDFY,YKCKRGKAF,KRGKAFIDF,RGKAFIDFYS,KRGKAFIDFY,KPYKCKRGKA,CKRGKAFIDF	TGCT
ZNF804B	c.1930_1931CC>AG	p.P6445	NDIDEDLSFPSYISRFKKHKLIPCS[p.P6445]SHLEFEDERQFNCKSSPCTVGGHSDHG	KLIPCSSHL,IPCSSHLEF,HKLIPCSSH,LIPCSSHLEF,HKLIPCSSHL	TGCT
ZNF814	c.959_960GG>AA	p.G320E	KHECGECGKSFSKYVSFSNHQRVHT[p.G320E]EKRPYECGECGKSFSKYASFSNHQRVH	HQRVHTEKR,RVHTEKRPY,RVHTEKRPYE,QRVHTEKRPY	KIRP
ZNF814	c.968C>A	p.P323H	CGECGKSFSKYVSFSNHQRVHTGKR[p.P323H]HYECGECGKSFSKYASFSNHQRVHTE	RVHTGKRHY,RVHTGKRHYE,HQRVHTGKRH,QRVHTGKRHY	KIRP
ZNF814	c.970T>C	p.Y324H	GECGKSFSKYVSFSNHQRVHTGKRP[p.Y324H]HECGECGKSFSKYASFSNHQRVHTEK	RVHTGKRPH,RVHTGKRPHE	TGCT
ZNF823	c.1640G>T	p.R547I	SGEKPYECKECGKAFSWLTCLLRHE[p.R547I]IIHTGEKPYECLQCGKAFTRSRFLRG	WLTCLLRHEI	UCEC
ZNF831	c.146_147insC	p.A49fs	PGGQASPHLTLGPVLLPPEQGLAPP[p.A49fs]HCVPEGPAHPTVPHGASRGPPAPRPASDGQPRWGQRALHTQPCAAA*	ALHTQPCAA,HGASRGPPA,ASRGPPAPR,RALHTQPCA,DGQPRWGQR,QPRWGQRAL,ALHTQPCAAA,RALHTQPCAA,VPEGPAHPTV,GQPRWGQRAL,GQRALHTQPC,RPASDGQPRW	STAD
ZNF831	c.1849C>A	p.Q617K	AREAMAGKGRAGGRKCGQRRLKMFS[p.Q617K]KEKWQVYGDETFKRIYQKMKASPHGG	RLKMFSKEK,MFSKEKWQV,QRRLKMFSK,FSKEKWQVY,LKMFSKEKW,KMFSKEKWQV,GQRRLKMFSK,RRLKMFSKEK,MFSKEKWQVY,RLKMFSKEKW	LUAD
ZNF831	c.2847G>T	p.E949D	QAPRVLSALADNAFSPKYLLRLPQA[p.E949D]DTPLPLPIPWGPRHSQDSLCSSGWPE	RLPQADTPL,PQADTPLPL,LPQADTPLPL,LRLPQADTPL	CRC
ZNF831	c.4178G>A	p.R1393Q	EGDCRQTLGTLSLGTSSRIVREMDK[p.R1393Q]QTVKDISPSAGEHGDCTTHSTAATSG	REMDKQTVK,QTVKDISPSA	SKCM
ZNF836	c.1712T>A	p.I571N	RIHTGEQPYKCNVCGKVFNYSGNLS[p.I571N]NHKRIHTGEKPFQCNECGTVFRNYSC	YSGNLSNHK,FNYSGNLSNH	CLL
ZNF836	c.1822A>C	p.K608Q	QCNECGTVFRNYSCLARHLRIHTGQ[p.K608Q]QPYKCNVCGKVFNDSGNLSNHKRIHT	RIHTGQQPY,GQQPYKCNV,RIHTGQQPYK,LRIHTGQQPY	CLL
ZNF836	c.1889G>T	p.R630I	TGQKPYKCNVCGKVFNDSGNLSNHK[p.R630I]IIHTGEKPFQCNECGKVFSYYSCLAR	KIIHTGEKPF	UCEC
ZNF836	c.2561G>T	p.R854I	TGDKPYKCNECGKAFIERSKLVYHQ[p.R854I]INHTGEKPYKCIECGKAFGRFSCLNK	KLVYHQINH,HQINHTGEK,RSKLVYHQI,INHTGEKPY,KLVYHQINHT,RSKLVYHQIN,INHTGEKPYK,QINHTGEKPY	UCEC
ZNF841	c.2270G>T	p.R757I	TGEMPYKCIECGKVFNSTTTLARHR[p.R757I]IIHTGEKPYKCNECGKVFRYRSGLAR	TTTLARHRI	UCEC
ZNF845	c.1269G>A	p.M423I	LTRHRRLHTGEKPYKCNDCGKTFSQ[p.M423I]ISSLVYHRRLHTGEKPYKCEECDEAF	FSQISSLVY,KTFSQISSL,QISSLVYHR,ISSLVYHRR,TFSQISSLV,SQISSLVYH,KTFSQISSLV,SQISSLVYHR,QISSLVYHRR,TFSQISSLVY,GKTFSQISSL	CLL
ZNF845	c.2774G>A	p.R925H	AHLACHHRIHTGEKPYKCNECGKTF[p.R925H]HHNSVLVIHKTIHTGEKPYKCNECGK	KTFHHNSVL,GKTFHHNSV,FHHNSVLVI,KTFHHNSVLV,TFHHNSVLVI,CGKTFHHNSV,HHNSVLVIHK,GKTFHHNSVL,FHHNSVLVIH	PRAD
ZNF880	c.1217A>G	p.Q406R	ECKECGKVFRHKFCLTNHHRMHTGE[p.Q406R]RPYKCNECGKAFRDCSGLTAHLIHT	HHRMHTGER,HRMHTGERPY	KIRC
ZP3	c.1085_1086insG	p.V362fs	VMSQWSRSASRNRRHVTEEADVTVG[p.V362fs]ATDLPGQEG*	EEADVTVGA,EEADVTVGAT,TEEADVTVGA	KIRC
ZPBP	c.460C>T	p.R154C	NFEESMSGIYTCFLEYKPTVEEIVK[p.R154C]CLQLKYAIYAYREPHYYYQFTARYHA	IVKCLQLKY,CLQLKYAIY,EEIVKCLQL,CLQLKYAIYA,IVKCLQLKYA,KCLQLKYAIY,VEEIVKCLQL	GBM

gene	cDNA Change	Protein Change	Mutation_Context_Sequence	Peptides	Exemplary Diseases
ZSCAN18	c.674_675insC	p.P225fs	SSILSDGVYERHMDPLLLPGELASP[p.P225fs]QPGPWSWGDPGTF*	WSWGDPGTF,LASPQPGPW,SPQPGPWSW,GELASPQPG	STAD
ZSWIM2	c.641C>A	p.S214Y	TSMLKCPLCRKEFAPLKLILEEFKN[p.S214Y]YSKLVAAAEKERLDKHLGIPCNNCKQ	KNYSKLVAA,LILEEFKNY,FKNYSKLVA,EEFKNYSKL,ILEEFKNYSK,YSKLVAAAEK,KNYSKLVAAA,KLILEEFKNY,FKNYSKLVAA,LEEFKNYSKL,EEFKNYSKLV	LUAD
ZSWIM4	c.1219G>A	p.E407K	GPSLQPTMAPAPELLQKGSTCITNT[p.E407K]KGWVGHPLDPIGCLCRALLEACRLEE	GSTCITNTK,TKGWVGHPL,KGSTCITNTK,NTKGWVGHPL	CESC
ZSWIM6	c.1829delA	p.Q610fs	LAIAIVNTLRRQQQKQLEMFRTQKK[p.Q610fs]SYPIKT*	RTQKKSYPI,TQKKSYPIK,MFRTQKKSY,RTQKKSYPIK,EMFRTQKKSY,FRTQKKSYPI	KICH
ZZEF1	c.89T>C	p.V30A	PSHSSEDEAAAAGGEGWGPHQDWAA[p.V30A]ASGTTPGPGVAAPALPPAAALLEPAR	GPHQDWAAA,WAAASGTTPG	ACC
ZZZ3	c.14G>A	p.R5Q	MAAS[p.R5Q]QSTRVTRSTVGLNGLDESFCGRTLRN	MAASQSTRV,ASQSTRVTR,SQSTRVTRST	HNSC
ZZZ3	c.485G>A	p.R162Q	IKSDKESVEQRSTVVDNDADFQGTK[p.R162Q]QACRCLILDDCEKREIKKVNVSEEGP	KQACRCLIL,GTKQACRCLI,DFQGTKQACR,TKQACRCLIL	LUSC

Example 5

[00418] Recurrent Mutations for Cancer Subtype Specific Immunogenic compositions. The Cancer Genome Atlas (TCGA) contains comprehensive large-scale genome sequencing data from tumor samples to catalogue genetic mutations responsible for cancer. Tumor-specific neoantigenic peptides for use in an immunogenic composition can be selected based on a number of criteria. The first criteria is based on gene expression. The fraction of patients (per tumor type) who express the gene at >10 transcripts per million was determined. Estimates assume a random assortment of HLA type vs. mutation status of each gene vs. gene expression (per tumor type). National yearly incidence was used to quantify the population that could be treated with each peptide. Peptides were ranked by expected population. The results of the analysis is shown in Table 9.

Table 9

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
RBM14 p.AAAAAAA286del (uc009yrj.2)	VTAASTSYY	19282	Pancreatic Cancer	HLA.A01.01 HLA.A03.01 HLA.A11.01 HLA.A26.01 HLA.A26.02 HLA.A26.03 HLA.A29.02 HLA.A68.01 HLA.A80.01 HLA.B15.01 HLA.B15.03 HLA.B15.17 HLA.B58.01
HRAS p.G12D (uc001lpv.2) KRAS p.G12D (uc001rgp.1) NRAS p.G12D (uc009wgu.2)	KLVVVGADGV	16466	Colorectal Cancer Pancreatic Cancer Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
NRAS p.G12V (uc009wgu.2) KRAS p.G12V (uc001rgp.1)	KLVVVGAVGV	13995	Colorectal Cancer Lung Adenocarcinoma Pancreatic Cancer Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
NRAS p.G12V (uc009wgu.2) KRAS p.G12V (uc001rgp.1)	VVGAVGVGK	11278	Colorectal Cancer Lung Adenocarcinoma Pancreatic Cancer Uterine Corpus Endometrial Carcinoma	HLA.A03.01 HLA.A11.01
KRAS p.G12C (uc001rgp.1) NRAS p.G12C (uc009wgu.2) HRAS p.G12C (uc001lpv.2)	KLVVVGACGV	7538	Colorectal Cancer Lung Adenocarcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
KRAS p.G12C (uc001rgp.1) NRAS p.G12C (uc009wgu.2) HRAS p.G12C (uc001lpv.2)	VVGACGVGK	5751	Colorectal Cancer Lung Adenocarcinoma	HLA.A03.01 HLA.A11.01
NRAS p.G12V (uc009wgu.2) KRAS p.G12V (uc001rgp.1)	VVVGAVGVGK	5535	Colorectal Cancer Lung Adenocarcinoma Pancreatic Cancer	HLA.A11.01 HLA.A68.01
TP53 p.R248W (uc002gim.2)	GMNWRPILTI	5006	Breast Cancer Colorectal Cancer Pancreatic Cancer	HLA.A02.01 HLA.A02.03
PIK3CA p.E542K (uc003fjk.2)	AISTRDPLSK	4852	Bladder Cancer Breast Cancer	HLA.A03.01 HLA.A11.01

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
FRG1B p.I10T (uc010ztl.1)	KLSDSRTAL	4782	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.B07.02 HLA.B15.03
GATA3 p.H435fs (uc001ijz.2)	KIMFATLQR	4535	Breast Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01 HLA.A68.01
HRAS p.G12D (uc001lpv.2) KRAS p.G12D (uc001rgp.1) NRAS p.G12D (uc009wgu.2)	VVGADGVGK	4530	Colorectal Cancer Pancreatic Cancer	HLA.A11.01
NRAS p.Q61R (uc009wgu.2) KRAS p.Q61R (uc001rgp.1) HRAS p.Q61R (uc001lpv.2)	ILDTAGREEY	4433	Melanoma Thyroid Cancer	HLA.A01.01
NRAS p.Q61K (uc009wgu.2) HRAS p.Q61K (uc001lpv.2) KRAS p.Q61K (uc001rgp.1)	ILDTAGKEEY	4203	Colorectal Cancer Melanoma	HLA.A01.01
GATA3 p.H435fs (uc001ijz.2)	MLTGPPARV	4113	Breast Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01
RBM47 p.495_502AAAAAAAA>A (uc003gvc.2)	AAAAVIPTV	4035	Pancreatic Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01 HLA.B15.17
RBM47 p.495_502AAAAAAAA>A (uc003gvc.2)	AAAAAVIPTV	3864	Pancreatic Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06 HLA.A68.02
GATA3 p.H435fs (uc001ijz.2)	YMFLKAESK	3832	Breast Cancer	HLA.A03.01 HLA.A11.01 HLA.A68.01
GATA3 p.H435fs (uc001ijz.2)	SMLTGPPARV	3718	Breast Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
GATA3 p.H435fs (uc001ijz.2)	YMFLKAESKI	3718	Breast Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
GATA3 p.H435fs (uc001ijz.2)	TLQRSSLWCL	3621	Breast Cancer	HLA.A02.01 HLA.A02.03

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
AP3S1 p.K41fs (uc003krl.2)	LVSEMKMFV	3603	Pancreatic Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01
PIK3CA p.H1047R (uc003fjk.2)	FMKQMNDAR	3582	Breast Cancer	HLA.A31.01 HLA.A33.01 HLA.A68.01
KRAS p.Q61L (uc001rgp.1) NRAS p.Q61L (uc009wgu.2) HRAS p.Q61L (uc001lpv.2)	LLDILDTAGL	3563	Colorectal Cancer Lung Adenocarcinoma Melanoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
GATA3 p.H435fs (uc001ijz.2)	FATLQRSSL	3551	Breast Cancer	HLA.B07.02 HLA.B08.01 HLA.B39.01
AP3S1 p.K41fs (uc003krl.2)	HLVSEMKMFV	3524	Pancreatic Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06 HLA.A68.02
FRG1B p.L52S (uc010ztl.1)	ALSASNSCFI	3502	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
FRG1B p.L52S (uc010ztl.1)	FQNGKMALSA	3502	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
RBM14 p.AAAAAAA286del (uc009yrj.2)	AVTAASTSY	3477	Pancreatic Cancer	HLA.A26.02 HLA.A29.02 HLA.B15.01 HLA.B15.03 HLA.B15.17
KRAS p.G12R (uc001rgp.1) NRAS p.G12R (uc009wgu.2)	VVGARGVGK	3176	Pancreatic Cancer	HLA.A03.01 HLA.A11.01
PIK3CA p.E545K (uc003fjk.2)	SEITKQEKDF	3090	Breast Cancer	HLA.B44.02
FRG1B p.A53T (uc010ztl.1)	LLTSNSCFI	3016	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
FRG1B p.A53T (uc010ztl.1)	ALLTSNSCFI	2959	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
FRG1B p.I10T (uc010ztl.1)	RTALKSGYGK	2787	Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A68.01

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
FRG1B p.A50P (uc010ztl.1)	FQNGKMPLL	2781	Prostate Cancer Melanoma	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.B15.03 HLA.B39.01
PIK3CA p.H1047L (uc003fjk.2)	FMKQMNDAL	2610	Breast Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.B08.01 HLA.B15.01 HLA.B15.03
KRAS p.Q61L (uc001rgp.1) NRAS p.Q61L (uc009wgu.2) HRAS p.Q61L (uc001lpv.2)	ILDTAGLEEY	2555	Colorectal Cancer Lung Adenocarcinoma Melanoma	HLA.A01.01
FRG1B p.A11T (uc010ztl.1)	ITLKSGYGK	2523	Prostate Cancer Melanoma	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01 HLA.A68.01
ANAPC1 p.T537A (uc002thi.2)	VSAPKPLSK	2521	Pancreatic Cancer Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01
GATA3 p.H435fs (uc001ijz.2)	FLKAESKIM	2496	Breast Cancer	HLA.A02.03 HLA.B08.01 HLA.B15.01 HLA.B15.03
FRG1B p.A50P (uc010ztl.1)	FQNGKMPLLA	2486	Prostate Cancer Melanoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
PIK3CA p.H1047R (uc003fjk.2)	YFMKQMNDAR	2478	Breast Cancer	HLA.A33.01 HLA.A68.01
GATA3 p.S408fs (uc001ijz.2)	AIQPVLWTT	2371	Breast Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.06
RBM14 p.AAAAAAA286del (uc009yrj.2)	AVTAASTSYY	2363	Pancreatic Cancer	HLA.A11.01
FRG1B p.I10T (uc010ztl.1)	KLSDSRTALK	2356	Prostate Cancer	HLA.A03.01 HLA.A11.01
FRG1B p.A11T (uc010ztl.1)	KLSDSRITL	2328	Prostate Cancer Melanoma	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.B15.03
ANAPC1 p.T537A (uc002thi.2)	GVSAPKPLSK	2260	Pancreatic Cancer Prostate Cancer	HLA.A03.01 HLA.A11.01

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
TP53 p.Y220C (uc002gim.2)	VVVPCEPPEV	2200	Breast Cancer	HLA.A02.01 HLA.A02.06
TP53 p.R248W (uc002gim.2)	SSCMGGMNWR	2135	Colorectal Cancer	HLA.A11.01 HLA.A68.01
KRAS p.G12R (uc001rgp.1) NRAS p.G12R (uc009wgu.2)	GARGVGKSAL	2075	Pancreatic Cancer	HLA.B07.02
RAC1 p.P29S (uc003spx.2)	TTNAFSGEY	2042	Melanoma	HLA.A01.01 HLA.A11.01 HLA.A25.01 HLA.A26.01 HLA.A26.02 HLA.A26.03 HLA.A29.02 HLA.A68.01 HLA.A80.01 HLA.B15.01 HLA.B15.03 HLA.B15.17
GATA3 p.H435fs (uc001ijz.2)	GPPARVPAV	2039	Breast Cancer	HLA.B07.02
GATA3 p.H435fs (uc001ijz.2)	KPKRDGYMF	2039	Breast Cancer	HLA.B07.02
GATA3 p.H435fs (uc001ijz.2)	KPKRDGYMFL	2039	Breast Cancer	HLA.B07.02
KRAS p.G12A (uc001rgp.1) HRAS p.G12A (uc001lpv.2) NRAS p.G12A (uc009wgu.2)	KLVVVGAAGV	2034	Colorectal Cancer Lung Adenocarcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
SPOP p.F133L (uc002ipg.2)	FVQGKDWGL	2002	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01
GATA3 p.H435fs (uc001ijz.2)	CSMLTGPPAR	1995	Breast Cancer	HLA.A11.01 HLA.A33.01 HLA.A68.01
WASH3P p.G175S (uc002cdi.2) WASH2P p.G175S (uc002tkh.2)	SIRQAGGISK	1978	Prostate Cancer Melanoma	HLA.A03.01 HLA.A11.01
ARFGAP3 p.N299fs (uc003bdd.2)	EIAEVLFHI	1959	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A26.02 HLA.A26.03 HLA.A68.02 HLA.A69.01
GATA3 p.S408fs (uc001ijz.2)	ALQPLQPHA	1906	Breast Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
ARFGAP3 p.N299fs (uc003bdd.2)	SAWDLEIAEV	1892	Prostate Cancer	HLA.A02.01 HLA.A02.06 HLA.A68.02
FRG1B p.I59V (uc010ztl.1) FRG1 p.I157V (uc003izs.2)	LLASNSCFV	1824	Prostate Cancer Melanoma	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01
ARFGAP3 p.N299fs (uc003bdd.2)	KMLTQTDSA	1818	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
PTH2 p.L22del (uc002pnn.1) CTSA p.L37del (uc002xqh.2) AGPAT2 p.17_18insL (uc004cii.1)	LLLLLLLLV	1807	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
TP53 p.R248Q (uc002gim.2)	SSCMGGMNQR	1795	Bladder Cancer	HLA.A11.01 HLA.A68.01
KRAS p.G12C (uc001rgp.1) NRAS p.G12C (uc009wgu.2) HRAS p.G12C (uc001lpv.2)	VVVGACGVGK	1785	Colorectal Cancer Lung Adenocarcinoma	HLA.A11.01
PIK3CA p.N345K (uc003fjk.2)	KILCATYVK	1776	Breast Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01
FRG1B p.A11T (uc010ztl.1)	KLSDSRITLK	1749	Prostate Cancer	HLA.A03.01 HLA.A11.01
FRG1B p.A11T (uc010ztl.1)	RITLKSGYGK	1749	Prostate Cancer	HLA.A03.01 HLA.A11.01
GATA3 p.H435fs (uc001ijz.2)	AVPFDLHFCR	1749	Breast Cancer	HLA.A11.01 HLA.A68.01
PIK3CA p.E542K (uc003fjk.2)	ISTRDPLSK	1746	Breast Cancer	HLA.A11.01
TP53 p.G245S (uc002gim.2)	SSCMGSMNR	1732	Colorectal Cancer	HLA.A11.01 HLA.A31.01 HLA.A68.01
GATA3 p.H435fs (uc001ijz.2)	AESKIMFATL	1731	Breast Cancer	HLA.B40.01 HLA.B44.02
AKT1 p.E17K (uc001ypk.2) AKT2 p.E17K (uc002onf.2)	WLHKRGKYIK	1717	Breast Cancer	HLA.A03.01
PIK3CA p.N345K (uc003fjk.2)	ILCATYVKV	1715	Breast Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
FRG1B p.I59V (uc010ztl.1) FRG1 p.I157V (uc003izs.2)	ALLASNSCFV	1698	Prostate Cancer Melanoma	HLA.A02.01 HLA.A02.03 HLA.A02.06

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
FRG1B p.L52S (uc010ztl.1)	SASNSCFIR	1685	Prostate Cancer	HLA.A11.01 HLA.A31.01 HLA.A33.01 HLA.A68.01
PIK3CA p.N345K (uc003fjk.2)	KILCATYVKV	1679	Breast Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
AP3S1 p.K41fs (uc003krl.2)	ETFHLVSEM	1635	Pancreatic Cancer	HLA.A25.01 HLA.A26.01 HLA.A26.02 HLA.A26.03 HLA.A68.01 HLA.A68.02 HLA.A69.01 HLA.B15.17
PIK3CA p.N345K (uc003fjk.2)	KVNIRDIDK	1620	Breast Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01
KRAS p.G12A (uc001rgp.1) HRAS p.G12A (uc001ipv.2) NRAS p.G12A (uc009wgu.2)	VVGAAGVGK	1613	Colorectal Cancer Lung Adenocarcinoma	HLA.A03.01 HLA.A11.01
CDC27 p.D555E (uc002ile.3)	TLWHLQKEV	1577	Colorectal Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
GATA3 p.H435fs (uc001ijz.2)	ESKIMFATL	1573	Breast Cancer	HLA.A68.02 HLA.B08.01
TP53 p.P75fs (uc002gim.2)	KPTRAATVSV	1536	Colorectal Cancer	HLA.B07.02
CTNNB1 p.T41A (uc010hia.1)	ATAPSLSGK	1536	Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01 HLA.A68.01
CDC27 p.D555E (uc002ile.3)	HLQKEVALSV	1530	Colorectal Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
PIK3CA p.H1047L (uc003fjk.2)	ALHGGWTTK	1513	Breast Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01
UBC p.R73L (uc002gyy.3)	RLRGGMQIFV	1474	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
PEX1 p.I370fs (uc003uly.2)	KMRRPVCYK	1456	Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
TP53 p.C238Y (uc002gim.2)	TTIHYNYMY	1454	Colorectal Cancer	HLA.A01.01 HLA.A11.01 HLA.A25.01 HLA.A26.01 HLA.A26.02 HLA.A26.03 HLA.A29.02 HLA.A68.01 HLA.A80.01 HLA.B15.17
ANAPC1 p.T537A (uc002thi.2)	APKPLSKLL	1449	Pancreatic Cancer	HLA.B07.02
FRG1B p.A53T (uc010ztl.1)	LTSNSCFIR	1447	Prostate Cancer	HLA.A11.01 HLA.A31.01 HLA.A33.01 HLA.A68.01
RNF43 p.G659fs (uc002iwf.2)	TQLARFFPI	1442	Colorectal Cancer Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A23.01 HLA.A30.01 HLA.A31.01 HLA.A69.01 HLA.B08.01 HLA.B08.03 HLA.B15.03 HLA.B38.01 HLA.B39.01 HLA.B40.01 HLA.B40.02
AP3S1 p.K41fs (uc003krl.2)	ETFHLVSEMK	1440	Pancreatic Cancer	HLA.A11.01 HLA.A68.01
PIK3CA p.H1047R (uc003fjk.2)	ARHGGWTTK	1426	Breast Cancer	HLA.B27.05
PIK3CA p.H1047R (uc003fjk.2)	ARHGGWTTKM	1426	Breast Cancer	HLA.B27.05
GATA3 p.S408fs (uc001ijz.2)	QPVLWTTPPL	1421	Breast Cancer	HLA.B07.02
FRG1B p.A50P (uc010ztl.1)	MPLLASNSCF	1374	Prostate Cancer	HLA.B07.02
WASH3P p.G175S (uc002cdi.2) WASH2P p.G175S (uc002tkh.2)	ISKAKLRSM	1337	Prostate Cancer Melanoma	HLA.A30.01 HLA.B08.01 HLA.B15.17
HRAS p.G13R (uc001lpv.2) NRAS p.G13R (uc009wgu.2)	VVGAGRVGK	1324	Colorectal Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
ACADS p.R330H (uc001tza.3)	RLLTWHAAM	1321	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.B08.01 HLA.B15.01 HLA.B15.03 HLA.B15.17
HRAS p.G12D (uc001lpv.2) KRAS p.G12D (uc001rgp.1) NRAS p.G12D (uc009wgu.2)	LVVVGADGV	1284	Pancreatic Cancer	HLA.A02.06 HLA.A68.02 HLA.A69.01
KRAS p.G12S (uc001rgp.1) HRAS p.G12S (uc001lpv.2) NRAS p.G12S (uc009wgu.2)	KLVVVGASGV	1278	Colorectal Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
TP53 p.A159V (uc002gim.2)	RVRVMAIYK	1271	Bladder Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01
HLA-A p.Q78R (uc003nol.2)	IEREGPEYW	1271	Prostate Cancer	HLA.B44.02 HLA.B44.03
GATA3 p.H435fs (uc001ijz.2)	LQRSSLWCL	1248	Breast Cancer	HLA.A02.06 HLA.B15.01 HLA.B15.03
ZMIZ2 p.VAAAAATATATATAT153del (uc003tlr.2)	ALQEKQSQEL	1226	Pancreatic Cancer	HLA.A02.01 HLA.A02.03
GIGYF2 p.Q1005del (uc002vtj.3)	KLSGWGNVSK	1204	Pancreatic Cancer	HLA.A03.01 HLA.A11.01
FRG1B p.L52S (uc010ztl.1)	LSASNSCFIR	1190	Prostate Cancer	HLA.A11.01 HLA.A68.01
AKT1 p.E17K (uc001ypk.2) AKT2 p.E17K (uc002onf.2)	WLHKRGKYI	1172	Breast Cancer	HLA.A02.03 HLA.B08.01
PEX1 p.I370fs (uc003uly.2)	KLGQIIMKK	1165	Prostate Cancer	HLA.A03.01 HLA.A11.01
RAC1 p.P29S (uc003spx.2)	FSGEYIPTV	1152	Melanoma	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01
GATA3 p.H435fs (uc001ijz.2)	IMKPKRDGY	1151	Breast Cancer	HLA.B15.01 HLA.B15.03
AEBP1 p.K1133del (uc003tkb.2)	EEEIATGQAF	1143	Pancreatic Cancer	HLA.B44.02
FBXW7 p.R465H (uc003ims.2)	TVHCMHLHEK	1142	Colorectal Cancer	HLA.A03.01 HLA.A11.01 HLA.A68.01

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
TSPAN4 p.L92V (uc001lsd.1)	LTFFLLLLV	1140	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01 HLA.B15.17
TP53 p.R158L (uc002gim.2)	RVLAMAIYK	1136	Lung Squamous Cell Carcinoma	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01 HLA.A68.01
NRAS p.G12V (uc009wgu.2) KRAS p.G12V (uc001rgp.1)	LVVVGAVGV	1130	Pancreatic Cancer	HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01
GATA3 p.S408fs (uc001ijz.2)	HMSSLSHISA	1127	Breast Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
CTNNB1 p.S37F (uc010hia.1)	YLDSGIHFG	1121	Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.02 HLA.A02.06
CTNNB1 p.S37F (uc010hia.1)	YLDSGIHFGA	1120	Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
CTNNB1 p.S37C (uc010hia.1)	YLDSGIHCGA	1111	Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
SF3B1 p.K700E (uc002uue.2)	GLVDEQQEV	1099	Breast Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
KRAS p.G12R (uc001rgp.1) NRAS p.G12R (uc009wgu.2)	VVVGARGVGK	1082	Pancreatic Cancer	HLA.A11.01
EGFR p.L858R (uc003tqk.2)	KITDFGRAK	1054	Lung Adenocarcinoma	HLA.A03.01 HLA.A11.01 HLA.A30.01
TP53 p.E271K (uc002gim.2)	NLLGRNSFK	1046	Bladder Cancer	HLA.A03.01 HLA.A11.01 HLA.A68.01
TSPAN4 p.L92V (uc001lsd.1)	FLLLLVVFL	1044	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
TSPAN4 p.L92V (uc001lsd.1)	LLVVFLLEA	1044	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
TSPAN4 p.L92V (uc001isd.1)	LLLLVVFLL	1030	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.06
TSPAN4 p.L92V (uc001isd.1)	FLLLLVVFLL	1027	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
TSPAN4 p.L92V (uc001isd.1)	LLLVVFLLEA	1027	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
TSPAN4 p.L92V (uc001isd.1)	LLTFFLLLLV	1027	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
ARFGAP3 p.N299fs (uc003bdd.2)	LEIAEVLFHI	1024	Prostate Cancer	HLA.B40.01 HLA.B44.02
FRG1B p.I10T (uc010ztl.1)	TALKSGYGK	1020	Prostate Cancer	HLA.A11.01 HLA.A68.01
RBM14 p.AAAAAAA286del (uc009yrj.2)	ATAAAVTAA	1020	Pancreatic Cancer	HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01
KRAS p.G12S (uc001rgp.1) HRAS p.G12S (uc001ipv.2) NRAS p.G12S (uc009wgu.2)	VVGASGVGK	1019	Colorectal Cancer	HLA.A03.01 HLA.A11.01
UBC p.L149R (uc002gyy.3)	STLHLVLRR	1014	Prostate Cancer	HLA.A11.01 HLA.A31.01 HLA.A33.01 HLA.A68.01
PIK3CA p.N345K (uc003fjk.2)	ATYVKVNIR	1007	Breast Cancer	HLA.A11.01 HLA.A31.01 HLA.A33.01 HLA.A68.01
ERBB3 p.V104M (uc001sjh.2)	RMVRGTQVY	990	Colorectal Cancer	HLA.A03.01 HLA.A29.02 HLA.A80.01 HLA.B15.01 HLA.B15.03 HLA.B15.17
GATA3 p.H435fs (uc001ijz.2)	AESKIMFAT	984	Breast Cancer	HLA.B40.01 HLA.B40.02 HLA.B45.01
FRG1B p.L52S (uc010ztl.1)	ALSASNSCF	982	Prostate Cancer	HLA.B15.01 HLA.B15.03
TP53 p.E271K (uc002gim.2)	LLGRNSFKV	978	Bladder Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
TP53 p.E271K (uc002gim.2)	NLLGRNSFKV	969	Bladder Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
FRG1B p.A11T (uc010ztl.1)	TLKSGYGKY	969	Prostate Cancer	HLA.A26.02 HLA.A29.02 HLA.B15.01 HLA.B15.03
NFE2L2 p.E79Q (uc002ulh.3)	QLDEQTGEFL	966	Lung Squamous Cell Carcinoma	HLA.A02.01 HLA.A02.06
TP53 p.K132N (uc002gim.2)	ALNNMFCQL	955	Bladder Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.B15.01 HLA.B15.03
MAP2K1 p.P124S (uc010bhq.2)	NSSYIVGFY	943	Melanoma	HLA.A01.01 HLA.A26.01 HLA.A26.02 HLA.A29.02 HLA.A68.01 HLA.A80.01 HLA.B15.03 HLA.B15.17
TSPAN9 p.S50L (uc001qlp.2)	ATFSPSFPL	937	Melanoma	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A11.01 HLA.A30.01 HLA.A31.01 HLA.A68.02 HLA.A69.01 HLA.B15.03 HLA.B15.17 HLA.B58.01
SF3B1 p.K700E (uc002uue.2)	QEVRTISAL	936	Breast Cancer	HLA.B15.03 HLA.B39.01 HLA.B40.01 HLA.B40.02 HLA.B44.02 HLA.B44.03
ZNF91 p.R333H (uc002nre.2)	FSHSSTLAK	907	Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A68.01
FNBP4 p.TT58del (uc009ylv.2)	APSAATTTA	905	Prostate Cancer	HLA.B07.02
FNBP4 p.TT58del (uc009ylv.2)	APSAATTTAV	905	Prostate Cancer	HLA.B07.02

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
RAC1 p.P29S (uc003spx.2)	YTTNAFSGEY	901	Melanoma	HLA.A01.01 HLA.A68.01
ACADS p.R330H (uc001tza.3)	LTWHAAMLK	896	Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01 HLA.A68.01
TP53 p.C242F (uc002gim.2)	SSFMGGMNR	889	Lung Squamous Cell Carcinoma	HLA.A03.01 HLA.A11.01 HLA.A31.01 HLA.A33.01 HLA.A68.01
CNPY3 p.17_18LL>L (uc003ota.3)	LLLLPAPEL	878	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.06
CNPY3 p.17_18LL>L (uc003ota.3)	LLLLLLLLPA	876	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
CNPY3 p.17_18LL>L (uc003ota.3)	LLLLLLLPA	876	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
CNPY3 p.17_18LL>L (uc003ota.3)	LLLLLPAPEL	876	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
ZMIZ2 p.VAAAAATATATATAT153del (uc003tlr.2)	AAAAAVAAL	855	Pancreatic Cancer	HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.B07.02 HLA.B15.03 HLA.B15.17
PODXL p.28_30PSP>P (uc003vqw.3)	SPSPSQNAT	852	Prostate Cancer	HLA.B07.02
PODXL p.28_30PSP>P (uc003vqw.3)	SPSQNATQTT	852	Prostate Cancer	HLA.B07.02
AP3S1 p.K41fs (uc003krl.2)	HLVSEMKMF	849	Pancreatic Cancer	HLA.A26.02 HLA.B15.01 HLA.B15.03
STK19 p.D89N (uc003nyv.2)	NPIFRFSSL	849	Melanoma	HLA.A26.02 HLA.B07.02 HLA.B08.01 HLA.B39.01
NUF2 p.S340L (uc001gcq.1)	NLFKRLMIV	845	Colorectal Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.B08.01
FRG1B p.A53T (uc010ztl.1)	ALLTSNSCF	833	Prostate Cancer	HLA.B15.01 HLA.B15.03

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
UBC p.L149R (uc002gyy.3)	LVLRRRGGM	829	Prostate Cancer	HLA.B08.01
TP53 p.A159P (uc002gim.2)	RVRPMAIYK	820	Lung Adenocarcinoma	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01 HLA.A68.01
FRG1B p.K13N (uc010ztl.1)	IALNSGYGK	791	Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01 HLA.A68.01
GATA3 p.H435fs (uc001ijz.2)	VPFDLHFCR	791	Breast Cancer	HLA.A33.01 HLA.A68.01
UBC p.L149R (uc002gyy.3)	STLHLVLRRR	789	Prostate Cancer	HLA.A11.01 HLA.A33.01 HLA.A68.01
ACADS p.R330H (uc001tza.3)	LLTWHAAML	789	Prostate Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
GATA3 p.H435fs (uc001ijz.2)	ATLQRSSLW	782	Breast Cancer	HLA.B15.17 HLA.B57.01 HLA.B58.01
MAP2K1 p.P124S (uc010bhq.2)	VLHECNSSYI	779	Melanoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
ACADS p.R330H (uc001tza.3)	RLLTWHAAML	773	Prostate Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
RXRA p.S427F (uc004cfb.2) RXRG p.S428F (uc001gda.2)	RLPALRFIGL	771	Bladder Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06
ERBB3 p.V104M (uc001sjh.2)	LPLPNLRMV	765	Colorectal Cancer	HLA.B07.02
TSPAN9 p.S50L (uc001qlp.2)	LLSAANLVI	759	Melanoma	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.B15.01 HLA.B15.03 HLA.B15.17
CTNNB1 p.S33F (uc010hia.1)	YLDFGIHSGA	755	Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
CTNNB1 p.S33F (uc010hia.1)	YLDFGIHSG	754	Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.02 HLA.A02.06

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
PTEN p.R130G (uc001kfb.2)	GTGVMICAY	751	Uterine Corpus Endometrial Carcinoma	HLA.A29.02 HLA.B15.01 HLA.B15.17
RXRA p.S427F (uc004cfb.2) RXRG p.S428F (uc001gda.2)	LPALRFIGL	748	Bladder Cancer	HLA.B07.02 HLA.B08.01
NOTCH2 p.P6fs (uc001eik.2)	MPALRRSAV	747	Bladder Cancer	HLA.B07.02 HLA.B08.01
JMY p.PPPPPPPPPPP811del (uc003kfx.3)	LPPTPPPLPV	733	Pancreatic Cancer	HLA.B07.02
JMY p.PPPPPPPPPPP811del (uc003kfx.3)	SPLPPTPPPL	733	Pancreatic Cancer	HLA.B07.02
ACADS p.R330H (uc001tza.3)	LLTWHAAMLK	729	Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A68.01
GATA3 p.H435fs (uc001ijz.2)	RSSIMKPKR	703	Breast Cancer	HLA.A30.01 HLA.A31.01
OGFOD1 p.G477fs (uc002ejb.2)	FLLLTLPKV	702	Pancreatic Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
HERC2P3 p.A803V (uc001ytg.2)	RVRDMKCLM	699	Pancreatic Cancer	HLA.A30.01 HLA.B07.02 HLA.B15.17
C1QB p.GPKGPMGPKGGPGAPGAP90del (uc001bgd.2)	ESGDYKATQK	697	Pancreatic Cancer	HLA.A68.01
SLC38A10 p.1071_1072ll>l (uc002jzz.1)	GLNPLPDVQV	689	Pancreatic Cancer	HLA.A02.01 HLA.A02.03
UBB p.I188fs (uc002gpx.2) UBC p.I191T (uc002gyy.3)	IPPTSRGSSL	686	Prostate Cancer	HLA.B07.02
UBB p.I188fs (uc002gpx.2) UBC p.I191T (uc002gyy.3)	PPTSRGSSL	686	Prostate Cancer	HLA.B07.02
CTNNB1 p.D32N (uc010hia.1)	YLNSGIHSGA	672	Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
FRG1B p.K13N (uc010ztl.1)	ALNSGYGKYL	670	Prostate Cancer	HLA.A02.01 HLA.A02.03
NBPF14 p.R25C (uc001eqf.2)	KLCPQLAENK	667	Pancreatic Cancer	HLA.A03.01 HLA.A11.01
IARS2 p.R832C (uc001hmc.2)	VIVCSFAPI	662	Melanoma	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.A69.01 HLA.B15.03
PIK3CA p.H1047R (uc003fjk.2)	KQMNDARHG	661	Breast Cancer	HLA.B15.03

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
CTNNB1 p.D32N (uc010hia.1)	YLNSGIHSG	658	Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.02 HLA.A02.03
SIK3 p.950_951QQ>Q (uc001ppy.2)	QEYQELFRHM	653	Pancreatic Cancer	HLA.B40.01 HLA.B44.02
IARS2 p.R832C (uc001hmc.2)	ILDVIVCSFA	651	Melanoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
AP3S1 p.K41fs (uc003krl.2)	RETFHLVSEM	650	Pancreatic Cancer	HLA.B40.01
PPP2R1A p.P179R (uc002pyp.2)	RMVRRAAASK	649	Uterine Corpus Endometrial Carcinoma	HLA.A03.01 HLA.A11.01
ZMIZ2 p.VAAAAATATATATAT153del (uc003tlr.2)	AAAAAAVAAL	641	Pancreatic Cancer	HLA.B07.02
HSD17B7P2 p.N175S (uc010qex.1)	SARKSNFSL	637	Prostate Cancer	HLA.A30.01 HLA.B07.02 HLA.B08.01 HLA.B15.17
ARL16 p.G6R (uc002kbf.2)	RVAGRRALSR	632	Melanoma	HLA.A03.01 HLA.A11.01 HLA.A33.01 HLA.A68.01
GATA3 p.S408fs (uc001ijz.2)	TTPPLQHGHR	623	Breast Cancer	HLA.A33.01 HLA.A68.01
AP3S1 p.K41fs (uc003krl.2)	FHLVSEMKM	619	Pancreatic Cancer	HLA.B38.01 HLA.B39.01
PLEKHA6 p.V328fs (uc001hau.2)	SIMMSWMPPL	613	Colorectal Cancer	HLA.A02.01 HLA.A02.03 HLA.A02.06 HLA.A68.02 HLA.B07.02
LZTS1 p.RTQDLEGALRTKGLEL432del (uc003wzr.2)	KLEGLELEV	609	Pancreatic Cancer	HLA.A02.01 HLA.A02.02 HLA.A02.03 HLA.A02.06
HSD17B7P2 p.N175S (uc010qex.1)	WTSSRSARK	607	Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A68.01
RBM14 p.AAAAAAA286del (uc009yrj.2)	GAAATAAAV	606	Pancreatic Cancer	HLA.A02.03 HLA.A68.02
TP53 p.R249M (uc002gim.2)	MPILTIITL	606	Lung Adenocarcinoma	HLA.A69.01 HLA.B07.02 HLA.B08.01 HLA.B15.03 HLA.B39.01 HLA.B53.01

Mutation	Mutant Sequence	Estimated Yearly Population	Relevant Tumor Types (>500 patients per year)	Presenting HLAs (predicted <500nM)
IRF2BPL p.114_115QQ>Q (uc001xsy.2)	QLNHVDGSSK	605	Prostate Cancer	HLA.A03.01 HLA.A11.01
POLI p.D17del (uc002lfj.3)	EEDAEAWAM	599	Prostate Cancer	HLA.B40.01 HLA.B44.02 HLA.B44.03
ZNF780A p.Q600H (uc010xvh.1)	HMHLIRHQK	594	Prostate Cancer	HLA.A03.01 HLA.A11.01 HLA.A30.01 HLA.A31.01 HLA.A33.01 HLA.A68.01
FRG1B p.I10T (uc010ztl.1)	LSDSRTALK	589	Prostate Cancer	HLA.A11.01
PARG p.A584T (uc001jih.2)	EETEAQHLY	585	Prostate Cancer	HLA.B44.02 HLA.B44.03
GATA3 p.S408fs (uc001ijz.2)	SSLSHISAL	573	Breast Cancer	HLA.A02.06 HLA.B08.01 HLA.B15.03 HLA.B15.17 HLA.B39.01
EGFR p.L858R (uc003tqk.2)	FGRAKLLGA	564	Lung Adenocarcinoma	HLA.B08.01
TP53 p.R249M (uc002gim.2)	RMPILTIITL	563	Lung Adenocarcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
PARG p.A584T (uc001jih.2)	TEAQHLYQSI	557	Prostate Cancer	HLA.B40.01 HLA.B44.02
CDC27 p.D555E (uc002ile.3)	EVALSVLSK	557	Colorectal Cancer	HLA.A11.01 HLA.A68.01
GATA3 p.H435fs (uc001ijz.2)	MFLKAESKI	554	Breast Cancer	HLA.A23.01
FRG1B p.K13N (uc010ztl.1)	RIALNSGYGK	546	Prostate Cancer	HLA.A03.01 HLA.A11.01
CTNNB1 p.G34R (uc010hia.1)	YLDSRIHSGA	530	Uterine Corpus Endometrial Carcinoma	HLA.A02.01 HLA.A02.03 HLA.A02.06
FRG1B p.L52S (uc010ztl.1)	LSASNSCFI	528	Prostate Cancer	HLA.A68.02 HLA.B15.17 HLA.B58.01
AXIN2 p.W663fs (uc002jfi.2)	TPAPPPVPT	520	Colorectal Cancer	HLA.B07.02
AXIN2 p.W663fs (uc002jfi.2)	VPTCSPRTL	520	Colorectal Cancer	HLA.B07.02
FCGBP p.A2493V (uc002omp.3)	RPGLHRFVV	504	Pancreatic Cancer	HLA.B07.02 HLA.B08.01

Example 6

[00419] Therapeutic targeting of recurrent mutations expressed in genes containing extracellular domains. Tumor-specific mutations present in greater than 1% of a population of cancer patients may be targeted with a drug or therapy that recognizes the tumor-specific neoepitope resulting from the mutation. The mutation is preferably within an extracellular domain. The drug or therapy is an antibody, antibody fragment, antibody drug conjugate, aptamer, CAR, or T cell receptor. The antibody or fragment thereof may be humanized, fully humanized, or chimeric. The antibody fragment may be a nanobody, Fab, Fab', (Fab')2, Fv, ScFv, diabody, triabody, tetrabody, Bis-scFv, minibody, Fab2, or Fab3 fragment.

[00420] A recurrent mutation that may be targeted is FGFR3:p.S249C. Fibroblast growth factor receptor 3 (FGFR3) is a protein that in humans is encoded by the FGFR3 gene. FGFR3 has also been designated as CD333 (cluster of differentiation 333). The full-length protein includes an extracellular region, composed of three immunoglobulin-like domains, a single hydrophobic membrane-spanning segment and a cytoplasmic tyrosine kinase domain. The mutation occurs in the extracellular domain of the protein. The mutation is present in 6.92% of bladder cancer (BLCA) patients analyzed and 1.12% of lung squamous cell carcinoma (LUSC) patients analyzed.

[00421] Another recurrent mutation that may be targeted is ERBB3:p.V104M. Receptor tyrosine-protein kinase erbB-3, also known as HER3 (human epidermal growth factor receptor 3), is a membrane bound protein that in humans is encoded by the ERBB3 gene. ErbB3 is a member of the epidermal growth factor receptor (EGFR/ERBB) family of receptor tyrosine kinases. The mutation is present in 1.72% of colorectal cancer (CRC), 2.86% of colon adenocarcinoma (COAD), 2.42% of stomach adenocarcinoma (STAD), and 2.06% of cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC) patients analyzed.

[00422] Another recurrent mutation that may be targeted is EGFR:p.L858R. The epidermal growth factor receptor (EGFR; ErbB-1; HER1 in humans) is the cell-surface receptor for members of the epidermal growth factor family (EGF-family) of extracellular protein ligands. The mutation is present in 3.24% of lung adenocarcinoma (LUAD) patients analyzed.

[00423] Another recurrent mutation that may be targeted is MUC4:p.H4205Q. Mucin 4 (MUC 4) is a mucin protein that in humans is encoded by the MUC4 gene. This gene encodes an integral membrane glycoprotein found on the cell surface, although secreted isoforms may exist.

The mutation is present in 2.3% of prostate adenocarcinoma (PRAD), 2.31% of bladder urothelial carcinoma (BLCA), and 7.14% of uterine carcinosarcoma (UCS) patients analyzed.

[00424] Another recurrent mutation that may be targeted is PDGFRA:p.R483fs. Platelet-derived growth factor receptor, alpha polypeptide is a protein that in humans is encoded by the PDGFRA gene. This gene encodes a cell surface tyrosine kinase receptor for members of the platelet-derived growth factor family. The mutation is present in 1.92% of prostate adenocarcinoma (PRAD) patients analyzed.

[00425] Another recurrent mutation that may be targeted is TMEM52 23_26LLPL>L. Transmembrane protein 52 is encoded by the TMEM52 gene. The mutation is present in 1.53% of prostate adenocarcinoma (PRAD) patients analyzed.

[00426] Another recurrent mutation that may be targeted is PODXL 28_30PSP>P. Podocalyxin-like protein 1 is a protein that in humans is encoded by the PODXL gene. The mutation is present in 1.53% of prostate adenocarcinoma (PRAD), 15.56% of adrenocortical carcinoma (ACC), and 3.57% of uterine carcinosarcoma (UCS) patients analyzed.

* * *

[00427] Having thus described in detail preferred embodiments of the present invention, it is to be understood that the invention defined by the above paragraphs is not to be limited to particular details set forth in the above description as many apparent variations thereof are possible without departing from the spirit or scope of the present invention.

WHAT IS CLAIMED IS:

1. A pharmaceutical composition comprising at least one neoantigenic peptide and a pharmaceutically acceptable carrier, each at least one neoantigenic peptide comprising a tumor-specific neoepitope capable of binding to an HLA protein in a subject, each tumor-specific neoepitope comprising a tumor-specific mutation present in a tumor, wherein:

(a) the composition comprises at least one neoantigenic peptide comprising a tumor-specific mutation present in a tumor in at least 1% of subjects in a population of subjects suffering from cancer;

(b) the composition comprises at least one neoantigenic peptide comprising a tumor-specific neoepitope which binds to an HLA protein present in at least 5% of subjects in the population of subjects suffering from cancer; and

(c) the composition comprises at least one neoantigenic peptide capable of eliciting an immune response against a tumor present in at least 5% of the subjects in the population of subjects suffering from cancer.

2. The pharmaceutical composition according to claim 1, wherein the population of subjects is suffering from adrenocortical carcinoma (ACC), bladder urothelial carcinoma (BLCA), breast invasive carcinoma (BRCA), cervical squamous cell carcinoma and endocervical adenocarcinoma (CESC), colon adenocarcinoma (COAD), Chronic lymphocytic Leukaemia (CLL), colorectal cancer (CRC), Diffuse large B-cell lymphoma (DLBCL), glioblastoma multiforme (GBM), head and neck squamous cell carcinoma (HNSC), kidney chromophobe (KICH), kidney renal clear cell carcinoma (KIRC), kidney renal papillary cell carcinoma (KIRP), acute myeloid leukemia (LAML), liver hepatocellular carcinoma (LIHC), lung adenocarcinoma (LUAD), lung squamous cell carcinoma (LUSC), multiple myeloma (MM), ovarian serous cystadenocarcinoma (OV), pancreatic adenocarcinoma (PAAD), prostate adenocarcinoma (PRAD), rectum adenocarcinoma (READ), skin cutaneous melanoma (SKCM), stomach adenocarcinoma (STAD), testicular germ cell tumors (TGCT), thyroid adenocarcinoma (THCA), uterine corpus endometrioid carcinoma (UCEC), or uterine carcinosarcoma (UCS).

3. The pharmaceutical composition according to claim 1 or 2, wherein the population suffering from cancer was treated with, is being treated with, or is selected to be

treated with ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK inhibitor or antiestrogen therapy.

4. The pharmaceutical composition according to any of claims 1 to 3, wherein the tumor-specific mutations comprise splice-variant mutations, point mutations, and/or frameshift mutations.

5. The pharmaceutical composition according to any of claims 1 to 4, wherein the at least one neoantigenic peptide comprises at least one neoantigenic peptide derived from a long peptide region flanking and including the tumor specific mutation, and wherein all contiguous segments within the long peptide are included.

6. The pharmaceutical composition according to any of claims 1 to 5, wherein the tumor-specific mutations are present in one or more genes listed in any of the Tables.

7. The pharmaceutical composition according to any of claims 1 to 6, wherein the composition comprises at least one neoantigenic peptide as defined in any of the Tables.

8. The pharmaceutical composition according to any of claims 1 to 7, wherein the tumor-specific mutations are present in one or more genes encoding a protein selected from the group consisting of Programmed Death-Ligand 1 (PD-L1), androgen receptor (AR), Bruton's Tyrosine Kinase (BTK), Epidermal Growth Factor Receptor (EGFR), BCR-Abl, c-kit, PIK3CA, HER2, EML4-ALK, KRAS, ALK, ROS1, AKT1, BRAF, MEK1, MEK2, NRAS, RAC1, and ESR1.

9. The pharmaceutical composition according to claim 8, wherein at least one tumor-specific mutation is derived from alternative splicing of PD-L1 or AR.

10. The pharmaceutical composition according to claim 9, wherein at least one tumor-specific mutation is derived from splice variant sPD-L1, AR-V1 or AR-V7.

11. The pharmaceutical composition according to any of claim 1 to 8, wherein the tumor-specific mutations comprise drug resistance mutations.

12. The pharmaceutical composition according to claim 11, wherein at least one tumor-specific mutation is a drug resistance mutation selected from the group consisting of BTK/C481S, EGFR/T790M, BCR-Abl/T315I, BCR-Abl/Y253H, BCR-Abl/E255K, BCR-Abl/E255V, c-kit/T670I, PIK3CA/E545K, PIK3CA/E542K, HER2/G776(YVMA), HER2/E545K, EML4-ALK/G1269A, KRAS/G12V/D, ALK/L1196M, ALK/G1202R, ALK/S1206Y, ALK/1151T(ins), ALK/F1174C, ROS1/G2032R, AKT1/E17K, BRAF/V600E, MEK1/Q56P, MEK1/E203K, MEK1/C121S, MEK1/V60E, MEK1/G128V, MEK1/V154I, MEK1/P124S, MEK1/P124L, NRAS/Q61K/L/R, NRAS/T58I, MEK2/C125S, RAC1/P29S, ESR1/S463P, AR/V534E, AR/P535H, AR/L536Q, AR/L536R, AR/Y537C, AR/Y537S, AR/Y537N, AR/D538G and AR/F876L.

13. The pharmaceutical composition according to any of claims 1 to 12, wherein the at least one tumor-specific mutation has an incidence of at least 500 patients a year in the population of subjects suffering from cancer, and wherein the at least one mutation comprises a mutation listed for the population in Table 9.

14. The pharmaceutical composition according to claim 13, wherein the at least one neoantigenic peptide comprises at least one peptide listed in Table 9.

15. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from CLL; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of SF3B1:p.K700E, MYD88:p.L273P, NOTCH1:p.P2514fs, ABCA11P:p.E901D, AHNAK:p.D3823E, ZNF814:p.E348D, AHNAK:p.V1220I, AHNAK:p.H1203N, ANKRD30A:p.A232V, APOOL:p.I138L, EGR2:p.H397N, MKI67:p.H2213D, NRAS:p.Q61R, PLIN4:p.M691V, XPO1:p.E571K, ZCRB1:p.L76F, ZNF700:p.N652H, ZNF700:p.Q654R, ZNF844:p.D458H, AHNAK:p.A4046V, ANKRD36:p.P337R, C1orf170:p.T203I, CAST:p.D639E, EGR2:p.E369K, GPR123:p.L630P, IKZF3:p.L162R, MUC4:p.P4224R, OR9Q1:p.M34L, PKD2:p.Y486F, PRAMEF11:p.R104Q, SYNJ1:p.I681F, TP53:p.R248Q, TP53:p.R248W, TRPV2:p.L627del, ZNF254:p.S498A, ZNF732:p.A459T, ZNF749:p.E530Q, ZNF845:p.M423I, ABCA11P:p.G900E, ACRC:p.E243D, ACRC:p.A244V, ACSL3:p.T188S, ADAMTS2:p.D948N, AGAP6:p.S127I,

AHNAK:p.A2114G, ANKRD36:p.D1014Y, ARID3A:p.G550fs, ARID4A:p.D1154E, ATP2B4:p.R183H, ATRNL1:p.L1244F, BNC1:p.Y937N, BRAF:p.K601N, BTLA:p.Q86K, C14orf177:p.G90V, C2orf44:p.N456K, C3orf15:p.R552Q, CACNA2D1:p.Y376N, CALD1:p.E340K, CCDC15:p.P488H, CCDC79:p.N440T, CCNB3:p.A932T, CD109:p.L470Q, CD209:p.Q189L, CKAP2:p.*684K, CMA1:p.I81K, CMIP:p.A230T, CNTNAP4:p.I12F, CRYM:p.*315K, DICER1:p.E1705K, DPCR1:p.L716P, EIF3A:p.M1093L, EIF4G3:p.R8H, ETFDH:p.I281F, EWSR1:p.Y656C, F5:p.L1332P, F5:p.L1253F, FAM50A:p.H317R, FBXL13:p.S102R, FBXW7:p.R465H, FHL1:p.D184E, FILIP1:p.I522K, FRG1B:p.Q39K, GNB1:p.I80T, GPR110:p.R443G, GPR98:p.Y6152F, HDGFL1:p.188_189insA, IGF2BP2:p.T186S, IL1R2:p.L364fs, KIAA1109:p.L4680P, KRAS:p.G13D, KRTAP19-1:p.G61S, MAF:p.G53fs, MAGEC1:p.L609H, MAP2K1:p.K57N, MED12:p.L36R, MED12:p.G44S, METAP2:p.Y137N, METTL9:p.Y57F, MGP:p.V15L, MKI67:p.R2222K, MUC16:p.T11005I, MUC4:p.S3941N, MUC4:p.S3941G, MUC4:p.V3091L, MUC4:p.S2951Y, MUC4:p.A2841S, MUC4:p.S2760A, MUC4:p.T2335M, MUC4:p.T1627K, MUC4:p.T1547S, MUC4:p.H1133Q, MYD88:p.M240T, NEDD4L:p.P194del, NEFH:p.S704T, NRG4:p.G21fs, OR2A25:p.S105C, OR4C16:p.Y63F, OR4N4:p.L150fs, PABPC1:p.K254fs, PIWIL1:p.P372fs, PLCD3:p.E499fs, PLEKHB1:p.S146P, PPIL4:p.S382R, PRDM4:p.*802K, PRG4:p.N675H, PRKAB1:p.P104H, R3HDM2:p.S592G, R3HDM2:p.S588N, R3HDM2:p.R206W, RPS2:p.R200G, RPTN:p.G364S, SF3B1:p.K666E, SF3B1:p.N626Y, SF3B1:p.Y623C, SIX3:p.I27L, SLC39A7:p.L456fs, SLC6A9:p.R94K, TFG:p.A382V, TGOLN2:p.K83R, TGOLN2:p.T80S, TLR2:p.D327V, TNKS2:p.T619fs, TP53:p.R273H, TP53:p.C242F, TP53:p.R175H, TWISTNB:p.H306Q, UBXN7:p.A276V, WDR78:p.N110K, XIRP2:p.V3008E, ZNF382:p.H186Q, ZNF578:p.R306H, ZNF578:p.G311S, ZNF578:p.H334R, ZNF700:p.S649C, ZNF705A:p.D298N, ZNF836:p.K608Q, and ZNF836:p.I571N.

16. The pharmaceutical composition according to claim 15, wherein at least 17.49% of subjects in the population have the at least one tumor-specific mutation.

17. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from BLCA; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of PIK3CA:p.E545K, FGFR3:p.S249C, TP53:p.R248Q, PIK3CA:p.E542K, RXRA:p.S427F, ZNF814:p.D404E, FBXW7:p.R505G, NOTCH2:p.P6fs, TP53:p.E285K, ANKRD30A:p.A353P, C3orf70:p.S6L, EFCAB6:p.R379K, ERCC2:p.N238S, FAM47C:p.Q225E, FOXQ1:p.S135L, HLA-A:p.Q78R, MUC4:p.H4205Q, OTUD4:p.T909I, SLAMF1:p.S277fs, SPRED3:p.S128del, TMCO2:p.S15fs, TP53:p.R280T, TP53:p.E271K, TP53:p.A159V, ZNF706:p.I8N, ZNF706:p.R3P, ACACB:p.E2318Q, ACPP:p.E321K, ACRC:p.A264V, ADAMTS2:p.23_24insL, AFF3:p.E919K, AHNAK:p.S4150F, AHNAK:p.D2889H, AHNAK:p.V1940A, ALX4:p.R126Q, ANKRD12:p.E627K, ANKRD32:p.T999N, ARID1A:p.S614L, ASXL2:p.117_118SS>S, ATP12A:p.R858C, ATP9A:p.R519Q, BCAS3:p.T214M, BPI:p.M255I, CACNG8:p.V146G, CAMSAP1:p.T466fs, CDC27:p.I91fs, CDKN1A:p.E44fs, CEP192:p.S2058L, CGB8:p.T18A, CHRNA3:p.L23del, CHST4:p.D352N, CLIP1:p.S1018fs, COX6A1:p.S8L, CREBBP:p.D1435H, CRIPAK:p.M48fs, CSPG5:p.D119N, CUL1:p.E485K, DLC1:p.S741T, DLL3:p.D318H, DOPEY2:p.E1196K, ECM1:p.E266K, EEF1A2:p.Y418S, EEF2K:p.E673K, EMILIN1:p.R27G, ERBB2:p.S310F, ERBB3:p.M91I, ERBB3:p.V104L, ERBB3:p.D297Y, ERCC2:p.Y14C, FAM155A:p.Q86del, FAM43B:p.E272del, FASTKD3:p.Q625E, FBXW7:p.S546L, FGFR3:p.R248C, FGFR3:p.G380R, FGFRL1:p.H479fs, GBE1:p.M587I, GIMAP1-GIMAP5:p.S311C, GNA13:p.R200G, H1FOO:p.A214fs, HEATR7B2:p.E1109K, HIST1H1D:p.I81M, HRAS:p.G12D, HRCT1:p.H92P, ILF3:p.E484K, KCNK2:p.S6W, KIAA0907:p.Q446P, KIF23:p.E350K, KLF5:p.S118L, KLHL15:p.D185G, LAMA4:p.E639K, LILRA1:p.H410Y, LILRB1:p.L479del, LLGL2:p.P955fs, LPIN1:p.S974L, LRRC16A:p.D227N, LRTM2:p.S139L, LURAP1L:p.55_56insGGG, MAGEC1:p.P553del, MCL1:p.E171del, MN1:p.S472L, MUC7:p.A191V, MVP:p.E412K, NBPF10:p.E3455K, NFE2L2:p.E79K, NFE2L2:p.R34G, NOS1AP:p.Q306del, OR2T35:p.V319fs, OR4N2:p.L150fs, PABPC3:p.K333fs, PAX3:p.S197L, PBX2:p.E70K, PBXIP1:p.H729del, PCDP1:p.E537K, PEX1:p.I370fs, PHLDA3:p.E82K, PLEKHM2:p.S459L, PLVAP:p.A321V, POLR3B:p.L372F, POTEC:p.R477Q, PPL:p.H326Y, PPP1R15A:p.E196K, PRDM16:p.E271Q, PRIC285:p.E1289Q, PRMT8:p.S31P, PUF60:p.S396L, RAB11FIP4:p.S596L, RAD51C:p.D167N, RAD51C:p.Y224H, RALGPS1:p.R381Q, RARS2:p.R6C, RBM26:p.P644A, RERE:p.K176N, RXRA:p.S427Y, SERPINA12:p.R211G, SF3B1:p.E902K,

SLC6A9:p.R243W, SLC9A5:p.L447F, SPESP1:p.F121L, SRPRB:p.G14S, SYN2:p.A34del, SYTL2:p.I440M, TAB3:p.R211T, TAF1B:p.R292C, TAOK2:p.L981del, TAS1R3:p.E525K, TAS2R9:p.E163Q, TBC1D1:p.S71F, TBC1D2B:p.R920Q, TFPI2:p.R222C, TM6SF1:p.S15W, TMEM131:p.K640fs, TMEM19:p.G331fs, TP53:p.R273C, TP53:p.R248W, TP53:p.R175H, TP53:p.K132N, TRAM1:p.E41Q, TSKS:p.E513K, TTN:p.C20935G, UBOX5:p.S417L, UGP2:p.D262H, VGF:p.E433K, XAB2:p.E782K, XYLB:p.S87F, ZC3H4:p.E798K, ZNF208:p.K852E, ZNF208:p.I647S, ZNF626:p.G198E, ZNF749:p.Q457E, ZNF761:p.H373R, ZNF799:p.T43A, ZNF799:p.W41G, ZNF799:p.E589G, ZNF844:p.P503R, ZNF845:p.M423T, ZNF845:p.T479M, ZNF860:p.H464R, ZNF878:p.S181R, ZNF91:p.R333H, and ZNF91:p.H305R.

18. The pharmaceutical composition according to claim 17, wherein at least 26.92% of subjects in the population have the at least one tumor-specific mutation.

19. The pharmaceutical composition according to any of claims 1 to 14, wherein:

(a) the population of subjects is suffering from a neoplasia; and

(b) the at least one tumor-specific mutation comprises a frameshift mutation resulting from an insertion of at least one nucleotide in the coding sequence of GATA3.

20. The pharmaceutical composition according to claim 19, wherein:

(a) the population of subjects is suffering from BRCA; and

(b) the at least one tumor-specific mutation comprises any combination of frameshift mutations selected from the group consisting of GATA3:p.L328fs, GATA3:p.N334fs, GATA3:p.L344fs, GATA3:p.H400fs, GATA3:p.S408fs, GATA3:p.S430fs, GATA3:p.H434fs, GATA3:p.H435fs, and GATA3:p.S408fs.

21. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from BRCA; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of PIK3CA:p.H1047R, PIK3CA:p.E545K, PIK3CA:p.E542K, AKT1:p.E17K, TP53:p.R175H, PIK3CA:p.N345K, PIK3CA:p.H1047L, SF3B1:p.K700E, GATA3:p.S408fs, PIK3CA:p.E726K, TP53:p.Y220C, TP53:p.H193R,

PIK3CA:p.Q546R, TP53:p.R273C, TP53:p.R248W, TP53:p.R273H, TP53:p.I195T, TP53:p.H179R, FGFR2:p.N549K, NUP93:p.E14K, PIK3CA:p.C420R, PIK3CA:p.E453K, PIK3CA:p.Q546K, TP53:p.V216M, TP53:p.C176F, CDH1:p.E243K, ERBB2:p.L755S, KRAS:p.G12V, PIK3CA:p.E545A, TBL1XR1:p.I141fs, TP53:p.G266E, TP53:p.R248Q, TP53:p.Y163C, TP53:p.C141Y, TP53:p.G108fs, ACPP:p.R43W, AKT2:p.I289M, ARHGAP9:p.R137C, C9orf174:p.R136W, CDC42BPA:p.P675T, COL12A1:p.S395L, CRISPLD1:p.R222W, CT47B1:p.234_243EKLTEEATEE>E, CYP1A2:p.V483M, DAB2IP:p.E161K, DGKB:p.S13L, DMD:p.K1772N, DPEP1:p.V11L, ERBB2:p.S310F, ERBB2:p.D769Y, ERBB3:p.E928G, ESYT1:p.R816W, FAM179A:p.A831T, FAM58BP:p.A70T, FMN2:p.S751F, GALNTL6:p.K567del, GATA3:p.L328fs, GATA3:p.N334fs, GATA3:p.L344fs, GATA3:p.H400fs, GATA3:p.S408fs, GATA3:p.S430fs, GATA3:p.H434fs, GATA3:p.H435fs, GDAP1:p.T307A, GRB14:p.A300T, GUCY2C:p.G549C, IL17B:p.R34W, KCNB2:p.R231H, KIF1B:p.R1320W, KIF26B:p.V1113M, KLF4:p.K434Q, LY9:p.I69L, MAP2K4:p.S184L, MAP2K4:p.S251I, MAP2K4:p.T261fs, MAP3K1:p.L318fs, MAP3K1:p.I761fs, MAP3K1:p.V1346del, MAP3K1:p.L1384fs, MAPK13:p.E315K, MAPK4:p.V100M, MARCH5:p.R170C, MBP:p.E120K, MEFV:p.R377H, METTL15:p.Q53E, MS4A4A:p.V99M, MUC17:p.R4415H, MYH6:p.T847M, MYO5B:p.A405V, NARS2:p.P240R, NLGN4X:p.D382N, NLRC4:p.R288W, OR13G1:p.R258H, OR2AK2:p.V45I, OTOF:p.T388M, PACSIN2:p.Q331H, PALM2-AKAP2:p.A299T, PCDH19:p.R286C, PCDHGC5:p.D664N, PIK3CA:p.R88Q, PIK3CA:p.E110del, PIK3CA:p.K111del, PIK3CA:p.PVPHGLEDL447del, PIK3CA:p.L455fs, PIK3CA:p.M1004I, PIK3CA:p.M1043I, PIK3CA:p.N1044Y, PIK3R1:p.KPDL567del, PREX2:p.R363Q, PRRX1:p.A196V, PTEN:p.V317fs, RGSL1:p.V222I, RUNX1:p.R142fs, RUNX1:p.D96fs, SCN2A:p.R36K, SLC25A32:p.Q83E, SLC25A45:p.G106C, STRA6:p.Q68R, STX6:p.H153D, TBX3:p.H187Y, TFPT:p.S252C, TINAG:p.R332W, TMEM71:p.R63Q, TP53:p.E286K, TP53:p.R282W, TP53:p.V272M, TP53:p.S241fs, TP53:p.C238fs, TP53:p.C238F, TP53:p.C238Y, TP53:p.Y234C, TP53:p.Y220S, TP53:p.R209fs, TP53:p.G199V, TP53:p.L194R, TP53:p.H193L, TP53:p.H193Y, TP53:p.V173L, TP53:p.V173M, TP53:p.K132N, TP53:p.R110fs, TUBD1:p.A200V, VLDLR:p.R231H, VWA3A:p.V955I, VWF:p.K1720N, XPO1:p.E571K, and ZNF268:p.F901del.

22. The pharmaceutical composition according to claim 21, wherein at least 36.04% of subjects in the population have the at least one tumor-specific mutation.

23. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from COAD; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting ofKRAS:p.G12D, BRAF:p.V600E, KRAS:p.G12V, ACVR2A:p.K435fs, GRB14:p.KKK295del, SEC63:p.L532fs, TGFBR2:p.E125fs, ATR:p.K771fs, ICA1:p.N204fs, KRAS:p.G12C, TP53:p.R175H, ABCA8:p.R842Q, ACTL7B:p.R354H, ACVR2A:p.K435fs, AIM2:p.K340fs, ALG2:p.S302Y, ANKIB1:p.K144fs, ARSG:p.V131I, ATP10D:p.R311H, AXIN2:p.W663fs, C5orf30:p.D4N, CACNG3:p.V134I, CASP5:p.K78fs, CC2D2A:p.R1284C, CDH10:p.E349K, DNMT1:p.E432K, DOCK2:p.G170R, DOCK5:p.E177K, EGR2:p.R390H, ERBB3:p.V104M, FAM135B:p.R884H, FBXW7:p.R505C, FBXW7:p.R465H, FHDC1:p.R254W, FOXL1:p.N89K, HCN4:p.R525H, HLA-DMA:p.E84K, HTR3B:p.R236C, ITGA4:p.T673M, KIF18A:p.R17C, KIF20B:p.E991K, KLHL5:p.R326C, KRAS:p.A146T, KRAS:p.G13D, LPHN3:p.R1183Q, MAP2K4:p.R287H, MAPK8IP1:p.L217fs, MFSD5:p.R280Q, MUC16:p.R8606H, MYO6:p.D1180N, NAA25:p.S807Y, NBPF14:p.V44L, NRAS:p.Q61K, NRAS:p.G13R, PAX3:p.T424M, PGAM1:p.R240H, PHF3:p.R1410I, PIK3CA:p.R88Q, PIK3CA:p.E545K, PIK3CA:p.H1047R, PLXNA3:p.V14fs, POSTN:p.R508C, PTPRU:p.D1434N, PYGO2:p.Q150fs, RBBP7:p.E274K, SFPQ:p.R611Q, SGSM1:p.F1117L, SLC25A40:p.R96Q, SLC8A1:p.R431H, SLITRK3:p.S298L, SPATA22:p.S150L, SUN3:p.E128K, TGFBR1:p.S241L, TP53:p.R273H, TP53:p.R273C, TP53:p.R248W, TRPV5:p.R492H, USP40:p.S851L, VPS13C:p.D1359Y, ZBTB24:p.L607I, ZNF434:p.R306C, ZNF443:p.R301I, ZNF484:p.R138C, and ZNF770:p.S441P.

24. The pharmaceutical composition according to claim 23, wherein at least 27.14% of subjects in the population have the at least one tumor-specific mutation.

25. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from GBM; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of HSD17B7P2:p.N175S, IDH1:p.R132H, EGFR:p.A289V, EGFR:p.G598V, WASH3P:p.G175S, ZNF814:p.D404E, RPSA:p.Q111E, NBPF10:p.E3455K, TP53:p.R248Q, BRAF:p.V600E, EGFR:p.A289T, PRB2:p.N230del, RGPD5:p.P1760A, TP53:p.R175H, CHEK2:p.K373E, EGFR:p.R108K, EGFR:p.R222C, PIK3CA:p.E545K, PIK3R1:p.G376R, POTEC:p.K507E, SDHAP2:p.V195E, SLC6A10P:p.K88N, TP53:p.R282W, TP53:p.R273H, CD3EAP:p.K219del, DST:p.R146C, EGFR:p.A289D, EGFR:p.H304Y, FRG1B:p.S71N, GOLGA8DP:p.A116E, KRTAP4-11:p.R121K, KRTAP4-11:p.S48R, MAP3K1:p.P324L, OGDH:p.I78fs, PODXL:p.S162fs, PSPH:p.V145I, SPINT1:p.A316V, TP53:p.R248W, TP53:p.G245S, TP53:p.Y220C, TP53:p.R158H, TSHZ2:p.A222T, UBC:p.L149R, ZDHHC4:p.R300H, ZNF844:p.R447P, AASS:p.T878fs, ABCC10:p.R570W, ADAM29:p.V205I, ADAMTS8:p.V524M, AGAP3:p.R766W, AICDA:p.Y144F, AK7:p.A159V, AK8:p.D243A, ANO2:p.R334C, AOX1:p.A507V, ARHGAP5:p.M691L, CALN1:p.V231I, CARM1:p.A202V, CD163L1:p.V721M, CD1D:p.L25fs, CD209:p.A283T, CDH18:p.A195T, CILP2:p.V553M, CIZ1:p.L89P, CLOCK:p.L123fs, COL6A5:p.T2224M, CSF2RB:p.G298S, CSMD3:p.E171K, CYP2D6:p.H352R, DCAF12L1:p.R335H, DCAF12L2:p.R246H, DPP10:p.V183I, DPY19L2P1:p.R378Q, DQX1:p.R505H, DRD5:p.S275R, DVL2:p.V66G, EFCAB6:p.R379K, EGFR:p.L62R, EGFR:p.R252C, EGFR:p.P596S, EGFR:p.P596L, EGFR:p.G598A, EGFR:p.E709K, EPHA1:p.A184T, ERC2:p.R20H, ESPNP:p.R627Q, FAM126B:p.R382H, FBN3:p.V886I, FGF14:p.T229M, FLG2:p.H1901fs, FLG:p.R2886H, FLNA:p.V1240M, FOXG1:p.H57del, FPR2:p.R54Q, FRG1B:p.K13N, FRG1B:p.A53T, GABRA6:p.V314I, GJB3:p.R160H, GLT8D2:p.A178V, GRM3:p.R183C, HERC1:p.R2330H, HNF1B:p.T417M, HTRA3:p.Q403R, IDH1:p.R132G, IFNA10:p.L80F, IFNA10:p.V79A, JHDM1D:p.R313H, JPH1:p.A395T, KEL:p.V411M, KIAA0907:p.R516fs, KIAA1704:p.D88del, KLK6:p.R120H, KRAS:p.G12D, KRTAP4-7:p.L121V, KRTAP4-7:p.L148V, KRTAP5-4:p.S131C, LAT2:p.L18W, LIMK2:p.R203H, LUM:p.R330C, MCOLN3:p.V141I, MGAT4B:p.T444P, MUC17:p.V77M, MUC17:p.3204_3205insP, MYO1D:p.T109M, MYO6:p.Q914fs, NAP1L5:p.140_141EE>E, NF1:p.F1658fs, NHP2L1:p.R84C, NLRP5:p.R737W, NPTX1:p.A263T, NUFIP2:p.Q29del, ODF4:p.R61C, OR11H12:p.H154P, OR2A7:p.V18I, OR2H1:p.V287I, OR2T12:p.R184H, OR5D13:p.R236C, OR5P2:p.A100V, OR6N2:p.R293C,

PASD1:p.A236del, PCDH11X:p.T486M, PCDHB13:p.P221L, PDGFRA:p.E229K, PDGFRB:p.S650L, PHC3:p.T35del, PIK3C2B:p.R287fs, PIK3CA:p.M1V, PIK3CA:p.R88Q, PIK3CA:p.M1043V, PIK3CA:p.H1047R, PIK3R1:p.K379N, PODNL1:p.A150V, POTEE:p.V166M, POTEG:p.R136H, PRKCD:p.G432fs, PROKR2:p.V297I, PTEN:p.C136Y, PTEN:p.S170N, PTEN:p.R173H, PTEN:p.T277I, PTEN:p.V317fs, PTPN14:p.E716del, R3HDM2:p.412_413QQ>Q, RAB11FIP5:p.R170H, RASAL3:p.R82H, RB1:p.N316fs, RDH8:p.A198V, REN:p.15_16LL>L, RIMBP2:p.R830H, SCAF11:p.E926fs, SCN7A:p.R1358H, SCNN1G:p.R564H, SDHAP2:p.R31C, SDHAP3:p.A66T, SEMG2:p.R292C, SH3RF2:p.R318C, SHB:p.A460T, SIGLEC10:p.T250M, SLC13A5:p.Q273P, SLC17A9:p.V324I, SLC22A9:p.R407Q, SLC26A3:p.V88I, SLC5A3:p.A302fs, SLC9A4:p.R631H, SPAM1:p.R346Q, SPEN:p.E803fs, SPTA1:p.A2011V, SUSD5:p.T513M, SYNE1:p.R8468H, TARSL2:p.G366D, TAS2R41:p.A255T, TAT:p.R367H, TFPI2:p.R206C, THSD7B:p.R90C, TMEM147:p.A92V, TMEM156:p.R81C, TMPRSS6:p.V302I, TNFSF9:p.A232T, TP53:p.C238F, TP53:p.C238Y, TP53:p.Y234C, TP53:p.V216M, TP53:p.H179R, TP53:p.T155N, TRAPPC10:p.K133fs, TTN:p.R21402W, TTN:p.V16403M, TUBBP5:p.V102M, TYRP1:p.T352fs, UBC:p.R73L, UGT2B28:p.P289H, USH2A:p.R3719H, WASH6P:p.L211V, ZFP42:p.V227I, ZFP42:p.T264M, ZNF181:p.V305G, ZNF280B:p.E400K, ZNF534:p.N583K, ZNF563:p.W208fs, ZNF844:p.F487L, and ZPBP:p.R154C.

26. The pharmaceutical composition according to claim 25, wherein at least 34.36% of subjects in the population have the at least one tumor-specific mutation.

27. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from HNSC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting ofPIK3CA:p.E545K, PIK3CA:p.E542K, TP53:p.R175H, PIK3CA:p.H1047R, TP53:p.R282W, TP53:p.R248Q, TP53:p.R273H, TP53:p.R248W, TP53:p.G245S, RHOA:p.E40Q, EP300:p.D1399N, HRAS:p.G13V, MB21D2:p.Q311E, NFE2L2:p.E79Q, TP53:p.H179Y, FBXW7:p.R505G, HIST1H2BF:p.E77K, HRAS:p.G12D, MAPK1:p.E322K, NFE2L2:p.D29H, TP53:p.P278S, TP53:p.C242F, TP53:p.Y220C, TP53:p.H193L, TP53:p.H179R, TP53:p.V157F, TP53:p.R110L,

AKNAD1:p.K620R, ANXA6:p.R231Q, AP1G2:p.D243N, ATAD5:p.D441N, ATP6AP2:p.E119Q, B2M:p.M1I, BCL11A:p.E579K, C1orf172:p.Y30fs, C7orf57:p.E30K, CCDC135:p.E313K, CDH12:p.P706T, CDH7:p.Q225K, CDK11B:p.E79del, CDKN2A:p.H83Y, CHCHD4:p.T79M, CIRH1A:p.S250I, CLSTN2:p.P759L, CRB1:p.L628fs, DENND5B:p.G1023E, DNAH5:p.Q1797E, DSP:p.R160G, EDA:p.L58F, EFCAB6:p.E1002K, ELF4:p.S415L, EP300:p.C1164Y, EPHA3:p.T802R, EPHA6:p.D952H, ERBB2:p.M916I, ESRRA:p.D219N, FAM101A:p.I89del, FBXO24:p.M553V, FCAR:p.V233M, GPANK1:p.Y351fs, GPR20:p.V300I, GPRASP1:p.S706L, GPRIN3:p.R633fs, GRID2:p.T649fs, GRM3:p.F682L, GUCY2F:p.S404L, HCRTR2:p.D100Y, HIST1H3C:p.K37M, HIST1H4C:p.R68P, HLX:p.S12T, HOXD10:p.Y151C, HPS3:p.K812N, HRAS:p.G12A, HRAS:p.G12S, IFT140:p.E664K, INPPL1:p.T493M, ITGA10:p.R669Q, ITGB1:p.D158N, KIAA1429:p.D1526N, KIAA1429:p.S138F, KPRP:p.E553fs, KSR2:p.T555M, LINGO2:p.P410T, LPCAT1:p.V187del, MAGEB3:p.V75A, MAP3K7:p.E524Q, MAP4K3:p.P657fs, MAP9:p.K485N, MARS2:p.R481Q, MBOAT7:p.R424W, MUC16:p.R12774H, MUC5B:p.T4388M, MYH11:p.E993K, MYOCD:p.T493M, MYOM1:p.R63Q, NANOS3:p.S183L, NCOR1:p.R1561Q, NCOR1:p.Q169E, NCR1:p.D213N, NFE2L2:p.E79K, ODZ1:p.R366M, OPN1MW:p.A285T, OR2M2:p.A95fs, OR2M3:p.M273I, OR2T33:p.R120S, OR6V1:p.I248fs, PABPC5:p.P58L, PACSIN1:p.E359K, PIK3CA:p.M1043V, PIK3CA:p.H1047L, PIWIL1:p.V699M, PLIN5:p.430_431insNG, PLXNA3:p.P58S, PRB1:p.R274fs, PRSS1:p.D107N, RAC1:p.A159V, RGS7:p.L21fs, RPA1:p.R31H, RPL18:p.R178fs, SFI1:p.R821Q, SLC35D3:p.*417S, SLC5A7:p.G336C, SMARCA4:p.P913L, STAT3:p.D661V, SYCP2:p.K474N, SYT6:p.R249H, TBX21:p.E494K, THSD7A:p.R1046C, THSD7A:p.C728F, TMC3:p.R934S, TMTC2:p.T409R, TP53:p.E285K, TP53:p.C275F, TP53:p.R273C, TP53:p.G266E, TP53:p.G262V, TP53:p.R249S, TP53:p.G245V, TP53:p.C238F, TP53:p.M237I, TP53:p.Y236C, TP53:p.Y236D, TP53:p.R196P, TP53:p.PHHERC177del, TP53:p.V173L, TP53:p.V173M, TP53:p.Y163C, TP53:p.P151T, TP53:p.V143M, TP53:p.P58fs, URI1:p.S13fs, ZNF177:p.K384N, ZNF750:p.S96fs, and ZZZ3:p.R5Q.

28. The pharmaceutical composition according to claim 27, wherein at least 21.61% of subjects in the population have the at least one tumor-specific mutation.

29. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from KIRC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of WASH3P:p.G175S, VHL:p.L89H, VHL:p.S111N, WDR52:p.V1227G, KRT1:p.552_559YGSGGSSY>Y, KRTAP1-1:p.S34C, PALM2-AKAP2:p.1075_1076insEA, ZNF814:p.D404E, DOPEY2:p.Y2048S, KAT2B:p.W111fs, PABPC1:p.E156fs, PCDHGC5:p.G599V, PIK3CA:p.E545K, RRAD:p.A278E, SIRPA:p.D131del, UQCRFS1:p.I83V, VHL:p.P45L, VHL:p.V74D, VHL:p.R82P, VHL:p.L116fs, VHL:p.L158V, VHL:p.L169P, WDR73:p.DGTRSQ315del, ABCA3:p.E95D, ABCC5:p.L1090fs, ACADS:p.R330H, ACAN:p.G952E, ACSM2A:p.L402fs, ADAM23:p.K380M, ADH1A:p.D154V, AFF3:p.SA620del, AGAP6:p.D69fs, AGAP7:p.E71fs, AHNAK:p.5_6insE, AIDA:p.K247M, ALAS1:p.G302R, ANAPC16:p.R95fs, ANK2:p.N453S, ANKRD36:p.K378R, ARHGEF5:p.E487G, ARSD:p.AGV234del, ARSD:p.A234G, ATP2A1:p.G704C, ATP7A:p.Q990fs, AVIL:p.G299fs, AXDND1:p.EQ991del, BAP1:p.N78S, BAP1:p.M1I, BLM:p.H660Q, BMPER:p.RIAL444del, BRK1:p.K70Q, BTRC:p.I416M, C16orf55:p.D118A, C19orf33:p.K102E, C20orf132:p.E382D, C2orf71:p.1225_1226insS, C6orf132:p.173_182PPPLLLEPPP>P, CASP5:p.R23fs, CATSPER4:p.T425M, CCDC120:p.I8V, CCR5:p.S185I, CCZ1:p.E214D, CD7:p.P174fs, CDAN1:p.L646fs, CDH23:p.F1132Y, CDK5RAP2:p.H1592Q, CENPB:p.E410V, CERCAM:p.A85fs, CHEK2:p.K373E, CHIT1:p.P284fs, CLCN2:p.645_645R>RR, CLUL1:p.G463R, CNTNAP4:p.Y436S, CUL9:p.D1726E, CWC25:p.K364E, CXorf51B:p.V43I, DDX39B:p.F149fs, DIRAS1:p.G79C, DISP2:p.F1021S, DNMBP:p.T78P, DOCK8:p.A177fs, DPCR1:p.H383N, DPCR1:p.L768del, EGFR:p.L838M, ENPEP:p.F289C, ESPNP:p.W122fs, FAM105A:p.H126N, FAM186A:p.IPPQAQELEIPL1556del, FAM194B:p.EEEEYL135del, FAM22F:p.S691del, FAM22F:p.P690fs, FAM47A:p.LRPEPPETGVSH235del, FAM47C:p.P388S, FAM78A:p.W192L, FBXO34:p.Q294fs, FGFR3:p.R571fs, FGFR3:p.P716H, FMN2:p.AIPPPPPLPGA956del, FOXD4L4:p.C405fs, FUT6:p.S140fs, GJA1:p.A311fs, GOLGA5:p.L492I, GPM6A:p.A50V, GPRIN1:p.231_239RKEDPGSLR>R, GRAMD1B:p.P356H, GREB1:p.S344Y, GRM6:p.A718fs, GUSB:p.L501V, GUSB:p.C500R, HBB:p.F86C, HDAC6:p.G977D, HEXDC:p.T482P, HNF1B:p.N302K, HNRPLL:p.M327V,

HRC:p.P439fs, HSFX2:p.D92E, IL1RAP:p.F50C, IVL:p.EQQEGQLKHP167del, KANK4:p.S253P, KCNJ18:p.E378K, KIAA1751:p.K97N, KRT1:p.SSYGSGG557del, KRT2:p.L299W, KRT4:p.F154fs, KRTAP10-6:p.49_49P>PSCCAP, KRTAP5-7:p.C120Y, KRTAP9-2:p.CCQP140del, LARS:p.P185fs, LCP1:p.P445fs, LOC338651:p.PHRSHSPPWS102del, LRCH2:p.D717G, LTA4H:p.F107L, LYST:p.Q710H, MAFA:p.207_208HH>H, MAGEC1:p.P239del, MAP2K5:p.Q445R, MAPKAPK2:p.T214fs, MARCKS:p.K152fs, MED12L:p.P2071S, MEGF6:p.A582fs, MGST3:p.G143fs, MLXIPL:p.S790R, MOCOS:p.S849P, MST1R:p.M464V, MTOR:p.C1483F, MTOR:p.L1460P, MUC16:p.P11260A, MUC17:p.R1227fs, MUC17:p.H1228fs, MUC2:p.1480_1481insI, MUC6:p.P1569fs, MYO3A:p.N525S, NBPF3:p.D491V, NCOR1P1:p.L52P, NDUFA4L2:p.G3fs, NEFH:p.651_651K>KAKSPEK, NES:p.V611L, NFAT5:p.Q906E, NOXO1:p.G3fs, NR2C1:p.S270I, NSMCE2:p.Q31fs, NUDT21:p.W13fs, ODZ2:p.W628fs, ONECUT1:p.L424M, OR10A3:p.F73V, OR4F4:p.E15G, OR4N2:p.L150fs, OR51B5:p.A66fs, OR7C1:p.F104fs, PABPC1:p.Y408F, PABPC1:p.K333fs, PABPC1:p.A181T, PABPC3:p.P191T, PALLD:p.A996T, PALM2-AKAP2:p.G1118fs, PARD6A:p.G84fs, PASK:p.T62I, PCDH15:p.C1713F, PCNT:p.G136S, PGM5:p.G426fs, PGPEP1L:p.R164fs, PIK3C2B:p.F1473L, PIK3CA:p.N1044K, PIK3R5:p.L371R, PITRM1:p.P816T, PLIN4:p.T347I, PODXL:p.28_30PSP>P, POLR1C:p.K332Q, POTED:p.I214V, PPM1E:p.R311W, PRKCE:p.Q157fs, PROX1:p.V225D, PRRC2C:p.P1883T, PRX:p.P549L, PSD3:p.T563P, PTCH1:p.P689H, RANBP3:p.L386W, RASGEF1C:p.A188T, RGPD6:p.F946L, RHEB:p.Y35N, RIMBP3:p.A396del, RIN3:p.L449V, RLIM:p.S501L, RNF17:p.S351C, RUNX2:p.P466H, SCAF1:p.P208fs, SDK1:p.K508fs, SECISBP2:p.D608E, SERPINB3:p.S209C, SESTD1:p.I306M, SFRP4:p.P325fs, SH3KBP1:p.P563fs, SIPA1L3:p.G777A, SLC13A2:p.L493fs, SLC16A9:p.CVLLGG470del, SLC25A5:p.A118T, SLC44A5:p.V70F, SLC4A8:p.N229K, SLC52A1:p.G370del, SLC52A2:p.G399fs, SLC6A10P:p.K88N, SLC6A14:p.A85fs, SLC9B1:p.V446fs, SON:p.VLESSAVT1359del, SP8:p.G165del, SPAG1:p.353_354insD, SPATA9:p.C189F, SPEG:p.A992fs, SPTB:p.T1864I, SRA1:p.V110L, STAT6:p.P354fs, STK11IP:p.A155E, STXBP3:p.E279G, SVIL:p.M93T, SYNE1:p.R8468S, SYNJ2:p.K832T, SYNPO:p.G619fs, TAOK2:p.Q899fs, TAS2R38:p.I311T, TBC1D12:p.F608Y, TBC1D1:p.H277R, TBC1D3:p.A556fs, TBC1D3C:p.A495fs, TBC1D3F:p.A556fs, TCF7:p.H140P, TDRD10:p.W276C, THRAP3:p.K551R,

TMEM102:p.A110P, TMEM161B:p.L142P, TMEM230:p.D140G, TMEM47:p.G87S, TRDN:p.*730Y, TTBK1:p.T1065S, UBE2O:p.R1118fs, UBR5:p.T1306fs, UPK3A:p.G272fs, VHL:p.G39S, VHL:p.S65L, VHL:p.N78D, VHL:p.R79P, VHL:p.W88L, VHL:p.L89P, VHL:p.R107P, VHL:p.S111R, VHL:p.H115N, VHL:p.D121Y, VHL:p.G123fs, VHL:p.D126fs, VHL:p.L128H, VHL:p.L135F, VHL:p.I151T, VHL:p.L153P, VHL:p.L158P, VHL:p.Q164fs, VHL:p.L184P, VHL:p.L188P, WASH6P:p.315_316insAPP, WASH6P:p.T201M, WWP2:p.G458A, ZCCHC6:p.K937N, ZFAND2B:p.I149T, ZFR2:p.Y107N, ZNF273:p.N319K, ZNF462:p.S650T, ZNF516:p.A256D, ZNF519:p.H431Y, ZNF687:p.F858C, ZNF732:p.E227Q, ZNF880:p.Q406R, ZP3:p.V362fs, and ZRANB1:p.*735fs.

30. The pharmaceutical composition according to claim 29, wherein at least 6% of subjects in the population have the at least one tumor-specific mutation.

31. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from LAML; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of NPM1:p.W288fs, DNMT3A:p.R882H, NPM1:p.L287fs, IDH2:p.R140Q, IDH1:p.R132C, FLT3:p.D835Y, DNMT3A:p.R882C, FLT3:p.600_601insFREYEYD, IDH1:p.R132H, NRAS:p.G13D, U2AF1:p.S34F, KIT:p.D816V, FLT3:p.D835E, IDH2:p.R172K, NRAS:p.G12D, WT1:p.S381fs, ABTB1:p.L249fs, DNMT3A:p.R736H, FLT3:p.D835H, KRAS:p.G12D, NPM1:p.L287fs, NRAS:p.Q61H, NRAS:p.Q61K, PHACTR1:p.V251fs, RBBP4:p.E330K, RUNX1:p.R135G, and U2AF1:p.S34Y.

32. The pharmaceutical composition according to claim 31, wherein at least 47.45% of subjects in the population have the at least one tumor-specific mutation.

33. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from LUAD; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of KRAS:p.G12C, KRAS:p.G12V, EGFR:p.L858R, U2AF1:p.S34F, KRAS:p.G12A, TP53:p.R158L, KRAS:p.G12D, PIK3CA:p.E545K, TP53:p.R273L, EGFR:p.ELREA746del, KRAS:p.G13D, A2ML1:p.S654fs,

BRAF:p.G469V, CTNNB1:p.S37F, EGFR:p.G719A, KRAS:p.G13C, MYOF:p.G165fs, EGFR:p.S768I, FAM47C:p.G948W, KRAS:p.Q61L, MYH10:p.L1091fs, NRAS:p.Q61L, OR4C3:p.H130fs, PI15:p.V22F, RAD50:p.D69Y, RIT1:p.M90I, TP53:p.C275F, TP53:p.R249M, TP53:p.R249G, TP53:p.R248P, TP53:p.R175H, TP53:p.Y163C, TP53:p.A159P, TP53:p.V157F, TP53:p.G154V, ABCB1:p.R467L, ACBD3:p.R224L, ACTA1:p.G275C, ACTN2:p.D893Y, ADAM30:p.Q741H, ADAMTS14:p.G238C, ADAMTS20:p.R1251S, ADAMTS20:p.R541L, ADAMTS5:p.L549M, ADAMTS9:p.G659W, ADCY2:p.P1016T, ADCY5:p.G623C, AFP:p.A182G, AHDC1:p.P155Q, AKAP1:p.LDRNEEG317del, ALKBH1:p.K137E, ANK2:p.Q3076L, ANKRD44:p.G339C, ANO3:p.A41S, AP1G1:p.R723L, APBB2:p.T243fs, APOB:p.L973M, APOBR:p.R840L, AQP10:p.Q261L, ARAP3:p.R1226L, ARFIP2:p.R86L, ARHGAP36:p.P16H, ARL13B:p.R358L, ASCC2:p.R365L, ASPM:p.S240F, ASXL3:p.P1470Q, ATRN:p.P197Q, AVIL:p.G64W, AXDND1:p.W101R, B3GAT1:p.R125L, BARX2:p.R68P, BCL9L:p.G980C, BCOR:p.N1459S, BEND2:p.P536Q, BMS1:p.G455V, BRAF:p.V600E, BRAF:p.G466V, BRD9:p.G330W, BRF1:p.V469L, BRWD3:p.H160N, BTRC:p.G260W, C11orf68:p.V135L, C15orf2:p.V753F, C15orf2:p.G906W, C18orf8:p.M61I, C1GALT1:p.G299V, C1orf173:p.G1454S, C1orf173:p.S688Y, C1orf87:p.R541L, C2orf53:p.P272H, C3orf20:p.R740L, C7:p.R687S, C7orf58:p.G140W, C7orf58:p.R238L, CACNA1A:p.S772Y, CACNA1D:p.R1073L, CACNA1E:p.R2089Q, CACNA2D1:p.A352E, CACNG3:p.R232W, CADPS:p.R959S, CALB2:p.R258C, CAMK2B:p.G131V, CARD11:p.I1065M, CCDC111:p.R417L, CCDC141:p.E1204V, CCDC19:p.R279L, CCDC19:p.R207L, CCKAR:p.L271M, CD1B:p.W41L, CDH10:p.S577R, CDH10:p.R472C, CDH10:p.R128S, CDH18:p.A721S, CDH20:p.P433H, CDH6:p.Q237K, CDK13:p.R880S, CDK4:p.R24L, CELF4:p.A309P, CFDP1:p.P129fs, CHN1:p.K264N, CHRNA4:p.S396R, CHRNA9:p.P361Q, CLCNKA:p.P124Q, CLEC12B:p.W217L, CLK4:p.R68L, CNTFR:p.D252Y, CNTN6:p.R807M, CNTNAP2:p.F395L, COL19A1:p.P538Q, COL5A2:p.G612W, COL5A2:p.G516W, COL9A1:p.P211Q, CPE:p.P290Q, CPNE8:p.Q127H, CPSF4:p.P219Q, CRIPAK:p.S180fs, CROT:p.Q580H, CRTC3:p.S363L, CSMD2:p.P1855Q, CSMD3:p.T2810N, CSMD3:p.P2727T, CSMD3:p.Q174H, CUBN:p.G596C, CUL4B:p.R91S, CUL7:p.L371F, CXCL9:p.K122N, CXCR4:p.E345Q, CXorf59:p.R198M, CYP11B1:p.R498G, CYP27A1:p.P112Q, CYP2B6:p.A444E, DACH2:p.R539L, DCC:p.R446H, DDX56:p.R329L, DEFA1:p.W90C,

DENND2A:p.R688Q, DENND2A:p.R499L, DMBT1:p.R1521L, DNAH5:p.R3822L, DNAH9:p.S2993R, DNAI2:p.V231L, DPP6:p.L757F, DSG4:p.R128L, DST:p.A4410S, DZIP3:p.M322L, EBF3:p.R231S, EFCAB4B:p.E265Q, EHHADH:p.Q704H, ELAVL2:p.L263F, EMR1:p.R493H, ENAH:p.R514L, ENPP1:p.G738E, EPB41L3:p.A896S, EPG5:p.R2289L, EPHA1:p.G111V, EPHB6:p.R337H, EPRS:p.V1151L, ERBB2:p.S310Y, ERBB2:p.774_775insAYVM, ERBB2:p.776_776G>VC, ERN2:p.T295K, FAM120B:p.P467H, FAM127C:p.F52L, FAM135B:p.W240C, FAM210B:p.L112F, FAM47A:p.R690L, FAM47B:p.W163C, FAM47B:p.L567F, FAM5C:p.R457G, FAM70B:p.P277T, FAM71B:p.L583M, FAM75A6:p.R304S, FAM75A6:p.P54L, FAM75D1:p.R1265S, FARP1:p.R299L, FAT1:p.R4359L, FAT3:p.R1266H, FAT3:p.G1899V, FAT3:p.H3574N, FBXO18:p.M144I, FBXO31:p.G443fs, FCGBP:p.A1022S, FCRL2:p.V505L, FERD3L:p.P92H, FGB:p.E339Q, FGFR2:p.E116K, FGFRL1:p.R243L, FGFRL1:p.V274L, FKBPL:p.R320L, FLG2:p.G1545V, FLG2:p.L572F, FLG:p.P3254H, FLG:p.P2466Q, FMN2:p.P992T, FOLH1:p.A643S, FOXRED1:p.R136L, FRAS1:p.C382F, FRG2B:p.D142Y, FRMPD1:p.E1093Q, FSHB:p.T43N, GABRA5:p.Q224K, GADL1:p.L352I, GAL3ST3:p.A271S, GALNT14:p.D234E, GAS8:p.R313S, GATA3:p.M443I, GCDH:p.R82C, GEM:p.R268L, GFRAL:p.Q308K, GIT2:p.R123L, GJB4:p.R22S, GLB1L2:p.I407M, GLOD4:p.Q223fs, GNAO1:p.P283Q, GPNMB:p.I174M, GPR137B:p.G240C, GPR158:p.P762T, GPR98:p.G4307W, GRB7:p.R239L, GRHL1:p.G608W, GRID1:p.R683L, GRIK1:p.R368Q, GRM5:p.P895fs, GTF2E1:p.R192L, H3F3C:p.R131L, HAO2:p.H12N, HCN1:p.P231Q, HECW1:p.A183S, HGF:p.M686T, HIP1:p.R940L, HIST1H1E:p.R25P, HLA-DMA:p.A236fs, HOXA5:p.G11C, HS3ST3A1:p.G399W, HSD17B6:p.F209L, HSPA13:p.V85L, HSPBAP1:p.R282L, HTR5A:p.W298C, IGHMBP2:p.R615S, IL2:p.R103M, IL2RA:p.G61W, IL32:p.P215T, ING1:p.A220S, INMT:p.G56V, ITGA8:p.G616C, ITGAD:p.L528fs, ITGAX:p.R283H, ITIH1:p.G254W, ITIH2:p.L842V, ITK:p.R29L, ITPR2:p.P358Q, JMJD1C:p.R1198S, KCNA1:p.G376C, KCNH8:p.M455I, KCNJ3:p.L430F, KCNK18:p.G23V, KCNK2:p.R166L, KEAP1:p.G603W, KEAP1:p.R260L, KEAP1:p.S144F, KHDRBS2:p.S203L, KIAA1211:p.P1203Q, KIAA1549:p.L1272F, KIAA1755:p.Q108H, KIF15:p.E252Q, KIF9:p.G480R, KIRREL:p.G604C, KLF5:p.E419Q, KRAS:p.Q61H, KRTAP10-12:p.R64P, KRTAP27-1:p.M124I, KRTAP4-5:p.C91F, KRTAP5-1:p.S193Y, L1CAM:p.R632S, L3MBTL4:p.W162L, LAMA1:p.D1030Y, LAMB1:p.T1610fs,

LAMB4:p.G1239W, LAMB4:p.G588W, LEF1:p.I53V, LEKR1:p.Q450K, LIM2:p.S150T, LIPJ:p.P236Q, LPHN3:p.E740D, LPPR4:p.R527S, LRFN5:p.N132K, LRP1B:p.G3563C, LRP2:p.M4039I, LRRC4C:p.Q10L, LRRIQ1:p.W792L, LRRTM4:p.S243Y, MAGEA10:p.R7H, MAGEC2:p.W109C, MAGI1:p.G1156V, MAGI2:p.P1044T, MAK:p.P373Q, MAP2K1:p.K57N, MARCH11:p.R193L, MEPE:p.G142C, MKI67:p.R1081S, MKRN3:p.P448H, MLL3:p.N393K, MLL3:p.Q356K, MMRN1:p.A1013S, MOGAT2:p.Q66fs, MXRA5:p.D324Y, MYH4:p.T790M, MYH8:p.R1117C, MYH8:p.H1006N, MYO5B:p.R708L, MYO7B:p.P2040H, MYO9B:p.R94L, MYT1L:p.P351Q, NAA11:p.T184K, NAB1:p.L72F, NAV1:p.R938L, NBPF15:p.G665E, NCAM2:p.G698C, NCAPD2:p.R220L, NDST3:p.V427I, NEK2:p.R239S, NFIA:p.L294F, NLRP3:p.R157C, NOTCH2:p.R2105L, NR4A2:p.R314L, NRG1:p.V481L, NRXN1:p.R813S, NRXN1:p.A660S, NRXN3:p.P23H, NRXN3:p.R103C, NTM:p.G333C, NUAK1:p.G173C, NYAP2:p.P437L, ODZ3:p.P218Q, OIT3:p.R508S, OOEP:p.R101C, OPN1LW:p.P283H, OR10H4:p.M199I, OR10J1:p.L157Q, OR10X1:p.L298I, OR10Z1:p.L205F, OR14A16:p.G160C, OR2A25:p.M80I, OR2AG2:p.G249W, OR2AK2:p.W37C, OR2H2:p.L205F, OR2J2:p.G234W, OR2L13:p.M106I, OR2L13:p.T242A, OR2L3:p.M1I, OR2L3:p.L67I, OR2L8:p.R121C, OR2L8:p.R171S, OR2M2:p.F177L, OR2M2:p.F323L, OR2M5:p.V205L, OR2T12:p.M258L, OR2T27:p.D11Y, OR2T33:p.P165Q, OR2T34:p.C246F, OR2T6:p.V213L, OR4C12:p.D309Y, OR4C12:p.M279I, OR4C16:p.L162M, OR4M2:p.A119S, OR4M2:p.A161S, OR51V1:p.P298T, OR5AS1:p.M39I, OR5B12:p.S289C, OR5B17:p.M266I, OR5D14:p.H246N, OR5D16:p.P264T, OR5D18:p.R123H, OR5F1:p.G44V, OR5J2:p.A36S, OR5L1:p.T275N, OR6C65:p.I154fs, OR6C75:p.G94W, OR6K2:p.P79Q, OR8D2:p.R306M, OR9A2:p.R289W, OR9G9:p.R169L, P2RX7:p.P142Q, P2RY10:p.T10K, P2RY10:p.V196L, PABPC5:p.R99S, PAPPA2:p.P917T, PAPPA2:p.P1706H, PBLD:p.P55Q, PCDH10:p.R587S, PCDH10:p.V986L, PCDH11X:p.R1010I, PCDHAC2:p.A742V, PCDHB5:p.P649S, PCDHGC5:p.K12N, PCDHGC5:p.P684H, PCLO:p.P3946T, PCMTD1:p.R271M, PDPR:p.G793W, PDYN:p.G191W, PDZD2:p.R565S, PDZD8:p.S980G, PFKM:p.R118S, PIGM:p.R225L, PIK3CA:p.E542K, PIK3CG:p.V165I, PILRA:p.S291fs, PLCE1:p.G564C, PLCL1:p.M564I, PLEKHA6:p.R110L, PNKP:p.G174W, POGZ:p.G75W, POLE:p.R573L, POM121L12:p.P231T, POM121L12:p.P242H, POTEE:p.V288M, POTEM:p.S78R, POU3F3:p.D321Y, PPT2:p.R265L, PRDM16:p.P1036L, PRELP:p.D201Y, PRPF40B:p.R160S, PRPF6:p.R763L, PTEN:p.R234L, PTPN11:p.G503V, PTPN13:p.E2067K,

PTPRJ:p.G334W, PTPRT:p.R928L, PTPRU:p.P559S, PXDNL:p.P1456T, QSOX1:p.R401L, QSOX2:p.R683L, RAB13:p.R167L, RAB8A:p.G20W, RAPGEFL1:p.R356L, RBM19:p.G390W, RCL1:p.P112Q, REG1B:p.W57L, REG3A:p.S150L, REG4:p.G110V, RIMS2:p.R55L, RIT2:p.R85L, RLN2:p.S138C, RNF20:p.P529Q, RORB:p.G94W, RPL10L:p.K187T, RPRD2:p.R97S, RTN1:p.S103W, RUNX2:p.R337M, RYR2:p.K2413N, RYR2:p.M4334I, RYR3:p.P1670T, S100PBP:p.R5L, S1PR1:p.L104F, SAGE1:p.H298Q, SALL1:p.E965K, SALL1:p.R898W, SALL4:p.R187L, SBSPON:p.G133W, SCAF8:p.G740C, SCG2:p.P252Q, SCML4:p.L261F, SCN2A:p.T155K, SEC24D:p.A50fs, SEC61A2:p.G126V, SERPINA12:p.D253Y, SERPINA9:p.M414I, SERPINC1:p.R45L, SGIP1:p.R502L, SH3GL3:p.R174L, SH3PXD2A:p.S759L, SI:p.V1217F, SKOR1:p.Y883C, SLC1A2:p.F348fs, SLC24A5:p.R35S, SLC25A48:p.R101S, SLC35E2:p.R201L, SLC39A12:p.C628S, SLC39A6:p.R53L, SLC4A5:p.I533V, SLC5A1:p.G53W, SLC5A7:p.G442V, SLC6A11:p.W299L, SLC6A2:p.S354C, SLC8A1:p.G433C, SLIT1:p.R1460L, SLITRK5:p.R68L, SLITRK5:p.R468M, SLITRK6:p.N741K, SORL1:p.R205L, SOS1:p.N233Y, SOX9:p.E75K, SPAG16:p.V439L, SPIN4:p.Y171C, SPRR2D:p.P30fs, SPTA1:p.G2367C, SPTA1:p.D2243Y, SSX3:p.P127T, ST18:p.H778Q, STAC3:p.G117W, STOML3:p.D86Y, STX2:p.R107L, SUMF2:p.G110E, SUN3:p.P339Q, SV2C:p.P60Q, SYNDIG1:p.D135Y, SYNE1:p.K8632E, TARS2:p.E199K, TAS2R16:p.Q177H, TCOF1:p.K264R, TCTE1:p.S127I, TDO2:p.Q197H, THSD7A:p.G810W, THSD7A:p.R801L, TIFAB:p.D43E, TIGD4:p.S312F, TLL1:p.P53Q, TMPRSS11E:p.G259C, TMTC1:p.A864D, TMTC1:p.G212V, TMX3:p.R151C, TNNI1:p.R67L, TNR:p.L692I, TOP2A:p.R736L, TP53:p.R337L, TP53:p.E285K, TP53:p.R283P, TP53:p.D281N, TP53:p.C277F, TP53:p.V274F, TP53:p.R273H, TP53:p.I255F, TP53:p.R249S, TP53:p.M237I, TP53:p.S215I, TP53:p.C176F, TP53:p.R110L, TP53:p.G105C, TP53:p.P72fs, TPO:p.E558K, TRAF6:p.R502S, TRIM42:p.Q127K, TRIM48:p.A93D, TRIM4:p.R398L, TRIM51:p.W131C, TRIM9:p.R337S, TRIML1:p.H399Q, TRPM3:p.G298W, TSC1:p.G378C, TSG101:p.R276S, TSHZ1:p.K501N, TSHZ3:p.G677V, TTF2:p.R761S, TUBA3C:p.Q176fs, UBAC1:p.K330N, UBE2J2:p.G193W, UBR1:p.G1647W, UGT2B7:p.M214I, VMP1:p.E369Q, VPS13B:p.G2575W, VSTM2A:p.G75V, VWA3B:p.R557L, WBP11:p.P227fs, WDR52:p.G612C, WDR59:p.R837S, WDR75:p.P287Q, WDR88:p.G100W, ZCCHC5:p.G335W, ZFHX4:p.L811F, ZFHX4:p.T1663N, ZFHX4:p.H2511Q, ZFP14:p.Q17L, ZIC1:p.A112E, ZNF154:p.T408N, ZNF223:p.G23W,

ZNF295:p.S732C, ZNF322:p.K106N, ZNF385D:p.T226S, ZNF454:p.S190I, ZNF492:p.P392H, ZNF521:p.G640C, ZNF521:p.P270H, ZNF536:p.G186C, ZNF536:p.G663W, ZNF644:p.G21W, ZNF716:p.H263L, ZNF71:p.V411L, ZNF782:p.G484W, ZNF831:p.Q617K, ZNF98:p.C492F, and ZSWIM2:p.S214Y.

34. The pharmaceutical composition according to claim 33, wherein at least 33.42% of subjects in the population have the at least one tumor-specific mutation.

35. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from LUSC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of PIK3CA:p.E545K, TP53:p.R158L, KRTAP5-5:p.GCG47del, NFE2L2:p.E79Q, CDKN2A:p.D108Y, DHX9:p.V40G, MAFA:p.207_208HH>H, NFE2L2:p.R34Q, PBX2:p.Y262F, PIK3CA:p.E542K, TP53:p.R273L, TP53:p.C242F, TP53:p.R175G, TP53:p.Y163C, TP53:p.V157F, AICDA:p.R131G, ALPK2:p.D53N, ANKFN1:p.M280I, ARPC1A:p.F212L, ASXL2:p.S1081L, C1orf74:p.D254N, C3orf30:p.D227E, CCDC121:p.W397L, CHN2:p.I43M, CLEC4C:p.R179L, CLN3:p.G206S, CNTN5:p.T178N, COL12A1:p.G2753C, CPS1:p.T855K, CSMD3:p.T1094K, CSMD3:p.Q691K, DDX11:p.R167T, EGFR:p.L861Q, EME1:p.D570H, EP300:p.D1399N, ESYT3:p.S574F, FAM135B:p.L648M, FAM135B:p.Q285H, FAM47A:p.G372W, FBXW7:p.R505G, FGFR3:p.S249C, GALNT13:p.G358C, GNL3L:p.K20N, GPC5:p.R347L, HCN1:p.A714S, HCN1:p.R659L, HCN1:p.G499V, HCN1:p.P326T, HERC2P3:p.A803V, HEXDC:p.T482P, HIST1H3B:p.E74K, HIST2H2BE:p.G54D, IFNA10:p.V79A, IL7R:p.S54L, INADL:p.P1340A, ISX:p.C2F, ITGAX:p.R685H, ITPR1:p.E1883Q, KCNN3:p.80_81insQQ, KEAP1:p.G480W, KEAP1:p.R470C, KEAP1:p.V155F, KIAA1751:p.L63F, KIAA2022:p.C345F, KIR3DL2:p.K229E, KLF5:p.E419Q, LAMA4:p.M1293I, LMLN:p.G199C, LRP2:p.A516V, LRRC66:p.F458L, LSG1:p.R517L, LUM:p.R310L, MB21D2:p.Q311E, MCHR1:p.S306F, MKRN3:p.G270V, MUC16:p.N11594K, NFE2L2:p.G81S, NFE2L2:p.G31A, NFE2L2:p.L30F, NFE2L2:p.D29H, OR2B11:p.G10V, OR2T2:p.F13V, OR4K2:p.C254F, OR51F2:p.R67P, OR51S1:p.R159Q, OR5D18:p.T271K, OR8H2:p.L166F, OR8J3:p.S160L, OR8K3:p.K235N, PCDHB1:p.N568K, PHIP:p.I1681M,

PIK3CA:p.E726K, PIK3CA:p.H1047R, PLCE1:p.G439C, PRSS57:p.E39Q, PYHIN1:p.G148A, RANBP6:p.I984L, RBMXL1:p.G305C, REG1B:p.M67I, RGS6:p.W366L, RNF5:p.T136I, RP1:p.S1771L, RRP15:p.L214F, RYR2:p.E711K, SAMD3:p.Q206H, SLITRK3:p.R214L, SON:p.S908L, SP4:p.E11del, STK11:p.G279fs, TARBP1:p.L782V, TBCD:p.R476C, TMPRSS11F:p.R274Q, TP53:p.R337L, TP53:p.E271K, TP53:p.R267P, TP53:p.G245V, TP53:p.Y234C, TP53:p.Y220C, TP53:p.H214R, TP53:p.H193L, TP53:p.H179L, TPTE:p.M541I, TRIM7:p.L332I, TTN:p.T32425M, ZFP36L2:p.D240N, ZNF208:p.H883Q, ZNF48:p.R235H, ZNF626:p.K473R, ZNF676:p.P43T, ZZZ3:p.R162Q.

36. The pharmaceutical composition according to claim 35, wherein at least 7.87% of subjects in the population have the at least one tumor-specific mutation.

37. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from OV; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of TP53:p.R273H, TP53:p.Y220C, TP53:p.R248Q, TP53:p.R175H, TP53:p.R273C, TP53:p.I195T, TP53:p.R248W, TP53:p.R282W, TP53:p.C176Y, TP53:p.V157F, TP53:p.S241F, TP53:p.H179R, TP53:p.G245S, TP53:p.H193R, ADCY2:p.V888I, B2M:p.M1V, BAP1:p.R227C, CYP4A11:p.V185F, DNAH5:p.R3197Q, GART:p.K807fs, GRIN2B:p.R519Q, HRNR:p.M1fs, KLHL29:p.L716fs, KRAS:p.G12V, MGA:p.R2435Q, MYO3A:p.N525S, NPAS2:p.Q201R, NRAS:p.Q61R, PDAP1:p.K55fs, PGAP1:p.F565C, TP53:p.S315fs, TP53:p.C275Y, TP53:p.R273L, TP53:p.V272M, TP53:p.G266V, TP53:p.G266R, TP53:p.D259Y, TP53:p.P250L, TP53:p.G245D, TP53:p.G245V, TP53:p.G244C, TP53:p.C238fs, TP53:p.Y236C, TP53:p.Y234C, TP53:p.V216M, TP53:p.S215R, TP53:p.Y205C, TP53:p.L194R, TP53:p.P191del, TP53:p.Y163C, TP53:p.A159V, TP53:p.K132N, TRPC7:p.D210V, UXS1:p.V100L, WNT11:p.C344Y, and ZNF295:p.E885A.

38. The pharmaceutical composition according to claim 37, wherein at least 22.78% of subjects in the population have the at least one tumor-specific mutation.

39. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from READ; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of KRAS:p.G12V, TP53:p.R273H, KRAS:p.A146T, KRAS:p.G12D, TP53:p.R175H, AKAP9:p.L3482I, APBA1:p.E624K, BAG5:p.D439N, C17orf97:p.E230D, CDH23:p.F177L, CERS3:p.E95D, DNAH5:p.R982H, ERBB2:p.V842I, GABRB3:p.D500N, KRAS:p.G13D, KRAS:p.G12C, KRAS:p.G12S, LRP6:p.R675Q, MACF1:p.F722L, MBOAT2:p.R43Q, MYO1D:p.E246K, NLRC4:p.E409K, NRAP:p.E327K, NRAS:p.Q61K, PCDH15:p.R1552I, PIK3CA:p.N345K, PIK3CA:p.E545K, POLE:p.S459F, PPP2R2B:p.P326L, SMAD4:p.R361H, TP53:p.R248W, ZFP2:p.R150I, and ZNF563:p.K26N.

40. The pharmaceutical composition according to claim 39, wherein at least 20.51% of subjects in the population have the at least one tumor-specific mutation.

41. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from SKCM; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of BRAF:p.V600E, NRAS:p.Q61R, NRAS:p.Q61K, HSD17B7P2:p.N175S, BRAF:p.V600K, DISP1:p.G732L, IDH1:p.R132C, NRAS:p.Q61L, MUC16:p.P5119S, RAC1:p.P29S, WASH3P:p.G175S, AGAP9:p.M248V, C15orf23:p.S24F, DNAH5:p.D3236N, SPTLC3:p.R97K, TMC5:p.R276C, CFB:p.R314M, FRG1B:p.A50P, INMT:p.S212F, LOC649330:p.G93E, MAP2K1:p.P124S, RGS7:p.R44C, STK19:p.D89N, ADAM30:p.G97L, ARL16:p.G6R, ARMC4:p.E22K, BRAF:p.K601E, CAPN13:p.P405S, CD1C:p.R89C, CLCC1:p.P406Q, CNTN5:p.S379F, DNAH5:p.R742Q, EEF1B2:p.S43G, FRG1B:p.I59V, GABRG1:p.E205K, IARS2:p.R832C, IL32:p.D218fs, ISX:p.R86C, KLHDC7A:p.E635K, NAP1L4:p.P285Q, NBPF10:p.Q908E, OR2A5:p.S71L, OR4E2:p.R226Q, OR4M1:p.G41E, OR4M2:p.S268F, OR4N2:p.G41E, OR51B2:p.S163L, PCDHGC5:p.R293C, PCLO:p.R4133C, PHGDH:p.G173L, POTEG:p.D51N, PPP6C:p.R301C, PRAMEF11:p.C84S, PSG9:p.E404K, PTPRB:p.D1560N, RNF152:p.P95S, SPAG16:p.P488S, SPATA8:p.E18K, TAF1A:p.R172M, TCEB3C:p.E308K, THSD7B:p.E126K, TTN:p.E12129K, XIRP2:p.D2439N, and ZNF831:p.R1393Q.

42. The pharmaceutical composition according to claim 41, wherein at least 90.91% of subjects in the population have the at least one tumor-specific mutation.

43. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from UCEC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of RPL22:p.K15fs, PTEN:p.R130G, PTEN:p.R130Q, KRAS:p.G12D, KRAS:p.G12V, PIK3CA:p.H1047R, PIK3CA:p.R88Q, PIK3CA:p.E545K, PTEN:p.V317fs, FGFR2:p.S252W, PIK3CA:p.E542K, CTNNB1:p.S37F, POLE:p.P286R, PPP2R1A:p.P179R, CTNNB1:p.S37C, KRAS:p.G13D, CTNNB1:p.D32N, CTNNB1:p.S33F, CTNNB1:p.G34R, KIAA2026:p.R574C, LIMCH1:p.R806fs, PIK3CA:p.H1047L, ALPK2:p.K523fs, CTNNB1:p.S33C, FBXW7:p.R505C, HPD:p.R284fs, KRAS:p.G12A, PIK3CA:p.R93Q, POLE:p.V411L, TP53:p.R248W, ABCA11P:p.R385I, ABI1:p.K445N, ACSM2B:p.K195N, APOB:p.F3102L, ASCC3:p.R136Q, C12orf4:p.R335Q, CCDC132:p.R838C, CHD4:p.R975H, CSDE1:p.R220C, CTNNB1:p.D32Y, CTNNB1:p.S33Y, CTNNB1:p.T41I, EXOC1:p.R588C, FBXW7:p.R465H, FGFR2:p.N549K, FUBP1:p.R430C, GEN1:p.S509L, IK:p.E90fs, KIF20B:p.E54K, MAX:p.H28R, MBOAT2:p.R43Q, METTL14:p.R298P, MFGE8:p.D170N, MS4A8B:p.S3L, NSMCE1:p.D244N, OXR1:p.E122K, PCDH19:p.E530K, PIK3CA:p.R108H, PIK3CA:p.N345K, PIK3CA:p.C420R, PIK3CA:p.Q546P, PIK3CA:p.Q546R, PTEN:p.R130L, RBL2:p.E127K, RXFP1:p.S223Y, SF3B1:p.R957Q, SLC20A1:p.P328fs, SOX17:p.S403I, TNS1:p.Q659del, TP53:p.R273H, TP53:p.R273C, TP53:p.R248Q, TTN:p.D16823N, TXNL1:p.R234C, ZFHX3:p.R1893fs, ZNF180:p.R625I, ZNF257:p.R392I, ZNF354B:p.D609N, ZNF43:p.R280C, ZNF709:p.R468I, ZNF765:p.S254L, ABCA5:p.R1476Q, ACVR1:p.R206H, ADAD1:p.S11L, ADAM9:p.R256Q, ADD3:p.E570K, ADGB:p.S1124L, AGXT2:p.R502C, AMBN:p.S225Y, ANKDD1A:p.R24H, ARHGEF33:p.R46I, ATP10B:p.L1304I, ATP2C1:p.E724K, ATP9A:p.R290Q, ATR:p.R1814fs, AVL9:p.F34L, BMPER:p.R241Q, BTN3A2:p.E153K, C14orf118:p.R279I, C14orf166B:p.F230L, C3orf23:p.R217C, C3orf62:p.R185Q, CACNA1C:p.S710L, CAGE1:p.E539K, CARD10:p.KE272del, CCDC144A:p.S1264L, CCDC168:p.D5020Y, CCDC36:p.R209I, CD55:p.E156K, CEP44:p.S253L, CIITA:p.E728K, CREBBP:p.P2094L, CTNNB1:p.S37A, CTTNBP2:p.S420L, DCT:p.R532Q, DIAPH2:p.E121K, DLG2:p.S624L,

DNAH10:p.R1888Q, DNAH14:p.R1367C, DNAH7:p.R2961Q, DNAH8:p.R1347H, DNAJC13:p.E1248K, DNMT1:p.E51K, DST:p.S1767Y, DYNC2H1:p.E883D, EMR1:p.R631Q, EPHX4:p.R282Q, ERCC6L2:p.L445I, F10:p.E117K, FAM155B:p.E158K, FAM83B:p.R206Q, FARP1:p.S383L, FAT3:p.A4159T, FBXW7:p.R689W, FBXW7:p.R465C, FBXW7:p.G423V, FN1:p.R290C, FZD6:p.R416Q, GABRA3:p.R73H, GABRA4:p.R460Q, GALNTL2:p.E395K, GFAP:p.A233T, GGA2:p.A63V, GIGYF2:p.R227H, GNPTAB:p.R1189Q, GPR112:p.S1283Y, GPR98:p.R4142W, GRIA3:p.S646Y, GRM6:p.E363D, HMCN1:p.S133Y, HSPA4L:p.R483C, HTR2A:p.S219L, INTS7:p.R940C, INTS7:p.R106I, ITM2C:p.E167K, JAKMIP2:p.R283I, KCND3:p.S438L, KCNS2:p.D211N, KDM1B:p.F361L, KIAA0556:p.L330I, KIAA1147:p.A149V, KIF23:p.R150Q, KIF27:p.K925N, KIF9:p.R594Q, KLHL13:p.E213K, KLHL28:p.E33K, LIN9:p.R183W, LRBA:p.E2103K, LRP2:p.R2432I, MAGI2:p.L450M, MC5R:p.A109T, MEGF10:p.S1053L, MKI67:p.T1664fs, MKLN1:p.F485L, MMRN1:p.F917L, MSH4:p.E730K, MTOR:p.S2215Y, MUC7:p.S336L, MYBPC2:p.R646H, N4BP2L2:p.R506C, NAPSA:p.R121Q, NCOA7:p.E369D, NCR1:p.R258W, NEK11:p.R374Q, NHEJ1:p.R109Q, NNMT:p.E233K, NOTCH4:p.15_16LL>L, NPY1R:p.A371T, NRAS:p.Q61R, OGDHL:p.R57C, OMA1:p.R445Q, OPRM1:p.R462C, OR4C12:p.F248L, OR5AK2:p.K89N, OSBPL6:p.R577Q, PCDHAC2:p.K138N, PCDHB12:p.R289C, PCDHGC5:p.A70T, PIK3CA:p.R38H, PIK3CA:p.E39K, PIK3CA:p.E110del, PIK3CA:p.K111E, PIK3CA:p.Q546K, PIK3CA:p.M1043V, PIK3CA:p.M1043I, PLA2G3:p.R201Q, PLXNA1:p.E1295K, PON1:p.R306Q, POTEE:p.R303I, POTEF:p.K674N, PPP2R1A:p.S256F, PPP2R3B:p.F310L, PRAM1:p.A268T, PREX1:p.E1246K, PRKCQ:p.A324V, PTEN:p.R130P, PVRL4:p.A358T, RAI2:p.S385Y, RBM39:p.T353I, RELN:p.F2722L, RFPL1:p.R148Q, ROBO2:p.D1018N, ROS1:p.R245I, RPS6KA6:p.S394Y, RSBN1:p.E572K, RYR1:p.A2576T, SACS:p.R2906Q, SCAPER:p.R366Q, SELP:p.R429W, SENP7:p.S673Y, SEPHS1:p.E13K, SFRP4:p.R232Q, SGK1:p.K367del, SIX1:p.E191K, SLC10A7:p.S261L, SLC12A2:p.R828Q, SLC16A14:p.R495Q, SLC7A2:p.R322W, SMCR8:p.E175K, SOS1:p.N233Y, SPOP:p.E50K, STRN3:p.K218N, STXBP6:p.D92N, SULT1E1:p.R77Q, SUN3:p.L124I, SUSD1:p.R343C, SYNM:p.R516Q, TAF1:p.R843W, TDRD3:p.R322Q, THADA:p.S1941L, TLN2:p.S208L, TMEM161B:p.R315Q, TMPRSS3:p.R16Q, TP53:p.Y220C, TPTE:p.S423L, TRANK1:p.E846K, TRPC5:p.S490L, TRPM3:p.R429W, TSSK1B:p.E301K, TTLL7:p.R751H, TTN:p.S20317L, TTN:p.E6404K, TTN:p.R4434Q, TTN:p.R2506Q, UGT8:p.E102K,

USF1:p.R52Q, USP16:p.R455Q, USP25:p.R873H, USP33:p.R36Q, VPRBP:p.R802Q, VPS13B:p.R692Q, WDR65:p.F110C, YTHDC2:p.E185K, ZFYVE1:p.R266Q, ZKSCAN1:p.R541fs, ZNF117:p.R157I, ZNF180:p.R569I, ZNF195:p.R59Q, ZNF254:p.K179N, ZNF263:p.R510I, ZNF333:p.R554Q, ZNF354B:p.R402I, ZNF442:p.R309Q, ZNF454:p.R376I, ZNF485:p.R374I, ZNF488:p.R206Q, ZNF559:p.E284K, ZNF594:p.R287I, ZNF611:p.R390I, ZNF645:p.R154C, ZNF649:p.R338Q, ZNF649:p.R198I, ZNF674:p.R405I, ZNF675:p.R220I, ZNF678:p.R564I, ZNF732:p.R354I, ZNF780A:p.R466Q, ZNF823:p.R547I, ZNF836:p.R854I, ZNF836:p.R630I, ZNF841:p.R757I, and ZNF98:p.R370I.

44. The pharmaceutical composition according to claim 43, wherein at least 67.74% of subjects in the population have the at least one tumor-specific mutation.

45. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from ACC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of ZFPM1:p.EPL444del, GARS:p.P42A, ZNF517:p.V349A, LRIG1:p.L24V, CCDC102A:p.R96W, OPRD1:p.C27F, SOWAHA:p.R124P, LACTB:p.M5L, TOR3A:p.F13L, ZFPM1:p.E444fs, ZNF787:p.D367del, LRIG1:p.L26V, IRX3:p.L422P, TRIOBP:p.H1300R, TUBA1C:p.L146F, ZFPM1:p.P445fs, ZFPM1:p.446_447LA>P, TPO:p.S398T, USP42:p.R779P, ERCC2:p.D312N, GLTPD2:p.D209E, OTOP1:p.LLW104del, RINL:p.P402L, AMDHD1:p.S3G, ASPDH:p.Q266R, KCNK17:p.S21G, TMEM247:p.Q128E, MUC5B:p.D682G, OBSCN:p.R4516W, FAM184B:p.R784W, SEMA5B:p.V840D, ZNF598:p.E25G, ADAD2:p.G44E, C1orf106:p.R538C, ZAR1:p.Q42H, PANK2:p.G126A, PODXL:p.28_30PSP>P, SALL3:p.L593V, THEM4:p.L17R, C2orf81:p.T315P, CLDN23:p.V210M, FAM109A:p.GGG156del, FPGS:p.I22V, HHIPL1:p.V692A, MUC5B:p.M2869T, PLEC:p.R1386Q, SYT8:p.R373W, TAF5:p.S130A, TMEM189-UBE2V1:p.N6D, UQCRFS1:p.S6A, B3GNT6:p.L316fs, CCDC105:p.P499T, CLIC6:p.Q298E, IDUA:p.T374P, NOTCH2:p.C19W, RGS9BP:p.A96S, RREB1:p.G783V, SP8:p.G165del, WDR34:p.W60G, C19orf10:p.G12R, CELSR2:p.16_17insP, FAM75C1:p.71_71H>HLVSQRH, GPRIN2:p.R446H, KBTBD13:p.A81V, OGFR:p.S557T, PODXL:p.30_30P>PSP,

BHLHE22:p.L62Q, C4orf32:p.G32E, C5orf65:p.Q245R, KNDC1:p.V806D, KRTAP10-6:p.49_49P>PSCCAP, LRP11:p.P92R, MAP1S:p.S411C, NOL9:p.S58A, RASIP1:p.R601C, RGMB:p.S63R, SARM1:p.R23P, TSC22D2:p.A419T, ZNF628:p.T230A, ZNF814:p.A337V, AATK:p.A541T, BTBD11:p.G265A, CRIPAK:p.C143R, KCTD3:p.F9V, KRT8:p.S59A, MUC5B:p.S681G, NCOR2:p.1846_1847insSSG, OGFR:p.E556K, APOE:p.C130R, C10orf95:p.A85S, C13orf33:p.R59G, CRIPAK:p.C174R, FAM18B2:p.C51Y, GLI3:p.P998L, GLTSCR2:p.Q389R, HECTD2:p.P19A, IRF2BPL:p.123_125QQQ>Q, MEX3C:p.179_182AAAA>A, NEFH:p.EE658del, RNF149:p.S9G, RNF222:p.A133T, SEZ6L2:p.R74P, TNIP2:p.R73G, ARRDC4:p.T79A, B3GNT6:p.P330fs, BAG1:p.G45R, C22orf26:p.P28L, CHDH:p.E40A, COQ2:p.V66L, CTGF:p.H83D, DLEU7:p.A83V, EPPK1:p.D2378H, FAM86C1:p.R30P, FZD1:p.93_94insP, GPRIN2:p.V241M, GPX1:p.11_13AAA>A, HES3:p.P96T, JMJD4:p.A11V, KANK3:p.R359H, LPPR2:p.A186S, NEFH:p.665_666insEE, NOM1:p.R24G, RNF39:p.G263C, SCRT1:p.S133A, SNED1:p.L1228P, TTLL11:p.122_123insKA, ZCCHC3:p.A159del, ZNF219:p.QP233del, ASB16:p.T249A, ASB2:p.H515P, ATP9B:p.S39G, AVL9:p.G7fs, C17orf96:p.L63V, C19orf29:p.A499V, CRB2:p.T1110M, CRIPAK:p.P173R, CRIPAK:p.I190L, CSGALNACT2:p.L362F, CTBS:p.LAL31del, CTNNB1:p.S45P, DMRT1:p.S45T, DOK7:p.G461D, FBRSL1:p.A836V, FEZ2:p.P50L, FRG1:p.S169N, HSD17B1:p.G313S, IBA57:p.S130R, KIF1A:p.E917D, KRTAP9-1:p.160_160Q>QPSCGSSCCQ, LURAP1L:p.55_56insGGG, NMU:p.A19E, NMU:p.A18E, NOXA1:p.D6E, NPTX1:p.G100D, PLIN5:p.R306W, TBP:p.95_96insQ, TMEM200C:p.S498G, TNXB:p.V706fs, VARS:p.P51S, ZC3H12D:p.P405S, and ZZEF1:p.V30A.

46. The pharmaceutical composition according to claim 45, wherein at least 20% of subjects in the population have the at least one tumor-specific mutation.

47. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from CESC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of PIK3CA:p.E545K, PIK3CA:p.E542K, MAPK1:p.E322K, EP300:p.D1399N, ERBB2:p.S310F, ERBB3:p.V104M, KRAS:p.G12D,

ANKRD12:p.E721Q, ANKRD36:p.M1144T, MICA:p.G318fs, PIK3CA:p.E726K, PTEN:p.R130Q, ABCD1:p.S606P, ACTL7B:p.E211K, ADAM21:p.F129C, ADAMTS12:p.P1053A, AKT1:p.E17K, ANKLE1:p.V643L, ANO3:p.M956I, AOAH:p.R326T, APOD:p.S115L, ASCC1:p.H207Y, ATM:p.S800F, AURKA:p.S387L, BAG5:p.M286I, C12orf43:p.E28Q, C16orf3:p.G65S, C3orf70:p.S6L, C4orf21:p.E800Q, CALB2:p.K60N, CALCB:p.R81T, CCDC152:p.E153Q, CCDC53:p.R58C, CDC27:p.P242S, CFHR5:p.R441H, CLOCK:p.L123fs, CMYA5:p.E2733K, CNTRL:p.P185S, CSHL1:p.R117Q, CSMD3:p.H952Y, CTNNB1:p.D32G, CTSH:p.E254Q, DHPS:p.F49L, DMPK:p.R44H, DNAH14:p.F622fs, DNAH3:p.E3367Q, DNAH8:p.E587D, DNASE1L1:p.D212N, ECE2:p.D254N, FAM71B:p.H445D, FAM73A:p.G23V, FAS:p.E261K, FBXW7:p.R505G, FBXW7:p.R465C, FEZF2:p.E82K, FKBPL:p.E161Q, FMNL1:p.E927Q, GPATCH3:p.E275Q, GPR142:p.R304T, GPRIN2:p.T100P, GRAMD2:p.I123M, HERC2:p.S329F, HGF:p.G229A, HIF3A:p.A72T, HIST1H1B:p.K188N, HIST1H2AL:p.R30P, HIST2H2AC:p.R30P, HLA-C:p.N104K, HLA-DPB1:p.G114fs, HRNR:p.G2539S, INVS:p.R799K, JPH3:p.Q433H, JUP:p.S627L, KIAA1211:p.R308fs, KIAA1211:p.E309fs, KLK2:p.E161K, KRAS:p.G13D, KRAS:p.G12V, LIN9:p.E231K, LOC151174:p.P90S, LRRC37A3:p.A406D, LRTM2:p.L176V, MEPE:p.S30T, MUC12:p.R2634C, MUC4:p.S2936L, MYOM2:p.D988N, NFE2L2:p.D29H, NOTCH2:p.R2298W, NPIPL1:p.P250L, NR5A2:p.E80K, NYAP2:p.R197Q, OBSL1:p.E1642K, OR13C2:p.L9V, OSBP:p.Q721H, PAOX:p.H107Y, PDILT:p.E500K, PIAS3:p.D460N, PLEKHO2:p.E351Q, PNRC1:p.R73C, PPP4R1:p.L597F, PREP:p.F469L, PRKDC:p.Q3568E, PSME3:p.R231W, RANBP6:p.R915W, RCAN2:p.D440N, RNPC3:p.E116fs, SDHAP1:p.H66Y, SDHAP2:p.S37fs, SERPINA3:p.K158N, SERPINA4:p.R98C, SF1:p.R255W, SGSM1:p.E818K, SIM1:p.V213M, SLC10A4:p.F281L, SLC25A5:p.I79F, SLC35G2:p.K62fs, SLC4A9:p.R617C, SLCO2A1:p.M479I, SND1:p.Q38E, SPATA17:p.R72K, SRSF12:p.S150C, TADA2B:p.E67K, TCTEX1D2:p.S74L, TEDDM1:p.M166I, TEX15:p.E1652Q, TMC2:p.E92D, TMEM131:p.E1319Q, TNKS2:p.T619fs, TNS1:p.Q659del, TP53:p.E285K, TRAF3:p.S9F, TRIM61:p.K98N, TRPM1:p.M996I, TUFT1:p.L101F, U2AF1:p.S34F, UNC93B1:p.V498M, USP4:p.L259V, VCAN:p.S1308C, WDR17:p.P278S, ZBED4:p.S385L, ZEB2:p.E1094K, ZFYVE9:p.M1147I, ZNF16:p.R452W, ZNF677:p.R131T, and ZSWIM4:p.E407K.

48. The pharmaceutical composition according to claim 47, wherein at least 23.71% of subjects in the population have the at least one tumor-specific mutation.

49. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from CRC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of KRAS:p.G12D, KRAS:p.G12V, BRAF:p.V600E, KRAS:p.G13D, TP53:p.R175H, PIK3CA:p.E545K, FBXW7:p.R465H, KRAS:p.A146T, PIK3CA:p.H1047R, TP53:p.R248W, CDC27:p.D555E, SMAD4:p.R361H, TP53:p.R273H, KRAS:p.G12C, NRAS:p.Q61K, ERBB2:p.V842I, ERBB3:p.V104M, FBXW7:p.R465C, PIK3CA:p.R88Q, PIK3CA:p.E542K, TP53:p.R273C, TP53:p.G245S, AXIN2:p.G665fs, C16orf45:p.T106N, C20orf26:p.R1088Q, DNMT1:p.E432K, FBXW7:p.R505C, HLCS:p.E362K, HPSE2:p.K58N, KIF14:p.R598Q, KIF18A:p.R17C, KIF20B:p.E991K, KLHL5:p.R326C, KLK2:p.P57T, KRAS:p.G12A, KRAS:p.G12S, LPHN3:p.R1183Q, LRP6:p.R675Q, MYH8:p.R1048Q, NRAP:p.E327K, NRAS:p.G12C, PIK3CA:p.N345K, POSTN:p.R508C, PPP2R1A:p.R183W, PTEN:p.R130Q, RAF1:p.S257L, SDK1:p.T1181M, SGSM1:p.F1117L, TCF7L2:p.R482fs, TP53:p.R282W, TRIM23:p.R289Q, UGT8:p.E102K, ZNF491:p.R343Q, A2M:p.R732Q, AADACL4:p.A266T, ABCA8:p.E1158K, ABCA8:p.R842Q, ABCA8:p.A696T, ABCB8:p.R345H, ACACA:p.R1731C, ACADM:p.F48C, ACOT9:p.R50Q, ACPP:p.R105Q, ACTL7B:p.R354H, ACTL9:p.R331H, ACVR1:p.S290L, ADAM30:p.S314Y, ADAM32:p.R559Q, ADAMTS16:p.D817N, ADAMTS4:p.R156W, ADCY5:p.R661H, AGMAT:p.V313M, AGPAT4:p.A212T, AKAP12:p.E1282K, AKAP9:p.L3482I, ALB:p.S294L, ALDH1L1:p.A870T, ALG2:p.S302Y, AMOTL1:p.R676Q, AMPD1:p.K502N, AMPH:p.R292W, ANKRD6:p.R479C, APBA1:p.K730N, APBA1:p.E624K, APC:p.E847fs, APC:p.F1354fs, APC:p.M1413fs, APOB:p.R3136C, APOB:p.A43V, APPL1:p.R668W, AQPEP:p.A309T, ARF4:p.R149H, ARFGEF1:p.D1632N, ARHGAP32:p.E1253K, ARHGAP36:p.R128C, ARHGAP36:p.A147V, ARHGAP5:p.D890fs, ARNTL:p.T395M, ARPP21:p.R338H, ARSG:p.V131I, ASCC3:p.R1197Q, ATP10D:p.R311H, ATP6V0A4:p.R191Q, ATP9B:p.R265Q, AXDND1:p.E930D, AXIN2:p.W663fs, B2M:p.L13fs, B3GALNT1:p.R145Q, BACH1:p.R538Q, BAG5:p.D439N, BBOX1:p.F176V, BCL2L11:p.R91Q, BCL7A:p.T52M, BCLAF1:p.R37fs, BEND5:p.R198C, BICD2:p.R162H,

BLVRA:p.S44L, BMP3:p.R344W, BNC2:p.R512W, BRPF1:p.R66C, BRWD3:p.R787C, BTBD7:p.S436L, BUB1B:p.F996L, BZRAP1:p.V1627I, C11orf30:p.R1111C, C14orf101:p.E295K, C14orf102:p.D115N, C14orf105:p.R100I, C15orf2:p.V488I, C15orf33:p.D340N, C16orf87:p.R151I, C1RL:p.L351fs, C22orf40:p.P32fs, C3orf39:p.R333W, C5orf30:p.D4N, C5orf4:p.R114Q, C6orf170:p.K724T, C7orf63:p.A10T, CACHD1:p.S720Y, CACNA1A:p.T665M, CACNA2D3:p.A332T, CACNB2:p.R608H, CACNG3:p.V134I, CACNG3:p.A138V, CACNG5:p.G121R, CADM1:p.S190L, CADPS:p.A1073T, CAPRIN2:p.E13K, CARD11:p.R423Q, CASC1:p.R54Q, CASP14:p.R5W, CBFB:p.E152K, CC2D2A:p.R1284C, CCDC18:p.K615N, CCDC60:p.R230H, CCDC81:p.R259I, CCDC88C:p.P1851fs, CCKBR:p.V236M, CD101:p.D283Y, CD101:p.R594Q, CD180:p.N228T, CDC14B:p.R375C, CDCA7L:p.P405fs, CDH10:p.E349K, CDH12:p.D674N, CDH20:p.A134V, CDH23:p.F177L, CDH2:p.D547Y, CDH9:p.F523L, CDK16:p.R108C, CEACAM5:p.L640I, CEP152:p.E21K, CERS3:p.E95D, CHD4:p.R975H, CHD5:p.A801T, CIZ1:p.V668A, CLEC18A:p.R423H, CLTCL1:p.R481W, CMAS:p.R110Q, CNRIP1:p.R102W, COBLL1:p.K732N, COL14A1:p.R1082I, COL17A1:p.P1004L, COL4A6:p.L550I, COL6A3:p.D2792N, COPB1:p.R425C, CORO2A:p.*526R, COX15:p.L86I, CSMD1:p.S781Y, CTCFL:p.E423K, CTDNEP1:p.E126K, CTTNBP2:p.R164C, CYP4B1:p.E434D, DACH2:p.R539C, DBC1:p.V216I, DBF4B:p.S254Y, DCHS2:p.F2149L, DCLK2:p.S549Y, DDI1:p.R275Q, DENND4A:p.P357H, DENND4C:p.R1081Q, DHTKD1:p.R410Q, DISP1:p.R763C, DKK2:p.R230H, DKK4:p.R203Q, DLC1:p.A350V, DLC1:p.E222D, DMD:p.R3195H, DNAH5:p.R982H, DNAH5:p.R224Q, DNAH9:p.D1547N, DNAJC24:p.E61K, DNM1:p.A251T, DNMT1:p.E1531Q, DNMT3B:p.R92W, DOCK10:p.A1830V, DOCK1:p.E864K, DOCK2:p.G170R, DOCK3:p.R1183C, DOCK5:p.E177K, DOK5:p.R274W, DPP8:p.G165R, DPY19L1:p.F378L, DUOX2:p.F880L, DVL2:p.A601fs, EBAG9:p.E187K, EBF3:p.G255fs, EDNRB:p.L450R, EGR2:p.R390H, EHD3:p.E44K, EIF2C1:p.R139Q, ELF3:p.F305fs, ELMOD2:p.T141M, EMR2:p.S75L, ENAM:p.R373H, ENOX2:p.R356W, ENTPD7:p.E327K, EPG5:p.D369N, EPHB2:p.R392H, ERCC6:p.V780I, ERCC6L:p.R505Q, ERRFI1:p.A421T, ESCO1:p.R300Q, ETV6:p.R369W, F8:p.S2269Y, FAM123B:p.F173fs, FAM135B:p.R884H, FAM169B:p.K165N, FAM170A:p.E56K, FAM171B:p.D459N, FAM181A:p.R109H, FAM5B:p.R402C, FBXO11:p.A432V, FBXW7:p.R689W, FBXW7:p.S582L, FBXW7:p.R14Q, FGF14:p.A236V,

FHDC1:p.R254W, FHOD3:p.A225T, FHOD3:p.E813K, FMO3:p.F510L, FNDC1:p.R652H, FOXK1:p.R354W, FOXN3:p.P96fs, FPGT-TNNI3K:p.R455H, FZD3:p.D367N, GABRA4:p.R460Q, GABRA5:p.S126N, GABRB3:p.D500N, GALNTL5:p.R262I, GJA1:p.R362Q, GLRA3:p.L454I, GLRA3:p.F132L, GOLGA4:p.Q1536H, GP2:p.S41L, GPC6:p.A214T, GPLD1:p.R717Q, GPR125:p.R113Q, GPR156:p.F754L, GPR158:p.D566N, GPR21:p.R216H, GPR61:p.A62T, GPR98:p.R4142W, GPRC5A:p.V30I, GRAP2:p.E69D, GRIA1:p.R218C, GRIA2:p.R845Q, GRM7:p.R679Q, GTF3A:p.K306N, HAO1:p.R172C, HARS2:p.R168H, HBB:p.F42L, HCN4:p.R525H, HDAC5:p.A1044T, HGF:p.S467Y, HIPK4:p.R280H, HLA-DMA:p.E84K, HMG20A:p.E248D, HPS3:p.S468L, HRSP12:p.R120Q, HS3ST1:p.E287K, HTR3B:p.R236C, HTR5A:p.R152C, HTT:p.D1548N, HYDIN:p.R1187C, HYDIN:p.R939Q, HYDIN:p.R451Q, HYOU1:p.R158C, IFT172:p.A944V, IGJ:p.R77Q, IL17RA:p.Q803fs, IL1RAPL2:p.T647M, IL3:p.A90T, IL5RA:p.L47I, INPP5D:p.R523Q, INPP5K:p.R263C, IRAK3:p.R267Q, IREB2:p.R419Q, ITGA4:p.T673M, ITGA4:p.F900L, ITIH5:p.A912T, ITK:p.E196K, JAG1:p.A462T, JAK1:p.V310I, KAL1:p.V303I, KBTBD8:p.V549I, KCNA3:p.A415V, KCND3:p.S438L, KCNMB4:p.F209L, KCTD20:p.L314fs, KDELC1:p.L447I, KIAA0528:p.R181Q, KIAA0556:p.R1082W, KIAA1109:p.S4937Y, KIAA1804:p.V474M, KIAA1804:p.R477W, KIF16B:p.R145Q, KIF26B:p.A1114V, KPNA4:p.R29Q, KRAS:p.K117N, KRAS:p.Q61L, KRAS:p.Q61K, KRT6B:p.L197P, L1CAM:p.T186M, LALBA:p.A41T, LAMA4:p.A558V, LBX1:p.R176W, LPAR4:p.R145Q, LRP1B:p.K2623N, LRP2:p.R3043C, LRP2:p.S737L, LRRC18:p.R218W, LRRC31:p.K23T, LRRC7:p.R1389H, LZTS2:p.P100fs, MACF1:p.S292L, MACF1:p.F722L, MAEL:p.R345C, MAGEE1:p.V380M, MAGI1:p.R1198C, MAP1B:p.E2046D, MAP2:p.K530N, MAP2K4:p.R287H, MAP3K4:p.R275Q, MAP7D2:p.R487C, MAPK8IP1:p.L217fs, MBOAT2:p.R43Q, MCF2L2:p.R926Q, MECOM:p.R969C, METTL16:p.R200Q, METTL21A:p.R174Q, METTL6:p.F56L, MFF:p.R162C, MFSD5:p.R280Q, MIA3:p.Q356H, MMAA:p.R326C, MORC1:p.D113Y, MORC2:p.R740H, MPDZ:p.L804I, MR1:p.S46L, MRPL47:p.L234I, MS4A8B:p.S3L, MSH4:p.K464N, MSH6:p.T1085fs, MSH6:p.R1095H, MUC16:p.R8606H, MYH13:p.D311N, MYH7:p.R1689C, MYO1D:p.E246K, MYO3A:p.N525H, MYO6:p.D1180N, MYO9A:p.R2179Q, MYO9A:p.R167Q, MYOZ2:p.E251K, MYT1:p.E226K, NAA25:p.S807Y, NCAM1:p.R474W, NCOA4:p.R562Q, NEB:p.D5434N, NEB:p.L1591I, NEB:p.E1214K, NEDD9:p.A798T,

NEDD9:p.A316T, NEK1:p.R608C, NFASC:p.V256I, NINL:p.R1366C, NLRC4:p.D593N, NLRC4:p.E409K, NLRP4:p.V229I, NLRP5:p.R392H, NME9:p.E75K, NOLC1:p.T428M, NPC1:p.E451K, NPSR1:p.R235Q, NRAS:p.Q61L, NRAS:p.G13R, NRAS:p.G12D, NRG2:p.T246M, NTN4:p.E59K, NUB1:p.R373Q, NUDT15:p.S83Y, NUF2:p.S340L, NUP88:p.A302V, ODZ1:p.R2556W, OGDHL:p.A427T, OGFRL1:p.E427K, OLFM4:p.K132N, OPRM1:p.R353H, OR10A3:p.S93Y, OR2M3:p.R235H, OR52W1:p.R133C, OR5AU1:p.R312H, OR5B17:p.R163H, OR8S1:p.A99V, OSTN:p.R115Q, OTOL1:p.V431I, OTUD3:p.R277I, PAN3:p.S580N, PANK3:p.R260I, PAX3:p.T424M, PCBP1:p.L102Q, PCDH10:p.V477M, PCDH15:p.R1552I, PCDHAC2:p.A519T, PCDHAC2:p.E190K, PCDHAC2:p.A266T, PCDHAC2:p.A156V, PCDHAC2:p.E271K, PCDHAC2:p.A736V, PCDHB5:p.D51Y, PCDHB8:p.D235N, PCDHGC5:p.S289L, PCDHGC5:p.V662M, PCNXL2:p.R135Q, PCOLCE2:p.A348V, PCOLCE2:p.R87H, PDE4B:p.S417L, PGAM1:p.R240H, PHF3:p.R1410I, PIAS2:p.S519L, PIGR:p.A580T, PIK3CA:p.D350G, PIK3CA:p.E545A, PIK3CA:p.E545G, PIK3CA:p.Q546K, PIP4K2C:p.R204H, PKHD1L1:p.F1856L, PLA2G4A:p.E443K, PLCG2:p.E544K, PLCG2:p.D973N, PLEKHA6:p.V328fs, PLEKHG4B:p.E384K, PLK1:p.D233G, PLOD3:p.R297fs, PLSCR3:p.E77K, PLXNC1:p.S462L, PLXNC1:p.R819C, POLA1:p.E603D, POLE:p.S459F, POLE:p.V411L, POLQ:p.R860Q, PPP2R2B:p.P326L, PPP2R5C:p.S259Y, PRAMEF4:p.R248H, PREX1:p.V731I, PRKAA2:p.R407Q, PRKAR2B:p.S309L, PRKCI:p.R480C, PRKRA:p.K122N, PSG8:p.R397C, PSG8:p.R320C, PSMD12:p.R201Q, PTPDC1:p.R430W, PTPN12:p.R765Q, PTPN13:p.S887L, PTPRD:p.L1053I, PTPRU:p.D1434N, PXDN:p.P856fs, PXDNL:p.T1312M, QRSL1:p.S226L, RAB7L1:p.R79W, RALGAPA1:p.R398C, RANBP2:p.R1231C, RBBP7:p.E313K, RBBP7:p.E274K, RBFOX2:p.A340T, RBMXL1:p.R331Q, RHOBTB1:p.T464M, RIMS2:p.R599Q, RIN3:p.S708L, RLBP1:p.D281N, RLBP1:p.A72V, RNASET2:p.A127V, RNF113B:p.A172V, RNF150:p.R236Q, RNF150:p.S208L, RNF43:p.S216L, ROR2:p.D672N, RPL6:p.F193C, RPS6KA5:p.E166K, RSPO2:p.R28C, RUVBL1:p.E431K, RUVBL1:p.R117C, RWDD2B:p.R254H, RXFP3:p.R113C, RYR3:p.R2705Q, SAGE1:p.R229C, SCFD2:p.R545W, SCML4:p.R194Q, SCN10A:p.T1570M, SCN11A:p.A1688T, SCN11A:p.V1289I, SCN11A:p.V566I, SCUBE2:p.V342M, SEMA3A:p.D81N, SEMA4D:p.R252Q, SEPHS1:p.R371Q, SEZ6L:p.S207L, SFPQ:p.R611Q, SFSWAP:p.S617Y, SGCG:p.A220V,

SGCZ:p.I41M, SH3TC2:p.R89C, SIGLEC11:p.S363F, SIPA1L1:p.R1063Q, SIPA1L1:p.S1227Y, SLC12A1:p.S292L, SLC22A15:p.S201L, SLC24A2:p.A134V, SLC25A40:p.R96Q, SLC2A7:p.A65T, SLC30A9:p.R194H, SLC33A1:p.S542L, SLC35F3:p.A280T, SLC39A7:p.R382C, SLC43A1:p.P133L, SLC43A3:p.R216H, SLC44A5:p.R185H, SLC6A2:p.A562T, SLC8A1:p.R431H, SLFN12L:p.F232fs, SLITRK1:p.R52H, SLITRK3:p.S298L, SMAD2:p.R321Q, SMARCA4:p.R381Q, SOCS5:p.S464L, SORBS1:p.V1156M, SORBS1:p.F570L, SORCS2:p.R320W, SOX6:p.R719W, SPATA22:p.S150L, SPEG:p.A944V, SPTB:p.R86C, SPTBN4:p.A1993V, STIM2:p.R572Q, STT3B:p.D583Y, SULT1C4:p.R85Q, SUN3:p.E128K, SUPT6H:p.A957T, SYNE1:p.I1249L, SYNE1:p.R170W, SYNE2:p.K3103N, SYNGR4:p.R169Q, SYT7:p.T349M, TANK:p.S380L, TAS1R2:p.R270C, TAS2R1:p.F183L, TCF7L2:p.R488C, TDRD10:p.S322L, TECTB:p.L29I, TEKT5:p.R401H, TGFBR1:p.S241L, THAP5:p.S287Y, THSD7B:p.R90H, TLL1:p.T153M, TLL2:p.S872L, TM9SF2:p.R91H, TMCC3:p.R110H, TMEM132A:p.R481C, TMEM132D:p.R578W, TMEM55A:p.R189Q, TMEM74:p.R125Q, TMPRSS11A:p.S288L, TNIP2:p.A139T, TOP2B:p.R656H, TOX:p.S354L, TP53:p.G244D, TP53:p.R175C, TPO:p.A826T, TPR:p.S2155L, TPTE2:p.R258Q, TPTE:p.S423L, TRAK1:p.D627N, TRAPPC11:p.R568Q, TRIM23:p.R396Q, TRIM44:p.D331N, TRIO:p.R661W, TRPA1:p.K54N, TRPC5:p.S490L, TRPM6:p.R995H, TRPM7:p.R1862C, TRPM7:p.R843Q, TRPS1:p.R1125W, TRPV5:p.R492H, TRRAP:p.R3515W, TSHZ1:p.R881M, TTC21A:p.S270Y, TTN:p.R22795C, TTN:p.R3193Q, TTN:p.R328H, TUBA3D:p.R243Q, TUFT1:p.A340T, TXNDC15:p.R343Q, UBE2NL:p.R86I, UBIAD1:p.A97T, UGT2A1:p.N97fs, USH2A:p.F2369L, USP11:p.A286T, USP25:p.R1119Q, USP26:p.R861Q, USP29:p.F81L, USP31:p.D391N, USP40:p.S851L, UTP14A:p.V148I, VAV3:p.E685K, VCAN:p.R1125H, VPS13C:p.D1359Y, WBSCR17:p.R228C, WDR3:p.E841K, WDR52:p.A157T, XKR6:p.R268Q, XPOT:p.R541W, YTHDC1:p.R267Q, YTHDC2:p.E634K, ZBBX:p.R596I, ZBTB24:p.L607I, ZC3H13:p.R103Q, ZCWPW2:p.D144N, ZEB2:p.R156H, ZFHX4:p.E237D, ZFP14:p.R386C, ZFP28:p.R525I, ZFP2:p.R150I, ZFP3:p.R273I, ZFP90:p.R330Q, ZHX2:p.V790I, ZIC4:p.S305L, ZIM3:p.D352N, ZKSCAN4:p.R319Q, ZMYM4:p.R1446Q, ZNF117:p.R185I, ZNF167:p.R683I, ZNF180:p.R401I, ZNF19:p.R349I, ZNF205:p.R384C, ZNF236:p.S1480L, ZNF248:p.R568I, ZNF259:p.R174I, ZNF266:p.R512Q, ZNF266:p.R344Q, ZNF280B:p.E363K, ZNF283:p.R392Q, ZNF32:p.S62L, ZNF345:p.R82Q, ZNF345:p.R334I, ZNF350:p.R310Q,

ZNF434:p.R306C, ZNF439:p.E239D, ZNF439:p.R262I, ZNF443:p.R301I, ZNF445:p.L682M, ZNF470:p.R641I, ZNF471:p.R282I, ZNF484:p.R138C, ZNF528:p.R279Q, ZNF563:p.K26N, ZNF573:p.R350I, ZNF583:p.R344I, ZNF585A:p.E638K, ZNF585A:p.E491D, ZNF625:p.R235Q, ZNF652:p.K327N, ZNF677:p.R451I, ZNF678:p.R368I, ZNF699:p.R41I, ZNF70:p.R244I, ZNF770:p.S441P, ZNF774:p.R423Q, ZNF782:p.K247T, ZNF7:p.R337I, and ZNF831:p.E949D.

50. The pharmaceutical composition according to claim 49, wherein at least 56.65% of subjects in the population have the at least one tumor-specific mutation.

51. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from DLBCL; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of EZH2:p.Y641F, MYD88:p.L273P, BCL2:p.G33R, CARD11:p.E626K, ADCY2:p.A87V, BCL2:p.N172S, BCL2:p.H20Q, BRAF:p.K601E, BTG1:p.L31F, CACNA1E:p.R1458C, CARD11:p.E93D, CD79B:p.Y197D, CD79B:p.Y197H, CREBBP:p.R1446H, GRID1:p.E622K, HIST1H1C:p.A65V, HIST1H1E:p.G133A, HIST1H3B:p.A48S, KRAS:p.G13D, MYD88:p.S251N, PABPC1:p.R94C, PIM1:p.L164F, PIM1:p.L184F, POU2F2:p.T239A, POU2F2:p.T239S, RELN:p.R2971Q, SLC25A48:p.A67T, STAT6:p.D468H, TNF:p.L47F, and TRAF7:p.R11H.

52. The pharmaceutical composition according to claim 51, wherein at least 13.79% of subjects in the population have the at least one tumor-specific mutation.

53. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from KICH; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of ACR:p.W279C, AGRN:p.1284_1285VT>A, C7orf25:p.R384fs, CAMSAP1:p.T466fs, CBWD6:p.E102fs, DOCK8:p.L1111fs, EBPL:p.Q196P, EBPL:p.L189V, GFM1:p.A17fs, GOLGA6L6:p.D570E, ITGA5:p.A48D, LUZP2:p.S154fs, MTMR9:p.K193fs, MUC16:p.P10452fs, MUC4:p.S2832P, ODF2L:p.K407fs,

RHBDD3:p.G34fs, RILPL1:p.S358R, TAS2R30:p.L236fs, TRRAP:p.A973S, UBR5:p.K2120fs, URGCP:p.G639fs, ZNF98:p.A222T, and ZSWIM6:p.Q610fs.

54. The pharmaceutical composition according to claim 53, wherein at least 50% of subjects in the population have the at least one tumor-specific mutation.

55. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from KIRP; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of FAM18B2:p.C51Y, ZNF598:p.E25G, NEFH:p.E645K, EEF1B2:p.S43G, NEFH:p.AKSPEKEE652del, OBP2B:p.K61N, SKI:p.A62G, C14orf126:p.R6W, KRT8:p.S59A, ACSBG2:p.I250M, ASIC2:p.R46L, CSGALNACT2:p.L362F, FRG1B:p.A50P, IDUA:p.H33Q, KRTAP4-5:p.S74C, SCAF11:p.E926fs, SYN2:p.A34del, ZNF814:p.R322K, BMS1:p.E878D, JMY:p.P822T, KIF1A:p.E917D, KRTAP4-7:p.S57P, LAMA5:p.L2223R, LRP1:p.P1058T, MED16:p.H449Q, MUC2:p.T1488P, MUC5B:p.D682G, NACA2:p.R75K, NEFH:p.665_666insEE, OR2L8:p.S201fs, RGPD5:p.P1760A, RRN3:p.P11S, RRN3:p.R9C, STAG3L2:p.L81fs, ZNF814:p.G320E, ACP6:p.V29G, AHNAK2:p.S2166F, AHNAK2:p.P1215S, AP1G1:p.I782fs, AQP2:p.N68T, BAIAP2L2:p.V396M, BMP6:p.Q118L, BST1:p.G36A, CDR1:p.V31A, CLDN7:p.S172A, CLIP1:p.S1018fs, COL18A1:p.G884fs, CROCC:p.A355P, CTAGE15P:p.A364V, CUBN:p.I2816M, DMRT2:p.T106S, DPY19L1:p.V249L, DSPP:p.D1047N, EBPL:p.L189V, EIF4G1:p.E465del, EXOSC2:p.R11P, FAM216A:p.P36S, FCGR2A:p.V222G, FMOD:p.S331R, FOLR2:p.Q112R, FRG1B:p.L20P, GAGE2B:p.9_10insY, GDPD5:p.G593fs, GIMAP8:p.A544S, GLUD2:p.R300G, GLUD2:p.S496R, GPR135:p.Q5P, HOXD8:p.Q67H, IER5:p.R194G, IL25:p.C168fs, JSRP1:p.V92A, KRAS:p.G12D, KRTAP1-1:p.Y86C, KRTAP4-11:p.L161V, LTBP1:p.L163P, MAML2:p.Q591K, MAPK7:p.A501D, MEF2A:p.P99S, MET:p.H1094Y, MET:p.M1250T, MST1:p.N435fs, MUC2:p.T1582R, MUC2:p.T1722I, MUC4:p.A4222T, MUC4:p.T2335M, MUC4:p.P1138L, MUC5B:p.S1098A, MUC5B:p.S3431N, MYH7:p.A1487T, NBPF10:p.R39fs, NBPF10:p.Y638S, NEFH:p.654_654S>SPEKAKS, PARG:p.A584T, PBX2:p.Y262F, PIP4K2A:p.R219K, RLIM:p.S471P, RUNX2:p.Q71E, SGK223:p.R63S, SMARCB1:p.L365fs, SRCAP:p.Q1875fs,

TBC1D2B:p.R920Q, TCF7L2:p.R482fs, TMEM131:p.K640fs, TMEM60:p.K77fs, TPPP:p.R30K, TRPV3:p.A218E, TTBK2:p.C83W, UBXN11:p.S510G, UGT1A1:p.T4A, UTS2R:p.A289E, YBX1:p.P250L, ZNF514:p.V81G, ZNF516:p.A256D, ZNF681:p.K405Q, ZNF814:p.D404E, ZNF814:p.P323H, ZXDB:p.G206R.

56. The pharmaceutical composition according to claim 55, wherein at least 42.24% of subjects in the population have the at least one tumor-specific mutation.

57. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from LIHC; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of TP53:p.R249S, CTNNB1:p.D32V, CTNNB1:p.D32G, CTNNB1:p.S33P, CTNNB1:p.K335I, CTNNB1:p.H36P, EEF1A1:p.T432L, GNAS:p.R844C, OR2T4:p.V137L, TP53:p.H193R, ATXN1:p.Q217H, CSMD3:p.F2383fs, CTNNB1:p.D32N, CTNNB1:p.S33C, CTNNB1:p.G34V, CTNNB1:p.S45P, CTNNB1:p.N387K, DHRS4:p.I218T, DNM2:p.E378D, F5:p.Q426L, GALNTL5:p.A45T, GPX1:p.P77R, GRM8:p.R852C, IDH1:p.R132C, KIF26B:p.A2033T, KRT8:p.S59A, LOC100132247:p.T532P, NEB:p.D3854H, PIK3CA:p.H1047R, SOLH:p.R714H, TP53:p.R158H, TP53:p.V157F, and ZNF638:p.D400N.

58. The pharmaceutical composition according to claim 57, wherein at least 6.57% of subjects in the population have the at least one tumor-specific mutation.

59. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from MM; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of NRAS:p.Q61R, KRAS:p.Q61H, KRAS:p.G13D, NRAS:p.Q61K, BRAF:p.V600E, NRAS:p.Q61H, NRAS:p.G13R, ZNF717:p.W315C, ATP13A4:p.V431G, DNAJC12:p.R135K, IRF4:p.K123R, KRAS:p.A146T, KRAS:p.Q61R, KRAS:p.G12A, KRAS:p.G12D, ZNF717:p.N594I, ACTG1:p.A22P, ARL6IP1:p.M75L, BEND2:p.E630K, BRAF:p.G469A, CDHR1:p.R218G, DIS3:p.R780K, DMXL2:p.D2412E, DNAJC10:p.I80K, EGR1:p.Q9H, FGFR3:p.*807S, IDH1:p.R132C, IL6ST:p.P216H,

INTS12:p.M1V, KRAS:p.K117N, KRAS:p.A59G, KRAS:p.G12R, MAX:p.R36W, MLL5:p.G492E, NBPF1:p.E810K, NRAS:p.Q61L, NRAS:p.G12D, ODF2L:p.E294K, PADI2:p.T114P, PNLIP:p.T37M, PRDM1:p.S588C, PTPN11:p.E76K, PTPN14:p.E286K, RBM6:p.V675G, SCN10A:p.R1142H, SRGAP1:p.T61M, SUSD1:p.T168P, TAS2R16:p.V231I, TINAG:p.E403K, TRIP12:p.L1775P, and ZNF717:p.C844S.

60. The pharmaceutical composition according to claim 59, wherein at least 23.9% of subjects in the population have the at least one tumor-specific mutation.

61. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from PRAD; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of HSD17B7P2:p.N175S, RGPD5:p.P1760A, FRG1B:p.L52S, EEF1B2:p.S43G, FRG1B:p.I10T, FRG1B:p.A53T, LRRC37A2:p.T102S, NBPF10:p.E3455K, PTH2:p.L22V, CYP2D7P1:p.S32A, FAM47C:p.N648D, MAP3K9:p.E38del, MUC4:p.H4205Q, CHEK2:p.K373E, FRG1B:p.A11T, FRG1B:p.A50P, HLA-J:p.R124W, KRTAP1-5:p.I88T, KRTAP4-9:p.D18V, NPIP:p.A271V, PDGFRA:p.R483fs, ZNF780A:p.Q600H, ZNF845:p.R925H, ZNF91:p.R333H, ARFGAP3:p.N299fs, BTN2A3P:p.P3S, FNBP4:p.TT58del, HLA-A:p.Q78R, LOC554223:p.RAPWMEQ147del, PODXL:p.28_30PSP>P, POLI:p.D17del, SPOP:p.F133L, SYN2:p.A34del, TMEM52:p.23_26LLPL>L, UBC:p.L149R, ZNF208:p.I647S, ZNF799:p.E589G, ZNF814:p.D404E, ASTN2:p.L221del, B4GALNT1:p.G88fs, C16orf74:p.S21del, CCDC15:p.H458P, CD209:p.R129W, CNTNAP1:p.S1029I, DBR1:p.541_542DD>D, FAM22F:p.S691del, FRG1B:p.D32V, FRG1B:p.I34T, FRG1B:p.N55D, FRG1B:p.I59V, FRG1B:p.S71N, KIF25:p.W3R, KRTAP4-11:p.L161V, KRTAP4-11:p.M93V, KRTAP4-11:p.R51K, KRTAP4-6:p.S153Y, LILRB5:p.S598P, LMOD2:p.E124del, LOC645752:p.L40P, LRP1:p.P1058T, LRRIQ3:p.K244fs, LURAP1L:p.55_56insGGG, MLLT10:p.V463E, MYOCD:p.Q310del, NBPF10:p.N1369D, OTUD4:p.T909I, PARG:p.A584T, PEX1:p.I370fs, POTEC:p.K507E, POTEC:p.R477Q, POU4F2:p.68_69insG, PRG4:p.T417P, SDHAP2:p.R31C, SPOP:p.F133C, SPOP:p.W131G, TIMD4:p.T152del, TMEM121:p.P299del, TP53:p.G245S, UBC:p.R73L, UBC:p.I191T, WASH3P:p.G175S, ZMIZ1:p.D1048fs, ZNF709:p.T413I,

ACADS:p.R330H, ADAMTS7:p.K1357fs, AFF2:p.R597H, AGAP6:p.S127I, AK302238:p.A44T, AK302879:p.Q191R, ALDH1A2:p.R85C, ANAPC1:p.T537A, ANKRD36C:p.H438R, AP4B1:p.R276W, ARFGAP2:p.S38N, BBS9:p.F268fs, BC139719:p.L133R, BRAF:p.G469A, C22orf43:p.D171del, CANT1:p.K131R, CHD3:p.E35del, CLEC4A:p.R209H, CNOT3:p.E20K, CNPY3:p.17_18LL>L, CNTNAP3B:p.S317T, CNTNAP3B:p.M1247I, CTNNB1:p.T41A, DDX10:p.D788del, DLC1:p.S741T, DPY19L2:p.M210V, EDC4:p.S617del, EFCAB6:p.R379K, ERC2:p.927_928HH>H, FAM111B:p.S269fs, FEM1A:p.L620M, FHOD3:p.A632fs, FLJ43860:p.L850fs, FMN2:p.G59del, FNBP4:p.914_915PP>P, FRG1:p.E86del, FRG1B:p.K13N, FRG1B:p.P42Q, GABRB1:p.R416C, GABRR2:p.A368V, GAGE2B:p.9_10insY, GOLGA8DP:p.N84H, GOT2:p.R355W, GPATCH4:p.K210fs, HDGFL1:p.188_189insA, HLA-DQB2:p.G250S, HLA-DQB2:p.R247H, IDH1:p.R132H, IL27:p.E176del, IRF2BPL:p.123_125QQQ>Q, KANK3:p.DGDS489del, KIAA1462:p.858_859SS>S, KRTAP4-11:p.S48R, KRTAP4-7:p.S57P, KRTAP4-8:p.C95S, LPHN3:p.R826H, LRP10:p.L11del, LRP5:p.S1609P, LRRC16B:p.R787W, MAS1L:p.R324G, MECOM:p.R915Q, MED12:p.L1224F, MED12L:p.Q2115del, MESP2:p.GQGQGQGQ195del, MGAT4C:p.T345M, MLEC:p.E238del, MSLNL:p.T68P, MUC7:p.S173P, MYC:p.Q37del, NBPF10:p.N440D, NLRP6:p.E611del, NOX3:p.C404fs, OR1M1:p.V69I, OR7E24:p.L7fs, OTUD4:p.A153del, PANK2:p.T417fs, PCLO:p.S496P, PCNT:p.S162G, PCSK9:p.23_24insL, PHOSPHO1:p.S32del, POU4F1:p.H108del, PRAMEF8:p.R319H, PRDM7:p.M387L, PRG4:p.T597P, PTPRD:p.R1323C, PTPRF:p.R1174Q, ROBO3:p.RS1367del, ROCK1:p.T518S, RPTN:p.G296S, RTL1:p.152_152E>EE, SIRPA:p.V233I, SLC2A6:p.A230D, SLC8A2:p.E710del, SMG7:p.E846fs, SNAPC4:p.S542del, SP8:p.G165del, SPOP:p.F133I, SPOP:p.F133V, SPOP:p.F102C, SPOP:p.F102V, SRSF11:p.G17fs, SRSF4:p.K396del, SSPO:p.S4198fs, STAG3L2:p.L81fs, STK19:p.R18fs, TBC1D2B:p.R920Q, TBC1D9:p.P1233T, TCHH:p.P1158R, TCOF1:p.K1366del, TNRC18:p.2664_2665SS>S, TP53:p.R248Q, TP53:p.R175H, TP53:p.C141G, TSPAN4:p.L92V, UBXN11:p.GPGPGPSP504del, UTP3:p.E81del, WASH3P:p.L187V, ZAN:p.P717L, ZAN:p.L878P, ZFP90:p.R591fs, ZNF761:p.H373R, and ZNF91:p.H305R.

62. The pharmaceutical composition according to claim 61, wherein at least 39.85% of subjects in the population have the at least one tumor-specific mutation.

63. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from STAD; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of RNF43:p.G659fs, BZRAP1:p.P1416fs, XYLT2:p.Y526fs, LARP4B:p.T163fs, PGM5:p.I98V, ZBTB20:p.P692fs, ARID1A:p.G1848fs, FHOD3:p.P334fs, KIAA0182:p.T120fs, ATP6V1B1:p.Y383fs, PIK3CA:p.H1047R, FRMD4A:p.P1005fs, PIK3CA:p.E545K, CDC14A:p.N123fs, KRAS:p.G13D, MLL2:p.T172fs, BCORL1:p.S1679fs, PLEKHA6:p.V328fs, C9orf131:p.P342fs, CD4:p.Q164fs, FBXW7:p.R465C, GNG12:p.T68fs, IRS4:p.G591fs, JARID2:p.V422fs, KIAA0195:p.I902fs, MBD6:p.P732fs, MVK:p.P138fs, PAMR1:p.G101fs, WNT16:p.W165fs, ZNF43:p.N251fs, ABCA6:p.L306fs, ADAM28:p.K73fs, AOC3:p.L79fs, ATP2A1:p.R819fs, B2M:p.L13fs, C6orf89:p.P58fs, CNTLN:p.K1305fs, CR2:p.V206fs, DYRK4:p.K468fs, ERBB3:p.V104M, GLI1:p.W272fs, KRAS:p.G12D, MLL2:p.T172fs, MSH6:p.T1085fs, NLK:p.C190fs, OR5M3:p.T89fs, PAX6:p.P375fs, PTEN:p.L265fs, RABGAP1:p.K928fs, RAD51AP2:p.T316fs, SVIL:p.G1862fs, TP53:p.R273H, WNK4:p.G606fs, ARID1A:p.P2139fs, AXIN2:p.G665fs, C13orf33:p.R67fs, C1QTNF5:p.P308fs, CELSR1:p.G614fs, CRYGD:p.G159fs, DCHS1:p.R235fs, DDC:p.I433fs, EDNRB:p.Y383fs, EPHA2:p.P460fs, FOXN3:p.P96fs, HDAC4:p.P901fs, INF2:p.S527fs, KIRREL2:p.V649fs, KLF3:p.I104fs, KLHL14:p.P231fs, MAP7D3:p.Q308fs, OTX2:p.R44fs, PAFAH1B1:p.K302fs, PLAGL2:p.P10fs, POLM:p.P97fs, PRPF40B:p.I31fs, RALGAPB:p.T379fs, SBNO1:p.N1139fs, SERPINI1:p.L81fs, SH3KBP1:p.L574fs, SLC12A7:p.H686fs, SLC27A3:p.P643fs, TBX4:p.S370fs, TP53:p.R273C, TP53:p.R175H, TRAM1L1:p.R345fs, WBP1:p.P138fs, ABCC4:p.L883fs, AKAP13:p.K2785fs, ALDH3A1:p.P562fs, ALPK2:p.L356fs, ARFGEF1:p.P1552fs, ARID1A:p.G1848fs, AVPR1A:p.F351fs, BAX:p.M38fs, C14orf43:p.P313fs, C1QTNF5:p.G194fs, C7orf50:p.L179fs, CDC25C:p.K322fs, CETN3:p.K63fs, CHD3:p.P597fs, CTCF:p.K202fs, CTSC:p.F105fs, DDX17:p.G163fs, DLGAP3:p.G377fs, EBF3:p.G255fs, FHDC1:p.F100fs, FILIP1L:p.K749fs, FLNB:p.W529fs, GBP7:p.G431fs, GCC2:p.E700fs, GPR161:p.G517fs, IWS1:p.S802fs, KIAA0240:p.K895fs, KIAA1967:p.P415fs, LRRC43:p.D558fs, MACF1:p.R707fs,

MBD6:p.G780fs, MLL3:p.F4496fs, MPRIP:p.A351fs, MUC6:p.2129_2130SS>S, NOX5:p.P467fs, OPTN:p.P24fs, OR4K5:p.F177fs, PIK3CA:p.N345K, PIK3CA:p.E542K, PLXNA1:p.P1016fs, PNPLA7:p.P1199fs, PODN:p.I301fs, PPP2R3B:p.T389fs, PRSS36:p.L680fs, RGL2:p.G203fs, RHOQ:p.V190fs, RNF111:p.R771fs, RTN2:p.P313fs, SALL4:p.V995fs, SBF1:p.P1076fs, SETDB2:p.R715fs, SNAPC2:p.T292fs, SPG20:p.F232fs, SRCAP:p.P1876fs, STAT2:p.P489fs, TCHP:p.E172fs, TP53:p.R282W, TP53:p.R248Q, USP21:p.K474fs, WDR7:p.G262fs, ZBTB7C:p.E157fs, ZFC3H1:p.K385fs, ZNF124:p.T339fs, ZNF626:p.K115fs, ADNP2:p.S322fs, AGAP1:p.G127fs, ALDH2:p.L286fs, ARHGAP5:p.D890fs, ARHGEF17:p.A615fs, ARID1A:p.Y1324fs, ART1:p.I243fs, ASCL4:p.D35fs, ATXN2L:p.G998fs, B3GNT5:p.F30fs, BCKDHA:p.H37fs, BCL9L:p.P1127fs, BEND3:p.D265fs, BNC2:p.S575R, BRD3:p.P24fs, C12orf51:p.P4235fs, C1R:p.P216fs, C7orf49:p.G130fs, CA2:p.I145fs, CABP5:p.R145fs, CASD1:p.F781fs, CASP8:p.R471fs, CCDC153:p.P200fs, CD93:p.D280fs, CROT:p.L32fs, CSF3R:p.P468fs, CTCF:p.K202fs, ERBB2:p.S310F, FAM46D:p.S69R, FBN3:p.G601fs, FBXO21:p.F144fs, GAS6:p.G150fs, GLYR1:p.G380fs, GXYLT1:p.L223fs, HAUS6:p.S530fs, IGF2R:p.T1314fs, ITGB1:p.L378I, KDM3B:p.P1316fs, KIF13A:p.K1115fs, KLF3:p.S224fs, LARP1:p.A223fs, LRP1:p.G1488fs, LRP1:p.G1488fs, MAGEE2:p.Q45fs, MAMSTR:p.P162fs, MAPK15:p.Q511fs, MLL2:p.P647fs, MOCS2:p.P22fs, MTG1:p.L105fs, MTG1:p.H327fs, MTIF2:p.N109fs, NID2:p.R1035fs, PAX2:p.P395fs, PCCA:p.R230H, PDZD2:p.R101fs, PFKP:p.M593fs, PIK3CA:p.R88Q, PLA2G1B:p.L53fs, PLAU:p.R201fs, PMEPA1:p.P208fs, POP1:p.K750fs, PTCH1:p.P1307fs, PTPRT:p.P1075fs, RDBP:p.P6fs, RNMT:p.K392fs, ROBO2:p.P1080fs, RUNDC3B:p.L6fs, SDAD1:p.K275fs, SLC10A6:p.G109fs, SNAPC1:p.D211fs, SPATA5L1:p.C685fs, SPTA1:p.K1732T, STAT5B:p.P367fs, SYT4:p.M1fs, TAF1L:p.K851fs, TAP2:p.L75fs, TBL1XR1:p.N126fs, THEMIS:p.K406fs, TMEM79:p.P161fs, TP53:p.C176F, TP53BP2:p.K69fs, TP53RK:p.L174fs, UBQLN2:p.A523fs, UHRF1BP1:p.I1330fs, VPRBP:p.K939fs, VPS13B:p.T56fs, WASF3:p.P305fs, YLPM1:p.E1178fs, ZC3H13:p.K1006fs, ZC3H18:p.P825fs, ZC3H4:p.E779Q, ZNF48:p.P247fs, ZNF608:p.A465fs, ZNF878:p.S238fs, ZSCAN18:p.P225fs, ABCB1:p.R527fs, ABCB6:p.G318fs, ACACB:p.G255fs, ACP1:p.Q123fs, ACTL6A:p.L88fs, ADAMTSL4:p.G778fs, AGBL5:p.I420fs, AHI1:p.K303fs, AKAP9:p.M3743fs, AKD1:p.R1209fs, ANKRD40:p.D99E, ARHGEF5:p.S1512fs, ARID1A:p.K1071fs, ARID3A:p.S557G, ARPP21:p.I130fs, ASPN:p.F67fs, ASXL3:p.E873fs,

ATP6V1C2:p.R312fs, BEST3:p.P444fs, BRAF:p.P403fs, BRMS1:p.G107fs, BTBD11:p.T451fs, BTBD11:p.A561V, C11orf9:p.S261fs, C14orf102:p.R90fs, C14orf43:p.Q36fs, C15orf52:p.G98fs, C19orf21:p.R262C, C19orf70:p.P50fs, C20orf160:p.P46fs, C3:p.P890fs, CADPS2:p.N468fs, CASC3:p.S232F, CASC3:p.P603L, CASC3:p.P645L, CASC3:p.S658L, CASKIN2:p.P727fs, CBLL1:p.E138fs, CBLN3:p.P69fs, CCDC108:p.P1164fs, CCDC148:p.K420fs, CCDC153:p.P200fs, CCDC169-SOHLH2:p.K162R, CCDC88A:p.K677fs, CD1E:p.F85V, CD3EAP:p.K218fs, CDH11:p.K357T, CDH1:p.D254Y, CDH23:p.V403I, CFI:p.K37fs, CHPF2:p.D645fs, CIC:p.R507fs, CIC:p.A1114fs, CIC:p.A1114fs, CLSTN1:p.T615M, CNBD1:p.L396P, CNGA4:p.K510T, CNOT6:p.S248fs, CNTROB:p.R920fs, COL9A1:p.P283fs, CPAMD8:p.P784fs, CR1L:p.L79fs, CRB1:p.F630V, CSMD1:p.L3410V, CTNNA3:p.K856fs, CTNND1:p.I447fs, CTSD:p.P89fs, CUX1:p.A439fs, CYP7B1:p.K332T, DAB2IP:p.D994fs, DNAH11:p.T871fs, DNAH8:p.K1688fs, DNAJC1:p.K193fs, DNM2:p.P791fs, DSTN:p.F101fs, DYRK1B:p.Q545fs, EAF2:p.V109fs, EDNRB:p.A104V, EEA1:p.N570fs, EFHA1:p.F290fs, EGR1:p.P332fs, EIF4G3:p.K563fs, ELK3:p.S173fs, ENTPD2:p.G204fs, EOMES:p.G332fs, EPHA10:p.P868fs, EPHB6:p.G54fs, EPHX1:p.P132fs, EPPK1:p.G2015fs, ERBB4:p.M1fs, ESF1:p.T99fs, EXOSC8:p.L160fs, FAM113B:p.R51fs, FAM116A:p.L441fs, FAM135B:p.S645R, FAM151A:p.P117fs, FAM193A:p.D428fs, FAM193A:p.D428fs, FAM214B:p.A42fs, FAM40B:p.R740C, FAM70B:p.S19L, FASTKD1:p.K3fs, FBXW7:p.R479Q, FBXW9:p.G298fs, FER:p.L474fs, FERMT2:p.K152fs, FGGY:p.G138fs, FIGNL1:p.K309fs, FLG:p.K159fs, FLNB:p.W529fs, FOLH1:p.S501fs, FYB:p.G324fs, GABRD:p.Q412fs, GALNTL1:p.W317fs, GANAB:p.L23fs, GCDH:p.L389fs, GIMAP7:p.V276fs, GIPC3:p.G227fs, GLI3:p.P1033fs, GLIPR1L2:p.G92fs, GNPNAT1:p.F54fs, GON4L:p.M134fs, GPATCH4:p.K210fs, GRK4:p.K22fs, GTF3C1:p.S767fs, GTF3C4:p.E562fs, H2AFY2:p.K144fs, HCFC1R1:p.P83fs, HCRTR2:p.S9fs, HCRTR2:p.S9fs, HDLBP:p.G747fs, HECA:p.R333fs, HIVEP3:p.H554fs, HIVEP3:p.P534fs, HLA-C:p.P209fs, HOOK1:p.L361fs, HOXD8:p.P122fs, HTT:p.G697fs, IBTK:p.K1213fs, IDE:p.K37fs, IFT172:p.A837T, INPPL1:p.A974fs, INPPL1:p.P1154fs, INSM2:p.T533fs, INTS12:p.L14fs, INVS:p.R815fs, IPO11:p.S844fs, IRX6:p.A425V, ISG20L2:p.P288fs, ITGB8:p.A7fs, JARID2:p.G394fs, JHDM1D:p.R97fs, KBTBD6:p.G442fs, KCNC1:p.K455fs, KCNH2:p.G149A, KCNJ10:p.P102fs, KCNMB2:p.N151K, KCTD21:p.T6M, KIAA0586:p.A1592fs, KIAA1009:p.F406fs, KIAA1109:p.E1588fs, KIAA2026:p.K690fs,

KIF26B:p.S1065fs, KIF6:p.L204fs, KIRREL:p.P335fs, KLC2:p.T568fs, KRAS:p.Q61H, KRAS:p.G12S, MAN1C1:p.G431fs, MAP1A:p.P2063fs, MAP2:p.K1472fs, MAP3K12:p.R449del, MAP7D1:p.A80fs, MGST2:p.K102fs, MKI67:p.T1664fs, MKL1:p.P307fs, MLL2:p.P2354fs, MLL2:p.L656fs, MLL2:p.P647fs, MLL2:p.L1877fs, MMP3:p.I64fs, MPDZ:p.K1582fs, MTUS2:p.R1005W, MUC16:p.A6156T, MYB:p.R481fs, MYEOV:p.L269fs, MYH11:p.K1263del, MYO18A:p.P209fs, MYO7A:p.I539fs, MYOCD:p.G226fs, NAA16:p.H514fs, NBEA:p.V2247fs, NCAPD3:p.Q909fs, NCAPH:p.T466fs, NCOR2:p.P1308fs, NEFM:p.A213V, NEK8:p.V690fs, NF1:p.T676fs, NHLRC1:p.F204fs, NKD1:p.P286fs, NPR3:p.Y138H, NT5M:p.P206fs, NUFIP2:p.R224fs, NUP210:p.L135fs, NYNRIN:p.G113fs, OBSCN:p.G997fs, OGDH:p.Y948fs, OR4C16:p.S135R, OR51A7:p.L124R, OR7C1:p.C179fs, OSBP2:p.H627fs, OTOF:p.E1304K, P2RX1:p.R20fs, PALB2:p.M296fs, PALB2:p.N280fs, PANK1:p.K400fs, PAPD4:p.C225fs, PAPPA2:p.I1683fs, PARP15:p.K461fs, PARP4:p.K847fs, PCDH10:p.N118fs, PCDH10:p.P225fs, PCGF3:p.H63fs, PELI2:p.G197fs, PHACTR1:p.V251fs, PHACTR2:p.S237fs, PHACTR4:p.S354fs, PHKB:p.K642fs, PIAS3:p.H116fs, PIGO:p.P787fs, PIGT:p.A346fs, PIK3R3:p.M341fs, PITPNM1:p.P295fs, PKN2:p.K76fs, PLA2G15:p.W230fs, PLAG1:p.K184fs, PLEKHO1:p.T254fs, PLOD3:p.R297fs, PLOD3:p.P296fs, PLXNA2:p.P464fs, POLQ:p.L1430fs, PPARGC1B:p.P135fs, PPL:p.P454fs, PPM1H:p.P226fs, PPP1R12C:p.P372fs, PREX2:p.R562fs, PRICKLE4:p.Q109fs, PRKAR1B:p.P87fs, PRKCG:p.R345C, PRMT8:p.S28fs, PROX1:p.F592fs, PRRG3:p.R163fs, PSD2:p.G256fs, PTCHD3:p.F588fs, PTPN4:p.N319fs, PTPRC:p.Q895H, PWWP2B:p.S84fs, PYGO2:p.Q150fs, RABGAP1:p.K928fs, RB1CC1:p.N1171fs, RBM6:p.R96fs, RHOA:p.Y42C, RIMS1:p.R71G, RIMS2:p.V401fs, RING1:p.G171fs, RINT1:p.L107fs, RNF43:p.P116fs, ROBO2:p.K1293fs, RPS6KA6:p.K109fs, RRS1:p.N45fs, RSF1:p.K386fs, RUSC2:p.P486fs, RXFP3:p.A60V, SAFB:p.W798fs, SCARF1:p.R614Q, SCLT1:p.K109fs, SERPINB12:p.Q168fs, SGK3:p.L61fs, SGOL2:p.E407fs, SIGLEC1:p.P318fs, SIK1:p.Q678fs, SLC16A6:p.G98fs, SLC25A17:p.F28fs, SLC26A7:p.I629fs, SLC32A1:p.V494I, SLC4A3:p.L1061fs, SLC7A10:p.P157fs, SLC9A2:p.T746fs, SLITRK1:p.K45fs, SND1:p.H721fs, SOAT1:p.F64fs, SORBS2:p.E1158fs, SOX7:p.L309fs, SPAG17:p.Q1264fs, SPTY2D1:p.P485fs, SRCIN1:p.P865fs, SREBF2:p.H763fs, SRRT:p.G102fs, STAB1:p.P1120fs, STRADA:p.R333fs, STX2:p.K252fs, SV2A:p.E138fs, SYCP2:p.M176fs, SYNJ2:p.P1111fs, TAS2R10:p.L196fs,

TBC1D22B:p.A175fs, TEAD2:p.P298fs, TFE3:p.G482fs, TGM6:p.T358fs, TIMM44:p.K83fs, TIMP3:p.A199fs, TLR4:p.L498V, TMEM132D:p.P206fs, TMEM41A:p.F156fs, TMEM41B:p.F230fs, TMTC4:p.R611C, TNK2:p.P632fs, TOPBP1:p.I1381fs, TP53:p.E286K, TP53:p.P152fs, TRIP11:p.K541fs, TRPA1:p.T673fs, TRPM8:p.H765fs, TTF1:p.K336fs, TTI1:p.R707H, TTN:p.E15192D, U2AF2:p.L175fs, UBC:p.G684fs, UBR4:p.P2802fs, UPF2:p.E1033D, UPK2:p.P49fs, USP13:p.I116fs, USP15:p.K782fs, VASH1:p.G3fs, VEZF1:p.355_356insN, VPS13A:p.F2883fs, WAPAL:p.R522fs, WDFY3:p.L1842fs, WDR59:p.N160fs, WDR5:p.N214fs, WDR60:p.Q412fs, WDTC1:p.M287fs, WHSC1L1:p.K418fs, WNT1:p.W167fs, XIRP2:p.E1007D, YBX2:p.P226fs, YIF1A:p.R131fs, ZBBX:p.E151del, ZBTB40:p.L262fs, ZBTB7C:p.G342fs, ZBTB7C:p.D154fs, ZC3H18:p.T701fs, ZDHHC5:p.E651del, ZDHHC7:p.P316fs, ZFHX3:p.R1893fs, ZFHX3:p.E763fs, ZFHX4:p.L408fs, ZHX3:p.N249K, ZIM3:p.I384fs, ZKSCAN5:p.D13fs, ZMYM4:p.K345fs, ZNF236:p.T1410M, ZNF23:p.F122fs, ZNF334:p.K426fs, ZNF358:p.T130fs, ZNF701:p.L296fs, ZNF711:p.L737fs, and ZNF831:p.A49fs.

64. The pharmaceutical composition according to claim 63, wherein at least 48.79% of subjects in the population have the at least one tumor-specific mutation.

65. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from TGCT; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of FAM18B2:p.C51Y, BTN2A3P:p.P3S, MUC2:p.G1715S, NBPF10:p.L44V, SP8:p.G156S, DCP1B:p.Q252H, DEK:p.E41D, ERC1:p.K692R, FAM104B:p.D75H, FRG1B:p.M49V, KRTAP10-10:p.V234M, LRRCC1:p.A6V, NRAS:p.Q61R, PNPLA4:p.L223P, ANKLE1:p.C644fs, ANKLE1:p.C644fs, KIT:p.D816H, KIT:p.D816Y, MUC2:p.T1597I, PSMD11:p.A5V, RHPN2:p.V73M, RUNX2:p.Q71E, SP4:p.E7K, TUBA1C:p.L146F, ZNF814:p.Y324H, ADAMTS17:p.N572T, ATRX:p.K1936R, BCL11B:p.E535D, BMP2K:p.Q460H, BMP2K:p.H487Q, C12orf32:p.D60V, C22orf43:p.K19E, CDC27:p.N571I, CDC27:p.P242S, DDX11:p.K208fs, EBPL:p.L189V, EZH2:p.K510R, FAM86A:p.A141T, GAS2L2:p.D189A, GRID2IP:p.LS754del, HGC6.3:p.E171G, KIT:p.D816V, KIT:p.N822Y, KIT:p.N822K, KRAS:p.Q61R,

KRAS:p.G12V, KRTAP1-1:p.I116V, LRRC37BP1:p.Y166D, MEF2A:p.R127Q, MFF:p.S7F, MST1:p.R347W, MUC4:p.S3048L, MUC6:p.H2000Q, MUC6:p.P1977H, NAT10:p.I393T, OPLAH:p.A900D, PIEZO1:p.Q749E, PRAMEF4:p.F300V, RBM10:p.E184D, SERINC2:p.T121P, SPIN2A:p.M150V, SRRM2:p.A2257S, SSBP3:p.K6R, ZNF680:p.R501W, ABCC8:p.Y512C, ABCC9:p.L466P, ABCD1:p.H169Q, ABL2:p.P19T, ACVR2B:p.R48C, AHDC1:p.P33fs, AHNAK2:p.L1640M, ALPPL2:p.W31S, AMMECR1:p.G77C, ANK3:p.D1322E, ANKHD1-EIF4EBP3:p.G60S, ANKRD11:p.Y2015S, ANKRD11:p.K369R, ANKRD50:p.V637M, APBB3:p.L450P, ARHGAP24:p.T35A, ARID4B:p.G1076A, ARMC3:p.A514T, ARRB2:p.T99P, ATAD5:p.I305V, ATXN3:p.305_306insQQQQQQQ, AVPR1B:p.G39R, AXDND1:p.E994Q, BAI2:p.A231G, BEST3:p.P383L, BIRC6:p.V414L, BIRC8:p.A225M, BRWD1:p.K1319R, BTN2A2:p.L15F, C12orf51:p.A2644T, C12orf65:p.K143T, C16orf62:p.L244I, C1QBP:p.T225I, C1orf167:p.S123G, C5orf25:p.Y4F, CACNA1E:p.G2080S, CAPNS1:p.LV303del, CCDC159:p.A332S, CDKAL1:p.P409L, CDYL:p.V48A, CDYL:p.A60G, CELSR2:p.L17P, CHD4:p.E138D, CKAP5:p.G576A, CLCC1:p.K52R, CMTM8:p.S26T, CNKSR2:p.P249L, CNTN5:p.I501T, COG5:p.H617R, COL15A1:p.K708R, COL6A3:p.A2378D, CRYGB:p.R143G, CSGALNACT2:p.L362F, CUL4A:p.I438F, CXXC1:p.Q156H, CYP19A1:p.F406L, DCLRE1B:p.F28I, DDX11:p.A376T, DDX11:p.E680D, DEPDC5:p.R1525Q, DLC1:p.S741T, DNMT1:p.R995Q, DOCK11:p.Q169E, DSPP:p.D1047N, E2F7:p.I91S, EBF1:p.D353G, ECI2:p.K55R, EEF1A2:p.Y418S, EIF3J:p.A8G, EML6:p.K805R, EPAS1:p.S474T, EPRS:p.L1335I, ERICH1:p.E327K, FAM101B:p.L5P, FAM104A:p.M1R, FAM110D:p.R71H, FAM155A:p.Q95R, FAM186A:p.G1492E, FAM194B:p.Y139H, FAM21B:p.P1231S, FAM32A:p.K9R, FAM46B:p.H416R, FAM48B1:p.I499V, FAM48B1:p.A516P, FAM5C:p.S425W, FAM86C2P:p.C120Y, FBXL14:p.V48G, FRMPD3:p.Q832del, FRS2:p.L47S, GDF5:p.E105fs, GPNMB:p.C3fs, GPT2:p.R10P, H2AFV:p.Q125R, HDLBP:p.R503C, HERC2:p.R2129C, HIST1H2BJ:p.K13R, HLX:p.N231K, HMGB3:p.E198D, HSF4:p.R169W, HSF4:p.S491P, HYAL4:p.D222N, INO80E:p.P206fs, INTS4:p.S460A, IQCF6:p.R3H, ITPR1:p.M1569I, ITPR3:p.R1698G, KANSL3:p.G376E, KCNA4:p.E627del, KDM5A:p.P423S, KDM6A:p.Y362fs, KIAA0020:p.K63R, KIDINS220:p.N851S, KIT:p.W557G, KLHDC2:p.W321S, KRAS:p.A146T, KRAS:p.Q61H, KRAS:p.Q61L, KRAS:p.G12A, KRAS:p.G12R, KRBA1:p.R839G, KRTAP4-8:p.T63S, L2HGDH:p.P441del, LAMC3:p.P174Q,

LHCGR:p.L16Q, LOC401296:p.L144M, LPHN2:p.F906I, LRP12:p.G310C, LTB4R:p.F73L, LTBP3:p.L35del, LUC7L3:p.S148T, LYPD4:p.T64K, MAMLD1:p.Q572L, MAP4K2:p.R341G, MAPK7:p.A501D, MAT2A:p.E166G, MED12L:p.C1292Y, MESP2:p.Q182E, MEX3C:p.R534S, MIER2:p.L131F, MLL5:p.Y66C, MLLT3:p.177_178SS>S, MMS19:p.D1005N, MRPS25:p.E119del, MSH6:p.D576A, MTIF3:p.G65E, MUC17:p.M1807T, MUC17:p.T2279N, MUC17:p.G2474S, MUC2:p.TTPSPP1475del, MUC2:p.T1568M, MUC2:p.T1580N, MUC2:p.T1704I, MUC2:p.T1706M, MUC4:p.H1117D, MUC5B:p.R1097H, MYEF2:p.K323E, MYEOV:p.L302H, MYH8:p.A785V, MYO1A:p.N584K, NAP1L3:p.P353R, NAV1:p.I1433M, NCAM1:p.E131G, NEB:p.D3107N, NEFH:p.V670E, NELL2:p.G170D, NHS:p.D1561N, NKD2:p.H447del, NSD1:p.T461R, NT5C3:p.A3P, NYAP1:p.P480S, OBSCN:p.A908T, OR10J1:p.R244Q, OR1S2:p.M298I, OR2L3:p.K294R, OR6K6:p.F311L, PABPC3:p.V325fs, PBX2:p.Y262F, PCDHB4:p.P255F, PCMTD1:p.V281A, PCP4L1:p.K64R, PDE3A:p.A98E, PDIA6:p.N56K, PDS5A:p.L1309F, PHLDA2:p.R28S, PIGR:p.V183G, PIK3CA:p.E545K, PIK3CD:p.C381R, PKD1:p.T938M, PLEKHM1:p.A895V, PLEKHN1:p.A600D, PLXND1:p.R367L, PMS2:p.K651R, PNMA3:p.E200G, POTEF:p.S112G, PRAMEF8:p.I448V, PRDM2:p.E278D, PRODH:p.L527V, PRPF31:p.R289W, PSME4:p.N495D, PTGR1:p.E40A, PTPRB:p.Q726H, RABGEF1:p.N207D, RAC1:p.P34R, RANBP17:p.M900I, REV3L:p.A30S, RFC3:p.I82N, RFC3:p.K296N, RIMBP3:p.Q1154R, RPL19:p.R151C, RPL5:p.R58fs, RPTN:p.M538I, RRAD:p.A278E, RYR1:p.D668Y, RYR2:p.L2023F, SAFB:p.G799V, SCRIB:p.G332V, SDK1:p.Y2146C, SEC16A:p.T443K, SEC31B:p.P905S, SELO:p.R565Q, SELP:p.A297T, SI:p.I1681K, SLC2A7:p.H268Q, SLC37A1:p.V528I, SLC38A1:p.G100R, SMARCA2:p.D1158A, SMARCA5:p.T156fs, SMC3:p.E970Q, SMG1:p.P2696H, SNRNP200:p.A2129G, SPIN2B:p.M150V, ST6GALNAC1:p.S354N, STAMBPL1:p.Y143H, STARD8:p.G662A, STON1-GTF2A1L:p.N451S, SYMPK:p.A336G, TAS2R8:p.W98C, TCHH:p.W1016R, TET1:p.T1472S, TIAM1:p.G247M, TNS1:p.P183S, TOR1AIP2:p.G146R, TPRX1:p.S216P, TPRX1:p.S200P, TRMT61A:p.S244I, TSPAN4:p.L92V, TTF1:p.Q530R, UBE2M:p.G131D, UBR5:p.R2517S, UGT2B11:p.R447I, UMODL1:p.M559I, UNC93A:p.V445A, USP46:p.Q137R, VWA2:p.G317D, VWA7:p.V792G, WASH3P:p.L187V, WNT5B:p.K327E, WRN:p.E510D, XDH:p.P410S, ZAN:p.S755P, ZC3H11A:p.I777T, ZC3H7A:p.C575S, ZDHHC11:p.H250Q, ZFHX4:p.D3239N, ZKSCAN3:p.K200A, ZMYM4:p.T367I, ZNF174:p.P353T,

ZNF322:p.Y353C, ZNF592:p.K324Q, ZNF592:p.P500T, ZNF782:p.C145F, ZNF799:p.C453R, ZNF804B:p.P644S, and ZNRF3:p.R889W.

66. The pharmaceutical composition according to claim 65, wherein at least 51.61% of subjects in the population have the at least one tumor-specific mutation.

67. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from THCA; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of BRAF:p.V600E, NRAS:p.Q61R, HRAS:p.Q61R, NRAS:p.Q61K, OTUD4:p.T909I, HRAS:p.Q61K, NLRP6:p.E611G, AKT1:p.E17K, ANKMY1:p.N302I, ATP6V1A:p.L237P, CYP19A1:p.S113I, DCUN1D4:p.L275P, DGCR8:p.E518K, DLC1:p.S741T, DNAH10:p.C1853F, EIF1AX:p.G9D, FAM75D5:p.L222P, FCGRT:p.P40A, KRAS:p.Q61K, LMX1B:p.Q285del, MAS1L:p.R324G, MED15:p.S35I, MEGF6:p.Y393C, ODZ2:p.A1529V, OR5L1:p.R122H, OR6K6:p.F311L, OTX1:p.D315N, POTEE:p.S75G, SCN5A:p.D1978H, TOP2A:p.K1199E, and TSG101:p.K265R.

68. The pharmaceutical composition according to claim 67, wherein at least 69.88% of subjects in the population have the at least one tumor-specific mutation.

69. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from UCS; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of TP53:p.R248Q, ZNF814:p.D404E, BTN2A3P:p.P3S, FBXW7:p.R465C, FRG1B:p.G65E, MUC4:p.H4205Q, NBPF10:p.V99F, PIK3CA:p.E545K, PIK3CA:p.H1047R, PPP2R1A:p.P179R, DDX11L2:p.*128Q, FBXW7:p.R479Q, FRG1B:p.K13N, FRG1B:p.L52S, HSD17B7P2:p.N175S, KRAS:p.G12V, LOC283788:p.S37G, TP53:p.R273H, TP53:p.S241Y, ADAMTS12:p.E359K, BCL2L11:p.L187fs, CDC27:p.L460fs, CHEK2:p.K373E, ESPNP:p.W122fs, FBXW7:p.R689W, FBXW7:p.R505G, FBXW7:p.R465H, FCGBP:p.V4019M, FRG1B:p.I10T, FRG1B:p.D32V, FRG1B:p.R37K, KRAS:p.G12D, LOC100233156:p.R21C, LOC283788:p.I46M,

LRP1B:p.L1392F, MAMLD1:p.Q572L, MST1P9:p.L319P, MUC4:p.A2390T, MUC4:p.G2172S, NBPF10:p.E3455K, PIK3CA:p.G106V, PODXL:p.28_30PSP>P, POTEC:p.R477Q, PPP2R1A:p.R183W, PPP2R1A:p.S219L, PTPN18:p.TG378del, RGPD3:p.N756D, RPL13AP20:p.G107R, SAMD4B:p.R477W, SMAP1:p.E169fs, TP53:p.H193R, TP53:p.H179R, TP53:p.R175H, TUBBP5:p.R119H, and U2AF1:p.S34F.

70. The pharmaceutical composition according to claim 69, wherein at least 16.07% of subjects in the population have the at least one tumor-specific mutation.

71. The pharmaceutical composition according to any of claims 1 to 7, wherein:

(a) the population of subjects is suffering from PAAD; and

(b) the at least one tumor-specific mutation comprises any combination of mutations selected from the group consisting of RBM14:p.AAAAAAA286del, KRAS:p.G12D, JMY:p.PPPPPPPPPPPP811del, RIOK1:p.D69del, LCE2A:p.SSGGCCGSSSGGCC47del, KRAS:p.G12V, C1QB:p.GPKGPMGPKGGPGAPGAP90del, ZFHX3:p.V777del, DBR1:p.541_542DD>D, AEBP1:p.K1133del, KRAS:p.G12R, RBM47:p.495_502AAAAAAAA>A, , AP3S1:p.K41fs, MLL2:p.AEGPHLSPQPEELHLSPQ792del, RFX1:p.386_401GGGGGGGGGGGGGGSG>G, AXDND1:p.EQ991del, HERC2P3:p.A803V, RGPD3:p.N756D, FNDC1:p.D1180del, ANAPC1:p.T537A, IRS4:p.21_22AA>A, GIGYF2:p.Q1005del, NCOA3:p.Q1253fs, SIK3:p.950_951QQ>Q, GPR6:p.AAAAATAAGGPDTGEWGPPA36del, NBPF12:p.D1323fs, SHROOM4:p.1156_1157EE>E, ZMIZ2:p.VAAAAATATATATAT153del, DGKK:p.PAPP41del, LZTS1:p.RTQDLEGALRTKGLEL432del, CASQ2:p.395_396DD>D, DCP1B:p.251_252insH, ESPNP:p.296_317PPPPSFPPPPPPPPGTQLPPPPP>P, KBTBD6:p.T403K, NBPF16:p.D449fs, ANKRD36C:p.H438R, ESPN:p.PPPPPPSFPPPPPPPPGTQLPP430del, FCGBP:p.A2493V, KRAS:p.Q61H, NCOA3:p.Q1276del, OR2T2:p.C203fs, TMCC1:p.Q565L, BCKDHA:p.G129fs, ESPNP:p.H64fs, GNAS:p.R844H, NBPF14:p.R25C, OGFOD1:p.G477fs, RBM12:p.P693S, SLC38A10:p.1071_1072II>I, SORBS2:p.P866S, TP53:p.R248W, TP53:p.R175H, and UBAC1:p.E269del.

72. The pharmaceutical composition according to claim 71, wherein at least 50% of subjects in the population have the at least one tumor-specific mutation.

73. The pharmaceutical composition according to any of claims 1 to 72, wherein the composition comprises at least 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19 or 20 neoantigenic peptides.

74. The pharmaceutical composition according to claim 73, wherein the composition comprises 15 to 20 neoantigenic peptides.

75. The pharmaceutical composition according to any of claims 1 to 74, wherein each neoantigenic peptide is from about 5 to about 50 amino acids in length.

76. The pharmaceutical composition according to any of claims 1 to 75, wherein each tumor-specific neoepitope binds to HLA-A, -B or –C with a K_D of less than 500 nM.

77. The pharmaceutical composition according to any of claims 1 to 76, which is an immunogenic or vaccine composition.

78. The pharmaceutical composition according to claim 77, further comprising an immunomodulator or adjuvant.

79. The pharmaceutical composition according to claim 78, wherein the immunodulator or adjuvant is selected from the group consisting of poly-ICLC, 1018 ISS, aluminum salts, Amplivax, AS15, BCG, CP-870,893, CpG7909, CyaA, dSLIM, GM-CSF, IC30, IC31, Imiquimod, ImuFact IMP321, IS Patch, ISS, ISCOMATRIX, Juvlmmune, LipoVac, MF59, monophosphoryllipid A, Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, OK-432, OM-174, OM-197-MP-EC, ONTAK, PepTel®, vector system, PLGA microparticles, resiquimod, SRL172, Virosomes and other Virus-like particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, and Aquila's QS21 stimulon.

80. A method of treating or preventing a tumor in a subject in need thereof, comprising administering to the subject a pharmaceutical composition according to any of claims 1 to 79.

81. The method of claim 80, wherein the pharmaceutical composition is administered as a combination therapy with an additional cancer therapy.

82. The method of claim 81, wherein the additional thereapy is a check point inhibitor.

83. The method of claim 81, wherein the additional therapy is surgery, chemotherapy, or a targeted therapy.

84. A method of prophylactic cancer treatment comprising:

(a) selecting a cancer drug for a patient in need thereof, the drug selected from the group consisting of ibrutinib, erlotinib, imatinib, gefitinib, crizotinib, trastuzumab, vemurafenib, RAF/MEK inhibitors, and antiestrogen therapy; and

(b) administering prophylactically to the subject, a pharmaceutical composition according to any of claims 1 to 79 wherein the at least one neoantigenic peptide is derived from drug resistant mutations associated with the selected cancer drug.

85. A method of treating or preventing a tumor in a population of subjects in need thereof, comprising administering to a subject an agent comprising an extracellular ligand-binding domain recognizing a tumor-specific neoepitope comprising a tumor-specific mutation having an incidence of at least 1% of subjects in the population.

86. The method according to claim 85, wherein the agent comprises an antibody, antibody fragment, antibody drug conjugate, aptamer, CAR, or T cell receptor.

87. The method according to claim 86, wherein the antibody or antibody fragment is humanized, fully humanized, or chimeric.

88. The method according to claims 86 or 87, wherein the antibody fragment comprises a nanobody, Fab, Fab', (Fab')2, Fv, ScFv, diabody, triabody, tetrabody, Bis-scFv, minibody, Fab2, or Fab3 fragment.

89. The method according to any of claims 85 to 88, wherein the tumor-specific mutation comprises a mutation listed for any population in Table 9.

90. The method according to any of claims 85 to 88, wherein the tumor-specific mutation is within a gene containing an extracellular domain.

91. The method according to claim 90, wherein the tumor-specific mutation comprises FGFR3 S249C, ERBB3 V104M, EGFR L858R, MUC4 H4205Q, PDGFRA R483fs, TMEM52 23_26LLPL>L, or PODXL 28_30PSP>P.

92. The method according to claim 90, wherein the tumor-specific mutation is within the extracellular domain.

93. The method according to claim 92, wherein the tumor-specific mutation comprises FGFR3 S249C or ERBB3 V104M.