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(54) Titre : NOUVEAUX PEPTIDES ET COMBINAISON DE PEPTIDES POUR UNE UTILISATION DANS
L'IMMUNOTHERAPIE CONTRE LE LYMPHOME NON HODGKINIEN ET D'AUTRES CANCERS
(54) Title: NOVEL PEPTIDES AND COMBINATION OF PEPTIDES FOR USE IN IMMUNOTHERAPY AGAINST NHL
AND OTHER CANCERS

(57) **Abrégé/Abstract:**

The present invention relates to peptides, proteins, nucleic acids and cells for use in immunotherapeutic methods. In particular, the present invention relates to the immunotherapy of cancer. The present invention furthermore relates to tumor-associated T-cell peptide epitopes, alone or in combination with other tumor-associated peptides that can for example serve as active pharmaceutical ingredients of vaccine compositions that stimulate anti-tumor immune responses, or to stimulate T cells ex vivo and transfer into patients. Peptides bound to molecules of the major histocompatibility complex (MHC), or peptides as such, can also be targets of antibodies, soluble T-cell receptors, and other binding molecules.

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(57) Abstract: The present invention relates to peptides, proteins, nucleic acids and cells for use in immunotherapeutic methods. In particular, the present invention relates to the immunotherapy of cancer. The present invention furthermore relates to tumor-associated T-cell peptide epitopes, alone or in combination with other tumor-associated peptides that can for example serve as active pharmaceutical ingredients of vaccine compositions that stimulate anti-tumor immune responses, or to stimulate T cells ex vivo and transfer into patients. Peptides bound to molecules of the major histocompatibility complex (MHC), or peptides as such, can also be targets of antibodies, soluble T-cell receptors, and other binding molecules.

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Novel peptides and combination of peptides for use in immunotherapy against NHL and other cancers

The present invention relates to peptides, proteins, nucleic acids and cells for use in immunotherapeutic methods. In particular, the present invention relates to the immunotherapy of cancer. The present invention furthermore relates to tumor-associated T-cell peptide epitopes, alone or in combination with other tumor-associated peptides that can for example serve as active pharmaceutical ingredients of vaccine compositions that stimulate anti-tumor immune responses, or to stimulate T cells ex vivo and transfer into patients. Peptides bound to molecules of the major histocompatibility complex (MHC), or peptides as such, can also be targets of antibodies, soluble T-cell receptors, and other binding molecules.

The present invention relates to several novel peptide sequences and their variants derived from HLA class I molecules of human tumor cells that can be used in vaccine compositions for eliciting anti-tumor immune responses, or as targets for the development of pharmaceutically/immunologically active compounds and cells.

BACKGROUND OF THE INVENTION

Non-Hodgkin lymphomas (NHLs) are a heterogeneous group of lymphoproliferative diseases. NHL usually originates in lymphoid tissues and can spread to other organs (National Cancer Institute, 2015).

NHL is the seventh most common type of cancer and represents 4.3% of all new cancer cases in the U.S. (SEER Stat facts, 2014). It is the most common hematological malignancy both in Europe and the U.S. (Inoges et al., 2014).

The probability to develop NHL increases with age: The median age at the time point of diagnosis is 66 years. NHL is more common in people of Caucasian descent (21 cases per 100,000 persons), followed by Africans (15 cases per 100,000 persons) and Asians (14 cases per 100,000 persons). Men have a higher risk to develop NHL

than women (23.9 cases per 100,000 males vs. 16.3 cases per 100,000 females) (SEER Stat facts, 2014).

The 5-year relative survival of NHL patients is 70% and varies with the cancer stage at the time point of diagnosis. For localized disease, the 5-year relative survival is 82%. If NHL has spread to different parts of the body, the 5-year relative survival decreases to 73.8% for regional and 62.4% for distant stage disease (SEER Stat facts, 2014). Risk factors include (high) age, male gender, ethnicity (Caucasian), exposure to benzene or radiation, HIV, autoimmune diseases, infections with HTLV-1, EBV or HHV8, infections with *Helicobacter pylori*, *Chlamydia psittaci*, *Campylobacter jejuni* or HCV, (high) body weight and breast implants (American Cancer Society, 2015).

NHL has over 60 subtypes. The three most common subtypes are diffuse large B-cell lymphoma (DLBCL, the most common subtype), follicular lymphoma (FL, the second most common subtype) and small lymphocytic lymphoma/chronic lymphocytic lymphoma (SLL/CLL, the third most common subtype). DLBCL, FL and SLL/CLL account for about 85% of NHL (Li et al., 2015).

Diffuse large B-cell lymphoma (DLBCL) is the most common NHL type and comprises 30% of all NHLs. DLBCL belongs to the aggressive NHL subtypes and most patients show a quickly progressing disease. The International Prognostic Index (IPI) for aggressive NHL uses five significant risk factors prognostic for overall survival:

1. Age (≤ 60 years vs. > 60 years)
2. Serum lactate dehydrogenase (LDH) (normal vs. elevated)
3. Performance status (0 or 1 vs. 2-4)
4. Stage (stage I or II vs. stage III or IV)
5. Extranodal site involvement (0 or 1 vs. 2-4).

Patients with two or more risk factors have a less than 50% chance of relapse-free survival and overall survival at 5 years. Patients with rearrangements of the *bcl-2* and *myc* gene and/or overexpression of *myc* have a particularly poor prognosis. DLBCL patients co-expressing CD20 and CD30 have a more favorable prognosis and are predestined for an anti-CD30-specific therapy (National Cancer Institute, 2015).

Follicular lymphoma (FL) is the second most common NHL type and comprises 20% of all NHLs and 70% of all indolent lymphomas. More than 90% of the patients exhibit rearrangement of the bcl-2 gene. Most patients are 50 years or older at the time point of diagnosis and have advanced stage disease. The Follicular Lymphoma International Prognostic Index (FLIPI) uses five significant risk factors prognostic for overall survival:

1. Age (≤ 60 years vs. > 60 years)
2. Serum lactate dehydrogenase (LDH) (normal vs. elevated)
3. Stage (stage I or II vs. stage III or IV)
4. Hemoglobin level (≥ 120 g/L vs. < 120 g/L)
5. Number of nodal areas (≤ 4 vs. > 4).

Patients with none or one risk factor have an 85% 10-year survival rate. Patients with three or more risk factors have a 40% 10-year survival rate (National Cancer Institute, 2015).

Diagnosis of NHL is done on an excisional biopsy of an abnormal lymph node or an incisional biopsy of an involved organ. Besides immunohistochemistry, cytogenetics, molecular genetics and fluorescent in situ hybridization (FISH) are used to clarify the diagnosis (Armitage, 2007).

Staging is done after the evaluation of the patients' history, physical examination and laboratory studies including hematologic parameters, screening chemistry studies and especially a test for serum lactate dehydrogenase (LDH) level. Imaging studies include computed tomograms of the chest, abdomen and pelvis and a PET scan (Armitage, 2007).

Determining for prognosis and treatment decision is the differentiation between indolent NHL types and aggressive NHLs. Indolent NHLs progress slowly, have a good prognosis and respond in early stages to radiation therapy, chemotherapy and immunotherapy, but are not curable in advanced stages. Aggressive NHLs progress quickly, but are responsive to intensive combination chemotherapy (National Cancer Institute, 2015).

Depending on the disease stage at the time point of diagnosis patients are classified into prognostic groups (National Cancer Institute, 2015) as follows:

Stage	Prognostic groups
I	Involvement of a single lymphatic site (nodal region, Waldeyer ring, thymus or spleen (I).
	Localized involvement of a single extra-lymphatic organ or site in the absence of any lymph node involvement (IE).
II	Involvement of two or more lymph node regions on the same side of the diaphragm (II).
	Localized involvement of a single extra-lymphatic organ or site in association with regional lymph node involvement with or without involvement of other lymph node regions on the same side of the diaphragm (IIE). The number of regions involved may be indicated by a subscript Arabic numeral (for example II3).
III	Involvement of lymph node regions on both sides of the diaphragm (III), which also may be accompanied by extra-lymphatic extension in association with adjacent lymph node involvement (IIIE) or by involvement of the spleen (IIIS) or both (IIIE, IIIS).
IV	Diffuse or disseminated involvement of one or more extra-lymphatic organs, with or without associated lymph node involvement.
	Isolated extra-lymphatic organ involvement in the absence of adjacent regional lymph node involvement, but in conjunction with disease in distant site(s). Stage IV includes any involvement of the liver or bone marrow, lungs (other than by direct extension from another site), or cerebrospinal fluid.

The Ann Arbor staging system is usually used for patients with NHL. In this system, stage I, stage II, stage III and stage IV are sub-classified in to the categories A and B. Patients with well-defined generalized symptoms receive the designation B, while patients without these symptoms belong to category A. Category B symptoms include unexplained loss of more than 10% of body weight in the six months before diagnosis, unexplained fever with temperatures above 38°C and drenching night sweats. Specialized designations are used depending on the involvement of specific organs/ sites (National Cancer Institute, 2015) as follows:

Designation	Specific sites
E	Extranodal lymphoid malignancies near major lymphatic aggregates
N	Nodes
H	Liver
L	Lung
M	Bone marrow
S	Spleen
P	Pleura
O	Bone
D	Skin

To assign a precise stage, patients receive a clinical stage (CS) based on the findings of the clinical evaluation and a pathologic stage (PS) based on the findings of invasive procedures beyond the initial biopsy (National Cancer Institute, 2015).

Treatment of NHL depends on the histologic type and stage. Standard treatment options include (National Cancer Institute, 2015):

Stage	Standard treatment option
Indolent, stage I and contiguous stage II NHL	Radiation therapy
	Rituximab ± chemotherapy
	Watchful waiting
	Other therapies as designated for patients with advanced-stage disease
Indolent, non-contiguous stage II/III/IV NHL	Watchful waiting for asymptomatic patients
	Rituximab
	Purine nucleoside analogs
	Alkylating agents ± steroids
	Combination chemotherapy
	Yttrium-90-labeled ibritumomab tiuxetan
	Maintenance rituximab
Indolent, Recurrent NHL	Chemotherapy (single agent or combination)
	Rituximab

	Lenalidomide
	Radiolabeled anti-CD20 monoclonal antibodies
	Palliative radiation therapy
Aggressive, stage I and contiguous stage II NHL	R-CHOP ± (involved-field radiation therapy) IF-XRT
Aggressive, non-contiguous stage II/III/IV NHL	R-CHOP
	Other combination chemotherapy
Lymphoblastic lymphoma	Intensive therapy
	Radiation therapy
Diffuse, small, noncleaved-cell/ Burkitt lymphoma	Aggressive multi-drug regimens
	Central nervous system (CNS) prophylaxis
Aggressive, recurrent NHL	Bone marrow or stem cell transplantation
	Re-treatment with standard agents
	Palliative radiation therapy

Indolent, stage I and contiguous stage II NHL: Standard treatment options include radiation therapy, rituximab (anti-CD20 monoclonal antibody) ± chemotherapy, watchful waiting and other therapies as designated for patients with advanced-stage disease.

Indolent, non-contiguous stage II/III/IV NHL: Standard treatment options include watchful waiting for asymptomatic patients, rituximab, obinutuzumab (anti-CD20 monoclonal antibody), purine nucleoside analogs (fludarabine, 2-chlorodeoxyadenosine), alkylating agents (cyclophosphamide, chlorambucil) ± steroids, bendamustine, combination chemotherapy (CVP, C-MOPP (cyclophosphamide, vincristine, procarbazine, and prednisone), CHOP, FND (fludarabine, mitoxantrone ± dexamethasone)), yttrium-labeled ibritumomab tiuxetan and maintenance rituximab. Rituximab (R) is considered first-line therapy, either alone or in combination with other agents (R-Bendamustine, R-F (fludarabine), R-CVP (cyclophosphamide, vincristine, and prednisone), R-CHOP (cyclophosphamide, doxorubicin, vincristine, and prednisone), R-FM (fludarabine, mitoxantrone), R-FCM (fludarabine, cyclophosphamide, and mitoxantrone)). Under clinical evaluation are bone marrow transplantation (BMT) or peripheral stem cell transplantation (PSCT),

idiotype vaccines and radiolabeled monoclonal antibodies (ofatumumab: anti-CD20 monoclonal antibody).

Indolent, recurrent NHL: Standard treatment options include chemotherapy (single agent or combination), rituximab, lenalidomide, radiolabeled anti-CD20 monoclonal antibodies (yttrium-90 ibritumomab) and palliative radiation therapy. Treatment options under clinical evaluation include SCTs.

Aggressive, stage I and contiguous stage II NHL: Standard treatment options include R-CHOP ± IF-XRT. Treatment options under clinical evaluation include R-ACVBP (rituximab + doxorubicin, cyclophosphamide, vindesine, bleomycin, prednisone).

Aggressive, non-contiguous stage II/III/IV NHL: Standard treatment options include combination chemotherapy ± local-field radiation therapy. Drug combinations include ACVBP, CHOP, CNOP (cyclophosphamide, mitoxantrone, vincristine, prednisone), m-BACOD (methotrexate, bleomycin, doxorubicin, cyclophosphamide, vincristine, dexamethasone, leucovorin), MACOP-B (methotrexate, doxorubicin, cyclophosphamide, vincristine, prednisone fixed dose, bleomycin, leucovorin), ProMACE CytaBOM (prednisone, doxorubicin, cyclophosphamide, etoposide, cytarabine, bleomycin, vincristine, methotrexate, leucovorin), R-CHOP. Under clinical evaluation are BMT and SCT.

Lymphoblastic lymphoma: Standard treatment options include intensive therapy and radiation therapy.

Diffuse, small noncleaved-cell/ Burkitt lymphoma: Standard treatment options include aggressive multidrug regimens and CNS prophylaxis.

Aggressive, recurrent NHL: Standard treatment options include BMT or SCT, re-treatment with standard agents (rituximab, radiolabeled anti-CD20 monoclonal antibodies, denileukin diftitox (a fusion protein combining diphtheria toxin and interleukin-2)) and palliative radiation therapy. Treatment options under clinical evaluation include SCT (National Cancer Institute, 2015).

Spontaneous tumor regression can be observed in lymphoma patients. Therefore, active immunotherapy is a therapy option (Palomba, 2012). An important vaccination option includes Id vaccines. B lymphocytes express surface immunoglobulins with a specific amino acid sequence in the variable regions of their heavy and light chains, unique to each cell clone (= idiotype, Id). The idiotype functions as a tumor associated antigen.

Passive immunization includes the injection of recombinant murine anti-Id monoclonal antibodies alone or in combination with IFN alpha, IL2 or chlorambucil.

Active immunization includes the injection of recombinant protein (Id) conjugated to an adjuvant (KLH), given together with GM-CSF as an immune adjuvant. Tumor-specific Id is produced by hybridoma cultures or using recombinant DNA technology (plasmids) by bacterial, insect or mammalian cell culture.

Three phase III clinical trials have been conducted (Biovest, Genitope, Favril). In two trials patients had received rituximab. GM-CSF was administered in all three trials. Biovest used hybridoma-produced protein, Genitope and Favril used recombinant protein. In all three trials Id was conjugated to KLH. Only Biovest had a significant result.

Vaccines other than Id include the cancer-testis antigens MAGE, NY-ESO1 and PASD-1, the B-cell antigen CD20 or cellular vaccines. The vaccines consist of DCs pulsed with apoptotic tumor cells, tumor cell lysate, DC-tumor cell fusion or DCs pulsed with tumor-derived RNA. In situ vaccination involves the vaccination with intra-tumoral CpG in combination with chemotherapy or irradiated tumor cells grown in the presence of GM-CSF and collection/expansion/re-infusion of T cells.

Vaccinations with antibodies that alter immunologic checkpoints are comprised of anti-CD40, anti-OX40, anti-41BB, anti-CD27, anti-GITR (agonist antibodies that directly enhance anti-tumor response) or anti-PD1, anti-CTLA-4 (blocking antibodies that inhibit the checkpoint that would hinder the immune response). Examples are ipilimumab (anti-CTLA-4) and CT-011 (anti-PD1) (Palomba, 2012).

Considering the severe side-effects and expense associated with treating cancer, there is a need to identify factors that can be used in the treatment of cancer in general and NHL in particular. There is also a need to identify factors representing biomarkers for cancer in general and NHL in particular, leading to better diagnosis of cancer, assessment of prognosis, and prediction of treatment success.

Immunotherapy of cancer represents an option of specific targeting of cancer cells while minimizing side effects. Cancer immunotherapy makes use of the existence of tumor associated antigens.

The current classification of tumor associated antigens (TAAs) comprises the following major groups:

a) Cancer-testis antigens: The first TAAs ever identified that can be recognized by T cells belong to this class, which was originally called cancer-testis (CT) antigens because of the expression of its members in histologically different human tumors and, among normal tissues, only in spermatocytes/spermatogonia of testis and, occasionally, in placenta. Since the cells of testis do not express class I and II HLA molecules, these antigens cannot be recognized by T cells in normal tissues and can therefore be considered as immunologically tumor-specific. Well-known examples for CT antigens are the MAGE family members and NY-ESO-1.

b) Differentiation antigens: These TAAs are shared between tumors and the normal tissue from which the tumor arose. Most of the known differentiation antigens are found in melanomas and normal melanocytes. Many of these melanocyte lineage-related proteins are involved in biosynthesis of melanin and are therefore not tumor specific but nevertheless are widely used for cancer immunotherapy. Examples include, but are not limited to, tyrosinase and Melan-A/MART-1 for melanoma or PSA for prostate cancer.

c) Over-expressed TAAs: Genes encoding widely expressed TAAs have been detected in histologically different types of tumors as well as in many normal tissues, generally with lower expression levels. It is possible that many of the epitopes processed and potentially presented by normal tissues are below the threshold level for T-cell recognition, while their over-expression in tumor cells can trigger an anticancer response by breaking previously established tolerance. Prominent examples for this class of TAAs are Her-2/neu, survivin, telomerase, or WT1.

d) Tumor-specific antigens: These unique TAAs arise from mutations of normal genes (such as β -catenin, CDK4, etc.). Some of these molecular changes are associated with neoplastic transformation and/or progression. Tumor-specific antigens are generally able to induce strong immune responses without bearing the risk for autoimmune reactions against normal tissues. On the other hand, these TAAs are in most cases only relevant to the exact tumor on which they were identified and are usually not shared between many individual tumors. Tumor-specificity (or -association) of a peptide may also arise if the peptide originates from a tumor- (-associated) exon in case of proteins with tumor-specific (-associated) isoforms.

e) TAAs arising from abnormal post-translational modifications: Such TAAs may arise from proteins which are neither specific nor overexpressed in tumors but nevertheless become tumor associated by posttranslational processes primarily active in tumors. Examples for this class arise from altered glycosylation patterns leading to novel epitopes in tumors as for MUC1 or events like protein splicing during degradation which may or may not be tumor specific.

f) Oncoviral proteins: These TAAs are viral proteins that may play a critical role in the oncogenic process and, because they are foreign (not of human origin), they can evoke a T-cell response. Examples of such proteins are the human papilloma type 16 virus proteins, E6 and E7, which are expressed in cervical carcinoma.

T-cell based immunotherapy targets peptide epitopes derived from tumor-associated or tumor-specific proteins, which are presented by molecules of the major histocompatibility complex (MHC). The antigens that are recognized by the tumor specific T lymphocytes, that is, the epitopes thereof, can be molecules derived from all protein classes, such as enzymes, receptors, transcription factors, etc. which are expressed and, as compared to unaltered cells of the same origin, usually up-regulated in cells of the respective tumor.

There are two classes of MHC-molecules, MHC class I and MHC class II. MHC class I molecules are composed of an alpha heavy chain and beta-2-microglobulin, MHC class II molecules of an alpha and a beta chain. Their three-dimensional conformation results in a binding groove, which is used for non-covalent interaction with peptides.

MHC class I molecules can be found on most nucleated cells. They present peptides that result from proteolytic cleavage of predominantly endogenous proteins, defective ribosomal products (DRIPs) and larger peptides. However, peptides derived from endosomal compartments or exogenous sources are also frequently found on MHC class I molecules. This non-classical way of class I presentation is referred to as cross-presentation in the literature (Brossart and Bevan, 1997; Rock et al., 1990). MHC class II molecules can be found predominantly on professional antigen presenting cells (APCs), and primarily present peptides of exogenous or transmembrane proteins that are taken up by APCs e.g. during endocytosis, and are subsequently processed. Complexes of peptide and MHC class I are recognized by CD8-positive T cells bearing the appropriate T-cell receptor (TCR), whereas complexes of peptide and MHC class II molecules are recognized by CD4-positive-helper-T cells bearing the appropriate TCR. It is well known that the TCR, the peptide and the MHC are thereby present in a stoichiometric amount of 1:1:1.

CD4-positive helper T cells play an important role in inducing and sustaining effective responses by CD8-positive cytotoxic T cells. The identification of CD4-positive T-cell epitopes derived from tumor associated antigens (TAA) is of great importance for the development of pharmaceutical products for triggering anti-tumor immune responses (Gnjatic et al., 2003). At the tumor site, T helper cells, support a cytotoxic T cell-(CTL-) friendly cytokine milieu (Mortara et al., 2006) and attract effector cells, e.g. CTLs, natural killer (NK) cells, macrophages, and granulocytes (Hwang et al., 2007).

In the absence of inflammation, expression of MHC class II molecules is mainly restricted to cells of the immune system, especially professional antigen-presenting cells (APC), e.g., monocytes, monocyte-derived cells, macrophages, dendritic cells. In cancer patients, cells of the tumor have been found to express MHC class II molecules (Dengjel et al., 2006).

Elongated (longer) peptides of the invention can act as MHC class II active epitopes. T-helper cells, activated by MHC class II epitopes, play an important role in orchestrating the effector function of CTLs in anti-tumor immunity. T-helper cell epitopes that trigger a T-helper cell response of the TH1 type support effector functions of CD8-positive killer T cells, which include cytotoxic functions directed

against tumor cells displaying tumor-associated peptide/MHC complexes on their cell surfaces. In this way tumor-associated T-helper cell peptide epitopes, alone or in combination with other tumor-associated peptides, can serve as active pharmaceutical ingredients of vaccine compositions that stimulate anti-tumor immune responses.

It was shown in mammalian animal models, e.g., mice, that even in the absence of CD8-positive T lymphocytes, CD4-positive T cells are sufficient for inhibiting manifestation of tumors via inhibition of angiogenesis by secretion of interferon-gamma (IFN γ) (Beatty and Paterson, 2001; Mumberg et al., 1999). There is evidence for CD4 T cells as direct anti-tumor effectors (Braumuller et al., 2013; Tran et al., 2014).

Since the constitutive expression of HLA class II molecules is usually limited to immune cells, the possibility of isolating class II peptides directly from primary tumors was previously not considered possible. However, Dengjel et al. were successful in identifying a number of MHC Class II epitopes directly from tumors (WO 2007/028574, EP 1 760 088 B1).

Since both types of response, CD8 and CD4 dependent, contribute jointly and synergistically to the anti-tumor effect, the identification and characterization of tumor-associated antigens recognized by either CD8⁺ T cells (ligand: MHC class I molecule + peptide epitope) or by CD4-positive T-helper cells (ligand: MHC class II molecule + peptide epitope) is important in the development of tumor vaccines.

For an MHC class I peptide to trigger (elicit) a cellular immune response, it also must bind to an MHC-molecule. This process is dependent on the allele of the MHC-molecule and specific polymorphisms of the amino acid sequence of the peptide. MHC-class-I-binding peptides are usually 8-12 amino acid residues in length and usually contain two conserved residues ("anchors") in their sequence that interact with the corresponding binding groove of the MHC-molecule. In this way, each MHC allele has a "binding motif" determining which peptides can bind specifically to the binding groove.

In the MHC class I dependent immune reaction, peptides not only have to be able to bind to certain MHC class I molecules expressed by tumor cells, they subsequently also have to be recognized by T cells bearing specific T cell receptors (TCR).

For proteins to be recognized by T-lymphocytes as tumor-specific or -associated antigens, and to be used in a therapy, particular prerequisites must be fulfilled. The antigen should be expressed mainly by tumor cells and not, or in comparably small amounts, by normal healthy tissues. In a preferred embodiment, the peptide should be over-presented by tumor cells as compared to normal healthy tissues. It is furthermore desirable that the respective antigen is not only present in a type of tumor, but also in high concentrations (i.e. copy numbers of the respective peptide per cell). Tumor-specific and tumor-associated antigens are often derived from proteins directly involved in transformation of a normal cell to a tumor cell due to their function, e.g. in cell cycle control or suppression of apoptosis. Additionally, downstream targets of the proteins directly causative for a transformation may be up-regulated and thus may be indirectly tumor-associated. Such indirect tumor-associated antigens may also be targets of a vaccination approach (Singh-Jasuja et al., 2004). It is essential that epitopes are present in the amino acid sequence of the antigen, in order to ensure that such a peptide ("immunogenic peptide"), being derived from a tumor associated antigen, leads to an *in vitro* or *in vivo* T-cell-response.

Basically, any peptide able to bind an MHC molecule may function as a T-cell epitope. A prerequisite for the induction of an *in vitro* or *in vivo* T-cell-response is the presence of a T cell having a corresponding TCR and the absence of immunological tolerance for this particular epitope.

Therefore, TAAs are a starting point for the development of a T cell based therapy including but not limited to tumor vaccines. The methods for identifying and characterizing the TAAs are usually based on the use of T-cells that can be isolated from patients or healthy subjects, or they are based on the generation of differential transcription profiles or differential peptide expression patterns between tumors and normal tissues. However, the identification of genes over-expressed in tumor tissues or human tumor cell lines, or selectively expressed in such tissues or cell lines, does

not provide precise information as to the use of the antigens being transcribed from these genes in an immune therapy. This is because only an individual subpopulation of epitopes of these antigens are suitable for such an application, since a T cell with a corresponding TCR has to be present and the immunological tolerance for this particular epitope needs to be absent or minimal. In a very preferred embodiment of the invention it is therefore important to select only those over- or selectively presented peptides against which a functional and/or a proliferating T cell can be found. Such a functional T cell is defined as a T cell, which upon stimulation with a specific antigen can be clonally expanded and is able to execute effector functions ("effector T cell").

In case of targeting peptide-MHC by specific TCRs (e.g. soluble TCRs) and antibodies or other binding molecules (scaffolds) according to the invention, the immunogenicity of the underlying peptides is secondary. In these cases, the presentation is the determining factor.

SUMMARY OF THE INVENTION

In a first aspect of the present invention, the present invention relates to a peptide comprising an amino acid sequence selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 311 or a variant sequence thereof which is at least 77%, preferably at least 88%, homologous (preferably at least 77% or at least 88% identical) to SEQ ID NO: 1 to SEQ ID NO: 311, wherein said variant binds to MHC and/or induces T cells cross-reacting with said peptide, or a pharmaceutical acceptable salt thereof, wherein said peptide is not the underlying full-length polypeptide.

The present invention further relates to a peptide of the present invention comprising a sequence that is selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 311 or a variant thereof, which is at least 77%, preferably at least 88%, homologous (preferably at least 77% or at least 88% identical) to SEQ ID NO: 1 to SEQ ID NO: 311, wherein said peptide or variant thereof has an overall length of between 8 and 100, preferably between 8 and 30, and most preferred of between 8 and 14 amino acids.

The following tables show the peptides according to the present invention, their respective SEQ ID NOs, and the prospective source (underlying) genes for these peptides. All peptides in Table 1 and Table 2 bind to HLA-A*02. The peptides in Table 2 have been disclosed before in large listings as results of high-throughput screenings with high error rates or calculated using algorithms, but have not been associated with cancer at all before. The peptides in Table 3 are additional peptides that may be useful in combination with the other peptides of the invention. The peptides in Tables 4A and B are furthermore useful in the diagnosis and/or treatment of various other malignancies that involve an over-expression or over-presentation of the respective underlying polypeptide.

Table 1: Peptides according to the present invention.

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
1	LLSGQLPTI	84969	TOX2
2	LLSEETPSA	10765	KDM5B
3	LTIDTQYYL	5422	POLA1
4	TLLGFFLAKV	5422	POLA1
5	VLQGLTFTL	6890	TAP1
6	TLITLPLLFL	6890	TAP1
7	NLLGMIFSM	51398	WDR83OS
8	ALYAVIEKA	5293	PIK3CD
9	FLLDLDPLL	7915	ALDH5A1
10	FLLVGTQIDL	643751,998	CDC42P6, CDC42
11	GLDTVVALL	23203	PMPCA
12	GLLLLVPLL	145864	HAPLN3
13	HLVPASWKL	3718	JAK3
14	LLSDPTPGA	3718	JAK3
15	IIIEDLLEA	10985	GCN1L1
16	TLIAAILYL	5355	PLP2
17	VIPLLSSV	91526	ANKRD44
18	KLTDQPPLV	91526	ANKRD44
19	VLEAILPLV	2889	RAPGEF1
20	YLIAGGDRWL	2646	GCKR
21	ALFKEAYSL	55732	C1orf112
22	ALKKHLTSV	10773	ZBTB6
23	ALVEDIINL	92399	MRRF
24	AVLGFSFRL	80222	TARS2
25	FLDTSNQHLL	4064	CD180
26	FLGSFIDHV	91147	TMEM67
27	FLNQESFDL	6610	SMPD2
28	FLSNANPSL	7818	DAP3

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
29	ILSDVTQGL	55591	VEZT
30	ILSTLDVEL	10744,9232	PTTG2, PTTG1
31	KLYDEESLL	57680	CHD8
32	VLNEDELPSV	57680	CHD8
33	LLANIVPIAMLV	4539,6775071,8923201	MT-ND4L
34	LLWEDGVTEA	22916	NCBP2
35	SLSSERYYL	8320	EOMES
36	VILDIPLLFET	79877	DCAKD
37	VLGNALEGV	4678	NASP
38	YLTAEILELAGN	221613,3012,3013,3014,317772,55766,723790,8329,8330,8331,8332,8334,8335,8336,8337,8338,85235,8969,92815,9555	HIST1H2AA, HIST1H2AE, HIST1H2AD, H2AFX, HIST2H2AB, H2AFJ, HIST2H2AA4, HIST1H2AI, HIST1H2AK, HIST1H2AJ, HIST1H2AL, HIST1H2AC, HIST1H2AB, HIST1H2AM, HIST2H2AA3, HIST2H2AC, HIST1H2AH, HIST1H2AG, HIST3H2A, H2AFY
39	QLLPQGIVPAL	55374	TMCO6
40	FLNSVIVDL	6249	CLIP1
41	ILASIFETV	6574	SLC20A1
42	YLQDLVERA	10347	ABCA7
43	ALLEGVKNV	84678	KDM2B
44	FIIEEQSFL	10200	MPHOSPH6
45	FILDDSALYL	23130	ATG2A
46	FLVEEIFQT	8888	MCM3AP
47	GLLPKLTAL	22920	KIFAP3
48	KILDEDLYI	641	BLM
49	TILGDPQILL	23460	ABCA6
50	LLLDGLIYL	23460	ABCA6
51	SLLGNSPVL	23460	ABCA6
52	VLLEDVDAAFL	617	BCS1L
53	FLREYFERL	5573	PRKAR1A
54	DIFDAMFSV	5573	PRKAR1A
55	ILVEVDLVQA	4261	CIITA
56	GLQDLLFSL	4261	CIITA
57	LQIGDFVSV	51167	CYB5R4
58	QLAPFLPQL	23392	KIAA0368
59	RLHREVAQV	2802	GOLGA3
60	SLLIDVITV	51534	VTA1
61	SLLNKDLSL	1786	DNMT1
62	ALAPYLDLL	54093	SETD4

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
63	ALIEEAYGL	3836,3841	KPNA1, KPNA5
64	FLVEVSNDV	23224	SYNE2
65	NLTDVSPDL	23224	SYNE2
66	KLAPIPVEL	153241	CEP120
67	LLATVNVAL	23511	NUP188
68	QIAAFLFTV	56006	SMG9
69	TLLAFPLLL	84720	PIGO
70	VLIEILQKA	23633,3841	KPNA6, KPNA5
71	VLLDYVGNVQL	51676	ASB2
72	TLQEETAVYL	51676	ASB2
73	YLGEEYPEV	23451	SF3B1
74	SLDLRPLEV	43	ACHE
75	AALKYIPSV	1794	DOCK2
76	ALADLVPVDVVV	84188	FAR1
77	ALLDVSNNYGI	115752	DIS3L
78	AMEEAVAQV	22897	CEP164
79	AMKEEKEQL	9126	SMC3
80	YLFDEIDQA	9126	SMC3
81	FIFSYITAV	128338	DRAM2
82	FLIDGSSSV	1690	COCH
83	FLMDDNMSNTL	4603	MYBL1
84	FLQELQLEHA	8604	SLC25A12
85	GLAPAEVVVATVA	57591	MKL1
86	GLATIRAYL	2731	GLDC
87	GLFARIIMI	5250	SLC25A3
88	GLFDNRSGLP EA	79733	E2F8
89	GLTALHVAV	602	BCL3
90	HLDEVFLEL	55744	COA1
91	HLSSTTAQV	201633	TIGIT
92	KLLFEIASA	124460	SNX20
93	KLLGSLQLL	81603	TRIM8
94	LLAGQATTAYF	972	CD74
95	LLFDLIPVVS V	284114	TMEM102
96	LLNENESLFL	26156	RSL1D1
97	LLNFSPGNL	3929	LBP
98	MLQDGIARL	79697	C14orf169
99	QLYDGATALFL	147463	ANKRD29
100	RLIRTIAAI	140461	ASB8
101	SLDQSTWNV	23240	KIAA0922
102	SLFAAISGMIL	931	MS4A1
103	SLQDHLEKV	1756	DMD
104	VLLGLPLL V	9674	KIAA0040
105	VLTPVILQV	100499483,100499484	C9orf174

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
106	VL YELLQYI	51513	ETV7
107	VQAVSIPEV	55755	CDK5RAP2
108	YLAPENGYLM	6625	SNRNP70
109	YLFQFSAAL	130367	SGPP2
110	YQYPFVLGL	130367	SGPP2
111	YLLDTLLSL	57448	BIRC6
112	FLAILPEEV	7762	ZNF215
113	FVIDSFEEL	147945	NLRP4
114	GLSDISPST	26005	C2CD3
115	LLIDIIHFL	25914	RTTN
116	SLLDNLLTI	25914	RTTN
117	VLATILAQL	26271	FBXO5
118	VLDGMIYAI	54813	KLHL28
119	ELCDIILRV	54813	KLHL28
120	VLLGTTWAL	221188	GPR114
121	YLTGYNFTL	9521	EEF1E1
122	AISEAQESV	79882	ZC3H14
123	ALLSAFVQL	8295	TRRAP
124	FLGVVVPTV	56996	SLC12A9
125	FVAPPTAAV	162	AP1B1
126	GLSIFIYRL	10075	HUWE1
127	HLMEENMIVYV	65220	NADK
128	KLFDASPTFFA	3992,3995	FADS1, FADS3
129	SLFEASQQL	23347	SMCHD1
130	VIFSYYLGV	79004	CUEDC2
131	VLIEETDQL	6924	TCEB3
132	VLQDQVDEL	51199	NIN
133	ALEELTGFREL	4288	MKI67
134	ALGRLGILSV	22828,26230	SCAF8, TIAM2
135	ALTGLQFQL	22797	TFEC
136	FIFGIVHLL	64066	MMP27
137	FIQQERFFL	4012	LNPEP
138	NLINNIFEL	4012	LNPEP
139	FLASPLVAI	3593	IL12B
140	FLFEDFVEV	140775	SMCR8
141	FLGELTLQL	257218	SHPRH
142	FLYEDSKSVRL	696	BTN1A1
143	TLHAVDVTL	696	BTN1A1
144	GLITQVDKL	9183	ZW10
145	GLLHEVVSL	163486	DENND1B
146	GLLQQPPAL	1871	E2F3
147	GLSEYQRNFL	56890	MDM1
148	ICAGHVPGV	79019	CENPM
149	ILNPVTTKL	81691	LOC81691

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
150	ILSEKEYKL	127254	C1orf173
151	ILVKQSPML	940	CD28
152	KIMYTLVSV	3709	ITPR2
153	KLLKGIYAI	1235	CCR6
154	KLMNIQQQL	11214	AKAP13
155	KLMTSLVKV	10734	STAG3
156	KMLEDDLKL	2334	AFF2
157	KVLEFLAKV	139422,4113,4115	MAGEB10, MAGEB2, MAGEB4
158	KVQDVLHQV	83756	TAS1R3
159	LLLSDSGFYL	28557	TRBV30
160	LLPPPSPAA	83881	MIXL1
161	NLMLELETV	1063	CENPF
162	RLADLKVSI	2175	FANCA
163	SIFDAVLKGV	157680	VPS13B
164	SLFDGAVISTV	23049	SMG1
165	KLLEEIEFL	23049	SMG1
166	SLFSEVASL	22832	KIAA1009
167	SLFSITKSV	60468	BACH2
168	SLLSPLLSV	54949	SDHAF2
169	SSLEENLLHQV	80205	CHD9
170	STIELSENSL	55635	DEPDC1
171	TLLDVISAL	27340	UTP20
172	TLQDSLEFI	51735,96459	RAPGEF6, FNIP1
173	VILDSVASV	5890	RAD51B
174	VLVEITDVDFAA	79801	SHCBP1
175	VMESILLRL	342850	ANKRD62
176	YLHIYESQL	29851	ICOS
177	YLYEAAEEATTL	22798	LAMB4
178	YVLQGEFFL	84541	KBTBD8
179	FVDTNLYFL	81037	CLPTM1L
180	GILQLVESV	6050	RNH1
181	LLFDQNDKV	100653071,10491	CRTAP
182	LLPPPPPVA	23091,4784	ZC3H13, NFIX
183	VLFETVLTl	8906	AP1G2
184	AVLGTSWQL	23041	MON2
185	FIAQLNNVEL	6509	SLC1A4
186	FLDVSRDFV	54461	FBXW5
187	FLNSFVFKM	89910	UBE3B
188	GLEDEMYEV	285905,644619,92105	INTS4L1, INTS4L2, INTS4
189	SLSHLVPAL	285905,644619,92105	INTS4L1, INTS4L2, INTS4

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
190	GLIELVDQL	90410	IFT20
191	GLSDISAQV	5989	RFX1
192	GMAAEVPKV	348378	FAM159A
193	SLADSMPSL	8945	BTRC
194	SLAPFDREPFTL	3937	LCP2
195	ALIPDLNQI	51361	HOOK1
196	TLALAMIYL	100134301,28 5074,64682,73 0268	ANAPC1
197	YLLTDNVVKL	79810	PTCD2
198	GLLSAVSSV	9894	TELO2
199	SLNSTTWKV	1233	CCR4
200	YLLDFEDRL	23207	PLEKHM2
201	YLNISQVNV	9262	STK17B
202	ALAAGGYDV	3009	HIST1H1B
203	ILDTIFHKV	2829	XCR1
204	RLCDIVNV	84614	ZBTB37
205	TLFYESPHL	221908	PPP1R35
206	SAVSGQWEV	2326	FMO1
207	GLVGLLEQA	57572,81704,8 5440	DOCK6, DOCK8, DOCK7
208	FLAVSLPLL	3071	NCKAP1L
209	FLLDTISGL	84864	MINA
210	FLAEQFEFL	55610	CCDC132
211	FIDDLFAFV	1209	CLPTM1
212	FLIGQGAHV	4659	PPP1R12A
213	YINEDEYEV	7874	USP7
214	FLFDGSMSL	3683	ITGAL
215	QLFEEEEIEL	63906	GPATCH3
216	KVVSNLPAI	10199	MPHOSPH10
217	AQFGAVLEV	55131	RBM28
218	ALDQFLEGI	57169	ZNFX1
219	ALLELENSV	715,83481	C1R, EPPK1
220	FLAEAPTAL	9814	SFI1
221	FLAPDNSLLLA	22898	DENND3
222	FLIETGTLL	79705	LRRK1
223	FLQDIPDGLFL	206426,26697 1,8394	PIP5K1P1, PIPSL, PIP5K1A
224	FLSPLLPLL	10961	ERP29
225	GTYQDVGSLNIGD V	973	CD79A
226	GVIDPVPEV	8879	SGPL1
227	IIAEGIPEA	47	ACLY
228	IIAEYLSYV	51667	NUB1
229	ILSPWGAEV	142	PARP1

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
230	IMDDDSYGV	9874	TLK1
231	IVMGAIPSV	1902	LPAR1
232	KVMEGTVAA	1445	CSK
233	MLEVHIPSV	79856	SNX22
234	NLQRTVVTV	4297	MLL
235	SLDVYELFL	79586	CHPF
236	SLFDGFFLTA	25920	COBRA1
237	YLDRLIPQA	115209	OMA1
238	YQYGAVVTL	1380	CR2
239	VLIDDTVLL	116138	KLHDC3
240	ALVPTPALFYL	51528	JKAMP
241	FIPDFIPAV	56912	IFT46
242	GILDFZVFL	100124692,89 72,93432	MGAM
243	GLPDLDIYL	23334	SZT2
244	ILEPFLPAV	6894	TARBP1
245	KLIQLPVVYV	9875	URB1
246	KLPVPLESV	285190,40096 6,5903,653489 ,727851,72954 0,729857,8422 0	RGPD4, RGPD1, RANBP2, RGPD3, RGPD8, RGPD6, RGPD2, RGPD5
247	KVLEMETTV	9810	RNF40
248	NLLEQFILL	64708	COPS7B
249	VLLESLVEI	149371	EXOC8
250	VLTNVGAAL	129285	PPP1R21
251	VLVELFTYI	3717	JAK2
252	YLGDLIMAL	3930,7108	LBR, TM7SF2

Table 2: Additional peptides according to the present invention with no prior known cancer association.

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
253	YSDDDVPSV	29028	ATAD2
254	FLYSETWNI	4519,8923205	MT-CYB
255	GMWNP NAPVFL	9910	RABGAP1L
256	ALQETPPQV	146206	RLTPR
257	FLQEWEVYA	57001	ACN9
258	RIYPFLLMV	10299	MARCH6
259	TVLDGLEFKV	10592	SMC2
260	RLDEAFDFV	1844	DUSP2
261	FLPETRIMTSV	11319	ECD
262	LMGPVVHEV	5116	PCNT
263	GLMDNEIKV	8795	TNFRSF10B

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
264	ILTGTPPGV	151313,51011	FAHD2B, FAHD2A
265	ILWHFVASL	23077	MYCBP2
266	QLTEMLPSI	689	BTF3
267	SLLETGSDLLL	57176	VAR2S
268	VLFPLPTPL	11184	MAP4K1
269	VLQNVAFSV	597	BCL2A1
270	VVVDSDSLAFV	122961	ISCA2
271	YLLDQPVLEQRL	81887	LAS1L
272	KLDHTLSQI	4863	NPAT
273	AILLPQPPK	1761,6392,64147,642204,654434,84286,85363	DMRT1, SDHD, KIF9, LINC00338, TMEM175, TRIM5
274	KLLNLISKL	5366	PMAIP1
275	KLMDLEDCA	23269	MGA
276	NMISYVVHL	204801	NLRP11
277	FLIDLNSTHGTF	5511	PPP1R8
278	FLLFINHRL	4292	MLH1
279	NLAGENILNPL	56948	SDR39U1
280	SLLNHLPYL	201562	PTPLB
281	TLQTVPLTTV	1997	ELF1
282	YLLEQGAQV	55527	FEM1A
283	ALMPVTPQA	23683	PRKD3
284	KLQEQIHRV	196441	ZFC3H1
285	SITAVTPLL	63910	SLC17A9
286	HLTEDTPKV	50814	NSDHL
287	ILMGHSLYM	9786	KIAA0586
288	RLAPEIVSA	157285	SGK223
289	SLLAANNLL	9380	GRHPR
290	IASPVIAAV	127544	RNF19B
291	KIIDTAGLSEA	22954	TRIM32
292	KLINSQISL	5293	PIK3CD
293	GLAMVEAISYV	109	ADCY3
294	KLYGPEGLELV	3394	IRF8
295	SLAAVSQQL	7094	TLN1
296	FILEPLYKI	9343	EFTUD2
297	ILQNGLETL	89857	KLHL6
298	ALTDVILCV	89857	KLHL6
299	RLLEEEGVSL	64428	NARFL
300	IVLERNPEL	5257	PHKB
301	LQFDGIHVV	55294	FBXW7
302	SLAELDEKISA	51562	MBIP
303	FVWEASHYL	5442	POLRMT
304	ALIRLDDLFL	56902	PNO1

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
305	AMLAQQMQL	4154	MBNL1
306	AQVALVNEV	10075	HUWE1
307	FLLPVAVKL	3954	LETM1
308	SLLDQIPEM	9632	SEC24C
309	SLSFVSPSL	11108	PRDM4
310	VMAEAPPGV	9798	IST1
311	YLHRQVAHV	6890	TAP1

Table 3: Peptides useful for e.g. personalized cancer therapies.

SEQ ID No.	Sequence	GeneID(s)	Official Gene Symbol(s)
312	RLPDIPLRQV	55656	INTS8
313	ALSVRISNV	3766	KCNJ10
314	LIDDKGTIKL	983	CDK1
315	SLYDSIAFI	56978	PRDM8
316	SLSAFLPSL	54757	FAM20A
317	GLSNLGIKSI	122553	TRAPPC6B
318	KIQEMQHFL	4321	MMP12
319	SLYKGLLSV	25788	RAD54B
320	LLWGNLPEI	729533, 653820	FAM72A, FAM72B
321	KLLAVIHEL	25788	RAD54B
322	TLTNIIHNL	94101	ORMDL1
323	ILVDWLTVQV	9133	CCNB2
324	LLYDAVHIV	2899	GRIK3
325	FLFVDPELV	146850	PIK3R6
326	KLTDVGIATL	115701	ALPK2
327	MLFGHPLLVSV	8237	USP11
328	ILFPDIIARA	64110	MAGEF1

The present invention furthermore generally relates to the peptides according to the present invention for use in the treatment of proliferative diseases, such as, for example, non-small cell lung cancer, small cell lung cancer, renal cell cancer, brain cancer, gastric cancer, colorectal cancer, hepatocellular cancer, pancreatic cancer, leukemia, breast cancer, melanoma, ovarian cancer, urinary bladder cancer, uterine cancer, gallbladder and bile duct cancer.

Particularly preferred are the peptides – alone or in combination - according to the present invention selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 311. More preferred are the peptides – alone or in combination - selected from the

group consisting of SEQ ID NO: 1 to SEQ ID NO: 217 (see Table 1), and their uses in the immunotherapy of NHL, non-small cell lung cancer, small cell lung cancer, renal cell cancer, brain cancer, gastric cancer, colorectal cancer, hepatocellular cancer, pancreatic cancer, leukemia, breast cancer, melanoma, ovarian cancer, urinary bladder cancer, uterine cancer, gallbladder and bile duct cancer, and preferably NHL.

As shown in the following Tables 4A and B, many of the peptides according to the present invention are also found on other tumor types and can, thus, also be used in the immunotherapy of other indications. Also, refer to Figure 1 and Example 1.

The tables show for selected peptides on which additional tumor types they were found and either over-presented on more than 5% of the measured tumor samples, or presented on more than 5% of the measured tumor samples with a ratio of geometric means tumor vs normal tissues being larger than 3. Over-presentation is defined as higher presentation on the tumor sample as compared to the normal sample with highest presentation. Normal tissues against which over-presentation was tested were: adipose tissue, adrenal gland, artery, bone marrow, brain, central nerve, colon, duodenum, esophagus, eye, gallbladder, heart, kidney, liver, lung, lymph node, mononuclear white blood cells, pancreas, peripheral nerve, parathyroid gland, peritoneum, pituitary, pleura, rectum, salivary gland, skeletal muscle, skin, small intestine, spleen, stomach, thymus, thyroid gland, trachea, ureter, urinary bladder, and vein.

Table 4A: Peptides according to the present invention and their specific uses in other proliferative diseases, especially in other cancerous diseases.

SEQ ID No.	Sequence	Other relevant organs / diseases
1	LLSGQLPTI	CLL, Uterine Cancer
2	LLSEETPSA	NSCLC, SCLC, CLL, AML, BRCA, Melanoma, Urinary bladder cancer, Uterine Cancer
3	LTIDTQYYL	CLL, Uterine Cancer
5	VLQGLTFTL	SCLC, CLL, BRCA, Melanoma, OC, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer
6	TLITLPLLFL	CLL, Melanoma
7	NLLGMIFSM	CLL, AML, Melanoma, Urinary bladder cancer
8	ALYAVIEKA	CLL, AML

SEQ ID No.	Sequence	Other relevant organs / diseases
9	FLLDLDPLL	CLL
10	FLLVGTQIDL	CLL, BRCA, Uterine Cancer
11	GLDTVVALL	CRC, CLL, AML, BRCA, Uterine Cancer
12	GLLLLVP LL	Melanoma, Gallbladder Cancer, Bile Duct Cancer
13	HLVPASWKL	CLL, Melanoma
15	IIIEDLLEA	BRCA, Melanoma, Uterine Cancer
16	TLIAAILYL	CLL, AML, Gallbladder Cancer, Bile Duct Cancer
17	VIIPLLSSV	CLL, AML, BRCA, Melanoma
19	VLEAILPLV	CLL
20	YLIAGGDRWL	NSCLC, RCC, CLL, BRCA, Melanoma
21	ALFKEAYSL	Esophageal Cancer
23	ALVEDIINL	CRC, BRCA, Melanoma, Uterine Cancer
24	AVLGFSFRL	CLL
25	FLDTSNQHLL	CLL
26	FLGSFIDHV	Melanoma, OC, Uterine Cancer
27	FLNQESFDL	CLL, BRCA, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer
28	FLSNANPSL	CLL, BRCA, Uterine Cancer
29	ILSDVTQGL	CLL, BRCA, Uterine Cancer
30	ILSTLDVEL	CRC, Melanoma, Uterine Cancer
31	KLYDEESLL	CLL, AML, Melanoma, Esophageal Cancer, Uterine Cancer
32	VLNEDELPSV	CLL
33	LLANIVPIAMLV	CLL
34	LLWEDGVTEA	CRC, CLL, Melanoma, Esophageal Cancer, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer
35	SLSSERYYL	OC
36	VILDIPLLFET	CLL, BRCA, Melanoma, Uterine Cancer
37	VLGNALEGV	HCC, CLL, AML, Urinary bladder cancer, Uterine Cancer
38	YLTAEILELAGN	NSCLC, SCLC, CRC, HCC, BRCA, Melanoma, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer
39	QLLPQGIVPAL	CLL, BRCA, OC, Urinary bladder cancer, Uterine Cancer
40	FLNSVIVDL	CLL, Melanoma, Urinary bladder cancer
41	ILASIFETV	NSCLC, SCLC, RCC, CLL, AML, BRCA, Melanoma, Urinary bladder cancer, Gallbladder Cancer, Bile Duct Cancer
42	YLQDLVERA	CLL, Uterine Cancer
43	ALLEGVKNV	CLL, Melanoma, OC
44	FIIEEQSFL	CLL, Esophageal Cancer, Gallbladder

SEQ ID No.	Sequence	Other relevant organs / diseases
		Cancer, Bile Duct Cancer
45	FILDDSALYL	CLL, Uterine Cancer
46	FLVEEIFQT	SCLC, Gallbladder Cancer, Bile Duct Cancer
47	GLLPKLTAL	RCC, Brain Cancer, CRC, HCC, AML, Melanoma, Esophageal Cancer, OC, Uterine Cancer
48	KILDEDLYI	CLL, BRCA, Melanoma, Esophageal Cancer, Gallbladder Cancer, Bile Duct Cancer
50	LLLDGLIYL	CLL
53	FLREYFERL	CLL, Melanoma, Uterine Cancer
55	ILVEVDLVQA	CLL, Uterine Cancer
56	GLQDLLFSL	CLL, AML
57	LQIGDFVSV	SCLC, CLL
58	QLAPFLPQL	OC, Urinary bladder cancer
59	RLHREVAQV	Esophageal Cancer
60	SLLIDVITV	CLL, Melanoma, Urinary bladder cancer, Uterine Cancer
61	SLLNKDLSL	Uterine Cancer
62	ALAPYLDLL	AML, Melanoma, Urinary bladder cancer
63	ALIEEAYGL	CLL
64	FLVEVSNDV	CLL, Uterine Cancer
65	NLTDVSPDL	CLL, Uterine Cancer
67	LLATVNVAL	CLL, Uterine Cancer
68	QIAAFLFTV	CLL, Urinary bladder cancer, Uterine Cancer
69	TLLAFPLLL	HCC, CLL, AML, Melanoma, Gallbladder Cancer, Bile Duct Cancer
70	VLIEILQKA	AML, BRCA, OC, Urinary bladder cancer, Uterine Cancer
73	YLGEEYPEV	SCLC, CRC, CLL, Melanoma, Uterine Cancer
74	SLDLRPLEV	RCC, GC
76	ALADLVPVDVVV	SCLC, CLL, BRCA, Melanoma, Uterine Cancer
77	ALLDVSNNYGI	HCC, CLL, Esophageal Cancer, OC, Urinary bladder cancer
78	AMEEAVAQV	RCC, Gallbladder Cancer, Bile Duct Cancer
79	AMKEEKEQL	AML
80	YLFDEIDQA	CLL, AML, Uterine Cancer
81	FIFSYITAV	CLL
82	FLIDGSSSV	CLL
83	FLMDDNMSNTL	Melanoma
84	FLQELQLEHA	CLL
85	GLAPAEVVVATVA	CLL, Melanoma

SEQ ID No.	Sequence	Other relevant organs / diseases
86	GLATIRAYL	RCC, Melanoma, Uterine Cancer
87	GLFARIIMI	Gallbladder Cancer, Bile Duct Cancer
88	GLFDNRSGLPEA	Urinary bladder cancer, Uterine Cancer
90	HLDEVFLEL	SCLC
92	KLLFEIASA	CLL, AML
93	KLLGSLQLL	RCC, BRCA
94	LLAGQATTAYF	RCC
95	LLFDLIPVVS	AML, BRCA, Uterine Cancer
96	LLNENESLFL	HCC, CLL, BRCA, Melanoma, OC, Uterine Cancer
97	LLNFSPGNL	CRC
98	MLQDGIARL	CLL, Melanoma
100	RLIRTIAAI	RCC
101	SLDQSTWNV	CLL
102	SLFAAISGMIL	CLL
103	SLQDHLEKV	HCC, CLL
104	VLLGLPLL	CLL, AML
105	VLTPVILQV	CLL, AML
106	VLYELLOWYI	Gallbladder Cancer, Bile Duct Cancer
108	YLAPENGYLM	SCLC, CRC, HCC, BRCA, Melanoma, OC, Urinary bladder cancer, Gallbladder Cancer, Bile Duct Cancer
109	YLFQFSAAL	RCC, PC
110	YQYPFVLGL	Uterine Cancer
114	GLSDISPST	CLL, Uterine Cancer
116	SLLDNLLTI	HCC, CLL, AML, Melanoma
117	VLATILAQL	SCLC, AML, Uterine Cancer
118	VLDGMIYAI	Uterine Cancer
119	ELCDIILRV	Melanoma
120	VLLGTTWAL	AML
121	YLTGYNFTL	Uterine Cancer
122	AISEAQESV	RCC, CLL, BRCA, Uterine Cancer
124	FLGVVPTV	CLL, Melanoma, OC, Uterine Cancer
125	FVAPPTAAV	Melanoma, Urinary bladder cancer, Uterine Cancer
126	GLSIFIYRL	Melanoma, Urinary bladder cancer
127	HLMEENMIVYV	Melanoma
128	KLFDASPTFFA	CLL, Gallbladder Cancer, Bile Duct Cancer
129	SLFEASQQL	CLL, Melanoma, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer
130	VIFSIVLGV	AML, Uterine Cancer
131	VLIEETDQL	CLL, Melanoma
132	VLQDQVDEL	CLL, AML, Melanoma
133	ALEELTGFREL	Esophageal Cancer
138	NLINNIFEL	CLL, AML, Urinary bladder cancer

SEQ ID No.	Sequence	Other relevant organs / diseases
141	FLGELTLQL	Melanoma
144	GLITQVDKL	AML
146	GLLQQPPAL	AML
148	ICAGHVPGV	AML, Uterine Cancer
149	ILNPVTTKL	AML
152	KIMYTLVSV	HCC
161	NLMLELETV	Uterine Cancer
163	SIFDAVLKGV	RCC, CRC, BRCA, Uterine Cancer
164	SLFDGAVISTV	SCLC, Uterine Cancer
165	KLLEEIEFL	RCC, AML, BRCA, Melanoma, Esophageal Cancer, Gallbladder Cancer, Bile Duct Cancer
166	SLFSEVASL	Melanoma
169	SSLEENLLHQV	HCC, CLL
171	TLLDVISAL	AML
174	VLVEITDVFDA	Melanoma
179	FVDTNLYFL	RCC, CLL, Melanoma, Uterine Cancer
180	GILQLVESV	HCC, CLL, AML, Melanoma, OC
181	LLFDQNDKV	RCC, HCC, BRCA, Melanoma, Urinary bladder cancer, Uterine Cancer
182	LLPPPPPVA	SCLC, CLL, Melanoma
183	VLFETVLT	CLL, AML, Urinary bladder cancer, Uterine Cancer
184	AVLGTSWQL	CRC, CLL, AML
185	FIAQLNNVEL	Melanoma, OC
186	FLDVSRDFV	SCLC, CLL
188	GLEDEMYEV	CLL, Melanoma, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer
189	SLSHLVPAL	CLL
190	GLIELVDQL	HCC, CLL, AML, Melanoma, Uterine Cancer
191	GLSDISAQV	CLL, Melanoma, Esophageal Cancer, OC
193	SLADSMPSL	BRCA, Uterine Cancer
194	SLAPFDREPFTL	NSCLC
195	ALIPDLNQI	Uterine Cancer
197	YLLTDNVVKL	RCC, BRCA
198	GLLSAVSSV	AML, Gallbladder Cancer, Bile Duct Cancer
200	YLLDFEDRL	CLL
201	YLNISQVNV	CLL
203	ILDTIFHKV	Melanoma
204	RLCDIVNV	Melanoma
206	SAVSGQWEV	CLL
207	GLVGLLEQA	SCLC, HCC, CLL, AML, BRCA, Melanoma, OC, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer

SEQ ID No.	Sequence	Other relevant organs / diseases
208	FLAVSLPLL	CLL
209	FLLDTISGL	CRC, HCC, CLL, AML, BRCA, Melanoma, Urinary bladder cancer, Uterine Cancer
210	FLAEQFEFL	CLL
211	FIDDLFAFV	HCC, CLL, AML, Melanoma
212	FLIGQGAHV	CLL, AML, Melanoma
213	YINEDEYEV	CLL, OC
214	FLFDGMSL	AML
215	QLFEEEEIEL	RCC, Esophageal Cancer, OC, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer
216	KVVSNLPAI	AML, Gallbladder Cancer, Bile Duct Cancer
217	AQFGAVLEV	AML, Melanoma
218	ALDQFLEGI	CLL, BRCA, Urinary bladder cancer, Uterine Cancer
219	ALLELENSV	HCC, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer
221	FLAPDNSLLLA	Gallbladder Cancer, Bile Duct Cancer
222	FLIETGTLL	CLL, BRCA, Uterine Cancer
223	FLQDIPDGLFL	CLL
224	FLSPLLPLL	HCC, CLL
225	GTYQDVGSLNIGDV	CLL
226	GVIDPVPEV	HCC, CLL, AML, Melanoma, OC, Gallbladder Cancer, Bile Duct Cancer
227	IIAEGIPEA	SCLC, CLL, Melanoma, Uterine Cancer
228	IIAEYLSYV	CLL
229	ILSPWGAEV	CLL, AML, Melanoma, Urinary bladder cancer
230	IMDDDSYGV	CLL
232	KVMEGTVAA	CLL
233	MLEVHIPSV	CLL
234	NLQRTVVTV	RCC, CLL, Uterine Cancer
235	SLDVYELFL	CRC, BRCA, Melanoma, Esophageal Cancer, OC, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer
236	SLFDGFFLTA	CLL, AML, Melanoma, Uterine Cancer
237	YLDRLIPQA	HCC, AML, Melanoma
238	YQYGAVVTL	CLL
239	VLIDDTVLL	HCC, AML, Melanoma
240	ALVPTPALFYL	BRCA
241	FIPDFIPAV	SCLC
242	GILDFZVFL	AML
243	GLPDLDIYL	HCC, CLL, AML, Melanoma, Uterine Cancer

SEQ ID No.	Sequence	Other relevant organs / diseases
244	ILEPFLPAV	Melanoma, Uterine Cancer
245	KLIQLPVVYV	CLL, BRCA, OC, Urinary bladder cancer
246	KLPVPLESV	CLL, Melanoma
247	KVLEMETTV	Uterine Cancer
248	NLLEQFILL	NSCLC, SCLC, RCC, Brain Cancer, CRC, HCC, CLL, AML, Melanoma, Urinary bladder cancer, Uterine Cancer
249	VLLESLVEI	Melanoma, Gallbladder Cancer, Bile Duct Cancer
250	VLTNVGAAL	CLL, Uterine Cancer
251	VLYELFTYI	CLL
252	YLGDLIMAL	CLL
253	YSDDDVPSV	NSCLC, SCLC, CLL, Melanoma, Esophageal Cancer, OC, Urinary bladder cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer
254	FLYSETWNI	HCC, CLL, AML, Melanoma
255	GMWNP NAPVFL	HCC, CLL, Uterine Cancer
257	FLQEWEVYA	CLL, AML, Melanoma, Urinary bladder cancer
258	RIYPFLLMV	NSCLC, SCLC, RCC, HCC, CLL, AML, Melanoma, Urinary bladder cancer, Gallbladder Cancer, Bile Duct Cancer
259	TVLDGLEFKV	SCLC, CLL, AML, Melanoma, Uterine Cancer
260	RLDEAFDFV	Melanoma, Urinary bladder cancer, Uterine Cancer
261	FLPETRIMTSV	SCLC, CLL, Melanoma, OC, Urinary bladder cancer
263	GLMDNEIKV	NSCLC, RCC, HCC, PC, Melanoma, Gallbladder Cancer, Bile Duct Cancer
264	ILTGTPPGV	BRCA
265	ILWHFVASL	CLL, Uterine Cancer
266	QLTEMLPSI	SCLC, HCC, Melanoma, Gallbladder Cancer, Bile Duct Cancer
267	SLLETGSDLLL	HCC, Esophageal Cancer
268	VLFPLPTPL	CLL
270	VVVDSDSLAFV	SCLC, CLL, Melanoma, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer
271	YLLDQPVLEQRL	CLL, Melanoma
273	AILLPQPPK	RCC, CLL, Melanoma, OC
274	KLLNLISKL	AML
277	FLIDLNSTHGTF	CLL
278	FLLFINHRL	CLL
279	NLAGENILNPL	CLL, Urinary bladder cancer, Uterine Cancer
280	SLLNHLPYL	CLL

SEQ ID No.	Sequence	Other relevant organs / diseases
281	TLQTVPLTTV	CLL
282	YLLEQGAQV	SCLC, HCC, CLL, Melanoma
283	ALMPVTPQA	CLL
284	KLQEQIHRV	AML
285	SITAVTPLL	RCC, AML
287	ILMGHSLYM	Gallbladder Cancer, Bile Duct Cancer
288	RLAPEIVSA	HCC
289	SLLAANNLL	HCC, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer
290	IASPVIAAV	HCC, PC, CLL, AML, BRCA, Melanoma, Gallbladder Cancer, Bile Duct Cancer
291	KIIDTAGLSEA	CLL
292	KLINSQISL	CLL
293	GLAMVEAISYV	CLL, Urinary bladder cancer, Uterine Cancer
294	KLYGPEGLELV	CLL
296	FILEPLYKI	CLL, Esophageal Cancer, OC, Uterine Cancer
299	RLLEEEGVSL	CRC, AML, BRCA
301	LQFDGIHVV	SCLC, Brain Cancer
302	SLAELDEKISA	NSCLC, CLL, Melanoma, Esophageal Cancer, Urinary bladder cancer
303	FVWEASHYL	NSCLC, CLL, Esophageal Cancer, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer
304	ALIRLDDLFL	RCC, CLL, Melanoma
305	AMLAQQMQL	CLL, BRCA
306	AQVALVNEV	Urinary bladder cancer, Uterine Cancer
308	SLLDQIPEM	RCC, CLL, AML, BRCA, Melanoma, OC, Uterine Cancer, Gallbladder Cancer, Bile Duct Cancer
309	SLSFVSPSL	CLL, BRCA, Esophageal Cancer, Uterine Cancer
310	VMAEAPPGV	Uterine Cancer
311	YLHRQVAAV	SCLC, Melanoma, OC, Urinary bladder cancer

NSCLC= non-small cell lung cancer, SCLC= small cell lung cancer, RCC= kidney cancer, CRC= colon or rectum cancer, GC= stomach cancer, HCC= liver cancer, PC= pancreatic cancer, BRCA=breast cancer, OC=ovarian cancer, AML=acute myelogenous leukemia, CLL=chronic lymphocytic leukemia.

Table 4B: Peptides according to the present invention and their specific uses in other proliferative diseases, especially in other cancerous diseases (amendment of Table 4A). The table shows, like Table 4A, for selected peptides on

which additional tumor types they were found showing over-presentation (including specific presentation) on more than 5% of the measured tumor samples, or presentation on more than 5% of the measured tumor samples with a ratio of geometric means tumor vs normal tissues being larger than 3. Over-presentation is defined as higher presentation on the tumor sample as compared to the normal sample with highest presentation. Normal tissues against which over-presentation was tested were: adipose tissue, adrenal gland, artery, bone marrow, brain, central nerve, colon, duodenum, esophagus, eye, gallbladder, heart, kidney, liver, lung, lymph node, mononuclear white blood cells, pancreas, parathyroid gland, peripheral nerve, peritoneum, pituitary, pleura, rectum, salivary gland, skeletal muscle, skin, small intestine, spleen, stomach, thyroid gland, trachea, ureter, urinary bladder, vein.

SEQ ID NO.	Sequence	Other relevant organs / diseases
2	LLSEETPSA	HNSCC
3	LTIDTQYYL	HNSCC
5	VLQGLTFTL	HNSCC
11	GLDTVALL	HNSCC
12	GLLLLVP LL	OC, Esophageal Cancer, HNSCC
16	TLIAAILYL	SCLC, HNSCC
23	ALVEDIINL	Urinary Bladder Cancer, AML, HNSCC
24	AVLGFSFRL	AML
26	FLGSFIDHV	SCLC, AML
28	FLSNANPSL	SCLC, HNSCC
30	ILSTLDVEL	SCLC, Urinary Bladder Cancer, Gallbladder Cancer, Bile Duct Cancer, AML, HNSCC
33	LLANIVPIAMLV	Melanoma
36	VILDIPLLFET	SCLC, AML, HNSCC
37	VLGNALEGV	SCLC
38	YLTAEILELAGN	HNSCC
39	QLLPQGIVPAL	HCC
41	ILASIFETV	HNSCC
43	ALLEGVKNV	SCLC, BRCA
44	FIIEEQSFL	AML, HNSCC
46	FLVEEIFQT	AML
47	GLLPKLTAL	HNSCC
48	KILDEDLYI	AML, HNSCC
54	DIFDAMFSV	CLL
55	ILVEVDLVQA	Esophageal Cancer
56	GLQDLLFSL	Melanoma
60	SLLIDVITV	NSCLC, SCLC, GC, CRC, PC, BRCA, AML
61	SLLNKDLSL	Esophageal Cancer, AML, HNSCC

66	KLAPIPVEL	CLL, AML
67	LLATVNVAL	HNSCC
68	QIAAFLFTV	AML
69	TLLAFPLLL	HNSCC
70	VLIEILQKA	SCLC, HNSCC
71	VLLDYVGNVQL	HNSCC
73	YLGEEYPEV	HNSCC
76	ALADLVPVDVV V	HNSCC
88	GLFDNRSGLPE A	AML, HNSCC
95	LLFDLIPVVS	HNSCC
96	LLNENESLFL	HNSCC
99	QLYDGATALFL	HNSCC
103	SLQDHLEKV	Uterine Cancer
106	VLYELLOWYI	HNSCC
107	VQAVSIPEV	CLL, AML
108	YLAPENGYLM	Uterine Cancer, AML, HNSCC
109	YLFQFSAAL	HNSCC
110	YQYPFVLGL	HNSCC
111	YLLDTLLSL	AML, HNSCC
115	LLIDIIHFL	AML
121	YLTGYNFTL	AML
122	AISEAQESV	HNSCC
124	FLGVVVPTV	AML, HNSCC
128	KLFDASPTFFA	OC, HNSCC
131	VLIEETDQL	BRCA
144	GLITQVDKL	Esophageal Cancer
146	GLLQQPPAL	HNSCC
152	KIMYTLVSV	AML
163	SIFDAVLKGV	HCC, Urinary Bladder Cancer, HNSCC
166	SLFSEVASL	AML
168	SLLSPLLSV	HNSCC
171	TLLDVISAL	HNSCC
179	FVDTNLYFL	AML
182	LLPPPPPVA	HNSCC
183	VLFETVLT	HNSCC
185	FIAQLNNVEL	AML
188	GLEDEMYEV	HNSCC
191	GLSDISAQV	AML
194	SLAPFDREPFT L	Melanoma, Gallbladder Cancer, Bile Duct Cancer, HNSCC
198	GLLSAVSSV	HNSCC
201	YLNISQVNV	AML

205	TLFYESPHL	CLL
212	FLIGQGAHV	HCC
213	YINEDEYEV	HNSCC
214	FLFDGMSL	Urinary Bladder Cancer
216	KVVSNLPAI	RCC
217	AQFGAVLEV	RCC
218	ALDQFLEGI	HNSCC
220	FLAEAPTAL	AML
221	FLAPDNSLLLA	AML
224	FLSPLLPLL	AML
226	GVIDPVPEV	HNSCC
227	IIAEGIPEA	RCC, HNSCC
228	IIAEYLSYV	AML, HNSCC
235	SLDVYELFL	HNSCC
236	SLFDGFFLTA	RCC, GC
239	VLIDDTVLL	Uterine Cancer
240	ALVPTPALFYL	HNSCC
244	ILEPFLPAV	CLL, AML
246	KLPVPLESV	AML
247	KVLEMETTV	BRCA
248	NLLEQFILL	HNSCC
251	VLIELFTYI	AML, HNSCC
252	YLGDLIMAL	AML
253	YSDDDVPSV	AML, HNSCC
254	FLYSETWNI	HNSCC
255	GMWNP NAPVFL	HNSCC
256	ALQETPPQV	AML
258	RIYPFLLMV	CRC
259	TVLDGLEFKV	HNSCC
260	RLDEAFDFV	RCC, CLL
263	GLMDNEIKV	HNSCC
265	ILWHFVASL	AML
267	SLLETGSDLLL	Urinary Bladder Cancer, AML
268	VLFPPLPTPL	AML
280	SLLNHLPYL	HNSCC
281	TLQTVPLTTV	AML
282	YLLEQGAQV	AML, HNSCC
289	SLLAANNLL	AML
290	IASPVIAAV	NSCLC, SCLC, CRC, Uterine Cancer
291	KIIDTAGLSEA	HNSCC
292	KLINSQISL	AML
296	FILEPLYKI	AML
297	ILQNGLETL	Gallbladder Cancer, Bile Duct Cancer, AML

299	RLLEEEGVSL	Melanoma
300	IVLERNPEL	AML
301	LQFDGIHV	HNSCC
302	SLAELDEKISA	Uterine Cancer, HNSCC
303	FVWEASHYL	AML, HNSCC
306	AQVALVNEV	Esophageal Cancer, AML
307	FLLPVAVKL	HNSCC
308	SLLDQIPEM	HNSCC
309	SLSFVSPSL	AML, HNSCC
314	LIDDKGTIKL	Urinary Bladder Cancer

NSCLC= non-small cell lung cancer, SCLC= small cell lung cancer, RCC= kidney cancer, CRC= colon or rectum cancer, GC= stomach cancer, HCC= liver cancer, PC= pancreatic cancer, BRCA=breast cancer, CLL= chronic lymphocytic leukemia, AML= acute myeloid leukemia, OC= ovarian cancer, HNSCC= head and neck squamous cell carcinoma, head and neck cancer.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 1, 2, 3, 5, 6, 7, 8, 9, 10, 11, 13, 16, 17, 19, 20, 24, 25, 27, 28, 29, 31, 32, 33, 34, 36, 37, 39, 40, 41, 42, 43, 44, 45, 48, 50, 53, 54, 55, 56, 57, 59, 60, 63, 64, 65, 66, 67, 68, 69, 73, 76, 77, 80, 81, 82, 84, 85, 92, 96, 98, 101, 102, 103, 104, 105, 107, 114, 116, 122, 124, 128, 129, 131, 132, 138, 169, 179, 180, 182, 183, 184, 186, 188, 189, 190, 191, 195, 200, 201, 205, 206, 207, 208, 209, 210, 211, 212, 213, 218, 222, 223, 224, 225, 226, 227, 228, 229, 230, 232, 233, 234, 236, 238, 243, 244, 245, 246, 248, 250, 251, 252, 253, 254, 255, 257, 258, 259, 260, 261, 265, 268, 270, 271, 273, 277, 278, 279, 280, 281, 282, 283, 290, 291, 292, 293, 294, 296, 302, 303, 304, 305, 308, and 309 for the – in one preferred embodiment combined - treatment of CLL.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 1, 2, 3, 5, 10, 11, 15, 23, 26, 27, 28, 29, 30, 31, 34, 36, 37, 38, 39, 42, 45, 47, 53, 55, 60, 61, 64, 65, 67, 68, 70, 73, 76, 80, 86, 87, 88, 95, 96, 103, 108, 110, 114, 117, 118, 121, 122, 124, 125, 129, 130, 148, 161, 163, 164, 179, 181, 183, 188, 190, 193, 195, 207, 209, 215, 218, 219, 222, 227, 234, 235, 236, 239, 243, 244, 247, 248, 250, 253, 255, 259, 260, 265, 270, 279, 289, 290, 293, 296, 302, 303, 306, 308, 309, and 310 for the – in one preferred embodiment combined - treatment of uterine cancer.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 2, 20, 38, 41, 194, 248, 253, 258, 263, 302, and 303 for the – in one preferred embodiment combined - treatment of NSCLC.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 2, 7, 8, 11, 16, 17, 31, 37, 41, 47, 56, 62, 69, 70, 79, 80, 92, 95, 104, 105, 116, 117, 120, 130, 132, 138, 144, 146, 148, 149, 165, 171, 180, 183, 184, 190, 198, 207, 209, 211, 212, 214, 216, 217, 226, 229, 236, 237, 239, 242, 243, 248, 254, 257, 258, 259, 274, 284, 285, 290, 299, 23, 24, 26, 30, 36, 44, 46, 48, 60, 61, 66, 68, 88, 107, 108, 111, 115, 121, 124, 152, 166, 179, 185, 191, 201, 220, 221, 224, 228, 244, 246, 251, 252, 253, 256, 265, 267, 268, 281, 282, 289, 292, 296, 297, 300, 303, 306, 309 and 308 for the – in one preferred embodiment combined - treatment of AML.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 2, 5, 10, 11, 15, 17, 20, 23, 27, 28, 29, 36, 38, 39, 41, 43, 48, 60, 70, 76, 93, 95, 96, 108, 122, 131, 163, 165, 181, 193, 197, 207, 209, 218, 222, 235, 240, 245, 247, 264, 290, 299, 305, 308, and 309 for the – in one preferred embodiment combined - treatment of BRCA.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 2, 5, 6, 7, 12, 13, 15, 17, 20, 23, 26, 30, 31, 33, 34, 36, 38, 40, 41, 43, 47, 48, 53, 56, 60, 62, 69, 73, 76, 83, 85, 86, 96, 98, 108, 116, 119, 124, 125, 126, 127, 129, 131, 132, 141, 165, 166, 174, 179, 180, 181, 182, 185, 188, 190, 191, 194, 203, 204, 207, 209, 211, 212, 217, 226, 227, 229, 235, 236, 237, 239, 243, 244, 246, 248, 249, 253, 254, 257, 258, 259, 260, 261, 263, 266, 270, 271, 273, 282, 290, 299, 302, 304, 308, and 311 for the – in one preferred embodiment combined - treatment of melanoma.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 2, 5,

7, 27, 34, 35, 37, 38, 39, 40, 41, 58, 60, 62, 68, 70, 77, 88, 108, 125, 126, 138, 181, 183, 209, 218, 229, 235, 245, 248, 253, 257, 258, 260, 261, 279, 293, 302, 306, 23, 30, 163, 214, 267, 314 and 311 for the – in one preferred embodiment combined - treatment of urinary bladder cancer.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 5, 12, 16, 30, 34, 38, 41, 44, 46, 48, 69, 78, 87, 106, 108, 128, 129, 165, 188, 194, 198, 207, 215, 216, 219, 221, 226, 235, 249, 253, 258, 263, 266, 270, 287, 289, 290, 297, 303, and 308 for the – in one preferred embodiment combined - treatment of gallbladder cancer and/or bile duct cancer.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 5, 12, 26, 35, 39, 43, 47, 58, 70, 77, 96, 108, 124, 128, 180, 185, 191, 207, 213, 215, 226, 235, 245, 253, 261, 273, 296, 308, and 311 for the – in one preferred embodiment combined - treatment of OC.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 11, 23, 30, 34, 38, 47, 60, 73, 97, 108, 163, 184, 209, 235, 248, 258, 290, and 299 for the – in one preferred embodiment combined - treatment of CRC.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 12, 21, 27, 31, 34, 44, 47, 48, 55, 59, 61, 77, 133, 144, 165, 191, 215, 235, 253, 267, 296, 302, 303, 306, and 309 for the – in one preferred embodiment combined - treatment of esophageal cancer.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 20, 41, 47, 74, 78, 86, 93, 94, 100, 109, 122, 163, 165, 179, 181, 197, 215, 234, 248, 258, 263, 273, 285, 304, 216, 217, 227, 236, 260, and 308 for the – in one preferred embodiment combined - treatment of RCC.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 37, 38, 39, 47, 69, 77, 96, 103, 108, 116, 152, 163, 169, 180, 181, 190, 207, 209, 211, 212, 219, 224, 226, 237, 239, 243, 248, 254, 255, 258, 263, 266, 267, 282, 288, 289, and 290 for the – in one preferred embodiment combined - treatment of HCC.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 60, 109, 263, and 290 for the – in one preferred embodiment combined - treatment of PC.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 47, 248, and 301 for the – in one preferred embodiment combined - treatment of brain cancer.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 2, 3, 5, 11, 12, 16, 23, 28, 30, 36, 38, 41, 44, 47, 48, 61, 67, 69, 70, 71, 73, 76, 88, 95, 96, 99, 106, 108, 109, 110, 111, 122, 124, 128, 146, 163, 168, 171, 182, 183, 188, 194, 198, 213, 218, 226, 227, 228, 235, 240, 248, 251, 253, 254, 255, 259, 263, 280, 282, 291, 301, 302, 303, 307, 308, and 309 for the – in one preferred embodiment combined - treatment of HNSCC.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 2, 5, 16, 26, 28, 30, 36, 37, 38, 41, 43, 46, 60, 70, 73, 76, 90, 108, 117, 164, 182, 186, 207, 227, 241, 248, 253, 258, 259, 261, 266, 270, 282, 301, 311, and 290 for the – in one preferred embodiment combined - treatment of SCLC.

Thus, another aspect of the present invention relates to the use of at least one peptide according to the present invention according to any one of SEQ ID No. 60, 74 and 236 for the – in one preferred embodiment combined - treatment of GC.

Thus, another aspect of the present invention relates to the use of the peptides according to the present invention for the - preferably combined - treatment of a proliferative disease selected from the group of NHL, non-small cell lung cancer, small cell lung cancer, renal cell cancer, brain cancer, gastric cancer, colorectal cancer, hepatocellular cancer, pancreatic cancer, leukemia, breast cancer, melanoma, ovarian cancer, urinary bladder cancer, uterine cancer, gallbladder and bile duct cancer.

The present invention furthermore relates to peptides according to the present invention that have the ability to bind to a molecule of the human major histocompatibility complex (MHC) class-I or - in an elongated form, such as a length-variant - MHC class -II.

The present invention further relates to the peptides according to the present invention wherein said peptides (each) consist or consist essentially of an amino acid sequence according to SEQ ID NO: 1 to SEQ ID NO: 311.

The present invention further relates to the peptides according to the present invention, wherein said peptide is modified and/or includes non-peptide bonds.

The present invention further relates to the peptides according to the present invention, wherein said peptide is part of a fusion protein, in particular fused to the N-terminal amino acids of the HLA-DR antigen-associated invariant chain (Ii), or fused to (or into the sequence of) an antibody, such as, for example, an antibody that is specific for dendritic cells.

The present invention further relates to a nucleic acid, encoding the peptides according to the present invention. The present invention further relates to the nucleic acid according to the present invention that is DNA, cDNA, PNA, RNA or combinations thereof.

The present invention further relates to an expression vector capable of expressing and/or expressing a nucleic acid according to the present invention.

The present invention further relates to a peptide according to the present invention, a nucleic acid according to the present invention or an expression vector according to the present invention for use in the treatment of diseases and in medicine, in particular in the treatment of cancer.

The present invention further relates to antibodies that are specific against the peptides according to the present invention or complexes of said peptides according to the present invention with MHC, and methods of making these.

The present invention further relates to T-cell receptors (TCRs), in particular soluble TCR (sTCRs) and in particular cloned TCRs engineered into autologous or allogeneic T cells, and methods of making these, as well as NK cells or other cells expressing and/or bearing said TCR or cross-reacting with said TCRs.

The antibodies and TCRs are additional embodiments of the immunotherapeutic use of the peptides according to the invention at hand.

The present invention further relates to a host cell comprising a nucleic acid according to the present invention or an expression vector as described before. The present invention further relates to the host cell according to the present invention that is an antigen presenting cell, and preferably is a dendritic cell.

The present invention further relates to a method for producing a peptide according to the present invention, said method comprising culturing the host cell according to the present invention, and isolating the peptide from said host cell or its culture medium.

The present invention further relates to said method according to the present invention, wherein the antigen is loaded onto class I or II MHC molecules expressed on the surface of a suitable antigen-presenting cell or artificial antigen-presenting cell by contacting a sufficient amount of the antigen with an antigen-presenting cell.

The present invention further relates to the method according to the present invention, wherein the antigen-presenting cell comprises an expression vector capable of expressing or expressing said peptide containing SEQ ID No. 1 to SEQ ID No.: 311, preferably containing SEQ ID No. 1 to SEQ ID No. 217, or a variant amino acid sequence.

The present invention further relates to activated T cells, produced by the method according to the present invention, wherein said T cell selectively recognizes a cell which expresses a polypeptide comprising an amino acid sequence according to the present invention.

The present invention further relates to a method of killing target cells in a patient which target cells aberrantly express a polypeptide comprising any amino acid sequence according to the present invention, the method comprising administering to the patient an effective number of T cells as produced according to the present invention.

The present invention further relates to the use of any peptide as described, the nucleic acid according to the present invention, the expression vector according to the present invention, the cell according to the present invention, the activated T lymphocyte, the T cell receptor or the antibody or other peptide- and/or peptide-MHC-binding molecules according to the present invention as a medicament or in the manufacture of a medicament. Preferably, said medicament is active against cancer.

Preferably, said medicament is a cellular therapy, a vaccine or a protein based on a soluble TCR or antibody.

The present invention further relates to a use according to the present invention, wherein said cancer cells are NHL, non-small cell lung cancer, small cell lung cancer, renal cell cancer, brain cancer, gastric cancer, colorectal cancer, hepatocellular cancer, pancreatic cancer, leukemia, breast cancer, melanoma, ovarian cancer, urinary bladder cancer, uterine cancer, gallbladder and bile duct cancer, and preferably NHL cells.

The present invention further relates to biomarkers based on the peptides according to the present invention, herein called “targets” that can be used in the diagnosis of cancer, preferably NHL. The marker can be over-presentation of the peptide(s) themselves, or over-expression of the corresponding gene(s). The markers may also be used to predict the probability of success of a treatment, preferably an immunotherapy, and most preferred an immunotherapy targeting the same target that is identified by the biomarker. For example, an antibody or soluble TCR can be used to stain sections of the tumor to detect the presence of a peptide of interest in complex with MHC.

Optionally the antibody carries a further effector function such as an immune stimulating domain or toxin.

The present invention also relates to the use of these novel targets in the context of cancer treatment.

Both therapeutic and diagnostic uses against additional cancerous diseases are disclosed in the following description of the underlying expression products (polypeptides) of the peptides according to the invention.

ACHE encodes acetylcholinesterase which hydrolyzes the neurotransmitter, acetylcholine at neuromuscular junctions and brain cholinergic synapses, and thus terminates signal transmission (RefSeq, 2002). ACHE may be a marker and regulator of apoptosis. It is involved in cell adhesion, differentiation, and proliferation and it is a promising tumor suppressor (Greig et al., 2013; Xi et al., 2015). ACHE and BCHE are involved in tumorigenesis but their relationship is not clear yet (Shan, 2004a). ACHE is abnormally expressed in meningioma, glioma, acoustic neurinoma, lung cancer, colon cancer, fibrosarcoma and ovarian cancer (Russo et al., 2006; Shan, 2004a; Shan, 2004b). Treatment of the Lambert-Eaton myasthenic syndrome, which has an idiopathic and a tumor-associated form, includes the usage of acetylcholinesterase inhibitors (Mareska and Gutmann, 2004; Verschuuren et al., 2006). Peptides spliced from the ACHE parent molecule as well as the parent protein itself can act independently as signaling molecule (Bukowska, 2005; Halliday and Greenfield, 2012).

ACN9 (also known as succinate dehydrogenase complex assembly factor 3 (SDHAF3)) encodes ACN9 homolog and is located on chromosome 7q21.3 (RefSeq, 2002). Wrong or absent SDH complex assembly can result in cancer and neurodegenerative syndromes (Van Vranken et al., 2015). Various SNPs in ACN9 are associated with breast cancer (Kibriya et al., 2009).

CDC42 encodes cell division cycle 42 which is a small GTPase of the Rho-subfamily, which regulates signaling pathways that control diverse cellular functions including cell morphology, migration, endocytosis and cell cycle progression (RefSeq, 2002). CDC42 controls epithelial as well as migratory polarity in combination with other regulators (Gandalovicova et al., 2016). c-Cbl is inhibited in glioblastomas and basal-like breast cancer through alteration of Cool-1/betapix and CDC42 (Noble et al., 2015). Exchange factors of CDC42, so called Dock family proteins, are involved in cancer (Gadea and Blangy, 2014). CDC42 is a RhoGTPase located at epithelial tight junctions (Lane et al., 2014; Zihni and Terry, 2015). CDC42 is able to activate STAT3 which is over-expressed in a variety of cancers (Raptis et al., 2011). CDC42 de-regulation is involved in cancer. It was shown that CDC42 signaling is involved in cellular transformation, cell division, cell invasion, migration, invadopodia formation, enzyme activity, filopodia formation, actin cytoskeleton alteration, and cell polarity. CDC42 regulates the invasion in glioblastoma (Stengel and Zheng, 2011; Albergaria et al., 2011; Kwiatkowska and Symons, 2013; Qadir et al., 2015; Lin and Zheng, 2015). Activated CDC42-associate kinase 1 (ACK1/TNK2) is an oncogenic kinase. p21-activated kinase (PAK) 5 is a downstream effector kinase of CDC42 and it is over-expressed in several cancer entities. PAK1 is up-regulated in cancer and is associated with tumor progression. Myotonic dystrophy-related CDC42-binding kinases (MRCK) are associated with human cancer (Mahajan and Mahajan, 2010; Eswaran et al., 2012; Maruta, 2014; Unbekandt and Olson, 2014; Dammann et al., 2014; Wen et al., 2014; Mahajan and Mahajan, 2015). CDC42 controls polarized atypical protein kinase C activity (Prehoda, 2009). The CDC42-IQGAP1 axis may drive *H. pylori*-induced gastric carcinoma by negatively regulating the tumor suppressors E-cadherin and beta1-integrin (White et al., 2009; Osman et al., 2013). CDC42 is regulated via mTORC2 signaling and maybe via Notch signaling (Dotto, 2008; Zhou and Huang, 2011). Tiam1, GEFs, and RhoA are activators of CDC42

whereas Slit2 and Robo1 are inhibitors. CDC42 is regulated by CXCL12 and DLC-1 (Boissier and Huynh-Do, 2014; Sinha and Yang, 2008; Kim et al., 2009; Ben-Baruch, 2009; Xu et al., 2010; O'Connor and Chen, 2013). CDC42 is a downstream effector of CD44 and HMGB1 resulting in angiogenesis, unlimited replicative potential, tissue invasion, and metastasis (Bourguignon, 2008; Hu et al., 2014). CDC42 is over-expressed in several cancer entities and may be correlated with poor prognosis. CDC42 over-expression in breast cancer may contribute to ErbB1 accumulation (Hirsch and Wu, 2007; Arias-Romero and Chernoff, 2013). The Golgi pool of CDC42 is regulated by a complex of GM130 and RasGRF. GM130 is progressively lost in colorectal cancer (Baschieri and Farhan, 2015).

DCAKD encodes dephospho-CoA kinase domain containing and is located on chromosome 17q21.31 (RefSeq, 2002). DCAKD is up-regulated in breast cancer (Riis et al., 2012).

HAPLN3 encodes hyaluronan and proteoglycan link protein 3 which may function in hyaluronic acid binding and cell adhesion (RefSeq, 2002). A three-gene signature including HAPLN3 can be used as methylation marker in prostate cancer (Strand et al., 2014). A gene fusion product of MFGE8 and HAPLN3 has been reported in breast cancer (Varley et al., 2014). HAPLN3 is hyper-methylated in prostate cancer (Haldrup et al., 2013). HAPLN3 is up-regulated in breast cancer and may be used as biomarker (Kuo et al., 2010).

JAK3 encodes Janus Kinase 3, a member of the Janus kinase (JAK) family of tyrosine kinases involved in cytokine receptor-mediated intracellular signal transduction. It is predominantly expressed in immune cells and transduces a signal in response to its activation via tyrosine phosphorylation by interleukin receptors (RefSeq, 2002). JAK3 is de-regulated in different cancer types including cutaneous T-cell lymphoma, extranodal nasal-type natural killer cell lymphoma, acute lymphoblastic leukemia, renal cell carcinoma and colon carcinoma (Lin et al., 2005; de et al., 2013; Bouchekioua et al., 2014; Sibbesen et al., 2015; Losdyck et al., 2015). JAK3 expression affects its down-stream targets STAT3, STAT5, MAPK, pS6, the tumor suppressor microRNA miR-22, Bcl-2, Bcl-X, cyclin D2, p21 and p27.

Therefore, JAK2 controls cell growth, apoptosis and cell cycle progression (Lin et al., 2005; Sibbesen et al., 2015; Agarwal et al., 2015).

KDM2B encodes lysine demethylase 2B, a member of the F-box protein family which is characterized by an approximately 40 amino acid motif, the F-box. The F-box proteins constitute one of the four subunits of ubiquitin protein ligase complex called SCFs (SKP1-cullin-F-box), which function in phosphorylation-dependent ubiquitination (RefSeq, 2002). KDM2B over-expression leads to enhanced cell migration by binding to migration-associated genes (Rohde et al., 2016). MiR-448, which is over-expressed in gastric cancer, down-regulates KDM2B. Myc is a key target of KDM2B (Hong et al., 2016). KDM2B mediates hematopoietic cell development and shows opposing roles in tumor progression (Andricovich et al., 2016). KDM2B is a co-repressor of BCL6 (Oliviero et al., 2015). KDM2B is involved in PI3K/mTOR pathway and promotes cell proliferation and inhibits cell apoptosis in nasopharyngeal carcinoma (Ren et al., 2015). Local generation of fumarate inhibits KDM2B resulting in the activation of DNA repair (Jiang et al., 2015). Depletion of KDM2B results in a p53-dependent growth arrest (Penzo et al., 2015). BCOR PFUD internal tandem duplications can be found in pediatric kidney and brain tumors. BCORL1 is part of the Polycomb Group Complex 1 (PRC1.1) which is recruited by KDM2B to facilitate gene repression. The PRC1.1 is important for leukemic stem cells and down-regulation of complex members like KDM2B reduces cell proliferation (Yamamoto et al., 2014; He et al., 2013; Blackledge et al., 2014; van den Boom et al., 2016; Wong et al., 2016). KDM2B is a non-Yamanaka factor involved in cell reprogramming (Liang et al., 2012; Liu et al., 2015). In bladder cancer, KDM2B is involved in cell proliferation, migration, and angiogenesis (Kottakis et al., 2011). KDM2B is over-expressed in several entities including basal-like triple-negative breast cancer and pancreatic cancer and regulates cell proliferation, chromatin structure, and senescence in HeLa cells. It is a positive regulator of glycolysis, glutaminolysis, and pyrimidine synthesis (Tzatsos et al., 2011; Tzatsos et al., 2013; Kottakis et al., 2014; Bacalini et al., 2015; Yu et al., 2015). KDM2B is an oncogene involved in leukemia development by impairing Nsg2-mediated differentiation (He et al., 2011; Nakamura et al., 2013; Ueda et al., 2015). KDM2B is a NF-kappaB-dependent anti-apoptotic protein. KDM2B-dependent degradation of c-Fos negatively regulates cell proliferation (Ge et al., 2011; Han et al., 2016).

KDM5B encodes the protein JARID1B, a lysine-specific histone demethylase that is capable of repressing certain tumor suppressor genes by de-methylating lysine 4 of histone H3 (RefSeq, 2002). As epigenetic factor, KDM5B supports proliferation, migration and invasion of human OSCC, head and neck squamous cell carcinoma (HNSCC), breast cancer and lung cancer by suppressing p53 expression (Shen et al., 2015; Tang et al., 2015; Zhao and Liu, 2015; Lin et al., 2015). Also known as JARID1B, KDM5B promotes metastasis an epithelial-mesenchymal transition in various tumor types via PTEN/AKT signaling (Tang et al., 2015).

PTTG1 encodes pituitary tumor-transforming 1. The encoded protein is a homolog of yeast securing proteins, which prevent separins from promoting sister chromatid separation. It is an anaphase-promoting complex (APC) substrate that associates with a separin until activation of the APC (RefSeq, 2002). PTTG1 is over-expressed in different cancer types including oral cancer, cervical cancer, breast cancer, prostate cancer and skin cancer. High protein levels are associated with metastasis and poor clinical outcome (Noll et al., 2015; Yoon et al., 2012; Huang et al., 2012; Zhang et al., 2014; Chen et al., 2015). PTTG1 is up-regulated in an mTOR complex 1-dependent manner. PTTG1 inhibits TGFbeta1-dependent phosphorylation of SMAD3 to promote cell growth (Zhang et al., 2015; Chen et al., 2016).

PTTG2 encodes pituitary tumor-transforming 2 and it is located on chromosome 4p12 (RefSeq, 2002). Over-expression of the PTTG2 gene has been observed in high-grade glioma, whereas in liver cancer tissues from patients PTTG2 was not highly expressed (Yang et al., 2013; Cho-Rok et al., 2006). Elevated levels of PTTG2 were shown to promote cell proliferation and invasion during glioblastoma progression (Guo et al., 2016).

SMC2 (also called CAP-E or SMC2L1) encodes a member of the structural maintenance of chromosomes family which is critical for mitotic chromosome condensation and DNA repair (RefSeq, 2002). The SMC2 gene is altered by frameshift mutation and loss of expression in gastric and colorectal cancer with microsatellite instability suggesting that SMC2 might be involved in tumor pathogenesis (Je et al., 2014). SMC2 gene alterations can play a role in genome

instability, which accelerates the accumulation of other alterations in pyothorax-associated lymphomas (Ham et al., 2007).

TMEM67 encodes transmembrane protein 67 and is localized to the primary cilium and to the plasma membrane. The gene functions in centriole migration to the apical membrane and formation of the primary cilium. Defects in this gene are a cause of Meckel syndrome type 3 (MKS3) and Joubert syndrome type 6 (JBTS6) (RefSeq, 2002). TMEM67 is involved in cilia formation and defective cilia may cause ocular coloboma, tongue tumors, and medulloblastoma (Han et al., 2010; Parisi, 2009; Yang et al., 2015; Han and Alvarez-Buylla, 2010).

Stimulation of an immune response is dependent upon the presence of antigens recognized as foreign by the host immune system. The discovery of the existence of tumor associated antigens has raised the possibility of using a host's immune system to intervene in tumor growth. Various mechanisms of harnessing both the humoral and cellular arms of the immune system are currently being explored for cancer immunotherapy.

Specific elements of the cellular immune response are capable of specifically recognizing and destroying tumor cells. The isolation of T-cells from tumor-infiltrating cell populations or from peripheral blood suggests that such cells play an important role in natural immune defense against cancer. CD8-positive T-cells in particular, which recognize class I molecules of the major histocompatibility complex (MHC)-bearing peptides of usually 8 to 10 amino acid residues derived from proteins or defect ribosomal products (DRIPS) located in the cytosol, play an important role in this response. The MHC-molecules of the human are also designated as human leukocyte-antigens (HLA).

The term "T-cell response" means the specific proliferation and activation of effector functions induced by a peptide *in vitro* or *in vivo*. For MHC class I restricted cytotoxic T cells, effector functions may be lysis of peptide-pulsed, peptide-precursor pulsed or naturally peptide-presenting target cells, secretion of cytokines, preferably Interferon-gamma, TNF-alpha, or IL-2 induced by peptide, secretion of effector molecules, preferably granzymes or perforins induced by peptide, or degranulation.

The term “peptide” is used herein to designate a series of amino acid residues, connected one to the other typically by peptide bonds between the alpha-amino and carbonyl groups of the adjacent amino acids. The peptides are preferably 9 amino acids in length, but can be as short as 8 amino acids in length, and as long as 10, 11, 12, 13, or 14 or longer, and in case of MHC class II peptides (elongated variants of the peptides of the invention) they can be as long as 14, 15, 16, 17, 18, 19 or 20 or more amino acids in length.

Furthermore, the term “peptide” shall include salts of a series of amino acid residues, connected one to the other typically by peptide bonds between the alpha-amino and carbonyl groups of the adjacent amino acids. Preferably, the salts are pharmaceutical acceptable salts of the peptides, such as, for example, the chloride or acetate (trifluoroacetate) salts. It has to be noted that the salts of the peptides according to the present invention differ substantially from the peptides in their state(s) *in vivo*, as the peptides are not salts *in vivo*.

The term “peptide” shall also include “oligopeptide”. The term “oligopeptide” is used herein to designate a series of amino acid residues, connected one to the other typically by peptide bonds between the alpha-amino and carbonyl groups of the adjacent amino acids. The length of the oligopeptide is not critical to the invention, as long as the correct epitope or epitopes are maintained therein. The oligopeptides are typically less than about 30 amino acid residues in length, and greater than about 15 amino acids in length.

The term “polypeptide” designates a series of amino acid residues, connected one to the other typically by peptide bonds between the alpha-amino and carbonyl groups of the adjacent amino acids. The length of the polypeptide is not critical to the invention as long as the correct epitopes are maintained. In contrast to the terms peptide or oligopeptide, the term polypeptide is meant to refer to molecules containing more than about 30 amino acid residues.

A peptide, oligopeptide, protein or polynucleotide coding for such a molecule is “immunogenic” (and thus is an “immunogen” within the present invention), if it is

capable of inducing an immune response. In the case of the present invention, immunogenicity is more specifically defined as the ability to induce a T-cell response. Thus, an “immunogen” would be a molecule that is capable of inducing an immune response, and in the case of the present invention, a molecule capable of inducing a T-cell response. In another aspect, the immunogen can be the peptide, the complex of the peptide with MHC, oligopeptide, and/or protein that is used to raise specific antibodies or TCRs against it.

A class I T cell “epitope” requires a short peptide that is bound to a class I MHC receptor, forming a ternary complex (MHC class I alpha chain, beta-2-microglobulin, and peptide) that can be recognized by a T cell bearing a matching T-cell receptor binding to the MHC/peptide complex with appropriate affinity. Peptides binding to MHC class I molecules are typically 8-14 amino acids in length, and most typically 9 amino acids in length.

In humans, there are three different genetic loci that encode MHC class I molecules (the MHC-molecules of the human are also designated human leukocyte antigens (HLA)): HLA-A, HLA-B, and HLA-C. HLA-A*01, HLA-A*02, and HLA-B*07 are examples of different MHC class I alleles that can be expressed from these loci.

Table 5: Expression frequencies F of HLA-A*02 and HLA-A*24 and the most frequent HLA-DR serotypes. Frequencies are deduced from haplotype frequencies Gf within the American population adapted from Mori et al. (Mori et al., 1997) employing the Hardy-Weinberg formula $F = 1 - (1 - Gf)^2$. Combinations of A*02 or A*24 with certain HLA-DR alleles might be enriched or less frequent than expected from their single frequencies due to linkage disequilibrium. For details refer to Chanock et al. (Chanock et al., 2004).

Allele	Population	Calculated phenotype from allele frequency
A*02	Caucasian (North America)	49.1%
A*02	African American (North America)	34.1%
A*02	Asian American (North America)	43.2%
A*02	Latin American (North American)	48.3%
DR1	Caucasian (North America)	19.4%
DR2	Caucasian (North America)	28.2%
DR3	Caucasian (North America)	20.6%
DR4	Caucasian (North America)	30.7%

Allele	Population	Calculated phenotype from allele frequency
DR5	Caucasian (North America)	23.3%
DR6	Caucasian (North America)	26.7%
DR7	Caucasian (North America)	24.8%
DR8	Caucasian (North America)	5.7%
DR9	Caucasian (North America)	2.1%
DR1	African (North) American	13.20%
DR2	African (North) American	29.80%
DR3	African (North) American	24.80%
DR4	African (North) American	11.10%
DR5	African (North) American	31.10%
DR6	African (North) American	33.70%
DR7	African (North) American	19.20%
DR8	African (North) American	12.10%
DR9	African (North) American	5.80%
DR1	Asian (North) American	6.80%
DR2	Asian (North) American	33.80%
DR3	Asian (North) American	9.20%
DR4	Asian (North) American	28.60%
DR5	Asian (North) American	30.00%
DR6	Asian (North) American	25.10%
DR7	Asian (North) American	13.40%
DR8	Asian (North) American	12.70%
DR9	Asian (North) American	18.60%
DR1	Latin (North) American	15.30%
DR2	Latin (North) American	21.20%
DR3	Latin (North) American	15.20%
DR4	Latin (North) American	36.80%
DR5	Latin (North) American	20.00%
DR6	Latin (North) American	31.10%
DR7	Latin (North) American	20.20%
DR8	Latin (North) American	18.60%
DR9	Latin (North) American	2.10%
A*24	Philippines	65%
A*24	Russia Nenets	61%
A*24:02	Japan	59%
A*24	Malaysia	58%
A*24:02	Philippines	54%
A*24	India	47%
A*24	South Korea	40%
A*24	Sri Lanka	37%
A*24	China	32%
A*24:02	India	29%

Allele	Population	Calculated phenotype from allele frequency
A*24	Australia West	22%
A*24	USA	22%
A*24	Russia Samara	20%
A*24	South America	20%
A*24	Europe	18%

The peptides of the invention, preferably when included into a vaccine of the invention as described herein bind to A*02. A vaccine may also include pan-binding MHC class II peptides. Therefore, the vaccine of the invention can be used to treat cancer in patients that are A*02 positive, whereas no selection for MHC class II allotypes is necessary due to the pan-binding nature of these peptides.

If A*02 peptides of the invention are combined with peptides binding to another allele, for example A*24, a higher percentage of any patient population can be treated compared with addressing either MHC class I allele alone. While in most populations less than 50% of patients could be addressed by either allele alone, a vaccine comprising HLA-A*24 and HLA-A*02 epitopes can treat at least 60% of patients in any relevant population. Specifically, the following percentages of patients will be positive for at least one of these alleles in various regions: USA 61%, Western Europe 62%, China 75%, South Korea 77%, Japan 86% (calculated from www.allele frequencies.net).

In a preferred embodiment, the term “nucleotide sequence” refers to a heteropolymer of deoxyribonucleotides.

The nucleotide sequence coding for a particular peptide, oligopeptide, or polypeptide may be naturally occurring or they may be synthetically constructed. Generally, DNA segments encoding the peptides, polypeptides, and proteins of this invention are assembled from cDNA fragments and short oligonucleotide linkers, or from a series of oligonucleotides, to provide a synthetic gene that is capable of being expressed in a recombinant transcriptional unit comprising regulatory elements derived from a microbial or viral operon.

As used herein the term “a nucleotide coding for (or encoding) a peptide” refers to a nucleotide sequence coding for the peptide including artificial (man-made) start and stop codons compatible for the biological system the sequence is to be expressed by, for example, a dendritic cell or another cell system useful for the production of TCRs.

As used herein, reference to a nucleic acid sequence includes both single stranded and double stranded nucleic acid. Thus, for example for DNA, the specific sequence, unless the context indicates otherwise, refers to the single strand DNA of such sequence, the duplex of such sequence with its complement (double stranded DNA) and the complement of such sequence.

The term “coding region” refers to that portion of a gene which either naturally or normally codes for the expression product of that gene in its natural genomic environment, i.e., the region coding *in vivo* for the native expression product of the gene.

The coding region can be derived from a non-mutated (“normal”), mutated or altered gene, or can even be derived from a DNA sequence, or gene, wholly synthesized in the laboratory using methods well known to those of skill in the art of DNA synthesis.

The term “expression product” means the polypeptide or protein that is the natural translation product of the gene and any nucleic acid sequence coding equivalents resulting from genetic code degeneracy and thus coding for the same amino acid(s).

The term “fragment”, when referring to a coding sequence, means a portion of DNA comprising less than the complete coding region, whose expression product retains essentially the same biological function or activity as the expression product of the complete coding region.

The term “DNA segment” refers to a DNA polymer, in the form of a separate fragment or as a component of a larger DNA construct, which has been derived from DNA isolated at least once in substantially pure form, i.e., free of contaminating endogenous materials and in a quantity or concentration enabling identification, manipulation, and recovery of the segment and its component nucleotide sequences

by standard biochemical methods, for example, by using a cloning vector. Such segments are provided in the form of an open reading frame uninterrupted by internal non-translated sequences, or introns, which are typically present in eukaryotic genes. Sequences of non-translated DNA may be present downstream from the open reading frame, where the same do not interfere with manipulation or expression of the coding regions.

The term “primer” means a short nucleic acid sequence that can be paired with one strand of DNA and provides a free 3'-OH end at which a DNA polymerase starts synthesis of a deoxyribonucleotide chain.

The term “promoter” means a region of DNA involved in binding of RNA polymerase to initiate transcription.

The term “isolated” means that the material is removed from its original environment (e.g., the natural environment, if it is naturally occurring). For example, a naturally-occurring polynucleotide or polypeptide present in a living animal is not isolated, but the same polynucleotide or polypeptide, separated from some or all of the coexisting materials in the natural system, is isolated. Such polynucleotides could be part of a vector and/or such polynucleotides or polypeptides could be part of a composition, and still be isolated in that such vector or composition is not part of its natural environment.

The polynucleotides, and recombinant or immunogenic polypeptides, disclosed in accordance with the present invention may also be in “purified” form. The term “purified” does not require absolute purity; rather, it is intended as a relative definition, and can include preparations that are highly purified or preparations that are only partially purified, as those terms are understood by those of skill in the relevant art. For example, individual clones isolated from a cDNA library have been conventionally purified to electrophoretic homogeneity. Purification of starting material or natural material to at least one order of magnitude, preferably two or three orders, and more preferably four or five orders of magnitude is expressly contemplated. Furthermore, a claimed polypeptide which has a purity of preferably 99.999%, or at least 99.99% or 99.9%; and even desirably 99% by weight or greater is expressly encompassed.

The nucleic acids and polypeptide expression products disclosed according to the present invention, as well as expression vectors containing such nucleic acids and/or such polypeptides, may be in “enriched form”. As used herein, the term “enriched” means that the concentration of the material is at least about 2, 5, 10, 100, or 1000 times its natural concentration (for example), advantageously 0.01%, by weight, preferably at least about 0.1% by weight. Enriched preparations of about 0.5%, 1%, 5%, 10%, and 20% by weight are also contemplated. The sequences, constructs, vectors, clones, and other materials comprising the present invention can advantageously be in enriched or isolated form. The term “active fragment” means a fragment, usually of a peptide, polypeptide or nucleic acid sequence, that generates an immune response (i.e., has immunogenic activity) when administered, alone or optionally with a suitable adjuvant or in a vector, to an animal, such as a mammal, for example, a rabbit or a mouse, and also including a human, such immune response taking the form of stimulating a T-cell response within the recipient animal, such as a human. Alternatively, the “active fragment” may also be used to induce a T-cell response *in vitro*.

As used herein, the terms “portion”, “segment” and “fragment”, when used in relation to polypeptides, refer to a continuous sequence of residues, such as amino acid residues, which sequence forms a subset of a larger sequence. For example, if a polypeptide were subjected to treatment with any of the common endopeptidases, such as trypsin or chymotrypsin, the oligopeptides resulting from such treatment would represent portions, segments or fragments of the starting polypeptide. When used in relation to polynucleotides, these terms refer to the products produced by treatment of said polynucleotides with any of the endonucleases.

In accordance with the present invention, the term “percent identity” or “percent identical”, when referring to a sequence, means that a sequence is compared to a claimed or described sequence after alignment of the sequence to be compared (the “Compared Sequence”) with the described or claimed sequence (the “Reference Sequence”). The percent identity is then determined according to the following formula:

$$\text{percent identity} = 100 [1 - (C/R)]$$

wherein C is the number of differences between the Reference Sequence and the Compared Sequence over the length of alignment between the Reference Sequence and the Compared Sequence, wherein

- (i) each base or amino acid in the Reference Sequence that does not have a corresponding aligned base or amino acid in the Compared Sequence and
 - (ii) each gap in the Reference Sequence and
 - (iii) each aligned base or amino acid in the Reference Sequence that is different from an aligned base or amino acid in the Compared Sequence, constitutes a difference and
 - (iiii) the alignment has to start at position 1 of the aligned sequences;
- and R is the number of bases or amino acids in the Reference Sequence over the length of the alignment with the Compared Sequence with any gap created in the Reference Sequence also being counted as a base or amino acid.

If an alignment exists between the Compared Sequence and the Reference Sequence for which the percent identity as calculated above is about equal to or greater than a specified minimum Percent Identity then the Compared Sequence has the specified minimum percent identity to the Reference Sequence even though alignments may exist in which the herein above calculated percent identity is less than the specified percent identity.

As mentioned above, the present invention thus provides a peptide comprising a sequence that is selected from the group of consisting of SEQ ID NO: 1 to SEQ ID NO: 311 or a variant thereof which is 88% homologous to SEQ ID NO: 1 to SEQ ID NO: 311, or a variant thereof that will induce T cells cross-reacting with said peptide. The peptides of the invention have the ability to bind to a molecule of the human major histocompatibility complex (MHC) class-I or elongated versions of said peptides to class II.

In the present invention, the term "homologous" refers to the degree of identity (see percent identity above) between sequences of two amino acid sequences, i.e. peptide or polypeptide sequences. The aforementioned "homology" is determined by comparing two sequences aligned under optimal conditions over the sequences to be compared. Such a sequence homology can be calculated by creating an alignment

using, for example, the ClustalW algorithm. Commonly available sequence analysis software, more specifically, Vector NTI, GENETYX or other tools are provided by public databases.

A person skilled in the art will be able to assess, whether T cells induced by a variant of a specific peptide will be able to cross-react with the peptide itself (Appay et al., 2006; Colombetti et al., 2006; Fong et al., 2001; Zaremba et al., 1997).

By a "variant" of the given amino acid sequence the inventors mean that the side chains of, for example, one or two of the amino acid residues are altered (for example by replacing them with the side chain of another naturally occurring amino acid residue or some other side chain) such that the peptide is still able to bind to an HLA molecule in substantially the same way as a peptide consisting of the given amino acid sequence in consisting of SEQ ID NO: 1 to SEQ ID NO: 311. For example, a peptide may be modified so that it at least maintains, if not improves, the ability to interact with and bind to the binding groove of a suitable MHC molecule, such as HLA-A*02 or -DR, and in that way, it at least maintains, if not improves, the ability to bind to the TCR of activated T cells.

These T cells can subsequently cross-react with cells and kill cells that express a polypeptide that contains the natural amino acid sequence of the cognate peptide as defined in the aspects of the invention. As can be derived from the scientific literature and databases (Rammensee et al., 1999; Godkin et al., 1997), certain positions of HLA binding peptides are typically anchor residues forming a core sequence fitting to the binding motif of the HLA receptor, which is defined by polar, electrophysical, hydrophobic and spatial properties of the polypeptide chains constituting the binding groove. Thus, one skilled in the art would be able to modify the amino acid sequences set forth in SEQ ID NO: 1 to SEQ ID NO 311, by maintaining the known anchor residues, and would be able to determine whether such variants maintain the ability to bind MHC class I or II molecules. The variants of the present invention retain the ability to bind to the TCR of activated T cells, which can subsequently cross-react with and kill cells that express a polypeptide containing the natural amino acid sequence of the cognate peptide as defined in the aspects of the invention.

The original (unmodified) peptides as disclosed herein can be modified by the substitution of one or more residues at different, possibly selective, sites within the peptide chain, if not otherwise stated. Preferably those substitutions are located at the end of the amino acid chain. Such substitutions may be of a conservative nature, for example, where one amino acid is replaced by an amino acid of similar structure and characteristics, such as where a hydrophobic amino acid is replaced by another hydrophobic amino acid. Even more conservative would be replacement of amino acids of the same or similar size and chemical nature, such as where leucine is replaced by isoleucine. In studies of sequence variations in families of naturally occurring homologous proteins, certain amino acid substitutions are more often tolerated than others, and these are often show correlation with similarities in size, charge, polarity, and hydrophobicity between the original amino acid and its replacement, and such is the basis for defining "conservative substitutions."

Conservative substitutions are herein defined as exchanges within one of the following five groups: Group 1-small aliphatic, nonpolar or slightly polar residues (Ala, Ser, Thr, Pro, Gly); Group 2-polar, negatively charged residues and their amides (Asp, Asn, Glu, Gln); Group 3-polar, positively charged residues (His, Arg, Lys); Group 4-large, aliphatic, nonpolar residues (Met, Leu, Ile, Val, Cys); and Group 5-large, aromatic residues (Phe, Tyr, Trp).

Less conservative substitutions might involve the replacement of one amino acid by another that has similar characteristics but is somewhat different in size, such as replacement of an alanine by an isoleucine residue. Highly non-conservative replacements might involve substituting an acidic amino acid for one that is polar, or even for one that is basic in character. Such "radical" substitutions cannot, however, be dismissed as potentially ineffective since chemical effects are not totally predictable and radical substitutions might well give rise to serendipitous effects not otherwise predictable from simple chemical principles.

Of course, such substitutions may involve structures other than the common L-amino acids. Thus, D-amino acids might be substituted for the L-amino acids commonly found in the antigenic peptides of the invention and yet still be encompassed by the disclosure herein. In addition, non-standard amino acids (i.e., other than the common

Position	1	2	3	4	5	6	7	8	9
		M							
		M							V
		M							I
		M							L
		A							
		A							V
		A							I
		A							L
		V							
		V							V
		V							I
		V							L
		T							
		T							V
		T							I
		T							L
		Q							
		Q							V
		Q							I
		Q							L
Position	1	2	3	4	5	6	7	8	9
SEQ ID NO 5	V	L	Q	G	L	T	F	T	L
Variants									A
									I
									V
		M							
		M							A
		M							I
		M							V
		A							
		A							A
		A							I
		A							V
		V							
		V							A
		V							I
		V							V
		T							
		T							A
		T							I
		T							V
		Q							

Position	1	2	3	4	5	6	7	8	9
		Q							A
		Q							I
		Q							V
Position	1	2	3	4	5	6	7	8	9
SEQ ID NO. 8	A	L	Y	A	V	I	E	K	A
Variants									V
									I
									L
		M							
		M							V
		M							I
		M							L
		A							
		A							V
		A							I
		A							L
		V							
		V							V
		V							I
		V							L
		T							
		T							V
		T							I
		T							L
		Q							
		Q							V
		Q							I
		Q							L

Longer (elongated) peptides may also be suitable. It is possible that MHC class I epitopes, although usually between 8 and 11 amino acids long, are generated by peptide processing from longer peptides or proteins that include the actual epitope. It is preferred that the residues that flank the actual epitope are residues that do not substantially affect proteolytic cleavage necessary to expose the actual epitope during processing.

The peptides of the invention can be elongated by up to four amino acids, that is 1, 2, 3 or 4 amino acids can be added to either end in any combination between 4:0 and 0:4. Combinations of the elongations according to the invention can be found in Table 7.

Table 7: Combinations of the elongations of peptides of the invention

C-terminus	N-terminus
4	0
3	0 or 1
2	0 or 1 or 2
1	0 or 1 or 2 or 3
0	0 or 1 or 2 or 3 or 4
N-terminus	C-terminus
4	0
3	0 or 1
2	0 or 1 or 2
1	0 or 1 or 2 or 3
0	0 or 1 or 2 or 3 or 4

The amino acids for the elongation/extension can be the peptides of the original sequence of the protein or any other amino acid(s). The elongation can be used to enhance the stability or solubility of the peptides.

Thus, the epitopes of the present invention may be identical to naturally occurring tumor-associated or tumor-specific epitopes or may include epitopes that differ by no more than four residues from the reference peptide, as long as they have substantially identical antigenic activity.

In an alternative embodiment, the peptide is elongated on either or both sides by more than 4 amino acids, preferably to a total length of up to 30 amino acids. This may lead to MHC class II binding peptides. Binding to MHC class II can be tested by methods known in the art.

Accordingly, the present invention provides peptides and variants of MHC class I epitopes, wherein the peptide or variant has an overall length of between 8 and 100, preferably between 8 and 30, and most preferred between 8 and 14, namely 8, 9, 10, 11, 12, 13, 14 amino acids, in case of the elongated class II binding peptides the length can also be 15, 16, 17, 18, 19, 20, 21 or 22 amino acids.

Of course, the peptide or variant according to the present invention will have the ability to bind to a molecule of the human major histocompatibility complex (MHC) class I or II. Binding of a peptide or a variant to a MHC complex may be tested by methods known in the art.

Preferably, when the T cells specific for a peptide according to the present invention are tested against the substituted peptides, the peptide concentration at which the substituted peptides achieve half the maximal increase in lysis relative to background is no more than about 1 mM, preferably no more than about 1 μ M, more preferably no more than about 1 nM, and still more preferably no more than about 100 pM, and most preferably no more than about 10 pM. It is also preferred that the substituted peptide be recognized by T cells from more than one individual, at least two, and more preferably three individuals.

In a particularly preferred embodiment of the invention the peptide consists or consists essentially of an amino acid sequence according to SEQ ID NO: 1 to SEQ ID NO: 311.

“Consisting essentially of” shall mean that a peptide according to the present invention, in addition to the sequence according to any of SEQ ID NO: 1 to SEQ ID NO 311 or a variant thereof contains additional N- and/or C-terminally located stretches of amino acids that are not necessarily forming part of the peptide that functions as an epitope for MHC molecules epitope.

Nevertheless, these stretches can be important to provide an efficient introduction of the peptide according to the present invention into the cells. In one embodiment of the present invention, the peptide is part of a fusion protein which comprises, for example, the 80 N-terminal amino acids of the HLA-DR antigen-associated invariant chain (p33, in the following “Ii”) as derived from the NCBI, GenBank Accession number X00497. In other fusions, the peptides of the present invention can be fused to an antibody as described herein, or a functional part thereof, in particular into a sequence of an antibody, so as to be specifically targeted by said antibody, or, for example, to or into an antibody that is specific for dendritic cells as described herein.

In addition, the peptide or variant may be modified further to improve stability and/or binding to MHC molecules in order to elicit a stronger immune response. Methods for such an optimization of a peptide sequence are well known in the art and include, for example, the introduction of reverse peptide bonds or non-peptide bonds.

In a reverse peptide bond amino acid residues are not joined by peptide (-CO-NH-) linkages but the peptide bond is reversed. Such retro-inverso peptidomimetics may be made using methods known in the art, for example such as those described in Meziere et al (1997) (Meziere et al., 1997), incorporated herein by reference. This approach involves making pseudopeptides containing changes involving the backbone, and not the orientation of side chains. Meziere et al. (Meziere et al., 1997) show that for MHC binding and T helper cell responses, these pseudopeptides are useful. Retro-inverse peptides, which contain NH-CO bonds instead of CO-NH peptide bonds, are much more resistant to proteolysis.

A non-peptide bond is, for example, -CH₂-NH, -CH₂S-, -CH₂CH₂-, -CH=CH-, -COCH₂-, -CH(OH)CH₂-, and -CH₂SO-. US 4,897,445 provides a method for the solid phase synthesis of non-peptide bonds (-CH₂-NH) in polypeptide chains which involves polypeptides synthesized by standard procedures and the non-peptide bond synthesized by reacting an amino aldehyde and an amino acid in the presence of NaCNBH₃.

Peptides comprising the sequences described above may be synthesized with additional chemical groups present at their amino and/or carboxy termini, to enhance the stability, bioavailability, and/or affinity of the peptides. For example, hydrophobic groups such as carbobenzoxy, dansyl, or t-butyloxycarbonyl groups may be added to the peptides' amino termini. Likewise, an acetyl group or a 9-fluorenylmethoxycarbonyl group may be placed at the peptides' amino termini. Additionally, the hydrophobic group, t-butyloxycarbonyl, or an amido group may be added to the peptides' carboxy termini.

Further, the peptides of the invention may be synthesized to alter their steric configuration. For example, the D-isomer of one or more of the amino acid residues of the peptide may be used, rather than the usual L-isomer. Still further, at least one of the amino acid residues of the peptides of the invention may be substituted by one of the well-known non-naturally occurring amino acid residues. Alterations such as these may serve to increase the stability, bioavailability and/or binding action of the peptides of the invention.

Similarly, a peptide or variant of the invention may be modified chemically by reacting specific amino acids either before or after synthesis of the peptide. Examples for such modifications are well known in the art and are summarized e.g. in R. Lundblad, *Chemical Reagents for Protein Modification*, 3rd ed. CRC Press, 2004 (Lundblad, 2004), which is incorporated herein by reference. Chemical modification of amino acids includes but is not limited to, modification by acylation, amidination, pyridoxylation of lysine, reductive alkylation, trinitrobenzylation of amino groups with 2,4,6-trinitrobenzene sulphonic acid (TNBS), amide modification of carboxyl groups and sulphydryl modification by performic acid oxidation of cysteine to cysteic acid, formation of mercurial derivatives, formation of mixed disulphides with other thiol compounds, reaction with maleimide, carboxymethylation with iodoacetic acid or iodoacetamide and carbamoylation with cyanate at alkaline pH, although without limitation thereto. In this regard, the skilled person is referred to Chapter 15 of *Current Protocols In Protein Science*, Eds. Coligan et al. (John Wiley and Sons NY 1995-2000) (Coligan et al., 1995) for more extensive methodology relating to chemical modification of proteins.

Briefly, modification of e.g. arginyl residues in proteins is often based on the reaction of vicinal dicarbonyl compounds such as phenylglyoxal, 2,3-butanedione, and 1,2-cyclohexanedione to form an adduct. Another example is the reaction of methylglyoxal with arginine residues. Cysteine can be modified without concomitant modification of other nucleophilic sites such as lysine and histidine. As a result, a large number of reagents are available for the modification of cysteine. The websites of companies such as Sigma-Aldrich (<http://www.sigma-aldrich.com>) provide information on specific reagents.

Selective reduction of disulfide bonds in proteins is also common. Disulfide bonds can be formed and oxidized during the heat treatment of biopharmaceuticals. Woodward's Reagent K may be used to modify specific glutamic acid residues. N-(3-(dimethylamino)propyl)-N'-ethylcarbodiimide can be used to form intra-molecular crosslinks between a lysine residue and a glutamic acid residue. For example, diethylpyrocarbonate is a reagent for the modification of histidyl residues in proteins. Histidine can also be modified using 4-hydroxy-2-nonenal. The reaction of lysine

residues and other α -amino groups is, for example, useful in binding of peptides to surfaces or the cross-linking of proteins/peptides. Lysine is the site of attachment of poly(ethylene)glycol and the major site of modification in the glycosylation of proteins. Methionine residues in proteins can be modified with e.g. iodoacetamide, bromoethylamine, and chloramine T.

Tetranitromethane and N-acetylimidazole can be used for the modification of tyrosyl residues. Cross-linking via the formation of dityrosine can be accomplished with hydrogen peroxide/copper ions.

Recent studies on the modification of tryptophan have used N-bromosuccinimide, 2-hydroxy-5-nitrobenzyl bromide or 3-bromo-3-methyl-2-(2-nitrophenylmercapto)-3H-indole (BPNS-skatole).

Successful modification of therapeutic proteins and peptides with PEG is often associated with an extension of circulatory half-life while cross-linking of proteins with glutaraldehyde, polyethylene glycol diacrylate and formaldehyde is used for the preparation of hydrogels. Chemical modification of allergens for immunotherapy is often achieved by carbamylation with potassium cyanate.

A peptide or variant, wherein the peptide is modified or includes non-peptide bonds is a preferred embodiment of the invention.

Another embodiment of the present invention relates to a non-naturally occurring peptide wherein said peptide consists or consists essentially of an amino acid sequence according to SEQ ID No: 1 to SEQ ID No: 311 and has been synthetically produced (e.g. synthesized) as a pharmaceutically acceptable salt. Methods to synthetically produce peptides are well known in the art. The salts of the peptides according to the present invention differ substantially from the peptides in their state(s) *in vivo*, as the peptides as generated *in vivo* are no salts. The non-natural salt form of the peptide mediates the solubility of the peptide, in particular in the context of pharmaceutical compositions comprising the peptides, e.g. the peptide vaccines as disclosed herein. A sufficient and at least substantial solubility of the peptide(s) is required in order to efficiently provide the peptides to the subject to be

treated. Preferably, the salts are pharmaceutically acceptable salts of the peptides. These salts according to the invention include alkaline and earth alkaline salts such as salts of the Hofmeister series comprising as anions PO_4^{3-} , SO_4^{2-} , CH_3COO^- , Cl^- , Br^- , NO_3^- , ClO_4^- , I^- , SCN^- and as cations NH_4^+ , Rb^+ , K^+ , Na^+ , Cs^+ , Li^+ , Zn^{2+} , Mg^{2+} , Ca^{2+} , Mn^{2+} , Cu^{2+} and Ba^{2+} . Particularly salts are selected from $(\text{NH}_4)_3\text{PO}_4$, $(\text{NH}_4)_2\text{HPO}_4$, $(\text{NH}_4)\text{H}_2\text{PO}_4$, $(\text{NH}_4)_2\text{SO}_4$, $\text{NH}_4\text{CH}_3\text{COO}$, NH_4Cl , NH_4Br , NH_4NO_3 , NH_4ClO_4 , NH_4I , NH_4SCN , Rb_3PO_4 , Rb_2HPO_4 , RbH_2PO_4 , Rb_2SO_4 , $\text{Rb}_4\text{CH}_3\text{COO}$, Rb_4Cl , Rb_4Br , Rb_4NO_3 , Rb_4ClO_4 , Rb_4I , Rb_4SCN , K_3PO_4 , K_2HPO_4 , KH_2PO_4 , K_2SO_4 , KCH_3COO , KCl , KBr , KNO_3 , KClO_4 , KI , KSCN , Na_3PO_4 , Na_2HPO_4 , NaH_2PO_4 , Na_2SO_4 , NaCH_3COO , NaCl , NaBr , NaNO_3 , NaClO_4 , NaI , NaSCN , ZnCl_2 , Cs_3PO_4 , Cs_2HPO_4 , CsH_2PO_4 , Cs_2SO_4 , CsCH_3COO , CsCl , CsBr , CsNO_3 , CsClO_4 , CsI , CsSCN , Li_3PO_4 , Li_2HPO_4 , LiH_2PO_4 , Li_2SO_4 , LiCH_3COO , LiCl , LiBr , LiNO_3 , LiClO_4 , LiI , LiSCN , Cu_2SO_4 , $\text{Mg}_3(\text{PO}_4)_2$, Mg_2HPO_4 , $\text{Mg}(\text{H}_2\text{PO}_4)_2$, Mg_2SO_4 , $\text{Mg}(\text{CH}_3\text{COO})_2$, MgCl_2 , MgBr_2 , $\text{Mg}(\text{NO}_3)_2$, $\text{Mg}(\text{ClO}_4)_2$, MgI_2 , $\text{Mg}(\text{SCN})_2$, MnCl_2 , $\text{Ca}_3(\text{PO}_4)_2$, Ca_2HPO_4 , $\text{Ca}(\text{H}_2\text{PO}_4)_2$, CaSO_4 , $\text{Ca}(\text{CH}_3\text{COO})_2$, CaCl_2 , CaBr_2 , $\text{Ca}(\text{NO}_3)_2$, $\text{Ca}(\text{ClO}_4)_2$, CaI_2 , $\text{Ca}(\text{SCN})_2$, $\text{Ba}_3(\text{PO}_4)_2$, Ba_2HPO_4 , $\text{Ba}(\text{H}_2\text{PO}_4)_2$, BaSO_4 , $\text{Ba}(\text{CH}_3\text{COO})_2$, BaCl_2 , BaBr_2 , $\text{Ba}(\text{NO}_3)_2$, $\text{Ba}(\text{ClO}_4)_2$, BaI_2 , and $\text{Ba}(\text{SCN})_2$. Particularly preferred are NH acetate, MgCl_2 , KH_2PO_4 , Na_2SO_4 , KCl , NaCl , and CaCl_2 , such as, for example, the chloride or acetate (trifluoroacetate) salts.

Generally, peptides and variants (at least those containing peptide linkages between amino acid residues) may be synthesized by the Fmoc-polyamide mode of solid-phase peptide synthesis as disclosed by Lukas et al. (Lukas et al., 1981) and by references as cited therein. Temporary N-amino group protection is afforded by the 9-fluorenylmethyloxycarbonyl (Fmoc) group. Repetitive cleavage of this highly base-labile protecting group is done using 20% piperidine in N, N-dimethylformamide. Side-chain functionalities may be protected as their butyl ethers (in the case of serine threonine and tyrosine), butyl esters (in the case of glutamic acid and aspartic acid), butyloxycarbonyl derivative (in the case of lysine and histidine), trityl derivative (in the case of cysteine) and 4-methoxy-2,3,6-trimethylbenzenesulphonyl derivative (in the case of arginine). Where glutamine or asparagine are C-terminal residues, use is made of the 4,4'-dimethoxybenzhydryl group for protection of the side chain amido functionalities. The solid-phase support is based on a polydimethyl-acrylamide polymer constituted from the three monomers dimethylacrylamide (backbone-

monomer), bisacryloylethylene diamine (cross linker) and acryloylsarcosine methyl ester (functionalizing agent). The peptide-to-resin cleavable linked agent used is the acid-labile 4-hydroxymethyl-phenoxyacetic acid derivative. All amino acid derivatives are added as their preformed symmetrical anhydride derivatives with the exception of asparagine and glutamine, which are added using a reversed N, N-dicyclohexylcarbodiimide/1hydroxybenzotriazole mediated coupling procedure. All coupling and deprotection reactions are monitored using ninhydrin, trinitrobenzene sulphonic acid or isotin test procedures. Upon completion of synthesis, peptides are cleaved from the resin support with concomitant removal of side-chain protecting groups by treatment with 95% trifluoroacetic acid containing a 50 % scavenger mix. Scavengers commonly used include ethanedithiol, phenol, anisole and water, the exact choice depending on the constituent amino acids of the peptide being synthesized. Also a combination of solid phase and solution phase methodologies for the synthesis of peptides is possible (see, for example, (Bruckdorfer et al., 2004), and the references as cited therein).

Trifluoroacetic acid is removed by evaporation in vacuo, with subsequent trituration with diethyl ether affording the crude peptide. Any scavengers present are removed by a simple extraction procedure which on lyophilization of the aqueous phase affords the crude peptide free of scavengers. Reagents for peptide synthesis are generally available from e.g. Calbiochem-Novabiochem (Nottingham, UK).

Purification may be performed by any one, or a combination of, techniques such as re-crystallization, size exclusion chromatography, ion-exchange chromatography, hydrophobic interaction chromatography and (usually) reverse-phase high performance liquid chromatography using e.g. acetonitrile/water gradient separation.

Analysis of peptides may be carried out using thin layer chromatography, electrophoresis, in particular capillary electrophoresis, solid phase extraction (CSPE), reverse-phase high performance liquid chromatography, amino-acid analysis after acid hydrolysis and by fast atom bombardment (FAB) mass spectrometric analysis, as well as MALDI and ESI-Q-TOF mass spectrometric analysis.

In order to select over-presented peptides, a presentation profile is calculated showing the median sample presentation as well as replicate variation. The profile juxtaposes samples of the tumor entity of interest to a baseline of normal tissue samples. Each of these profiles can then be consolidated into an over-presentation score by calculating the p-value of a Linear Mixed-Effects Model (Pinheiro et al., 2015) adjusting for multiple testing by False Discovery Rate (Benjamini and Hochberg, 1995) (cf. Example 1, Figures 1A to P).

For the identification and relative quantitation of HLA ligands by mass spectrometry, HLA molecules from shock-frozen tissue samples were purified and HLA-associated peptides were isolated. The isolated peptides were separated and sequences were identified by online nano-electrospray-ionization (nanoESI) liquid chromatography-mass spectrometry (LC-MS) experiments. The resulting peptide sequences were verified by comparison of the fragmentation pattern of natural tumor-associated peptides (TUMAPs) recorded from NHL samples (N = 18 A*02-positive samples) with the fragmentation patterns of corresponding synthetic reference peptides of identical sequences. Since the peptides were directly identified as ligands of HLA molecules of primary tumors, these results provide direct evidence for the natural processing and presentation of the identified peptides on primary cancer tissue obtained from 18 NHL patients.

The discovery pipeline XPRESIDENT® v2.1 (see, for example, US 2013-0096016, which is hereby incorporated by reference in its entirety) allows the identification and selection of relevant over-presented peptide vaccine candidates based on direct relative quantitation of HLA-restricted peptide levels on cancer tissues in comparison to several different non-cancerous tissues and organs. This was achieved by the development of label-free differential quantitation using the acquired LC-MS data processed by a proprietary data analysis pipeline, combining algorithms for sequence identification, spectral clustering, ion counting, retention time alignment, charge state deconvolution and normalization.

Presentation levels including error estimates for each peptide and sample were established. Peptides exclusively presented on tumor tissue and peptides over-presented in tumor versus non-cancerous tissues and organs have been identified.

HLA-peptide complexes from NHL tissue samples were purified and HLA-associated peptides were isolated and analyzed by LC-MS (see examples). All TUMAPs contained in the present application were identified with this approach on primary NHL samples confirming their presentation on primary NHL.

TUMAPs identified on multiple NHL and normal tissues were quantified using ion-counting of label-free LC-MS data. The method assumes that LC-MS signal areas of a peptide correlate with its abundance in the sample. All quantitative signals of a peptide in various LC-MS experiments were normalized based on central tendency, averaged per sample and merged into a bar plot, called presentation profile. The presentation profile consolidates different analysis methods like protein database search, spectral clustering, charge state deconvolution (decharging) and retention time alignment and normalization.

Besides over-presentation of the peptide, mRNA expression of the underlying gene was tested. mRNA data were obtained via RNASeq analyses of normal tissues and cancer tissues (cf. Example 2, Figure 2). An additional source of normal tissue data was a database of publicly available RNA expression data from around 3000 normal tissue samples (Lonsdale, 2013). Peptides which are derived from proteins whose coding mRNA is highly expressed in cancer tissue, but very low or absent in vital normal tissues, were preferably included in the present invention.

The present invention provides peptides that are useful in treating cancers/tumors, preferably NHL that over- or exclusively present the peptides of the invention. These peptides were shown by mass spectrometry to be naturally presented by HLA molecules on primary human NHL samples.

Many of the source gene/proteins (also designated “full-length proteins” or “underlying proteins”) from which the peptides are derived were shown to be highly over-expressed in cancer compared with normal tissues – “normal tissues” in relation to this invention shall mean either healthy lymph node cells or other normal tissue cells, demonstrating a high degree of tumor association of the source genes (see Example 2). Moreover, the peptides themselves are strongly over-presented on

tumor tissue – “tumor tissue” in relation to this invention shall mean a sample from a patient suffering from NHL, but not on normal tissues (see Example 1).

HLA-bound peptides can be recognized by the immune system, specifically T lymphocytes. T cells can destroy the cells presenting the recognized HLA/peptide complex, e.g. NHL cells presenting the derived peptides.

The peptides of the present invention have been shown to be capable of stimulating T cell responses and/or are over-presented and thus can be used for the production of antibodies and/or TCRs, such as soluble TCRs, according to the present invention (see Example 3, Example 4). Furthermore, the peptides when complexed with the respective MHC can be used for the production of antibodies and/or TCRs, in particular sTCRs, according to the present invention, as well. Respective methods are well known to the person of skill, and can be found in the respective literature as well. Thus, the peptides of the present invention are useful for generating an immune response in a patient by which tumor cells can be destroyed. An immune response in a patient can be induced by direct administration of the described peptides or suitable precursor substances (e.g. elongated peptides, proteins, or nucleic acids encoding these peptides) to the patient, ideally in combination with an agent enhancing the immunogenicity (i.e. an adjuvant). The immune response originating from such a therapeutic vaccination can be expected to be highly specific against tumor cells because the target peptides of the present invention are not presented on normal tissues in comparable copy numbers, preventing the risk of undesired autoimmune reactions against normal cells in the patient.

The present description further relates to T-cell receptors (TCRs) comprising an alpha chain and a beta chain (“alpha/beta TCRs”). Also provided are peptides according to the invention capable of binding to TCRs and antibodies when presented by an MHC molecule. The present description also relates to nucleic acids, vectors and host cells for expressing TCRs and peptides of the present description; and methods of using the same.

The term “T-cell receptor” (abbreviated TCR) refers to a heterodimeric molecule comprising an alpha polypeptide chain (alpha chain) and a beta polypeptide chain

(beta chain), wherein the heterodimeric receptor is capable of binding to a peptide antigen presented by an HLA molecule. The term also includes so-called gamma/delta TCRs.

In one embodiment the description provides a method of producing a TCR as described herein, the method comprising culturing a host cell capable of expressing the TCR under conditions suitable to promote expression of the TCR.

The description in another aspect relates to methods according to the description, wherein the antigen is loaded onto class I or II MHC molecules expressed on the surface of a suitable antigen-presenting cell or artificial antigen-presenting cell by contacting a sufficient amount of the antigen with an antigen-presenting cell or the antigen is loaded onto class I or II MHC tetramers by tetramerizing the antigen/class I or II MHC complex monomers.

The alpha and beta chains of alpha/beta TCR's, and the gamma and delta chains of gamma/delta TCRs, are generally regarded as each having two "domains", namely variable and constant domains. The variable domain consists of a concatenation of variable region (V), and joining region (J). The variable domain may also include a leader region (L). Beta and delta chains may also include a diversity region (D). The alpha and beta constant domains may also include C-terminal transmembrane (TM) domains that anchor the alpha and beta chains to the cell membrane.

With respect to gamma/delta TCRs, the term "TCR gamma variable domain" as used herein refers to the concatenation of the TCR gamma V (TRGV) region without leader region (L), and the TCR gamma J (TRGJ) region, and the term TCR gamma constant domain refers to the extracellular TRGC region, or to a C-terminal truncated TRGC sequence. Likewise the term "TCR delta variable domain" refers to the concatenation of the TCR delta V (TRDV) region without leader region (L) and the TCR delta D/J (TRDD/TRDJ) region, and the term "TCR delta constant domain" refers to the extracellular TRDC region, or to a C-terminal truncated TRDC sequence.

TCRs of the present description preferably bind to an peptide-HLA molecule complex with a binding affinity (KD) of about 100 μ M or less, about 50 μ M or less, about 25

μM or less, or about 10 μM or less. More preferred are high affinity TCRs having binding affinities of about 1 μM or less, about 100 nM or less, about 50 nM or less, about 25 nM or less. Non-limiting examples of preferred binding affinity ranges for TCRs of the present invention include about 1 nM to about 10 nM; about 10 nM to about 20 nM; about 20 nM to about 30 nM; about 30 nM to about 40 nM; about 40 nM to about 50 nM; about 50 nM to about 60 nM; about 60 nM to about 70 nM; about 70 nM to about 80 nM; about 80 nM to about 90 nM; and about 90 nM to about 100 nM.

As used herein in connect with TCRs of the present description, “specific binding” and grammatical variants thereof are used to mean a TCR having a binding affinity (KD) for a peptide-HLA molecule complex of 100 μM or less.

Alpha/beta heterodimeric TCRs of the present description may have an introduced disulfide bond between their constant domains. Preferred TCRs of this type include those which have a TRAC constant domain sequence and a TRBC1 or TRBC2 constant domain sequence except that Thr 48 of TRAC and Ser 57 of TRBC1 or TRBC2 are replaced by cysteine residues, the said cysteines forming a disulfide bond between the TRAC constant domain sequence and the TRBC1 or TRBC2 constant domain sequence of the TCR.

With or without the introduced inter-chain bond mentioned above, alpha/beta heterodimeric TCRs of the present description may have a TRAC constant domain sequence and a TRBC1 or TRBC2 constant domain sequence, and the TRAC constant domain sequence and the TRBC1 or TRBC2 constant domain sequence of the TCR may be linked by the native disulfide bond between Cys4 of exon 2 of TRAC and Cys2 of exon 2 of TRBC1 or TRBC2.

TCRs of the present description may comprise a detectable label selected from the group consisting of a radionuclide, a fluorophore and biotin. TCRs of the present description may be conjugated to a therapeutically active agent, such as a radionuclide, a chemotherapeutic agent, or a toxin.

In an embodiment, a TCR of the present description having at least one mutation in the alpha chain and/or having at least one mutation in the beta chain has modified glycosylation compared to the unmutated TCR.

In an embodiment, a TCR comprising at least one mutation in the TCR alpha chain and/or TCR beta chain has a binding affinity for, and/or a binding half-life for, a peptide-HLA molecule complex, which is at least double that of a TCR comprising the unmutated TCR alpha chain and/or unmutated TCR beta chain. Affinity-enhancement of tumor-specific TCRs, and its exploitation, relies on the existence of a window for optimal TCR affinities. The existence of such a window is based on observations that TCRs specific for HLA-A2-restricted pathogens have KD values that are generally about 10-fold lower when compared to TCRs specific for HLA-A2-restricted tumor-associated self-antigens. It is now known, although tumor antigens have the potential to be immunogenic, because tumors arise from the individual's own cells only mutated proteins or proteins with altered translational processing will be seen as foreign by the immune system. Antigens that are upregulated or overexpressed (so called self-antigens) will not necessarily induce a functional immune response against the tumor: T-cells expressing TCRs that are highly reactive to these antigens will have been negatively selected within the thymus in a process known as central tolerance, meaning that only T-cells with low-affinity TCRs for self-antigens remain. Therefore, affinity of TCRs or variants of the present description to peptides can be enhanced by methods well known in the art.

The present description further relates to a method of identifying and isolating a TCR according to the present description, said method comprising incubating PBMCs from HLA-A*02-negative healthy donors with A2/peptide monomers, incubating the PBMCs with tetramer-phycoerythrin (PE) and isolating the high avidity T-cells by fluorescence activated cell sorting (FACS)–Calibur analysis.

The present description further relates to a method of identifying and isolating a TCR according to the present description, said method comprising obtaining a transgenic mouse with the entire human TCR $\alpha\beta$ gene loci (1.1 and 0.7 Mb), whose T-cells express a diverse human TCR repertoire that compensates for mouse TCR deficiency, immunizing the mouse with a peptide, incubating PBMCs obtained from

the transgenic mice with tetramer-phycoerythrin (PE), and isolating the high avidity T-cells by fluorescence activated cell sorting (FACS)–Calibur analysis.

In one aspect, to obtain T-cells expressing TCRs of the present description, nucleic acids encoding TCR-alpha and/or TCR-beta chains of the present description are cloned into expression vectors, such as gamma retrovirus or lentivirus. The recombinant viruses are generated and then tested for functionality, such as antigen specificity and functional avidity. An aliquot of the final product is then used to transduce the target T-cell population (generally purified from patient PBMCs), which is expanded before infusion into the patient.

In another aspect, to obtain T-cells expressing TCRs of the present description, TCR RNAs are synthesized by techniques known in the art, e.g., in vitro transcription systems. The in vitro-synthesized TCR RNAs are then introduced into primary CD8⁺ T-cells obtained from healthy donors by electroporation to re-express tumor specific TCR-alpha and/or TCR-beta chains.

To increase the expression, nucleic acids encoding TCRs of the present description may be operably linked to strong promoters, such as retroviral long terminal repeats (LTRs), cytomegalovirus (CMV), murine stem cell virus (MSCV) U3, phosphoglycerate kinase (PGK), β -actin, ubiquitin, and a simian virus 40 (SV40)/CD43 composite promoter, elongation factor (EF)-1a and the spleen focus-forming virus (SFFV) promoter. In a preferred embodiment, the promoter is heterologous to the nucleic acid being expressed.

In addition to strong promoters, TCR expression cassettes of the present description may contain additional elements that can enhance transgene expression, including a central polypurine tract (cPPT), which promotes the nuclear translocation of lentiviral constructs (Follenzi et al., 2000), and the woodchuck hepatitis virus posttranscriptional regulatory element (wPRE), which increases the level of transgene expression by increasing RNA stability (Zufferey et al., 1999).

The alpha and beta chains of a TCR of the present invention may be encoded by nucleic acids located in separate vectors, or may be encoded by polynucleotides located in the same vector.

Achieving high-level TCR surface expression requires that both the TCR-alpha and TCR-beta chains of the introduced TCR be transcribed at high levels. To do so, the TCR-alpha and TCR-beta chains of the present description may be cloned into bicistronic constructs in a single vector, which has been shown to be capable of overcoming this obstacle. The use of a viral intraribosomal entry site (IRES) between the TCR-alpha and TCR-beta chains results in the coordinated expression of both chains, because the TCR-alpha and TCR-beta chains are generated from a single transcript that is broken into two proteins during translation, ensuring that an equal molar ratio of TCR-alpha and TCR-beta chains are produced. (Schmitt et al. 2009).

Nucleic acids encoding TCRs of the present description may be codon optimized to increase expression from a host cell. Redundancy in the genetic code allows some amino acids to be encoded by more than one codon, but certain codons are less “optimal” than others because of the relative availability of matching tRNAs as well as other factors (Gustafsson et al., 2004). Modifying the TCR-alpha and TCR-beta gene sequences such that each amino acid is encoded by the optimal codon for mammalian gene expression, as well as eliminating mRNA instability motifs or cryptic splice sites, has been shown to significantly enhance TCR-alpha and TCR-beta gene expression (Scholten et al., 2006).

Furthermore, mispairing between the introduced and endogenous TCR chains may result in the acquisition of specificities that pose a significant risk for autoimmunity. For example, the formation of mixed TCR dimers may reduce the number of CD3 molecules available to form properly paired TCR complexes, and therefore can significantly decrease the functional avidity of the cells expressing the introduced TCR (Kuball et al., 2007).

To reduce mispairing, the C-terminus domain of the introduced TCR chains of the present description may be modified in order to promote interchain affinity, while decreasing the ability of the introduced chains to pair with the endogenous TCR. These

strategies may include replacing the human TCR-alpha and TCR-beta C-terminus domains with their murine counterparts (murinized C-terminus domain); generating a second interchain disulfide bond in the C-terminus domain by introducing a second cysteine residue into both the TCR-alpha and TCR-beta chains of the introduced TCR (cysteine modification); swapping interacting residues in the TCR-alpha and TCR-beta chain C-terminus domains ("knob-in-hole"); and fusing the variable domains of the TCR-alpha and TCR-beta chains directly to CD3 ζ (CD3 ζ fusion). (Schmitt et al. 2009).

In an embodiment, a host cell is engineered to express a TCR of the present description. In preferred embodiments, the host cell is a human T-cell or T-cell progenitor. In some embodiments the T-cell or T-cell progenitor is obtained from a cancer patient. In other embodiments the T-cell or T-cell progenitor is obtained from a healthy donor. Host cells of the present description can be allogeneic or autologous with respect to a patient to be treated. In one embodiment, the host is a gamma/delta T-cell transformed to express an alpha/beta TCR.

A "pharmaceutical composition" is a composition suitable for administration to a human being in a medical setting. Preferably, a pharmaceutical composition is sterile and produced according to GMP guidelines.

The pharmaceutical compositions comprise the peptides either in the free form or in the form of a pharmaceutically acceptable salt (see also above). As used herein, "a pharmaceutically acceptable salt" refers to a derivative of the disclosed peptides wherein the peptide is modified by making acid or base salts of the agent. For example, acid salts are prepared from the free base (typically wherein the neutral form of the drug has a neutral $-NH_2$ group) involving reaction with a suitable acid. Suitable acids for preparing acid salts include both organic acids, e.g., acetic acid, propionic acid, glycolic acid, pyruvic acid, oxalic acid, malic acid, malonic acid, succinic acid, maleic acid, fumaric acid, tartaric acid, citric acid, benzoic acid, cinnamic acid, mandelic acid, methane sulfonic acid, ethane sulfonic acid, p-toluenesulfonic acid, salicylic acid, and the like, as well as inorganic acids, e.g., hydrochloric acid, hydrobromic acid, sulfuric acid, nitric acid phosphoric acid and the like. Conversely, preparation of basic salts of acid moieties which may be present on

a peptide are prepared using a pharmaceutically acceptable base such as sodium hydroxide, potassium hydroxide, ammonium hydroxide, calcium hydroxide, trimethylamine or the like.

In an especially preferred embodiment, the pharmaceutical compositions comprise the peptides as salts of acetic acid (acetates), trifluoro acetates or hydrochloric acid (chlorides).

Preferably, the medicament of the present invention is an immunotherapeutic such as a vaccine. It may be administered directly into the patient, into the affected organ or systemically i.d., i.m., s.c., i.p. and i.v., or applied *ex vivo* to cells derived from the patient or a human cell line which are subsequently administered to the patient, or used *in vitro* to select a subpopulation of immune cells derived from the patient, which are then re-administered to the patient. If the nucleic acid is administered to cells *in vitro*, it may be useful for the cells to be transfected so as to co-express immune-stimulating cytokines, such as interleukin-2. The peptide may be substantially pure, or combined with an immune-stimulating adjuvant (see below) or used in combination with immune-stimulatory cytokines, or be administered with a suitable delivery system, for example liposomes. The peptide may also be conjugated to a suitable carrier such as keyhole limpet haemocyanin (KLH) or mannan (see WO 95/18145 and (Longenecker et al., 1993)). The peptide may also be tagged, may be a fusion protein, or may be a hybrid molecule. The peptides whose sequence is given in the present invention are expected to stimulate CD4 or CD8 T cells. However, stimulation of CD8 T cells is more efficient in the presence of help provided by CD4 T-helper cells. Thus, for MHC Class I epitopes that stimulate CD8 T cells the fusion partner or sections of a hybrid molecule suitably provide epitopes which stimulate CD4-positive T cells. CD4- and CD8-stimulating epitopes are well known in the art and include those identified in the present invention.

In one aspect, the vaccine comprises at least one peptide having the amino acid sequence set forth SEQ ID No. 1 to SEQ ID No. 311, and at least one additional peptide, preferably two to 50, more preferably two to 25, even more preferably two to 20 and most preferably two, three, four, five, six, seven, eight, nine, ten, eleven, twelve, thirteen, fourteen, fifteen, sixteen, seventeen or eighteen peptides. The

peptide(s) may be derived from one or more specific TAAs and may bind to MHC class I molecules.

A further aspect of the invention provides a nucleic acid (for example a polynucleotide) encoding a peptide or peptide variant of the invention. The polynucleotide may be, for example, DNA, cDNA, PNA, RNA or combinations thereof, either single- and/or double-stranded, or native or stabilized forms of polynucleotides, such as, for example, polynucleotides with a phosphorothioate backbone and it may or may not contain introns so long as it codes for the peptide. Of course, only peptides that contain naturally occurring amino acid residues joined by naturally occurring peptide bonds are encodable by a polynucleotide. A still further aspect of the invention provides an expression vector capable of expressing a polypeptide according to the invention.

A variety of methods have been developed to link polynucleotides, especially DNA, to vectors for example via complementary cohesive termini. For instance, complementary homopolymer tracts can be added to the DNA segment to be inserted to the vector DNA. The vector and DNA segment are then joined by hydrogen bonding between the complementary homopolymeric tails to form recombinant DNA molecules.

Synthetic linkers containing one or more restriction sites provide an alternative method of joining the DNA segment to vectors. Synthetic linkers containing a variety of restriction endonuclease sites are commercially available from a number of sources including International Biotechnologies Inc. New Haven, CN, USA.

A desirable method of modifying the DNA encoding the polypeptide of the invention employs the polymerase chain reaction as disclosed by Saiki RK, et al. (Saiki et al., 1988). This method may be used for introducing the DNA into a suitable vector, for example by engineering in suitable restriction sites, or it may be used to modify the DNA in other useful ways as is known in the art. If viral vectors are used, pox- or adenovirus vectors are preferred.

The DNA (or in the case of retroviral vectors, RNA) may then be expressed in a suitable host to produce a polypeptide comprising the peptide or variant of the invention. Thus, the DNA encoding the peptide or variant of the invention may be used in accordance with known techniques, appropriately modified in view of the teachings contained herein, to construct an expression vector, which is then used to transform an appropriate host cell for the expression and production of the polypeptide of the invention. Such techniques include those disclosed, for example, in US 4,440,859, 4,530,901, 4,582,800, 4,677,063, 4,678,751, 4,704,362, 4,710,463, 4,757,006, 4,766,075, and 4,810,648.

The DNA (or in the case of retroviral vectors, RNA) encoding the polypeptide constituting the compound of the invention may be joined to a wide variety of other DNA sequences for introduction into an appropriate host. The companion DNA will depend upon the nature of the host, the manner of the introduction of the DNA into the host, and whether episomal maintenance or integration is desired.

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, although such controls are generally available in the expression vector. The vector is then introduced into the host through standard techniques. Generally, not all of the hosts will be transformed by the vector. Therefore, it will be necessary to select for transformed host cells. One selection technique involves incorporating into the expression vector a DNA sequence, with any necessary control elements, that codes for a selectable trait in the transformed cell, such as antibiotic resistance.

Alternatively, the gene for such selectable trait can be on another vector, which is used to co-transform the desired host cell.

Host cells that have been transformed by the recombinant DNA of the invention are then cultured for a sufficient time and under appropriate conditions known to those skilled in the art in view of the teachings disclosed herein to permit the expression of the polypeptide, which can then be recovered.

Many expression systems are known, including bacteria (for example *E. coli* and *Bacillus subtilis*), yeasts (for example *Saccharomyces cerevisiae*), filamentous fungi (for example *Aspergillus spec.*), plant cells, animal cells and insect cells. Preferably, the system can be mammalian cells such as CHO cells available from the ATCC Cell Biology Collection.

A typical mammalian cell vector plasmid for constitutive expression comprises the CMV or SV40 promoter with a suitable poly A tail and a resistance marker, such as neomycin. One example is pSVL available from Pharmacia, Piscataway, NJ, USA. An example of an inducible mammalian expression vector is pMSG, also available from Pharmacia. Useful yeast plasmid vectors are pRS403-406 and pRS413-416 and are generally available from Stratagene Cloning Systems, La Jolla, CA 92037, USA. Plasmids pRS403, pRS404, pRS405 and pRS406 are Yeast Integrating plasmids (YIps) and incorporate the yeast selectable markers HIS3, TRP1, LEU2 and URA3. Plasmids pRS413-416 are Yeast Centromere plasmids (Ycps). CMV promoter-based vectors (for example from Sigma-Aldrich) provide transient or stable expression, cytoplasmic expression or secretion, and N-terminal or C-terminal tagging in various combinations of FLAG, 3xFLAG, c-myc or MAT. These fusion proteins allow for detection, purification and analysis of recombinant protein. Dual-tagged fusions provide flexibility in detection.

The strong human cytomegalovirus (CMV) promoter regulatory region drives constitutive protein expression levels as high as 1 mg/L in COS cells. For less potent cell lines, protein levels are typically ~0.1 mg/L. The presence of the SV40 replication origin will result in high levels of DNA replication in SV40 replication permissive COS cells. CMV vectors, for example, can contain the pMB1 (derivative of pBR322) origin for replication in bacterial cells, the b-lactamase gene for ampicillin resistance selection in bacteria, hGH polyA, and the f1 origin. Vectors containing the pre-pro-trypsin leader (PPT) sequence can direct the secretion of FLAG fusion proteins into the culture medium for purification using ANTI-FLAG antibodies, resins, and plates. Other vectors and expression systems are well known in the art for use with a variety of host cells.

In another embodiment two or more peptides or peptide variants of the invention are encoded and thus expressed in a successive order (similar to “beads on a string” constructs). In doing so, the peptides or peptide variants may be linked or fused together by stretches of linker amino acids, such as for example LLLLLL, or may be linked without any additional peptide(s) between them. These constructs can also be used for cancer therapy, and may induce immune responses both involving MHC I and MHC II.

The present invention also relates to a host cell transformed with a polynucleotide vector construct of the present invention. The host cell can be either prokaryotic or eukaryotic. Bacterial cells may be preferred prokaryotic host cells in some circumstances and typically are a strain of *E. coli* such as, for example, the *E. coli* strains DH5 available from Bethesda Research Laboratories Inc., Bethesda, MD, USA, and RR1 available from the American Type Culture Collection (ATCC) of Rockville, MD, USA (No ATCC 31343). Preferred eukaryotic host cells include yeast, insect and mammalian cells, preferably vertebrate cells such as those from a mouse, rat, monkey or human fibroblastic and colon cell lines. Yeast host cells include YPH499, YPH500 and YPH501, which are generally available from Stratagene Cloning Systems, La Jolla, CA 92037, USA. Preferred mammalian host cells include Chinese hamster ovary (CHO) cells available from the ATCC as CCL61, NIH Swiss mouse embryo cells NIH/3T3 available from the ATCC as CRL 1658, monkey kidney-derived COS-1 cells available from the ATCC as CRL 1650 and 293 cells which are human embryonic kidney cells. Preferred insect cells are Sf9 cells which can be transfected with baculovirus expression vectors. An overview regarding the choice of suitable host cells for expression can be found in, for example, the textbook of Paulina Balbás and Argelia Lorence “Methods in Molecular Biology Recombinant Gene Expression, Reviews and Protocols,” Part One, Second Edition, ISBN 978-1-58829-262-9, and other literature known to the person of skill.

Transformation of appropriate cell hosts with a DNA construct of the present invention is accomplished by well-known methods that typically depend on the type of vector used. With regard to transformation of prokaryotic host cells, see, for example, Cohen et al. (Cohen et al., 1972) and (Green and Sambrook, 2012) . Transformation of yeast cells is described in Sherman et al. (Sherman et al., 1986) . The method of

Beggs (Beggs, 1978) is also useful. With regard to vertebrate cells, reagents useful in transfecting such cells, for example calcium phosphate and DEAE-dextran or liposome formulations, are available from Stratagene Cloning Systems, or Life Technologies Inc., Gaithersburg, MD 20877, USA. Electroporation is also useful for transforming and/or transfecting cells and is well known in the art for transforming yeast cell, bacterial cells, insect cells and vertebrate cells.

Successfully transformed cells, i.e. cells that contain a DNA construct of the present invention, can be identified by well-known techniques such as PCR. Alternatively, the presence of the protein in the supernatant can be detected using antibodies.

It will be appreciated that certain host cells of the invention are useful in the preparation of the peptides of the invention, for example bacterial, yeast and insect cells. However, other host cells may be useful in certain therapeutic methods. For example, antigen-presenting cells, such as dendritic cells, may usefully be used to express the peptides of the invention such that they may be loaded into appropriate MHC molecules. Thus, the current invention provides a host cell comprising a nucleic acid or an expression vector according to the invention.

In a preferred embodiment, the host cell is an antigen presenting cell, in particular a dendritic cell or antigen presenting cell. APCs loaded with a recombinant fusion protein containing prostatic acid phosphatase (PAP) were approved by the U.S. Food and Drug Administration (FDA) on April 29, 2010, to treat asymptomatic or minimally symptomatic metastatic HRPC (Sipuleucel-T) (Rini et al., 2006; Small et al., 2006).

A further aspect of the invention provides a method of producing a peptide or its variant, the method comprising culturing a host cell and isolating the peptide from the host cell or its culture medium.

In another embodiment, the peptide, the nucleic acid or the expression vector of the invention are used in medicine. 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. Doses of e.g. between 50 µg and 1.5 mg, preferably 125 µg to 500 µg, of peptide or DNA may be given and will depend on the respective peptide or DNA. Dosages of this range were successfully used in previous trials (Walter et al., 2012).

The polynucleotide used for active vaccination may be substantially pure, or contained in a suitable vector or delivery system. The nucleic acid may be DNA, cDNA, PNA, RNA or a combination thereof. Methods for designing and introducing such a nucleic acid are well known in the art. An overview is provided by e.g. Teufel et al. (Teufel et al., 2005). Polynucleotide vaccines are easy to prepare, but the mode of action of these vectors in inducing an immune response is not fully understood. Suitable vectors and delivery systems include viral DNA and/or RNA, such as systems based on adenovirus, vaccinia virus, retroviruses, herpes virus, adeno-associated virus or hybrids containing elements of more than one virus. Non-viral delivery systems include cationic lipids and cationic polymers and are well known in the art of DNA delivery. Physical delivery, such as via a "gene-gun" may also be used. The peptide or peptides encoded by the nucleic acid may be a fusion protein, for example with an epitope that stimulates T cells for the respective opposite CDR as noted above.

The medicament of the invention may also include one or more adjuvants. Adjuvants are substances that non-specifically enhance or potentiate the immune response (e.g., immune responses mediated by CD8-positive T cells and helper-T (TH) cells to an antigen, and would thus be considered useful in the medicament of the present invention. Suitable adjuvants include, but are not limited to, 1018 ISS, aluminum salts, AMPLIVAX®, AS15, BCG, CP-870,893, CpG7909, CyaA, dSLIM, flagellin or TLR5 ligands derived from flagellin, FLT3 ligand, GM-CSF, IC30, IC31, Imiquimod (ALDARA®), resiquimod, ImuFact IMP321, Interleukins as IL-2, IL-13, IL-21, Interferon-alpha or -beta, or pegylated derivatives thereof, IS Patch, ISS, ISCOMATRIX, ISCOMs, JuvImmune®, LipoVac, MALP2, MF59, monophosphoryl lipid A, Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, water-in-oil and oil-in-water emulsions, OK-432, OM-174, OM-197-MP-EC, ONTAK, OspA, PepTel® vector system, poly(lactid co-glycolid) [PLG]-based and dextran microparticles, talactoferrin SRL172, Virosomes and other Virus-like

particles, YF-17D, VEGF trap, R848, beta-glucan, Pam3Cys, Aquila's QS21 stimulon, 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. Adjuvants such as Freund's or GM-CSF are preferred. Several immunological adjuvants (e.g., MF59) specific for dendritic cells and their preparation have been described previously (Allison and Krummel, 1995). Also cytokines may be used. Several cytokines have been directly linked to influencing dendritic cell migration to lymphoid tissues (e.g., TNF-), 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, IL-15, IL-23, IL-7, IFN-alpha, IFN-beta) (Gabrilovich et al., 1996).

CpG immunostimulatory oligonucleotides have also been reported to enhance the effects of adjuvants in a vaccine 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 TH1 cells and strong cytotoxic T-lymphocyte (CTL) generation, even in the absence of CD4 T cell help. The TH1 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, nanoparticles, 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 enable 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 (Krieg, 2006). US 6,406,705 B1 describes the combined use of CpG oligonucleotides, non-nucleic acid adjuvants and an antigen to induce an antigen-specific immune response. A 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.

Other examples for useful adjuvants include, but are not limited to chemically modified CpGs (e.g. CpR, Idera), dsRNA analogues such as Poly(I:C) and derivatives thereof (e.g. AmpliGen®, Hiltonol®, poly-(ICLC), poly(IC-R), poly(I:C12U), 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, sorafenib, temozolomide, temsirolimus, XL-999, CP-547632, pazopanib, VEGF Trap, ZD2171, AZD2171, anti-CTLA4, other antibodies targeting key structures of the immune system (e.g. anti-CD40, anti-TGFbeta, anti-TNFalpha receptor) 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.

Preferred adjuvants are anti-CD40, imiquimod, resiquimod, GM-CSF, cyclophosphamide, sunitinib, bevacizumab, interferon-alpha, CpG oligonucleotides and derivatives, poly-(I:C) and derivatives, RNA, sildenafil, and particulate formulations with PLG or virosomes.

In a preferred embodiment, the pharmaceutical composition according to the invention the adjuvant is selected from the group consisting of colony-stimulating factors, such as Granulocyte Macrophage Colony Stimulating Factor (GM-CSF, sargramostim), cyclophosphamide, imiquimod, resiquimod, and interferon-alpha.

In a preferred embodiment, the pharmaceutical composition according to the invention the adjuvant is selected from the group consisting of colony-stimulating factors, such as Granulocyte Macrophage Colony Stimulating Factor (GM-CSF, sargramostim), cyclophosphamide, imiquimod and resiquimod. In a preferred embodiment of the pharmaceutical composition according to the invention, the adjuvant is cyclophosphamide, imiquimod or resiquimod. Even more preferred

adjuvants are Montanide IMS 1312, Montanide ISA 206, Montanide ISA 50V, Montanide ISA-51, poly-ICLC (Hiltonol®) and anti-CD40 mAB, or combinations thereof.

This composition is used for parenteral administration, such as subcutaneous, intradermal, intramuscular or oral administration. For this, the peptides and optionally other molecules are dissolved or suspended in a pharmaceutically acceptable, preferably aqueous carrier. In addition, the composition can contain excipients, such as buffers, binding agents, blasting agents, diluents, flavors, lubricants, etc. The peptides can also be administered together with immune stimulating substances, such as cytokines. An extensive listing of excipients that can be used in such a composition, can be, for example, taken from A. Kibbe, Handbook of Pharmaceutical Excipients (Kibbe, 2000). The composition can be used for a prevention, prophylaxis and/or therapy of adenomatous or cancerous diseases. Exemplary formulations can be found in, for example, EP2112253.

It is important to realize that the immune response triggered by the vaccine according to the invention attacks the cancer in different cell-stages and different stages of development. Furthermore, different cancer associated signaling pathways are attacked. This is an advantage over vaccines that address only one or few targets, which may cause the tumor to easily adapt to the attack (tumor escape). Furthermore, not all individual tumors express the same pattern of antigens. Therefore, a combination of several tumor-associated peptides ensures that every single tumor bears at least some of the targets. The composition is designed in such a way that each tumor is expected to express several of the antigens and cover several independent pathways necessary for tumor growth and maintenance. Thus, the vaccine can easily be used “off-the-shelf” for a larger patient population. This means that a pre-selection of patients to be treated with the vaccine can be restricted to HLA typing, does not require any additional biomarker assessments for antigen expression, but it is still ensured that several targets are simultaneously attacked by the induced immune response, which is important for efficacy (Banchereau et al., 2001; Walter et al., 2012).

As used herein, the term "scaffold" refers to a molecule that specifically binds to an (e.g. antigenic) determinant. In one embodiment, a scaffold is able to direct the entity to which it is attached (e.g. a (second) antigen binding moiety) to a target site, for example to a specific type of tumor cell or tumor stroma bearing the antigenic determinant (e.g. the complex of a peptide with MHC, according to the application at hand). In another embodiment a scaffold is able to activate signaling through its target antigen, for example a T cell receptor complex antigen. Scaffolds include but are not limited to antibodies and fragments thereof, antigen binding domains of an antibody, comprising an antibody heavy chain variable region and an antibody light chain variable region, binding proteins comprising at least one Ankyrin repeat motif and single domain antigen binding (SDAB) molecules, aptamers, (soluble) TCRs and (modified) cells such as allogenic or autologous T cells. To assess whether a molecule is a scaffold binding to a target, binding assays can be performed.

"Specific" binding means that the scaffold binds the peptide-MHC-complex of interest better than other naturally occurring peptide-MHC-complexes, to an extent that a scaffold armed with an active molecule that is able to kill a cell bearing the specific target is not able to kill another cell without the specific target but presenting other peptide-MHC complex(es). Binding to other peptide-MHC complexes is irrelevant if the peptide of the cross-reactive peptide-MHC is not naturally occurring, i.e. not derived from the human HLA-peptidome. Tests to assess target cell killing are well known in the art. They should be performed using target cells (primary cells or cell lines) with unaltered peptide-MHC presentation, or cells loaded with peptides such that naturally occurring peptide-MHC levels are reached.

Each scaffold can comprise a labelling which provides that the bound scaffold can be detected by determining the presence or absence of a signal provided by the label. For example, the scaffold can be labelled with a fluorescent dye or any other applicable cellular marker molecule. Such marker molecules are well known in the art. For example, a fluorescence-labelling, for example provided by a fluorescence dye, can provide a visualization of the bound aptamer by fluorescence or laser scanning microscopy or flow cytometry. Each scaffold can be conjugated with a second active molecule such as for example IL-21, anti-CD3, and anti-CD28. For

further information on polypeptide scaffolds see for example the background section of WO 2014/071978A1 and the references cited therein.

The present invention further relates to aptamers. Aptamers (see for example WO 2014/191359 and the literature as cited therein) are short single-stranded nucleic acid molecules, which can fold into defined three-dimensional structures and recognize specific target structures. They have appeared to be suitable alternatives for developing targeted therapies. Aptamers have been shown to selectively bind to a variety of complex targets with high affinity and specificity.

Aptamers recognizing cell surface located molecules have been identified within the past decade and provide means for developing diagnostic and therapeutic approaches. Since aptamers have been shown to possess almost no toxicity and immunogenicity they are promising candidates for biomedical applications. Indeed aptamers, for example prostate-specific membrane-antigen recognizing aptamers, have been successfully employed for targeted therapies and shown to be functional in xenograft *in vivo* models. Furthermore, aptamers recognizing specific tumor cell lines have been identified.

DNA aptamers can be selected to reveal broad-spectrum recognition properties for various cancer cells, and particularly those derived from solid tumors, while non-tumorigenic and primary healthy cells are not recognized. If the identified aptamers recognize not only a specific tumor sub-type but rather interact with a series of tumors, this renders the aptamers applicable as so-called broad-spectrum diagnostics and therapeutics.

Further, investigation of cell-binding behavior with flow cytometry showed that the aptamers revealed very good apparent affinities that are within the nanomolar range.

Aptamers are useful for diagnostic and therapeutic purposes. Further, it could be shown that some of the aptamers are taken up by tumor cells and thus can function as molecular vehicles for the targeted delivery of anti-cancer agents such as siRNA into tumor cells.

Aptamers can be selected against complex targets such as cells and tissues and complexes of the peptides comprising, preferably consisting of, a sequence according to any of SEQ ID NO 1 to SEQ ID NO 311, according to the present invention with the MHC molecule, using the cell-SELEX (Systematic Evolution of Ligands by Exponential enrichment) technique.

The peptides of the present invention can be used to generate and develop specific antibodies against MHC/peptide complexes. These can be used for therapy, targeting toxins or radioactive substances to the diseased tissue. Another use of these antibodies can be targeting radionuclides to the diseased tissue for imaging purposes such as PET. This use can help to detect small metastases or to determine the size and precise localization of diseased tissues.

Therefore, it is a further aspect of the invention to provide a method for producing a recombinant antibody specifically binding to a human major histocompatibility complex (MHC) class I or II being complexed with a HLA-restricted antigen, the method comprising: immunizing a genetically engineered non-human mammal comprising cells expressing said human major histocompatibility complex (MHC) class I or II with a soluble form of a MHC class I or II molecule being complexed with said HLA-restricted antigen; isolating mRNA molecules from antibody producing cells of said non-human mammal; producing a phage display library displaying protein molecules encoded by said mRNA molecules; and isolating at least one phage from said phage display library, said at least one phage displaying said antibody specifically binding to said human major histocompatibility complex (MHC) class I or II being complexed with said HLA-restricted antigen.

It is a further aspect of the invention to provide an antibody that specifically binds to a human major histocompatibility complex (MHC) class I or II being complexed with a HLA-restricted antigen, wherein the antibody preferably is a polyclonal antibody, monoclonal antibody, bi-specific antibody and/or a chimeric antibody.

Respective methods for producing such antibodies and single chain class I major histocompatibility complexes, as well as other tools for the production of these antibodies are disclosed in WO 03/068201, WO 2004/084798, WO 01/72768, WO

03/070752, and in publications (Cohen et al., 2003a; Cohen et al., 2003b; Denkberg et al., 2003), which for the purposes of the present invention are all explicitly incorporated by reference in their entireties.

Preferably, the antibody is binding with a binding affinity of below 20 nanomolar, preferably of below 10 nanomolar, to the complex, which is also regarded as “specific” in the context of the present invention.

The present invention relates to a peptide comprising a sequence that is selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 311, or a variant thereof which is at least 88% homologous (preferably identical) to SEQ ID NO: 1 to SEQ ID NO: 311 or a variant thereof that induces T cells cross-reacting with said peptide, wherein said peptide is not the underlying full-length polypeptide.

The present invention further relates to a peptide comprising a sequence that is selected from the group consisting of SEQ ID NO: 1 to SEQ ID NO: 311 or a variant thereof which is at least 88% homologous (preferably identical) to SEQ ID NO: 1 to SEQ ID NO: 311, wherein said peptide or variant has an overall length of between 8 and 100, preferably between 8 and 30, and most preferred between 8 and 14 amino acids.

The present invention further relates to the peptides according to the invention that have the ability to bind to a molecule of the human major histocompatibility complex (MHC) class-I or -II.

The present invention further relates to the peptides according to the invention wherein the peptide consists or consists essentially of an amino acid sequence according to SEQ ID NO: 1 to SEQ ID NO: 311.

The present invention further relates to the peptides according to the invention, wherein the peptide is (chemically) modified and/or includes non-peptide bonds.

The present invention further relates to the peptides according to the invention, wherein the peptide is part of a fusion protein, in particular comprising N-terminal

amino acids of the HLA-DR antigen-associated invariant chain (Ii), or wherein the peptide is fused to (or into) an antibody, such as, for example, an antibody that is specific for dendritic cells.

The present invention further relates to a nucleic acid, encoding the peptides according to the invention, provided that the peptide is not the complete (full) human protein.

The present invention further relates to the nucleic acid according to the invention that is DNA, cDNA, PNA, RNA or combinations thereof.

The present invention further relates to an expression vector capable of expressing a nucleic acid according to the present invention.

The present invention further relates to a peptide according to the present invention, a nucleic acid according to the present invention or an expression vector according to the present invention for use in medicine, in particular in the treatment of NHL.

The present invention further relates to a host cell comprising a nucleic acid according to the invention or an expression vector according to the invention.

The present invention further relates to the host cell according to the present invention that is an antigen presenting cell, and preferably a dendritic cell.

The present invention further relates to a method of producing a peptide according to the present invention, said method comprising culturing the host cell according to the present invention, and isolating the peptide from said host cell or its culture medium.

The present invention further relates to the method according to the present invention, where-in the antigen is loaded onto class I or II MHC molecules expressed on the surface of a suitable antigen-presenting cell by contacting a sufficient amount of the antigen with an antigen-presenting cell.

The present invention further relates to the method according to the invention, wherein the antigen-presenting cell comprises an expression vector capable of expressing said peptide containing SEQ ID NO: 1 to SEQ ID NO: 311 or said variant amino acid sequence.

The present invention further relates to activated T cells, produced by the method according to the present invention, wherein said T cells selectively recognizes a cell which aberrantly expresses a polypeptide comprising an amino acid sequence according to the present invention.

The present invention further relates to a method of killing target cells in a patient which target cells aberrantly express a polypeptide comprising any amino acid sequence according to the present invention, the method comprising administering to the patient an effective number of T cells as according to the present invention.

The present invention further relates to the use of any peptide described, a nucleic acid according to the present invention, an expression vector according to the present invention, a cell according to the present invention, or an activated cytotoxic T lymphocyte according to the present invention as a medicament or in the manufacture of a medicament. The present invention further relates to a use according to the present invention, wherein the medicament is active against cancer.

The present invention further relates to a use according to the invention, wherein the medicament is a vaccine. The present invention further relates to a use according to the invention, wherein the medicament is active against cancer.

The present invention further relates to a use according to the invention, wherein said cancer cells are NHL cells or other solid or hematological tumor cells such as non-small cell lung cancer, small cell lung cancer, renal cell cancer, brain cancer, gastric cancer, colorectal cancer, hepatocellular cancer, pancreatic cancer, leukemia, breast cancer, melanoma, ovarian cancer, urinary bladder cancer, uterine cancer, gallbladder and bile duct cancer.

The present invention further relates to particular marker proteins and biomarkers based on the peptides according to the present invention, herein called “targets” that can be used in the diagnosis and/or prognosis of NHL. The present invention also relates to the use of these novel targets for cancer treatment.

The term “antibody” or “antibodies” is used herein in a broad sense and includes both polyclonal and monoclonal antibodies. In addition to intact or “full” immunoglobulin molecules, also included in the term “antibodies” are fragments (e.g. CDRs, Fv, Fab and Fc fragments) or polymers of those immunoglobulin molecules and humanized versions of immunoglobulin molecules, as long as they exhibit any of the desired properties (e.g., specific binding of a NHL marker (poly)peptide, delivery of a toxin to a NHL cell expressing a cancer marker gene at an increased level, and/or inhibiting the activity of a NHL marker polypeptide) according to the invention.

Whenever possible, the antibodies of the invention may be purchased from commercial sources. The antibodies of the invention may also be generated using well-known methods. The skilled artisan will understand that either full length NHL marker polypeptides or fragments thereof may be used to generate the antibodies of the invention. A polypeptide to be used for generating an antibody of the invention may be partially or fully purified from a natural source, or may be produced using recombinant DNA techniques.

For example, a cDNA encoding a peptide according to the present invention, such as a peptide according to SEQ ID NO: 1 to SEQ ID NO: 311 polypeptide, or a variant or fragment thereof, can be expressed in prokaryotic cells (e.g., bacteria) or eukaryotic cells (e.g., yeast, insect, or mammalian cells), after which the recombinant protein can be purified and used to generate a monoclonal or polyclonal antibody preparation that specifically bind the NHL marker polypeptide used to generate the antibody according to the invention.

One of skill in the art will realize that the generation of two or more different sets of monoclonal or polyclonal antibodies maximizes the likelihood of obtaining an antibody with the specificity and affinity required for its intended use (e.g., ELISA, immunohistochemistry, *in vivo* imaging, immunotoxin therapy). The antibodies are

tested for their desired activity by known methods, in accordance with the purpose for which the antibodies are to be used (e.g., ELISA, immunohistochemistry, immunotherapy, etc.; for further guidance on the generation and testing of antibodies, see, e.g., Greenfield, 2014 (Greenfield, 2014)). For example, the antibodies may be tested in ELISA assays or, Western blots, immunohistochemical staining of formalin-fixed cancers or frozen tissue sections. After their initial *in vitro* characterization, antibodies intended for therapeutic or *in vivo* diagnostic use are tested according to known clinical testing methods.

The term "monoclonal antibody" as used herein refers to an antibody obtained from a substantially homogeneous population of antibodies, i.e.; the individual antibodies comprising the population are identical except for possible naturally occurring mutations that may be present in minor amounts. The monoclonal antibodies herein specifically include "chimeric" antibodies in which a portion of the heavy and/or light chain is identical with or homologous to corresponding sequences in antibodies derived from a particular species or belonging to a particular antibody class or subclass, while the remainder of the chain(s) is identical with or homologous to corresponding sequences in antibodies derived from another species or belonging to another antibody class or subclass, as well as fragments of such antibodies, so long as they exhibit the desired antagonistic activity (US 4,816,567, which is hereby incorporated in its entirety).

Monoclonal antibodies of the invention may be prepared using hybridoma methods. In a hybridoma method, a mouse or other appropriate host animal is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in US 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies).

In vitro methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly Fab fragments, can be accomplished using routine techniques known in the art. For instance, digestion can be performed using papain. Examples of papain digestion are described in WO 94/29348 and US 4,342,566. Papain digestion of antibodies typically produces two identical antigen binding fragments, called Fab fragments, each with a single antigen binding site, and a residual Fc fragment. Pepsin treatment yields a F(ab')₂ fragment and a pFc' fragment.

The antibody fragments, whether attached to other sequences or not, can also include insertions, deletions, substitutions, or other selected modifications of particular regions or specific amino acids residues, provided the activity of the fragment is not significantly altered or impaired compared to the non-modified antibody or antibody fragment. These modifications can provide for some additional property, such as to remove/add amino acids capable of disulfide bonding, to increase its bio-longevity, to alter its secretory characteristics, etc. In any case, the antibody fragment must possess a bioactive property, such as binding activity, regulation of binding at the binding domain, etc. Functional or active regions of the antibody may be identified by mutagenesis of a specific region of the protein, followed by expression and testing of the expressed polypeptide. Such methods are readily apparent to a skilled practitioner in the art and can include site-specific mutagenesis of the nucleic acid encoding the antibody fragment.

The antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab' or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework (FR) residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the

recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin.

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed by substituting rodent CDRs or CDR sequences for the corresponding sequences of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (US 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Transgenic animals (e.g., mice) that are capable, upon immunization, of producing a full repertoire of human antibodies in the absence of endogenous immunoglobulin production can be employed. For example, it has been described that the homozygous deletion of the antibody heavy chain joining region gene in chimeric and germ-line mutant mice results in complete inhibition of endogenous antibody production. Transfer of the human germ-line immunoglobulin gene array in such germ-line mutant mice will result in the production of human antibodies upon antigen challenge. Human antibodies can also be produced in phage display libraries.

Antibodies of the invention are preferably administered to a subject in a pharmaceutically acceptable carrier. Typically, an appropriate amount of a pharmaceutically-acceptable salt is used in the formulation to render the formulation isotonic. Examples of the pharmaceutically-acceptable carrier include saline, Ringer's

solution and dextrose solution. The pH of the solution is preferably from about 5 to about 8, and more preferably from about 7 to about 7.5. Further carriers include sustained release preparations such as semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, e.g., films, liposomes or microparticles. It will be apparent to those persons skilled in the art that certain carriers may be more preferable depending upon, for instance, the route of administration and concentration of antibody being administered.

The antibodies can be administered to the subject, patient, or cell by injection (e.g., intravenous, intraperitoneal, subcutaneous, intramuscular), or by other methods such as infusion that ensure its delivery to the bloodstream in an effective form. The antibodies may also be administered by intratumoral or peritumoral routes, to exert local as well as systemic therapeutic effects. Local or intravenous injection is preferred.

Effective dosages and schedules for administering the antibodies may be determined empirically, and making such determinations is within the skill in the art. Those skilled in the art will understand that the dosage of antibodies that must be administered will vary depending on, for example, the subject that will receive the antibody, the route of administration, the particular type of antibody used and other drugs being administered. A typical daily dosage of the antibody used alone might range from about 1 ($\mu\text{g}/\text{kg}$ to up to 100 mg/kg of body weight or more per day, depending on the factors mentioned above. Following administration of an antibody, preferably for treating NHL, the efficacy of the therapeutic antibody can be assessed in various ways well known to the skilled practitioner. For instance, the size, number, and/or distribution of cancer in a subject receiving treatment may be monitored using standard tumor imaging techniques. A therapeutically-administered antibody that arrests tumor growth, results in tumor shrinkage, and/or prevents the development of new tumors, compared to the disease course that would occur in the absence of antibody administration, is an efficacious antibody for treatment of cancer.

It is a further aspect of the invention to provide a method for producing a soluble T-cell receptor (sTCR) recognizing a specific peptide-MHC complex. Such soluble T-cell receptors can be generated from specific T-cell clones, and their affinity can be

increased by mutagenesis targeting the complementarity-determining regions. For the purpose of T-cell receptor selection, phage display can be used (US 2010/0113300, (Liddy et al., 2012)). For the purpose of stabilization of T-cell receptors during phage display and in case of practical use as drug, alpha and beta chain can be linked e.g. by non-native disulfide bonds, other covalent bonds (single-chain T-cell receptor), or by dimerization domains (Boulter et al., 2003; Card et al., 2004; Willcox et al., 1999). The T-cell receptor can be linked to toxins, drugs, cytokines (see, for example, US 2013/0115191), and domains recruiting effector cells such as an anti-CD3 domain, etc., in order to execute particular functions on target cells. Moreover, it could be expressed in T cells used for adoptive transfer. Further information can be found in WO 2004/033685A1 and WO 2004/074322A1. A combination of sTCRs is described in WO 2012/056407A1. Additional methods for the production are disclosed in WO 2013/057586A1.

In addition, the peptides and/or the TCRs or antibodies or other binding molecules of the present invention can be used to verify a pathologist's diagnosis of a cancer based on a biopsied sample.

The antibodies or TCRs may also be used for *in vivo* diagnostic assays. Generally, the antibody is labeled with a radionucleotide (such as ^{111}In , ^{99}Tc , ^{14}C , ^{131}I , ^3H , ^{32}P or ^{35}S) so that the tumor can be localized using immunoscintigraphy. In one embodiment, antibodies or fragments thereof bind to the extracellular domains of two or more targets of a protein selected from the group consisting of the above-mentioned proteins, and the affinity value (K_d) is less than $1 \times 10\mu\text{M}$.

Antibodies for diagnostic use may be labeled with probes suitable for detection by various imaging methods. Methods for detection of probes include, but are not limited to, fluorescence, light, confocal and electron microscopy; magnetic resonance imaging and spectroscopy; fluoroscopy, computed tomography and positron emission tomography. Suitable probes include, but are not limited to, fluorescein, rhodamine, eosin and other fluorophores, radioisotopes, gold, gadolinium and other lanthanides, paramagnetic iron, fluorine-18 and other positron-emitting radionuclides. Additionally, probes may be bi- or multi-functional and be detectable by more than one of the methods listed. These antibodies may be directly or indirectly labeled with said

probes. Attachment of probes to the antibodies includes covalent attachment of the probe, incorporation of the probe into the antibody, and the covalent attachment of a chelating compound for binding of probe, amongst others well recognized in the art. For immunohistochemistry, the disease tissue sample may be fresh or frozen or may be embedded in paraffin and fixed with a preservative such as formalin. The fixed or embedded section contains the sample are contacted with a labeled primary antibody and secondary antibody, wherein the antibody is used to detect the expression of the proteins in situ.

Another aspect of the present invention includes an *in vitro* method for producing activated T cells, the method comprising contacting *in vitro* T cells with antigen loaded human MHC molecules expressed on the surface of a suitable antigen-presenting cell for a period of time sufficient to activate the T cell in an antigen specific manner, wherein the antigen is a peptide according to the invention. Preferably a sufficient amount of the antigen is used with an antigen-presenting cell.

Preferably the mammalian cell lacks or has a reduced level or function of the TAP peptide transporter. Suitable cells that lack the TAP peptide transporter include T2, RMA-S and Drosophila cells. TAP is the transporter associated with antigen processing.

The human peptide loading deficient cell line T2 is available from the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland 20852, USA under Catalogue No CRL 1992; the Drosophila cell line Schneider line 2 is available from the ATCC under Catalogue No CRL 19863; the mouse RMA-S cell line is described in Ljunggren et al. (Ljunggren and Karre, 1985).

Preferably, before transfection the host cell expresses substantially no MHC class I molecules. It is also preferred that the stimulator cell expresses a molecule important for providing a co-stimulatory signal for T-cells such as any of B7.1, B7.2, ICAM-1 and LFA 3. The nucleic acid sequences of numerous MHC class I molecules and of the co-stimulator molecules are publicly available from the GenBank and EMBL databases.

In case of a MHC class I epitope being used as an antigen, the T cells are CD8-positive T cells.

If an antigen-presenting cell is transfected to express such an epitope, preferably the cell comprises an expression vector capable of expressing a peptide containing SEQ ID NO: 1 to SEQ ID NO: 311, or a variant amino acid sequence thereof.

A number of other methods may be used for generating T cells in vitro. For example, autologous tumor-infiltrating lymphocytes can be used in the generation of CTL. Plebanski et al. (Plebanski et al., 1995) made use of autologous peripheral blood lymphocytes (PLBs) in the preparation of T cells. Furthermore, the production of autologous T cells by pulsing dendritic cells with peptide or polypeptide, or via infection with recombinant virus is possible. Also, B cells can be used in the production of autologous T cells. In addition, macrophages pulsed with peptide or polypeptide, or infected with recombinant virus, may be used in the preparation of autologous T cells. S. Walter et al. (Walter et al., 2003) describe the in vitro priming of T cells by using artificial antigen presenting cells (aAPCs), which is also a suitable way for generating T cells against the peptide of choice. In the present invention, aAPCs were generated by the coupling of preformed MHC:peptide complexes to the surface of polystyrene particles (microbeads) by biotin:streptavidin biochemistry. This system permits the exact control of the MHC density on aAPCs, which allows to selectively eliciting high- or low-avidity antigen-specific T cell responses with high efficiency from blood samples. Apart from MHC:peptide complexes, aAPCs should carry other proteins with co-stimulatory activity like anti-CD28 antibodies coupled to their surface. Furthermore, such aAPC-based systems often require the addition of appropriate soluble factors, e. g. cytokines, like interleukin-12.

Allogeneic cells may also be used in the preparation of T cells and a method is described in detail in WO 97/26328, incorporated herein by reference. For example, in addition to *Drosophila* cells and T2 cells, other cells may be used to present antigens such as CHO cells, baculovirus-infected insect cells, bacteria, yeast, and vaccinia-infected target cells. In addition plant viruses may be used (see, for example, Porta et al. (Porta et al., 1994) which describes the development of cowpea mosaic virus as a high-yielding system for the presentation of foreign peptides.

The activated T cells that are directed against the peptides of the invention are useful in therapy. Thus, a further aspect of the invention provides activated T cells obtainable by the foregoing methods of the invention.

Activated T cells, which are produced by the above method, will selectively recognize a cell that aberrantly expresses a polypeptide that comprises an amino acid sequence of SEQ ID NO: 1 to SEQ ID NO 311.

Preferably, the T cell recognizes the cell by interacting through its TCR with the HLA/peptide-complex (for example, binding). The T cells are useful in a method of killing target cells in a patient whose target cells aberrantly express a polypeptide comprising an amino acid sequence of the invention wherein the patient is administered an effective number of the activated T cells. The T cells that are administered to the patient may be derived from the patient and activated as described above (i.e. they are autologous T cells). Alternatively, the T cells are not from the patient but are from another individual. Of course, it is preferred if the individual is a healthy individual. By “healthy individual” the inventors mean that the individual is generally in good health, preferably has a competent immune system and, more preferably, is not suffering from any disease that can be readily tested for, and detected.

In vivo, the target cells for the CD8-positive T cells according to the present invention can be cells of the tumor (which sometimes express MHC class II) and/or stromal cells surrounding the tumor (tumor cells) (which sometimes also express MHC class II; (Dengjel et al., 2006)).

The T cells of the present invention may be used as active ingredients of a therapeutic composition. Thus, the invention also provides a method of killing target cells in a patient whose target cells aberrantly express a polypeptide comprising an amino acid sequence of the invention, the method comprising administering to the patient an effective number of T cells as defined above.

By "aberrantly expressed" the inventors also mean that the polypeptide is over-expressed compared to levels of expression in normal tissues or that the gene is silent in the tissue from which the tumor is derived but in the tumor it is expressed. By "over-expressed" the inventors mean that the polypeptide is present at a level at least 1.2-fold of that present in normal tissue; preferably at least 2-fold, and more preferably at least 5-fold or 10-fold the level present in normal tissue.

T cells may be obtained by methods known in the art, e.g. those described above.

Protocols for this so-called adoptive transfer of T cells are well known in the art. Reviews can be found in: Gattinoni et al. and Morgan et al. (Gattinoni et al., 2006; Morgan et al., 2006).

Another aspect of the present invention includes the use of the peptides complexed with MHC to generate a T-cell receptor whose nucleic acid is cloned and is introduced into a host cell, preferably a T cell. This engineered T cell can then be transferred to a patient for therapy of cancer.

Any molecule of the invention, i.e. the peptide, nucleic acid, antibody, expression vector, cell, activated T cell, T-cell receptor or the nucleic acid encoding it, is useful for the treatment of disorders, characterized by cells escaping an immune response. Therefore, any molecule of the present invention may be used as medicament or in the manufacture of a medicament. The molecule may be used by itself or combined with other molecule(s) of the invention or (a) known molecule(s).

The present invention is further directed at a kit comprising:

- (a) a container containing a pharmaceutical composition as described above, in solution or in lyophilized form;
- (b) optionally a second container containing a diluent or reconstituting solution for the lyophilized formulation; and
- (c) optionally, instructions for (i) use of the solution or (ii) reconstitution and/or use of the lyophilized formulation.

The kit may further comprise one or more of (iii) a buffer, (iv) a diluent, (v) a filter, (vi) a needle, or (v) a syringe. The container is preferably a bottle, a vial, a syringe or test tube; and it may be a multi-use container. The pharmaceutical composition is preferably lyophilized.

Kits of the present invention preferably comprise a lyophilized formulation of the present invention in a suitable container and instructions for its reconstitution and/or use. Suitable containers include, for example, bottles, vials (e.g. dual chamber vials), syringes (such as dual chamber syringes) and test tubes. The container may be formed from a variety of materials such as glass or plastic. Preferably the kit and/or container contain/s instructions on or associated with the container that indicates directions for reconstitution and/or use. For example, the label may indicate that the lyophilized formulation is to be reconstituted to peptide concentrations as described above. The label may further indicate that the formulation is useful or intended for subcutaneous administration.

The container holding the formulation may be a multi-use vial, which allows for repeat administrations (e.g., from 2-6 administrations) of the reconstituted formulation. The kit may further comprise a second container comprising a suitable diluent (e.g., sodium bicarbonate solution).

Upon mixing of the diluent and the lyophilized formulation, the final peptide concentration in the reconstituted formulation is preferably at least 0.15 mg/mL/peptide (=75 μ g) and preferably not more than 3 mg/mL/peptide (=1500 μ g). The kit may further include other materials desirable from a commercial and user standpoint, including other buffers, diluents, filters, needles, syringes, and package inserts with instructions for use.

Kits of the present invention may have a single container that contains the formulation of the pharmaceutical compositions according to the present invention with or without other components (e.g., other compounds or pharmaceutical compositions of these other compounds) or may have distinct container for each component.

Preferably, kits of the invention include a formulation of the invention packaged for use in combination with the co-administration of a second compound (such as adjuvants (e.g. GM-CSF), a chemotherapeutic agent, a natural product, a hormone or antagonist, an anti-angiogenesis agent or inhibitor, an apoptosis-inducing agent or a chelator) or a pharmaceutical composition thereof. The components of the kit may be pre-complexed or each component may be in a separate distinct container prior to administration to a patient. The components of the kit may be provided in one or more liquid solutions, preferably, an aqueous solution, more preferably, a sterile aqueous solution. The components of the kit may also be provided as solids, which may be converted into liquids by addition of suitable solvents, which are preferably provided in another distinct container.

The container of a therapeutic kit may be a vial, test tube, flask, bottle, syringe, or any other means of enclosing a solid or liquid. Usually, when there is more than one component, the kit will contain a second vial or other container, which allows for separate dosing. The kit may also contain another container for a pharmaceutically acceptable liquid. Preferably, a therapeutic kit will contain an apparatus (e.g., one or more needles, syringes, eye droppers, pipette, etc.), which enables administration of the agents of the invention that are components of the present kit.

The present formulation is one that is suitable for administration of the peptides by any acceptable route such as oral (enteral), nasal, ophthal, subcutaneous, intradermal, intramuscular, intravenous or transdermal. Preferably, the administration is s.c., and most preferably i.d. administration may be by infusion pump.

Since the peptides of the invention were isolated from NHL, the medicament of the invention is preferably used to treat NHL.

The present invention further relates to a method for producing a personalized pharmaceutical (composition) for an individual patient comprising manufacturing a pharmaceutical composition comprising at least one peptide selected from a warehouse of pre-screened TUMAPs, wherein the at least one peptide used in the pharmaceutical composition is selected for suitability in the individual patient. In one embodiment, the pharmaceutical composition is a vaccine. The method could also be

adapted to produce T cell clones for down-stream applications, such as TCR isolations, or soluble antibodies, and other treatment options.

A “personalized pharmaceutical” shall mean specifically tailored therapies for one individual patient that will only be used for therapy in such individual patient, including actively personalized cancer vaccines and adoptive cellular therapies using autologous patient tissue.

As used herein, the term “warehouse” shall refer to a group or set of peptides that have been pre-screened for immunogenicity and/or over-presentation in a particular tumor type. The term “warehouse” is not intended to imply that the particular peptides included in the vaccine have been pre-manufactured and stored in a physical facility, although that possibility is contemplated. It is expressly contemplated that the peptides may be manufactured *de novo* for each individualized vaccine produced, or may be pre-manufactured and stored. The warehouse (e.g. in the form of a database) is composed of tumor-associated peptides which were highly overexpressed in the tumor tissue of NHL patients with various HLA-A HLA-B and HLA-C alleles. It may contain MHC class I and MHC class II peptides or elongated MHC class I peptides. In addition to the tumor associated peptides collected from several NHL tissues, the warehouse may contain HLA-A*02 and HLA-A*24 marker peptides. These peptides allow comparison of the magnitude of T-cell immunity induced by TUMAPS in a quantitative manner and hence allow important conclusion to be drawn on the capacity of the vaccine to elicit anti-tumor responses. Secondly, they function as important positive control peptides derived from a “non-self” antigen in the case that any vaccine-induced T-cell responses to TUMAPs derived from “self” antigens in a patient are not observed. And thirdly, it may allow conclusions to be drawn, regarding the status of immunocompetence of the patient.

TUMAPs for the warehouse are identified by using an integrated functional genomics approach combining gene expression analysis, mass spectrometry, and T-cell immunology (XPresident®). The approach assures that only TUMAPs truly present on a high percentage of tumors but not or only minimally expressed on normal tissue, are chosen for further analysis. For initial peptide selection, NHL samples from patients and blood from healthy donors were analyzed in a stepwise approach:

1. HLA ligands from the malignant material were identified by mass spectrometry
2. Genome-wide messenger ribonucleic acid (mRNA) expression analysis was used to identify genes over-expressed in the malignant tissue (NHL) compared with a range of normal organs and tissues
3. Identified HLA ligands were compared to gene expression data. Peptides over-presented or selectively presented on tumor tissue, preferably encoded by selectively expressed or over-expressed genes as detected in step 2 were considered suitable TUMAP candidates for a multi-peptide vaccine.
4. Literature research was performed in order to identify additional evidence supporting the relevance of the identified peptides as TUMAPs
5. The relevance of over-expression at the mRNA level was confirmed by redetection of selected TUMAPs from step 3 on tumor tissue and lack of (or infrequent) detection on healthy tissues.
6. In order to assess, whether an induction of *in vivo* T-cell responses by the selected peptides may be feasible, *in vitro* immunogenicity assays were performed using human T cells from healthy donors as well as from NHL patients.

In an aspect, the peptides are pre-screened for immunogenicity before being included in the warehouse. By way of example, and not limitation, the immunogenicity of the peptides included in the warehouse is determined by a method comprising *in vitro* T-cell priming through repeated stimulations of CD8⁺ T cells from healthy donors with artificial antigen presenting cells loaded with peptide/MHC complexes and anti-CD28 antibody.

This method is preferred for rare cancers and patients with a rare expression profile. In contrast to multi-peptide cocktails with a fixed composition as currently developed, the warehouse allows a significantly higher matching of the actual expression of antigens in the tumor with the vaccine. Selected single or combinations of several “off-the-shelf” peptides will be used for each patient in a multitarget approach. In theory, an approach based on selection of e.g. 5 different antigenic peptides from a library of 50 would already lead to approximately 17 million possible drug product (DP) compositions.

In an aspect, the peptides are selected for inclusion in the vaccine based on their suitability for the individual patient based on the method according to the present invention as described herein, or as below.

The HLA phenotype, transcriptomic and peptidomic data is gathered from the patient's tumor material, and blood samples to identify the most suitable peptides for each patient containing "warehouse" and patient-unique (i.e. mutated) TUMAPs. Those peptides will be chosen, which are selectively or over-expressed in the patients' tumor and, where possible, show strong *in vitro* immunogenicity if tested with the patients' individual PBMCs.

Preferably, the peptides included in the vaccine are identified by a method comprising: (a) identifying tumor-associated peptides (TUMAPs) presented by a tumor sample from the individual patient; (b) comparing the peptides identified in (a) with a warehouse (database) of peptides as described above; and (c) selecting at least one peptide from the warehouse (database) that correlates with a tumor-associated peptide identified in the patient. For example, the TUMAPs presented by the tumor sample are identified by: (a1) comparing expression data from the tumor sample to expression data from a sample of normal tissue corresponding to the tissue type of the tumor sample to identify proteins that are over-expressed or aberrantly expressed in the tumor sample; and (a2) correlating the expression data with sequences of MHC ligands bound to MHC class I and/or class II molecules in the tumor sample to identify MHC ligands derived from proteins over-expressed or aberrantly expressed by the tumor. Preferably, the sequences of MHC ligands are identified by eluting bound peptides from MHC molecules isolated from the tumor sample, and sequencing the eluted ligands. Preferably, the tumor sample and the normal tissue are obtained from the same patient.

In addition to, or as an alternative to, selecting peptides using a warehousing (database) model, TUMAPs may be identified in the patient *de novo*, and then included in the vaccine. As one example, candidate TUMAPs may be identified in the patient by (a1) comparing expression data from the tumor sample to expression data from a sample of normal tissue corresponding to the tissue type of the tumor sample to identify proteins that are over-expressed or aberrantly expressed in the

tumor sample; and (a2) correlating the expression data with sequences of MHC ligands bound to MHC class I and/or class II molecules in the tumor sample to identify MHC ligands derived from proteins over-expressed or aberrantly expressed by the tumor. As another example, proteins may be identified containing mutations that are unique to the tumor sample relative to normal corresponding tissue from the individual patient, and TUMAPs can be identified that specifically target the mutation. For example, the genome of the tumor and of corresponding normal tissue can be sequenced by whole genome sequencing: For discovery of non-synonymous mutations in the protein-coding regions of genes, genomic DNA and RNA are extracted from tumor tissues and normal non-mutated genomic germline DNA is extracted from peripheral blood mononuclear cells (PBMCs). The applied NGS approach is confined to the re-sequencing of protein coding regions (exome re-sequencing). For this purpose, exonic DNA from human samples is captured using vendor-supplied target enrichment kits, followed by sequencing with e.g. a HiSeq2000 (Illumina). Additionally, tumor mRNA is sequenced for direct quantification of gene expression and validation that mutated genes are expressed in the patients' tumors. The resultant millions of sequence reads are processed through software algorithms. The output list contains mutations and gene expression. Tumor-specific somatic mutations are determined by comparison with the PBMC-derived germline variations and prioritized. The *de novo* identified peptides can then be tested for immunogenicity as described above for the warehouse, and candidate TUMAPs possessing suitable immunogenicity are selected for inclusion in the vaccine.

In one exemplary embodiment, the peptides included in the vaccine are identified by: (a) identifying tumor-associated peptides (TUMAPs) presented by a tumor sample from the individual patient by the method as described above; (b) comparing the peptides identified in a) with a warehouse of peptides that have been prescreened for immunogenicity and overpresentation in tumors as compared to corresponding normal tissue; (c) selecting at least one peptide from the warehouse that correlates with a tumor-associated peptide identified in the patient; and (d) optionally, selecting at least one peptide identified *de novo* in (a) confirming its immunogenicity.

In one exemplary embodiment, the peptides included in the vaccine are identified by: (a) identifying tumor-associated peptides (TUMAPs) presented by a tumor sample from the individual patient; and (b) selecting at least one peptide identified de novo in (a) and confirming its immunogenicity.

Once the peptides for a personalized peptide based vaccine are selected, the vaccine is produced. The vaccine preferably is a liquid formulation consisting of the individual peptides dissolved in between 20-40% DMSO, preferably about 30-35% DMSO, such as about 33% DMSO.

Each peptide to be included into a product is dissolved in DMSO. The concentration of the single peptide solutions has to be chosen depending on the number of peptides to be included into the product. The single peptide-DMSO solutions are mixed in equal parts to achieve a solution containing all peptides to be included in the product with a concentration of ~2.5 mg/ml per peptide. The mixed solution is then diluted 1:3 with water for injection to achieve a concentration of 0.826 mg/ml per peptide in 33% DMSO. The diluted solution is filtered through a 0.22 μ m sterile filter. The final bulk solution is obtained.

Final bulk solution is filled into vials and stored at -20°C until use. One vial contains 700 μ L solution, containing 0.578 mg of each peptide. Of this, 500 μ L (approx. 400 μ g per peptide) will be applied for intradermal injection.

In addition to being useful for treating cancer, the peptides of the present invention are also useful as diagnostics. Since the peptides were generated from NHL cells and since it was determined that these peptides are not or at lower levels present in normal tissues, these peptides can be used to diagnose the presence of a cancer.

The presence of claimed peptides on tissue biopsies in blood samples can assist a pathologist in diagnosis of cancer. Detection of certain peptides by means of antibodies, mass spectrometry or other methods known in the art can tell the pathologist that the tissue sample is malignant or inflamed or generally diseased, or can be used as a biomarker for NHL. Presence of groups of peptides can enable classification or sub-classification of diseased tissues.

The detection of peptides on diseased tissue specimen can enable the decision about the benefit of therapies involving the immune system, especially if T-lymphocytes are known or expected to be involved in the mechanism of action. Loss of MHC expression is a well described mechanism by which infected or malignant cells escape immuno-surveillance. Thus, presence of peptides shows that this mechanism is not exploited by the analyzed cells.

The peptides of the present invention might be used to analyze lymphocyte responses against those peptides such as T cell responses or antibody responses against the peptide or the peptide complexed to MHC molecules. These lymphocyte responses can be used as prognostic markers for decision on further therapy steps. These responses can also be used as surrogate response markers in immunotherapy approaches aiming to induce lymphocyte responses by different means, e.g. vaccination of protein, nucleic acids, autologous materials, adoptive transfer of lymphocytes. In gene therapy settings, lymphocyte responses against peptides can be considered in the assessment of side effects. Monitoring of lymphocyte responses might also be a valuable tool for follow-up examinations of transplantation therapies, e.g. for the detection of graft versus host and host versus graft diseases.

The present invention will now be described in the following examples which describe preferred embodiments thereof, and with reference to the accompanying figures, nevertheless, without being limited thereto. For the purposes of the present invention, all references as cited herein are incorporated by reference in their entireties.

FIGURES

Figures 1A to P show the over-presentation of various peptides in normal tissues (white bars) and NHL (black bars). Figure 1A) Gene symbol: TOX2, Peptide: LLSGQLPTI (SEQ ID NO.: 1); Tissues from left to right: 3 adipose tissues, 3 adrenal glands, 15 blood cell samples, 12 blood vessels, 10 bone marrows, 7 brains, 8 breasts, 2 cartilages, 2 eyes, 3 gallbladders, 6 hearts, 14 kidneys, 19 large intestines, 20 livers, 45 lungs, 8 lymph nodes, 7 nerves, 3 ovaries, 10 pancreases, 3 parathyroid glands, 1 peritoneum, 5 pituitary glands, 6 placentas, 3 pleuras, 3 prostates, 7

salivary glands, 5 skeletal muscles, 11 skins, 3 small intestines, 11 spleens, 5 stomachs, 6 testes, 2 thymi, 2 thyroid glands, 9 tracheas, 7 ureters, 8 urinary bladders, 5 uteri, 6 esophagi, 18 NHL samples. The peptide has additionally been detected on 1/84 lung cancers, 1/17 chronic lymphocytic leukemias, 1/20 pancreatic cancer cell lines, 1/20 ovarian cancers and 1/16 uterus cancers. Figure 1B) Gene symbol: TAP1, Peptide: VLQGLTFTL (SEQ ID NO.: 5); Tissues from left to right: 3 adipose tissues, 3 adrenal glands, 15 blood cell samples, 12 blood vessels, 10 bone marrows, 7 brains, 8 breasts, 2 cartilages, 2 eyes, 3 gallbladders, 6 hearts, 14 kidneys, 19 large intestines, 20 livers, 45 lungs, 8 lymph nodes, 7 nerves, 3 ovaries, 10 pancreases, 3 parathyroid glands, 1 peritoneum, 5 pituitary glands, 6 placentas, 3 pleuras, 3 prostates, 7 salivary glands, 5 skeletal muscles, 11 skins, 3 small intestines, 11 spleens, 5 stomachs, 6 testes, 2 thymi, 2 thyroid glands, 9 tracheas, 7 ureters, 8 urinary bladders, 5 uteri, 6 esophagi, 18 NHL samples. The peptide has additionally been detected on 4/101 lung cancers, 1/18 breast cancers, 1/17 chronic lymphocytic leukemias, 2/17 bile duct and gallbladder cancers, 2/16 melanomas, 2/20 ovarian cancers and 1/15 urinary bladder cancers. Figure 1C) Gene symbol: SLC20A1, Peptide: ILASIFETV (SEQ ID NO.: 41); Tissues from left to right: 3 adipose tissues, 3 adrenal glands, 15 blood cell samples, 12 blood vessels, 10 bone marrows, 7 brains, 8 breasts, 2 cartilages, 2 eyes, 3 gallbladders, 6 hearts, 14 kidneys, 19 large intestines, 20 livers, 45 lungs, 8 lymph nodes, 7 nerves, 3 ovaries, 10 pancreases, 3 parathyroid glands, 1 peritoneum, 5 pituitary glands, 6 placentas, 3 pleuras, 3 prostates, 7 salivary glands, 5 skeletal muscles, 11 skins, 3 small intestines, 11 spleens, 5 stomachs, 6 testes, 2 thymi, 2 thyroid glands, 9 tracheas, 7 ureters, 8 urinary bladders, 5 uteri, 6 esophagi, 18 NHL samples. The peptide has additionally been detected on 10/101 lung cancers, 4/18 acute myelogenous leukemias, 1/18 breast cancers, 1/17 chronic lymphocytic leukemias, 3/20 pancreatic cancer cell lines, 2/17 bile duct and gallbladder cancers, 4/16 melanomas, 1/20 ovarian cancers, 2/19 pancreas cancers, 1/38 prostate cancers, 2/22 kidney cancers and 1/15 urinary bladder cancers. Figure 1D) Gene symbol: COPS7B, Peptide: NLLEQFILL (SEQ ID NO.: 248); Samples from left to right: 4 cancer cell lines, 6 normal tissues (1 lymph node, 3 spleens, 1 stomach, 1 uterus), 55 cancer tissues (2 brain cancers, 1 breast cancer, 1 cecum cancer, 6 colon cancers, 6 leukocytic leukemia cancers, 2 liver cancers, 10 lung cancers, 8 lymph node cancers, 1 myeloid cell cancer, 3 ovarian cancers, 1 prostate cancer, 1 rectum cancer, 4 skin cancers, 2

stomach cancers, 3 urinary bladder cancers, 4 uterus cancers). Discrepancies regarding the list of tumor types between Figure 1D and Table 4A might be due to the more stringent selection criteria applied in Table 4A (for details please refer to Table 4A). The normal tissue panel and the cancer cell lines and xenografts tested were the same as in Figure 1A to C. Figure 1E) Gene symbol: KDM5B, Peptide: LLSEETPSA (SEQ ID NO.: 2); Samples from left to right: 1 primary culture, 40 cancer tissues (1 bone marrow cancer, 1 brain cancer, 2 breast cancers, 8 head and neck cancers, 4 leukocytic leukemia cancers, 1 liver cancer, 7 lung cancers, 6 lymph node cancers, 2 myeloid cell cancers, 1 ovarian cancer, 3 skin cancers, 3 urinary bladder cancers, 1 uterus cancer). Figure 1F) Gene symbol: CDC42, Peptide: FLLVGTQIDL (SEQ ID NO.: 10); Samples from left to right: 2 cell lines, 10 cancer tissues (2 breast cancers, 1 head and neck cancer, 1 leukocytic leukemia cancer, 1 lung cancer, 4 lymph node cancers, 1 uterus cancer). Figure 1G) Gene symbol: HAPLN3, Peptide: GLLLLVPLL (SEQ ID NO.: 12); Samples from left to right: 16 cancer tissues (1 breast cancer, 1 colon cancer, 1 colorectal cancer, 1 esophageal cancer, 1 gallbladder cancer, 1 head and neck cancer, 2 lung cancers, 5 lymph node cancers, 2 ovarian cancers, 1 skin cancer). Figure 1H) Gene symbol: JAK3, Peptide: HLVPASWKL (SEQ ID NO.: 13); Samples from left to right: 10 cancer tissues (1 leukocytic leukemia cancer, 1 lung cancer, 5 lymph node cancers, 1 ovarian cancer, 1 skin cancer, 1 testis cancer). Figure 1I) Gene symbol: TMEM67, Peptide: FLGSFIDHV (SEQ ID NO.: 26); Samples from left to right: 1 cell line, 9 cancer tissues (1 brain cancer, 1 lung cancer, 1 lymph node cancer, 1 myeloid cell cancer, 2 ovarian cancers, 2 skin cancers, 1 uterus cancer). Figure 1J) Gene symbols: PTTG1, PTTG2, Peptide: ILSTLDVEL (SEQ ID NO.: 30); Samples from left to right: 29 cancer tissues (1 bone marrow cancer, 2 colon cancers, 1 gallbladder cancer, 3 head and neck cancers, 1 kidney cancer, 5 lung cancers, 7 lymph node cancers, 1 ovarian cancer, 5 skin cancers, 2 urinary bladder cancers, 1 uterus cancer). Figure 1K) Gene symbol: DCAKD, Peptide: VILDIPLLFET (SEQ ID NO.: 36); Samples from left to right: 2 cell lines, 20 cancer tissues (1 brain cancer, 1 breast cancer, 1 colorectal cancer, 1 head and neck cancer, 1 leukocytic leukemia cancer, 1 liver cancer, 3 lung cancers, 4 lymph node cancers, 1 myeloid cell cancer, 1 ovarian cancer, 4 skin cancers, 1 uterus cancer). Figure 1L) Gene symbol: KDM2B, Peptide: ALLEGVKNV (SEQ ID NO.: 43); Samples from left to right: 13 cancer tissues (1 breast cancer, 1 leukocytic leukemia cancer, 1 lung cancer, 6 lymph node cancers, 3 ovarian cancers, 1 rectum cancer). Figure 1M)

Gene symbol: ACHE, Peptide: SLDLRPLEV (SEQ ID NO.: 74); Samples from left to right: 1 cell line, 2 normal tissues (1 lymph node, 1 spleen), 24 cancer tissues (3 brain cancers, 1 colon cancer, 1 gallbladder cancer, 1 kidney cancer, 1 lung cancer, 12 lymph node cancers, 1 ovarian cancer, 1 skin cancer, 2 stomach cancers, 1 testis cancer). Figure 1N) Gene symbol: CYTB, Peptide: FLYSETWNI (SEQ ID NO.: 254); Samples from left to right: 7 cell lines, 15 cancer tissues (1 colon cancer, 2 head and neck cancers, 3 leukocytic leukemia cancers, 1 liver cancer, 6 lymph node cancers, 1 myeloid cell cancer, 1 skin cancer). Figure 1O) Gene symbol: ACN9, Peptide: FLQEWVYA (SEQ ID NO.: 257); Samples from left to right: 2 cell lines, 11 cancer tissues (2 leukocytic leukemia cancers, 1 liver cancer, 4 lymph node cancers, 1 myeloid cells cancer, 2 skin cancers, 1 urinary bladder cancer). Figure 1P) Gene symbol: SMC2, Peptide: TVLDGLEFKV (SEQ ID NO.: 259); Samples from left to right: 1 primary culture, 14 cancer tissues (1 head and neck cancer, 3 leukocytic leukemia cancers, 3 lung cancers, 3 lymph node cancers, 1 myeloid cell cancer, 1 ovarian cancer, 2 skin cancers).

Figures 2A to C show exemplary expression profiles of source genes of the present invention that are highly over-expressed or exclusively expressed in NHL in a panel of normal tissues (white bars) and 10 NHL samples (black bars). Tissues from left to right: 6 arteries, 2 blood cell samples, 2 brains, 1 heart, 2 livers, 3 lungs, 2 veins, 1 adipose tissue, 1 adrenal gland, 5 bone marrows, 1 cartilage, 1 colon, 1 esophagus, 2 eyes, 2 gallbladders, 1 kidney, 6 lymph nodes, 4 pancreases, 2 peripheral nerves, 2 pituitary glands, 1 rectum, 2 salivary glands, 2 skeletal muscles, 1 skin, 1 small intestine, 1 spleen, 1 stomach, 1 thyroid gland, 7 tracheas, 1 urinary bladder, 1 breast, 5 ovaries, 5 placentas, 1 prostate, 1 testis, 1 thymus, 1 uterus, 10 NHL samples. Figure 2A) Gene symbol: MIXL1. Figure 2B) Gene symbol: CCR4. Figure 2C) Gene symbol: HIST1H1B.

Figure 3 shows exemplary immunogenicity data: flow cytometry results after peptide-specific multimer staining.

Figures 4A to C show exemplary results of peptide-specific *in vitro* CD8⁺ T cell responses of a healthy HLA-A*02⁺ donor. CD8⁺ T cells were primed using artificial APCs coated with anti-CD28 mAb and HLA-A*02 in complex with Seq ID No 253

peptide (A, left panel), Seq ID No 258 peptide (B, left panel) and Seq ID No 260 peptide (C, left panel), respectively. After three cycles of stimulation, the detection of peptide-reactive cells was performed by 2D multimer staining with A*02/Seq ID No 253 (A), A*02/Seq ID No 258 (B) or A*02/Seq ID No 260 (C). Right panels (A,B and C) show control staining of cells stimulated with irrelevant A*02/peptide complexes. Viable singlet cells were gated for CD8+ lymphocytes. Boolean gates helped excluding false-positive events detected with multimers specific for different peptides. Frequencies of specific multimer+ cells among CD8+ lymphocytes are indicated.

EXAMPLES

EXAMPLE 1

Identification and quantitation of tumor associated peptides presented on the cell surface

Tissue samples

Patients' tumor tissues were obtained from: Asterand (Detroit, MI, USA & Royston, Herts, UK); ProteoGenex Inc. (Culver City, CA, USA).

Normal tissues were obtained from Asterand (Detroit, MI, USA & Royston, Herts, UK); Bio-Options Inc. (Brea, CA, USA); BioServe (Beltsville, MD, USA); Capital BioScience Inc. (Rockville, MD, USA); Geneticist Inc. (Glendale, CA, USA); Kyoto Prefectural University of Medicine (KPUM) (Kyoto, Japan); ProteoGenex Inc. (Culver City, CA, USA); Tissue Solutions Ltd (Glasgow, UK); University Hospital Geneva (Geneva, Switzerland); University Hospital Heidelberg (Heidelberg, Germany); University Hospital Munich (Munich, Germany); and University Hospital Tübingen (Tübingen, Germany).

Written informed consents of all patients had been given before surgery or autopsy. Tissues were shock-frozen immediately after excision and stored until isolation of TUMAPs at -70°C or below.

Isolation of HLA peptides from tissue samples

HLA peptide pools from shock-frozen tissue samples were obtained by immune precipitation from solid tissues according to a slightly modified protocol (Falk et al., 1991; Seeger et al., 1999) using the HLA-A*02-specific antibody BB7.2, the HLA-A, -

B, C-specific antibody W6/32, CNBr-activated sepharose, acid treatment, and ultrafiltration.

Mass spectrometry analyses

The HLA peptide pools as obtained were separated according to their hydrophobicity by reversed-phase chromatography (nanoAcquity UPLC system, Waters) and the eluting peptides were analyzed in LTQ-velos and fusion hybrid mass spectrometers (ThermoElectron) equipped with an ESI source. Peptide pools were loaded directly onto the analytical fused-silica micro-capillary column (75 μm i.d. x 250 mm) packed with 1.7 μm C18 reversed-phase material (Waters) applying a flow rate of 400 nL per minute. Subsequently, the peptides were separated using a two-step 180 minute-binary gradient from 10% to 33% B at a flow rate of 300 nL per minute. The gradient was composed of Solvent A (0.1% formic acid in water) and solvent B (0.1% formic acid in acetonitrile). A gold coated glass capillary (PicoTip, New Objective) was used for introduction into the nanoESI source. The LTQ-Orbitrap mass spectrometers were operated in the data-dependent mode using a TOP5 strategy. In brief, a scan cycle was initiated with a full scan of high mass accuracy in the Orbitrap ($R = 30\,000$), which was followed by MS/MS scans also in the Orbitrap ($R = 7500$) on the 5 most abundant precursor ions with dynamic exclusion of previously selected ions. Tandem mass spectra were interpreted by SEQUEST and additional manual control. The identified peptide sequence was assured by comparison of the generated natural peptide fragmentation pattern with the fragmentation pattern of a synthetic sequence-identical reference peptide.

Label-free relative LC-MS quantitation was performed by ion counting i.e. by extraction and analysis of LC-MS features (Mueller et al., 2007). The method assumes that the peptide's LC-MS signal area correlates with its abundance in the sample. Extracted features were further processed by charge state deconvolution and retention time alignment (Mueller et al., 2008; Sturm et al., 2008). Finally, all LC-MS features were cross-referenced with the sequence identification results to combine quantitative data of different samples and tissues to peptide presentation profiles. The quantitative data were normalized in a two-tier fashion according to central tendency to account for variation within technical and biological replicates. Thus, each identified peptide can be associated with quantitative data allowing

relative quantification between samples and tissues. In addition, all quantitative data acquired for peptide candidates was inspected manually to assure data consistency and to verify the accuracy of the automated analysis. For each peptide a presentation profile was calculated showing the mean sample presentation as well as replicate variations. The profiles juxtapose NHL samples to a baseline of normal tissue samples. Presentation profiles of exemplary over-presented peptides are shown in Figure 1. Presentation scores for exemplary peptides are shown in Table 8.

Table 8: Presentation scores. The table lists peptides that are very highly over-presented on tumors compared to a panel of normal tissues (+++), highly over-presented on tumors compared to a panel of normal tissues (++) or over-presented on tumors compared to a panel of normal tissues (+). The panel of normal tissues considered relevant for comparison with tumors consisted of: adipose tissue, adrenal gland, artery, vein, bone marrow, brain, central and peripheral nerve, colon, rectum, small intestine incl. duodenum, esophagus, eye, gallbladder, heart, kidney, liver, lung, lymph node, mononuclear white blood cells, pancreas, parathyroid gland, peritoneum, pituitary, pleura, salivary gland, skeletal muscle, skin, spleen, stomach, thymus, thyroid gland, trachea, ureter, urinary bladder.

SEQ ID No.	Sequence	Peptide Presentation
1	LLSGQLPTI	+++
2	LLSEETPSA	+++
3	LTIDTQYYL	+++
5	VLQGLTFTL	+++
6	TLITLPLLFL	+++
7	NLLGMIFSM	+++
8	ALYAVIEKA	+++
9	FLLDLDPLL	+++
10	FLLVGTQIDL	+++
11	GLDTVVAL	+++
12	GLLLLVP	+++
13	HLVPASWKL	+++
15	IIIEDLLEA	+++
16	TLIAAILYL	+++
17	VIIPLLSSV	+++
18	KLTDQPPLV	+++
19	VLEAILPLV	+++
20	YLIAGGDRWL	+++
21	ALFKEAYSL	+++

SEQ ID No.	Sequence	Peptide Presentation
22	ALKKHLTSV	+++
23	ALVEDIINL	+++
24	AVLGFSFRL	+++
25	FLDTSNQHLL	+++
26	FLGSFIDHV	+++
27	FLNQESFDL	+++
28	FLSNANPSL	+++
29	ILSDVTQGL	+++
30	ILSTLDVEL	+++
31	KLYDEESLL	+++
32	VLNEDELPSV	+++
33	LLANIVPIAMLV	+++
34	LLWEDGVTEA	+++
35	SLSSERYYL	+++
36	VILDIPLLFET	+++
37	VLGNALEGV	+++
38	YLTAEILELAGN	+++
40	FLNSVIVDL	+
41	ILASIFETV	+++
43	ALLEGVKNV	+
44	FIIEEQSFL	+++
45	FILDDSALYL	+
46	FLVEEIFQT	++
47	GLLPKLTAL	+
49	TILGDPQILL	+++
50	LLLDGLIYL	+
53	FLREYFERL	+++
54	DIFDAMFSV	+++
55	ILVEVDLVQA	++
56	GLQDLLFSL	++
57	LQIGDFVSV	+
60	SLLIDVITV	+++
61	SLLNKDLSL	+
62	ALAPYLDLL	+++
64	FLVEVSNDV	++
65	NLTDVSPDL	+++
67	LLATVNVAL	+++
69	TLLAFPLLL	+
71	VLLDYVGNVQL	+++
72	TLQEETAVYL	+++
74	SLDLRPLEV	+
75	AALKYIPSV	+++
76	ALADLVPVDVVV	+++
77	ALLDVSNNYGI	+++

SEQ ID No.	Sequence	Peptide Presentation
78	AMEEAVAQV	+++
79	AMKEEKEQL	+++
80	YLFDEIDQA	+++
81	FIFSYITAV	+++
82	FLIDGSSSV	+++
83	FLMDDNMSNTL	+++
84	FLQELQLEHA	+++
85	GLAPAEVVVATVA	+++
86	GLATIRAYL	+++
87	GLFARIIMI	+++
88	GLFDNRSGLPEA	+++
89	GLTALHVAV	+++
90	HLDEVFLEL	+++
91	HLSSTTAQV	+++
92	KLLFEIASA	+++
93	KLLGSLQLL	+++
94	LLAGQATTAYF	+++
95	LLFDLIPVVS	+++
96	LLNENESLFL	+++
97	LLNFSPGNL	+++
98	MLQDGIARL	+++
99	QLYDGATALFL	+++
100	RLIRTIAAI	+++
101	SLDQSTWNV	+++
102	SLFAAISGMIL	+++
103	SLQDHLEKV	+++
104	VLLGLPLL	+++
105	VLTPVILQV	+++
106	VLYELLQYI	+++
107	VQAVSIPEV	+++
108	YLAPENGYLM	+++
109	YLFQFSAAL	+++
110	YQYPFVLGL	+++
111	YLLDTLLSL	+++
112	FLAILPEEV	+++
113	FVIDSFEEL	+++
114	GLSDISPST	+++
115	LLIDIIHFL	+++
116	SLLDNLLTI	+
117	VLATILAQL	+++
118	VLDGMIYAI	+++
119	ELCDIILRV	+++
120	VLLGTTWAL	+++
121	YLTGYNFTL	+++

SEQ ID No.	Sequence	Peptide Presentation
122	AISEAQESV	+
123	ALLSAFVQL	++
124	FLGVVVPTV	+++
125	FVAPPTAAV	+++
126	GLSIFIYRL	+++
128	KLFDASPTFFA	++
131	VLIEETDQL	+++
132	VLQDQVDEL	+++
133	ALEELTGFREL	+++
134	ALGRLGILSV	+++
135	ALTGLQFQL	+++
136	FIFGIVHLL	+++
137	FIQQERFFL	+++
138	NLINNIFEL	+
139	FLASPLVAI	+++
140	FLFEDFVEV	+++
141	FLGELTLQL	+++
142	FLYEDSKSVRL	+++
143	TLHAVDVTL	+++
144	GLITQVDKL	+++
145	GLLHEVVSL	+++
146	GLLQQPPAL	+++
147	GLSEYQRNFL	+++
148	ICAGHVPGV	+++
149	ILNPVTTKL	+++
150	ILSEKEYKL	+++
151	ILVKQSPML	+++
152	KIMYTLVSV	+++
153	KLLKGIYAI	+++
154	KLMNIQQQL	+++
155	KLMTSLVKV	+++
156	KMLEDDLKL	+++
157	KVLEFLAKV	+++
158	KVQDVLHQV	+++
159	LLLSDSGFYL	+++
160	LLPPPSPAA	+++
161	NLMLELETV	+++
162	RLADLKVSI	+++
163	SIFDAVLKGV	+++
164	SLFDGAVISTV	+++
165	KLLEEIEFL	++
166	SLFSEVASL	+++
167	SLFSITKSV	+++
168	SLLSPLLSV	+++

SEQ ID No.	Sequence	Peptide Presentation
169	SSLEENLLHQV	+++
170	STIELSENSL	+++
171	TLLDVISAL	+++
172	TLQDSLEFI	+++
173	VILDSVASV	+++
174	VLVEITDVDFAA	+++
175	VMESILLRL	+++
176	YLHIYESQL	+++
177	YLYEAEETTL	+++
178	YVLQGEFFL	+++
179	FVDTNLYFL	+++
180	GILQLVESV	++
182	LLPPPPVA	+
183	VLFETVLTl	+
185	FIAQLNNVEL	+
186	FLDVSRDFV	+
188	GLEDEMYEV	++
189	SLSHLVPAL	+
190	GLIELVDQL	++
191	GLSDISAQV	+++
194	SLAPFDREPFTL	+++
195	ALIPDLNQI	+++
196	TLALAMIYL	++
200	YLLDFEDRL	+
201	YLNISQVNV	++
203	ILDTIFHKV	+++
204	RLCDIVNV	+++
207	GLVGLLEQA	++
211	FIDDLFAFV	+++
212	FLIGQGAHV	+
213	YINEDEYEV	+
214	FLFDGMSL	++
215	QLFEEEEIEL	+
216	KVVSNLPAI	+++
217	AQFGAVLEV	+
218	ALDQFLEGI	+
219	ALLELENSV	+++
220	FLAEAPTAL	++
221	FLAPDNSLLLA	+++
222	FLIETGTLL	+
224	FLSPLLPLL	+
225	GTYQDVGSLNIGDV	+++
226	GVIDPVPEV	+
227	IIAEGIPEA	+

SEQ ID No.	Sequence	Peptide Presentation
231	IVMGAIPSV	+
232	KVMEGTVAA	++
233	MLEVHIPSV	++
236	SLFDGFFLTA	+
237	YLDRLIPQA	++
239	VLIDDTVLL	++
242	GILDFZVFL	+
243	GLPDLDIYL	+++
244	ILEPFLPAV	+
246	KLPVPLESV	+
249	VLLESLVEI	+++
252	YLGDLIMAL	+
253	YSDDDVPSV	+++
254	FLYSETWNI	+++
255	GMWNP NAPVFL	+++
256	ALQETPPQV	+++
257	FLQEWEVYA	+++
258	RIYPFLLMV	+++
259	TVLDGLEFKV	+++
260	RLDEAFDFV	++
263	GLMDNEIKV	+++
264	ILTGTPPGV	+++
265	ILWHFVASL	+++
266	QLTEMLPSI	+++
267	SLLETGSDLLL	+++
268	VLFPLPTPL	+++
269	VLQNVAFSV	+++
270	VVVDSDSLAFV	+++
271	YLLDQPVLEQRL	+++
272	KLDHTLSQI	+++
273	AILLPQPPK	+++
274	KLLNLISKL	+++
275	KLMDLED CAL	+++
276	NMISYVVHL	+++
277	FLIDLNSTHGTFL	+
279	NLAGENILNPL	++
280	SLLNHLPYL	+++
285	SITAVTPLL	+
287	ILMGHSLYM	++
289	SLLAANNLL	+++
290	IASPVIAAV	+++
291	KIIDTAGLSEA	+++
292	KLINSQISL	++
294	KLYGPEGLELV	+

SEQ ID No.	Sequence	Peptide Presentation
296	FILEPLYKI	++
298	ALTDVILCV	+
299	RLLEEEGVSL	+
302	SLAELDEKISA	+
303	FVWEASHYL	++
305	AMLAQQMQL	+
307	FLLPVAVKL	++
308	SLLDQIPEM	+

EXAMPLE 2

Expression profiling of genes encoding the peptides of the invention

Over-presentation or specific presentation of a peptide on tumor cells compared to normal cells is sufficient for its usefulness in immunotherapy, and some peptides are tumor-specific despite their source protein occurring also in normal tissues. Still, mRNA expression profiling adds an additional level of safety in selection of peptide targets for immunotherapies. Especially for therapeutic options with high safety risks, such as affinity-matured TCRs, the ideal target peptide will be derived from a protein that is unique to the tumor and not found on normal tissues.

RNA sources and preparation

Surgically removed tissue specimens were provided as indicated above (see Example 1) after written informed consent had been obtained from each patient. Tumor tissue specimens were snap-frozen immediately after surgery and later homogenized with mortar and pestle under liquid nitrogen. Total RNA was prepared from these samples using TRI Reagent (Ambion, Darmstadt, Germany) followed by a cleanup with RNeasy (QIAGEN, Hilden, Germany); both methods were performed according to the manufacturer's protocol.

Total RNA from healthy human tissues for RNASeq experiments was obtained from: Asterand (Detroit, MI, USA & Royston, Herts, UK); BioCat GmbH (Heidelberg, Germany); BioServe (Beltsville, MD, USA); Capital BioScience Inc. (Rockville, MD, USA); Geneticist Inc. (Glendale, CA, USA); Istituto Nazionale Tumori "Pascale" (Naples, Italy); ProteoGenex Inc. (Culver City, CA, USA); University Hospital Heidelberg (Heidelberg, Germany). Total RNA from tumor tissues for RNASeq

experiments was obtained from: Asterand (Detroit, MI, USA & Royston, Herts, UK); ProteoGenex Inc. (Culver City, CA, USA).

Quality and quantity of all RNA samples were assessed on an Agilent 2100 Bioanalyzer (Agilent, Waldbronn, Germany) using the RNA 6000 Pico LabChip Kit (Agilent).

RNAseq experiments

Gene expression analysis of - tumor and normal tissue RNA samples was performed by next generation sequencing (RNAseq) by CeGaT (Tübingen, Germany). Briefly, sequencing libraries are prepared using the Illumina HiSeq v4 reagent kit according to the provider's protocol (Illumina Inc., San Diego, CA, USA), which includes RNA fragmentation, cDNA conversion and addition of sequencing adaptors. Libraries derived from multiple samples are mixed equimolar and sequenced on the Illumina HiSeq 2500 sequencer according to the manufacturer's instructions, generating 50 bp single end reads. Processed reads are mapped to the human genome (GRCh38) using the STAR software. Expression data are provided on transcript level as RPKM (Reads Per Kilobase per Million mapped reads, generated by the software Cufflinks) and on exon level (total reads, generated by the software Bedtools), based on annotations of the ensembl sequence database (Ensembl77). Exon reads are normalized for exon length and alignment size to obtain RPKM values. Exemplary expression profiles of source genes of the present invention that are highly over-expressed or exclusively expressed in NHL are shown in Figure 2. Expression scores for further exemplary genes are shown in Table 9.

Table 9: Expression scores. The table lists peptides from genes that are very highly over-expressed in tumors compared to a panel of normal tissues (+++), highly over-expressed in tumors compared to a panel of normal tissues (++) or over-expressed in tumors compared to a panel of normal tissues (+). The baseline for this score was calculated from measurements of the following relevant normal tissues: adipose tissue, adrenal gland, artery, blood cells, bone marrow, brain, cartilage, colon, esophagus, eye, gallbladder, heart, kidney, liver, lung, lymph node, pancreas, pituitary, rectum, salivary gland, skeletal muscle, skin, small intestine, spleen, stomach, thyroid gland, trachea, urinary bladder, and vein. In case expression data

for several samples of the same tissue type were available, the arithmetic mean of all respective samples was used for the calculation.

SEQ ID No	Sequence	Gene Expression
9	FLLDLDPLL	++
21	ALFKEAYSL	+
25	FLDTSNQHLL	++
30	ILSTLDVEL	++
38	YLTAEILELAGN	++
43	ALLEGVKNV	+
55	ILVEVDLVQA	+
56	GLQDLLFSL	+
61	SLLNKDLSL	+
91	HLSSTTAQV	++
102	SLFAAISGMIL	+++
106	VL YELLQYI	+++
112	FLAILPEEV	++
113	FVIDSFEEL	+++
116	SLLDNLLTI	+
133	ALEELTGFREL	+
135	ALTGLQFQL	+++
142	FLYEDSKSVRL	+++
143	TLHAVDVTL	+++
146	GLLQQPPAL	+
148	ICAGHVPGV	+++
155	KLMTSLVKV	+++
157	KVLEFLAKV	+++
158	KVQDVLHQV	+++
159	LLLSDSGFYL	++
160	LLPPPSPAA	+++
161	NLMLELETV	+++
162	RLADLKVSI	+++
167	SLFSITKSV	+++
170	STIELSENSL	++
174	VLVEITDVDFAA	+
175	VMESILLRL	+++
178	YVLQGEFFL	+++
183	VL FETVLT I	+
192	GMAAEVPKV	+
199	SLNSTTWKV	+++
202	ALAAGGYDV	+++
222	FLIETGTLL	++
225	GTYQDVGSLNIGDV	++
229	ILSPWGAEV	++
238	YQYGAVVTL	++

SEQ ID No	Sequence	Gene Expression
256	ALQETPPQV	+
260	RLDEAFDFV	++
268	VLFPPLPTPL	+
276	NMISYVVHL	+++
294	KLYGPEGLELV	+++
297	ILQNGLETL	+++
298	ALTDVILCV	+++

EXAMPLE 3

In vitro immunogenicity for MHC class I presented peptides

In order to obtain information regarding the immunogenicity of the TUMAPs of the present invention, the inventors performed investigations using an *in vitro* T-cell priming assay based on repeated stimulations of CD8⁺ T cells with artificial antigen presenting cells (aAPCs) loaded with peptide/MHC complexes and anti-CD28 antibody. This way the inventors could show immunogenicity for HLA-A*0201 restricted TUMAPs of the invention, demonstrating that these peptides are T-cell epitopes against which CD8⁺ precursor T cells exist in humans (Table 10A).

In vitro priming of CD8⁺ T cells

In order to perform *in vitro* stimulations by artificial antigen presenting cells loaded with peptide-MHC complex (pMHC) and anti-CD28 antibody, the inventors first isolated CD8⁺ T cells from fresh HLA-A*02 leukapheresis products via positive selection using CD8 microbeads (Miltenyi Biotec, Bergisch-Gladbach, Germany) of healthy donors obtained from the University clinics Mannheim, Germany, after informed consent.

PBMCs and isolated CD8⁺ lymphocytes were incubated in T-cell medium (TCM) until use consisting of RPMI-Glutamax (Invitrogen, Karlsruhe, Germany) supplemented with 10% heat inactivated human AB serum (PAN-Biotech, Aidenbach, Germany), 100 U/ml Penicillin/100 µg/ml Streptomycin (Cambrex, Cologne, Germany), 1 mM sodium pyruvate (CC Pro, Oberdorla, Germany), 20 µg/ml Gentamycin (Cambrex). 2.5 ng/ml IL-7 (PromoCell, Heidelberg, Germany) and 10 U/ml IL-2 (Novartis Pharma, Nürnberg, Germany) were also added to the TCM at this step.

Generation of pMHC/anti-CD28 coated beads, T-cell stimulations and readout was performed in a highly defined *in vitro* system using four different pMHC molecules per stimulation condition and 8 different pMHC molecules per readout condition.

The purified co-stimulatory mouse IgG2a anti human CD28 Ab 9.3 (Jung et al., 1987) was chemically biotinylated using Sulfo-N-hydroxysuccinimidobiotin as recommended by the manufacturer (Perbio, Bonn, Germany). Beads used were 5.6 μm diameter streptavidin coated polystyrene particles (Bangs Laboratories, Illinois, USA).

pMHC used for positive and negative control stimulations were A*0201/MLA-001 (peptide ELAGIGILTV (SEQ ID NO. 329) from modified Melan-A/MART-1) and A*0201/DDX5-001 (YLLPAIVHI from DDX5, SEQ ID NO. 330), respectively.

800.000 beads/200 μl were coated in 96-well plates in the presence of 4 x 12.5 ng different biotin-pMHC, washed and 600 ng biotin anti-CD28 were added subsequently in a volume of 200 μl . Stimulations were initiated in 96-well plates by co-incubating 1×10^6 CD8⁺ T cells with 2×10^5 washed coated beads in 200 μl TCM supplemented with 5 ng/ml IL-12 (PromoCell) for 3 days at 37°C. Half of the medium was then exchanged by fresh TCM supplemented with 80 U/ml IL-2 and incubating was continued for 4 days at 37°C. This stimulation cycle was performed for a total of three times. For the pMHC multimer readout using 8 different pMHC molecules per condition, a two-dimensional combinatorial coding approach was used as previously described (Andersen et al., 2012) with minor modifications encompassing coupling to 5 different fluorochromes. Finally, multimeric analyses were performed by staining the cells with Live/dead near IR dye (Invitrogen, Karlsruhe, Germany), CD8-FITC antibody clone SK1 (BD, Heidelberg, Germany) and fluorescent pMHC multimers. For analysis, a BD LSRII SORP cytometer equipped with appropriate lasers and filters was used. Peptide specific cells were calculated as percentage of total CD8⁺ cells. Evaluation of multimeric analysis was done using the FlowJo software (Tree Star, Oregon, USA). *In vitro* priming of specific multimer⁺ CD8⁺ lymphocytes was detected by comparing to negative control stimulations. Immunogenicity for a given antigen was detected if at least one evaluable *in vitro* stimulated well of one healthy donor was found to contain a specific CD8⁺ T-cell line after *in vitro* stimulation (i.e. this well contained at least 1% of specific multimer⁺ among CD8⁺ T-cells and the

percentage of specific multimer+ cells was at least 10x the median of the negative control stimulations).

In vitro immunogenicity for NHL peptides

For tested HLA class I peptides, *in vitro* immunogenicity could be demonstrated by generation of peptide specific T-cell lines. Exemplary flow cytometry results after TUMAP-specific multimer staining for 2 peptides of the invention are shown in Figure 3 together with corresponding negative controls. Results for ten peptides from the invention are summarized in Tables 10A and 10B.

Table 10A: in vitro immunogenicity of HLA class I peptides of the invention

Exemplary results of *in vitro* immunogenicity experiments conducted by the applicant for the peptides of the invention. <20 % = +; 20 % - 49 % = ++; 50 % - 69 % = +++; >= 70 % = ++++

Seq ID	Sequence	wells
319	SLYKGLLSV	++
320	LLWGNLPEI	++
321	KLLAVIHEL	++
322	TLTNIIHNL	++
323	ILVDWLQV	++
324	LLYDAVHIV	++
325	FLFVDPELV	+++
326	KLTDVGIATL	++++
327	MLFGHPLLVS	++
328	ILFPDIIARA	++++

Table 10B In vitro immunogenicity of HLA class I peptides of the invention

Exemplary results of *in vitro* immunogenicity experiments conducted by the applicant for HLA-A*02 restricted peptides of the invention. Results of *in vitro* immunogenicity experiments are indicated. Percentage of positive wells and donors (among evaluable) are summarized as indicated <20 % = +; 20 % - 49 % = ++; 50 % - 69 % = +++; >= 70 % = ++++

SEQ ID NO:	Sequence	Wells positive [%]
1	LLSGQLPTI	"+++"
2	LLSEETPSA	"+"
3	LTIDTQYYL	"+"
5	VLQGLTFTL	"+++"

SEQ ID NO:	Sequence	Wells positive [%]
7	NLLGMIFSM	"++++"
8	ALYAVIEKA	"+"
9	FLLDLDPLL	"++"
12	GLLLLVPLL	"++++"
13	HLVPASWKL	"++++"
17	VIIPLLSSV	"++"
19	VLEAILPLV	"+"
21	ALFKEAYSL	"+"
22	ALKKHLTSV	"++++"
24	AVLGFSFRL	"++++"
25	FLDTSNQHLL	"+"
26	FLGSFIDHV	"+"
27	FLNQESFDL	"+"
28	FLSNANPSL	"++++"
29	ILSDVTQGL	"+"
30	ILSTLDVEL	"++"
33	LLANIVPIAMLV	"+"
35	SLSSERYYL	"++++"
36	VILDIPLL FET	"++"
37	VLGNALEGV	"+"
40	FLNSVIVDL	"++++"
41	ILASIFETV	"++++"
42	YLQDLVERA	"++++"
43	ALLEGVKNV	"++"
44	FIIEEQSFL	"+"
46	FLVEEIFQT	"+"
47	GLLPKLTAL	"++"
51	SLLGNSPVL	"++++"
52	VLLEDVDAAFL	"+"
53	FLREYFERL	"++++"
57	LQIGDFVSV	"++++"
59	RLHREVAQV	"+"
60	SLLIDVITV	"++++"
61	SLLNKDLSL	"+"
62	ALAPYLDLL	"++"
66	KLAPIPVEL	"++"
67	LLATVNVAL	"+"
68	QIAAFLFTV	"++++"
73	YLGEEYPEV	"+"
74	SLDLRPLEV	"++"
253	YSDDDVPSV	"++++"
254	FLYSETWNI	"+"
256	ALQETPPQV	"+"
258	RIYPFLLMV	"++++"

SEQ ID NO:	Sequence	Wells positive [%]
260	RLDEAFDFV	"++++"
261	FLPETRIMTSV	"+"
262	LMGPVVHEV	"++"

EXAMPLE 4

Synthesis of peptides

All peptides were synthesized using standard and well-established solid phase peptide synthesis using the Fmoc-strategy. Identity and purity of each individual peptide have been determined by mass spectrometry and analytical RP-HPLC. The peptides were obtained as white to off-white lyophilizates (trifluoro acetate salt) in purities of >50%. All TUMAPs are preferably administered as trifluoro-acetate salts or acetate salts, other salt-forms are also possible.

EXAMPLE 5

MHC Binding Assays

Candidate peptides for T cell based therapies according to the present invention were further tested for their MHC binding capacity (affinity). The individual peptide-MHC complexes were produced by UV-ligand exchange, where a UV-sensitive peptide is cleaved upon UV-irradiation, and exchanged with the peptide of interest as analyzed. Only peptide candidates that can effectively bind and stabilize the peptide-receptive MHC molecules prevent dissociation of the MHC complexes. To determine the yield of the exchange reaction, an ELISA was performed based on the detection of the light chain ($\beta 2m$) of stabilized MHC complexes. The assay was performed as generally described in Rodenko et al. (Rodenko et al., 2006).

96 well MAXISorp plates (NUNC) were coated over night with 2ug/ml streptavidin in PBS at room temperature, washed 4x and blocked for 1h at 37°C in 2% BSA containing blocking buffer. Refolded HLA-A*02:01/MLA-001 monomers served as standards, covering the range of 15-500 ng/ml. Peptide-MHC monomers of the UV-exchange reaction were diluted 100 fold in blocking buffer. Samples were incubated for 1h at 37°C, washed four times, incubated with 2ug/ml HRP conjugated anti- $\beta 2m$ for 1h at 37°C, washed again and detected with TMB solution that is stopped with NH_2SO_4 . Absorption was measured at 450nm. Candidate peptides that show a high exchange yield (preferably higher than 50%, most preferred higher than 75 %) are

generally preferred for a generation and production of antibodies or fragments thereof, and/or T cell receptors or fragments thereof, as they show sufficient avidity to the MHC molecules and prevent dissociation of the MHC complexes.

Table 11: MHC class I binding scores.

Binding of HLA-class I restricted peptides to HLA-A*02:01 was ranged by peptide exchange yield: $\geq 10\%$ = +; $\geq 20\%$ = ++; ≥ 50 = +++; $\geq 75\%$ = ++++

SEQ ID NO:	Sequence	Peptide exchange
1	LLSGQLPTI	"+++"
2	LLSEETPSA	"+++"
3	LTIDTQYYL	"+++"
4	TLLGFFLAKV	"++"
5	VLQGLTFTL	"+++"
6	TLITLPLLFL	"+++"
7	NLLGMIFSM	"++++"
8	ALYAVIEKA	"+++"
9	FLLDLDP LL	"+++"
10	FLLVGTQIDL	"+++"
11	GLDTV VALL	"+++"
12	GLLLL VPLL	"+++"
13	HLVPASWKL	"+++"
14	LLSDPTPGA	"++"
15	IIIEDLLEA	"++++"
16	TLIAAILYL	"++"
17	VIIPLLSSV	"+++"
18	KLTDQPPLV	"+++"
19	VLEAILPLV	"++++"
21	ALFKEAYSL	"+++"
22	ALKKHLTSV	"+++"
23	ALVEDIINL	"++++"
24	AVLGFSFRL	"+++"
25	FLDTSNQHLL	"+++"
26	FLGSFIDHV	"+++"
27	FLNQESFDL	"+++"
28	FLSNANPSL	"+++"
29	ILSDVTQGL	"+++"
30	ILSTLDVEL	"+++"
31	KLYDEESLL	"++++"
32	VLNEDELPSV	"+++"
33	LLANIVPIAMLV	"++++"
34	LLWEDGVTEA	"+++"
35	SLSSERYYL	"+++"
36	VILDIPLLFET	"+++"
37	VLGNALEGV	"+++"
38	YLTAEILELAGN	"++"
39	QLLPQGIVPAL	"+++"

40	FLNSVIVDL	"++++"
41	ILASIFETV	"++++"
42	YLQDLVERA	"++++"
43	ALLEGVKNV	"+++"
44	FIIEEQSFL	"+++"
45	FILDDSALYL	"+++"
46	FLVEEIFQT	"+++"
47	GLLPKLTAL	"+++"
48	KILDEDLYI	"+++"
49	TILGDPQILL	"++++"
50	LLLDGLIYL	"+++"
51	SLLGNSPVL	"++++"
52	VLLEDVDAAFL	"++++"
53	FLREYFERL	"++++"
54	DIFDAMFSV	"+"
55	ILVEVDLVQA	"++++"
56	GLQDLLFSL	"+++"
57	LQIGDFVSV	"++++"
58	QLAPFLPQL	"+++"
59	RLHREVAQV	"+++"
60	SLLIDVITV	"+++"
61	SLLNKDLSL	"++++"
62	ALAPYLDLL	"++++"
63	ALIEEAYGL	"+++"
64	FLVEVSNDV	"++++"
65	NLTDVSPDL	"+++"
66	KLAPIPVEL	"++++"
67	LLATVNVAL	"++++"
68	QIAAFLFTV	"++++"
69	TLLAFPLLL	"++++"
70	VLIEILQKA	"++++"
71	VLLDYVGNVQL	"++++"
72	TLQEETAVYL	"++"
73	YLGEEYPEV	"+++"
74	SLDLRPLEV	"++++"
75	AALKYIPSV	"+++"
76	ALADLVPVDVVV	"++++"
77	ALLDVSNNYGI	"++++"
78	AMEEAVAQV	"+++"
79	AMKEEKEQL	"++"
80	YLFDEIDQA	"+++"
81	FIFSYITAV	"++"
82	FLIDGSSSV	"+++"
83	FLMDDNMSNTL	"+++"
84	FLQELQLEHA	"+++"
85	GLAPAEVVVATVA	"+++"
86	GLATIRAYL	"+++"
87	GLFARIIMI	"++"
88	GLFDNRSGLPEA	"+++"

89	GLTALHVAV	"+++"
90	HLDEVFLEL	"+++"
91	HLSSTTAQV	"++"
92	KLLFEIASA	"+++"
93	KLLGSLQLL	"++++"
94	LLAGQATTAYF	"+++"
95	LLFDLIPVVS	"+++"
96	LLNENESLFL	"+++"
97	LLNFSPGNL	"+"
98	MLQDGIARL	"+++"
99	QLYDGATALFL	"++"
100	RLIRTIAAI	"+++"
101	SLDQSTWNV	"++++"
102	SLFAAISGMIL	"+++"
103	SLQDHLEKV	"+++"
104	VLLGLPLL	"+++"
105	VLTPVILQV	"+++"
106	VLYELLOWYI	"++++"
107	VQAVSIPEV	"+++"
108	YLAPENGYLM	"+++"
109	YLFQFSAAL	"+++"
110	YQYPFVLGL	"++++"
111	YLLDTLLSL	"+++"
112	FLAILPEEV	"+++"
113	FVIDSFEEL	"+++"
114	GLSDISPST	"++"
115	LLIDIIHFL	"++++"
116	SLLDNLLTI	"+++"
117	VLATILAQL	"++++"
118	VLDGMIYAI	"+++"
119	ELCDIILRV	"+++"
120	VLLGTTWAL	"+++"
121	YLTGYNFTL	"+++"
122	AISEAQESV	"++"
123	ALLSAFVQL	"+++"
124	FLGVVVPTV	"+++"
125	FVAPPTAAV	"+++"
127	HLMEENMIVYV	"+++"
128	KLFDASPTFFA	"+++"
129	SLFEASQQL	"+++"
130	VIFSYYVLGV	"+++"
131	VLIEETDQL	"++"
132	VLQDQVDEL	"++"
133	ALEELTGFREL	"++"
134	ALGRLGILSV	"+++"
135	ALTGLQFQL	"+++"
136	FIFGIVHLL	"+++"
137	FIQQERFFL	"+++"
138	NLINNIFEL	"++++"

139	FLASPLVAI	"++++"
140	FLFEDFVEV	"+++"
141	FLGELTLQL	"+++"
142	FLYEDSKSVRL	"+++"
143	TLHAVDVTL	"+++"
144	GLITQVDKL	"+++"
145	GLLHEVVSL	"+++"
146	GLLQQPPAL	"+++"
147	GLSEYQRNFL	"+++"
148	ICAGHVPGV	"+++"
149	ILNPVTTKL	"+++"
150	ILSEKEYKL	"+++"
151	ILVKQSPML	"+++"
152	KIMYTLVSV	"++"
153	KLLKGIYAI	"+++"
154	KLMNIQQQL	"+++"
155	KLMTSLVKV	"+++"
156	KMLEDDLKL	"+++"
157	KVLEFLAKV	"+++"
158	KVQDVLHQV	"+++"
159	LLSDDSGFYL	"+++"
160	LLPPPSPAA	"+++"
161	NLMLELETV	"+++"
162	RLADLKVSI	"++++"
163	SIFDAVLKGV	"++++"
164	SLFDGAVISTV	"+++"
165	KLLEEIEFL	"+++"
167	SLFSITKSV	"+++"
168	SLLSPLLSV	"+++"
169	SSLEENLLHQV	"+++"
171	TLLDVISAL	"++++"
172	TLQDSLEFI	"++++"
173	VILDSVASV	"++++"
174	VLVEITDVDFAA	"++++"
175	VMESILLRL	"+++"
176	YLHIYESQL	"+++"
177	YLYEAAEEATTL	"+++"
178	YVLQGEFFL	"+++"
179	FVDTNLYFL	"+++"
180	GILQLVESV	"+++"
181	LLFDQNDKV	"+++"
182	LLPPPPPVA	"++++"
183	VLFETVLTl	"+++"
184	AVLGTSWQL	"+++"
185	FIAQLNNVEL	"+"
186	FLDVSRDFV	"+++"
187	FLNSFVFKM	"++"
188	GLEDEMYEV	"++"
189	SLSHLVPAL	"+++"

190	GLIELVDQL	"+++"
191	GLSDISAQV	"+++"
192	GMAAEVPKV	"++"
193	SLADSMPSL	"++"
194	SLAPFDREPFTL	"++"
195	ALIPDLNQI	"+++"
197	YLLTDNVVKL	"++"
198	GLLSAVSSV	"+++"
199	SLNSTTWKV	"+++"
200	YLLDFEDRL	"++++"
201	YLNISQVNV	"+++"
202	ALAAGGYDV	"++"
203	ILDTIFHKV	"+++"
204	RLCDIVNVV	"++"
205	TLFYESPHL	"+++"
206	SAVSGQWEV	"++"
207	GLVGLLEQA	"++++"
208	FLAVSLPLL	"+++"
209	FLLDTISGL	"+++"
210	FLAEQFEFL	"+++"
211	FIDDLFAFV	"+++"
212	FLIGQGAHV	"+++"
213	YINEDEYEV	"++"
214	FLFDGSM SL	"+++"
215	QLFEEEEIEL	"++"
216	KVVS NLPAI	"++"
217	AQFGAVLEV	"+++"
218	ALDQFLEGI	"+++"
219	ALLELENSV	"++"
220	FLAEAPTAL	"++"
221	FLAPDNSLLLA	"++++"
222	FLIETGTLL	"+++"
223	FLQDIPDGLFL	"++"
224	FLSPLLPLL	"++"
226	GVIDPVPEV	"++"
227	IIAEGIPEA	"++"
228	IIAEYLSYV	"++"
229	ILSPWGAEV	"++++"
230	IMDDDSYGV	"++"
231	IVMGAIPSV	"+++"
232	KVMEGTVAA	"++"
233	MLEVHIPSV	"+++"
234	NLQRTVVTV	"++"
235	SLDVYELFL	"+++"
236	SLFDGFFLTA	"++++"
237	YLDRLIPQA	"+++"
238	YQYGAVVTL	"+++"
239	VLIDDTVLL	"+++"
240	ALVPTPALFYL	"+++"

241	FIPDFIPAV	"++"
242	GILDFZVFL	"++++"
243	GLPDLDIYL	"++++"
244	ILEPFLPAV	"+++"
245	KLIQLPVVYV	"+++"
246	KLPVPLESV	"+++"
247	KVLEMETTV	"+++"
248	NLLEQFILL	"+++"
249	VLLESLVEI	"++++"
250	VLTNVGAAL	"+++"
251	VLVELFTYI	"+++"
252	YLGDLIMAL	"+++"
253	YSDDDVPSV	"++++"
254	FLYSETWNI	"++++"
255	GMWNP NAPVFL	"++++"
256	ALQETPPQV	"+++"
257	FLQEW EVYA	"++++"
258	RIYPFLLMV	"+++"
259	TVLDGLEFKV	"++++"
260	RLDEAFDFV	"++++"
261	FLPETRIMTSV	"++++"
262	LMGPVVHEV	"++++"
263	GLMDNEIKV	"+++"
264	ILTGTPPGV	"+++"
265	ILWHFVASL	"++++"
266	QLTEMLPSI	"++++"
267	SLLETGSDLLL	"+++"
268	VLFPLPTPL	"++++"
269	VLQNVAFSV	"++++"
270	VVVDSDSLAFV	"++++"
271	YLLDQPVLEQRL	"++++"
272	KLDHTLSQI	"++++"
273	AILLPQPPK	"++"
274	KLLNLISKL	"++++"
275	KLMDLEDCAL	"++++"
276	NMISYVVHL	"++"
277	FLIDLNSTHGTF	"+++"
278	FLLFINHRL	"+++"
279	NLAGENILNPL	"+++"
280	SLLNHLPYL	"++++"
281	TLQTVPLTTV	"++++"
282	YLLEQGAQV	"++++"
283	ALMPVTPQA	"+++"
284	KLQEQIHRV	"+++"
285	SITAVTPLL	"+++"
286	HLTEDTPKV	"+++"
287	ILMGHSLYM	"++++"
288	RLAPEIVSA	"+++"
289	SLLAANNLL	"++++"

290	IASPVIAAV	"+++"
291	KIIDTAGLSEA	"+++"
292	KLINSQISL	"+++"
293	GLAMVEAISYV	"++++"
294	KLYGPEGLELV	"++++"
295	SLAAVSQQL	"+++"
296	FILEPLYKI	"++++"
297	ILQNGLETL	"+++"
298	ALTDVILCV	"++++"
299	RLLEEEGVSL	"+++"
300	IVLERNPEL	"+++"
301	LQFDGIHVV	"+++"
302	SLAELDEKISA	"+++"
303	FVWEASHYL	"++++"
304	ALIRLDDLFL	"+++"
305	AMLAQQMQL	"+++"
306	AQVALVNEV	"+++"
307	FLLPVAVKL	"+++"
308	SLLDQIPEM	"+++"
309	SLSFVSPSL	"+++"
310	VMAEAPPGV	"+++"
311	YLHRQVAAV	"+++"
314	LIDDKGTIKL	"++"

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CLAIMS

1. A peptide comprising an amino acid sequence selected from the group consisting of SEQ ID No. 1 to SEQ ID No. 311, and variant sequences thereof which are at least 88% homologous to SEQ ID No. 1 to SEQ ID No. 311, and wherein said variant binds to molecule(s) of the major histocompatibility complex (MHC) and/or induces T cells cross-reacting with said variant peptide; and a pharmaceutical acceptable salt thereof, wherein said peptide is not a full-length polypeptide.
2. The peptide according to claim 1, wherein said peptide has the ability to bind to an MHC class-I or –II molecule, and wherein said peptide, when bound to said MHC, is capable of being recognized by CD4 and/or CD8 T cells.
3. The peptide or variant thereof according to claim 1 or 2, wherein the amino acid sequence thereof comprises a continuous stretch of amino acids according to any one of SEQ ID No. 1 to SEQ ID No. 311.
4. The peptide or variant thereof according to any of claims 1 to 3, wherein said peptide or variant thereof has an overall length of from 8 to 100, preferably from 8 to 30, and more preferred from 8 to 16 amino acids, and most preferred wherein the peptide consists or consists essentially of an amino acid sequence according to any of SEQ ID No. 1 to SEQ ID No. 311.
5. The peptide or variant thereof according to any of Claims 1 to 4, wherein said peptide is modified and/or includes non-peptide bonds.
6. The peptide or variant thereof according to any of Claims 1 to 5, wherein said peptide is part of a fusion protein, in particular comprising N-terminal amino acids of the HLA-DR antigen-associated invariant chain (Ii).
7. A nucleic acid, encoding a peptide or variant thereof according to any one of claims 1 to 6, optionally linked to a heterologous promoter sequence.

8. An expression vector capable of expressing the nucleic acid according to claim 7.
9. A recombinant host cell comprising the peptide according to claim 1 to 6, the nucleic acid according to claim 7 or the expression vector according to claim 8, wherein said host cell preferably is an antigen presenting cell such as a dendritic cell.
10. The peptide or variant thereof according to any one of claims 1 to 6, the nucleic acid according to claim 7, the expression vector according to claim 8, or the host cell according to claim 9 for use in medicine.
11. A method for producing the peptide or variant thereof according to any one of claims 1 to 6, the method comprising culturing the host cell according to claim 9 that presents the peptide according to claim 1 to 6, or expresses the nucleic acid according to claim 7 or bears the expression vector according to claim 8, and isolating the peptide or variant thereof from the host cell or its culture medium.
12. An *in vitro* method for producing activated T lymphocytes, the method comprising contacting *in vitro* T cells with antigen loaded human class I or II MHC molecules expressed on the surface of a suitable antigen-presenting cell or an artificial construct mimicking an antigen-presenting cell for a period of time sufficient to activate said T cells in an antigen specific manner, wherein said antigen is a peptide according to any one of claims 1 to 4.
13. An activated T lymphocyte, produced by the method according to claim 12, that selectively recognizes a cell which presents a polypeptide comprising an amino acid sequence given in any one of claims 1 to 4.
14. A method for killing target cells in a patient which target cells present a polypeptide comprising an amino acid sequence given in any one of claims 1 to

- 4, the method comprising administering to the patient an effective number of activated T cells as defined in claim 13.
15. An antibody, in particular a soluble or membrane-bound antibody, that specifically recognizes the peptide or variant thereof according to any of claims 1 to 5, preferably the peptide or variant thereof according to any of claims 1 to 5 when bound to an MHC molecule.
16. Use of a peptide according to any one of claims 1 to 6, the nucleic acid according to claim 7, the expression vector according to claim 8, the cell according to claim 9, the activated T lymphocyte according to claim 13 or the antibody according to claim 15 for use in diagnosis and/or treatment of cancer, or for use in the manufacture of a medicament against cancer.
17. The use according to claim 16, wherein said cancer is selected from the group of NHL, non-small cell lung cancer, small cell lung cancer, renal cell cancer, brain cancer, gastric cancer, colorectal cancer, hepatocellular cancer, pancreatic cancer, leukemia, breast cancer, melanoma, ovarian cancer, urinary bladder cancer, uterine cancer, gallbladder and bile duct cancer and other tumors that show an overexpression of a protein from which a peptide SEQ ID No. 1 to SEQ ID No. 311 is derived from.
18. A kit comprising:
- (a) a container comprising a pharmaceutical composition containing the peptide(s) or the variant according to any one of claims 1 to 6, the nucleic acid(s) according to claim 7, the expression vector(s) according to claim 8, the cell(s) according to claim 10, the activated T lymphocyte(s) according to claim 13 or the antibody according to claim 15, in solution or in lyophilized form;
 - (b) optionally, a second container containing a diluent or reconstituting solution for the lyophilized formulation;
 - (c) optionally, at least one more peptide selected from the group consisting of SEQ ID No. 1 to SEQ ID No. 328, and
 - (d) optionally, instructions for (i) use of the solution or (ii) reconstitution and/or use of the lyophilized formulation.

19. The kit according to claim 18, further comprising one or more of (iii) a buffer, (iv) a diluent, (v) a filter, (vi) a needle, or (v) a syringe.
20. The kit according to claim 18 or 19, wherein said peptide is selected from the group consisting of SEQ ID No. 1 to SEQ ID No. 311.
21. A method for producing a personalized anti-cancer vaccine for a compound-based and/or cellular therapy for an individual patient, said method comprising:
 - a) identifying tumor-associated peptides (TUMAPs) presented by a tumor sample from said individual patient;
 - b) comparing the peptides as identified in a) with a warehouse of peptides that have been pre-screened for immunogenicity and/or over-presentation in tumors as compared to normal tissues
 - c) selecting at least one peptide from the warehouse that matches a TUMAP identified in the patient; and
 - d) manufacturing and/or formulating the personalized vaccine or compound-based or cellular therapy based on step c).
22. The method according to claim 21, wherein said TUMAPs are identified by:
 - a1) comparing expression data from the tumor sample to expression data from a sample of normal tissue corresponding to **the** tissue type of the tumor sample to identify proteins that are over-expressed or aberrantly expressed in the tumor sample; and
 - a2) correlating the expression data with sequences of MHC ligands bound to MHC class I and/or class II molecules in the tumor sample to identify MHC ligands derived from proteins over-expressed or aberrantly expressed by the tumor.
23. The method according to claim 21 or 22, wherein the sequences of MHC ligands are identified by eluting bound peptides from MHC molecules isolated from the tumor sample, and sequencing the eluted ligands.

24. The method according to any of claims 21 to 23, wherein the normal tissue corresponding to the tissue type of the tumor sample is obtained from the same patient.
25. The method according to any of claims 21 to 24, wherein the peptides included in the warehouse are identified based on the following steps:
- aa. Performing genome-wide messenger ribonucleic acid (mRNA) expression analysis by highly parallel methods, such as microarrays or sequencing-based expression profiling, comprising identify genes that over-expressed in a malignant tissue, compared with a normal tissue or tissues;
 - ab. Selecting peptides encoded by selectively expressed or over-expressed genes as detected in step aa, and
 - ac. Determining an induction of *in vivo* T-cell responses by the peptides as selected comprising *in vitro* immunogenicity assays using human T cells from healthy donors or said patient; or
 - ba. Identifying HLA ligands from said tumor sample using mass spectrometry;
 - bb. Performing genome-wide messenger ribonucleic acid (mRNA) expression analysis by highly parallel methods, such as microarrays or sequencing-based expression profiling, comprising identify genes that over-expressed in a malignant tissue, compared with a normal tissue or tissues;
 - bc. Comparing the identified HLA ligands to said gene expression data;
 - bd. Selecting peptides encoded by selectively expressed or over-expressed genes as detected in step bc;
 - be. Re-detecting of selected TUMAPs from step bd on tumor tissue and lack of or infrequent detection on healthy tissues and confirming the relevance of over-expression at the mRNA level; and
 - bf. Determining an induction of *in vivo* T-cell responses by the peptides as selected comprising *in vitro* immunogenicity assays using human T cells from healthy donors or said patient.
26. The method according to any of claims 21 to 25, wherein the immunogenicity of the peptides included in the warehouse is determined by a method comprising *in vitro* immunogenicity assays, patient immunomonitoring for individual HLA

binding, MHC multimer staining, ELISPOT assays and/or intracellular cytokine staining.

27. The method according to any of claims 21 to 26, wherein said warehouse comprises a plurality of peptides selected from the group consisting of SEQ ID No. 1 to SEQ ID No. 328.
28. The method according to any of claims 21 to 27, further comprising identifying at least one mutation that is unique to the tumor sample relative to normal corresponding tissue from the individual patient, and selecting a peptide that correlates with the mutation for inclusion in the vaccine or for the generation of cellular therapies.
29. The method according to claim 28, wherein said at least one mutation is identified by whole genome sequencing.
30. A T-cell receptor, preferably soluble or membrane-bound, that is reactive with an HLA ligand, wherein said ligand has at least 75% identity to an amino acid sequence selected from the group consisting of SEQ ID No. 1 to SEQ ID No. 311.
31. The T-cell receptor according to claim 30, wherein said amino acid sequence is at least 88% identical to SEQ ID No. 1 to SEQ ID No. 311.
32. The T-cell receptor according to claim 30 or 31, wherein said amino acid sequence consists any of SEQ ID No. 1 to SEQ ID No. 311.
33. The T-cell receptor according to any of claims 30 to 32, wherein said T-cell receptor is provided as a soluble molecule and optionally carries a further effector function such as an immune stimulating domain or toxin.
34. A nucleic acid, encoding for a TCR according to any one of claims 30 to 33, optionally linked to a heterologous promoter sequence.

35. An expression vector capable of expressing the nucleic acid according to claim 34.
36. A host cell comprising the nucleic acid according to claim 34 or the nucleic acid encoding an antibody according to claim 15 or the expression vector according to claim 35, wherein said host cell preferably is a T cell or NK cell.
37. A method for producing the T cell receptor according to any claims 30 to 33, said method comprising culturing a host cell according to Claim 36, and isolating said T cell receptor from said host cell and/or its culture medium.
38. A pharmaceutical composition comprising at least one active ingredient selected from the group consisting of
- a) a peptide selected from the group consisting of SEQ ID No. 1 to SEQ ID No. 311;
 - b) a T-cell receptor reactive with a peptide and/or the peptide-MHC complex according to a);
 - c) a fusion protein comprising a peptide according to a), and the N-terminal amino acids 1 to 80 of the HLA-DR antigen-associated invariant chain (Ii);
 - d) a nucleic acid encoding for any of a) to c) or an expression vector comprising said nucleic acid,
 - e) a host cell comprising the expression vector of d,
 - f) an activated T-lymphocyte, obtained by a method comprising contacting in vitro T cells with a peptide according to a) expressed on the surface of a suitable antigen presenting cell for a period of time sufficient to activate said T cell in an antigen specific manner, as well as a method to transfer these activated T cells into the autologous or other patients;
 - g) an antibody, or soluble T-cell receptor, reactive to a peptide and/or the peptide – MHC complex according to a) and/or a cell presenting a peptide according to a), and potentially modified by fusion with for example immune-activating domains or toxins,
 - h) an aptamer recognizing a peptide selected from the group consisting of SEQ ID No. 1 to SEQ ID No. 311 and/or a complex of a peptide selected from

the group consisting of SEQ ID No. 1 to SEQ ID No. 311 with an MHC molecule, and

i) a conjugated or labelled peptide or scaffold according to any of a) to h) and a pharmaceutically acceptable carrier, and optionally, pharmaceutically acceptable excipients and/or stabilizers.

39. An aptamer that specifically recognizes the peptide or variant thereof according to any of claims 1 to 5, preferably the peptide or variant thereof according to any of claims 1 to 5 that is bound to an MHC molecule.

Figure 1A

Peptide: LLSGQLPTI (A*02)

Seq ID NO: 1

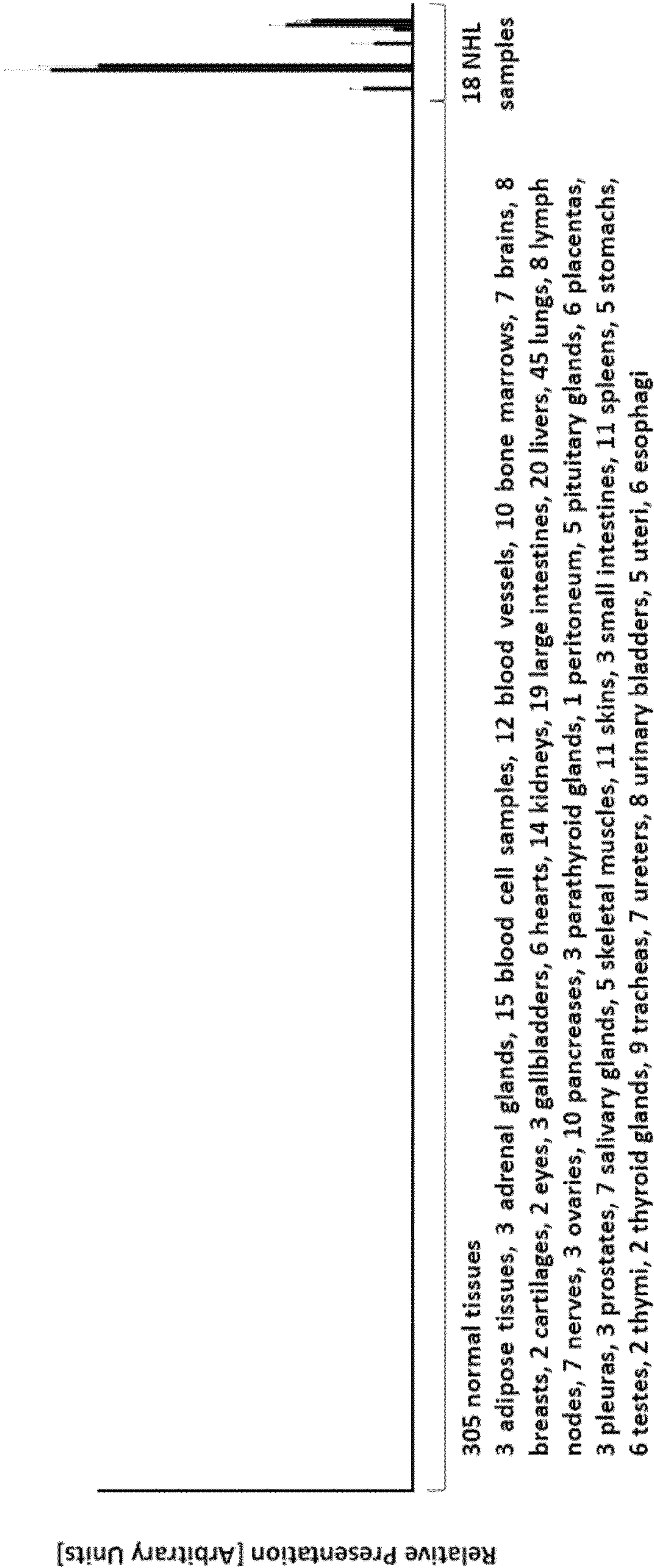


Figure 1B

Peptide: VLQGLTFTL (A*02)
Seq ID NO: 5

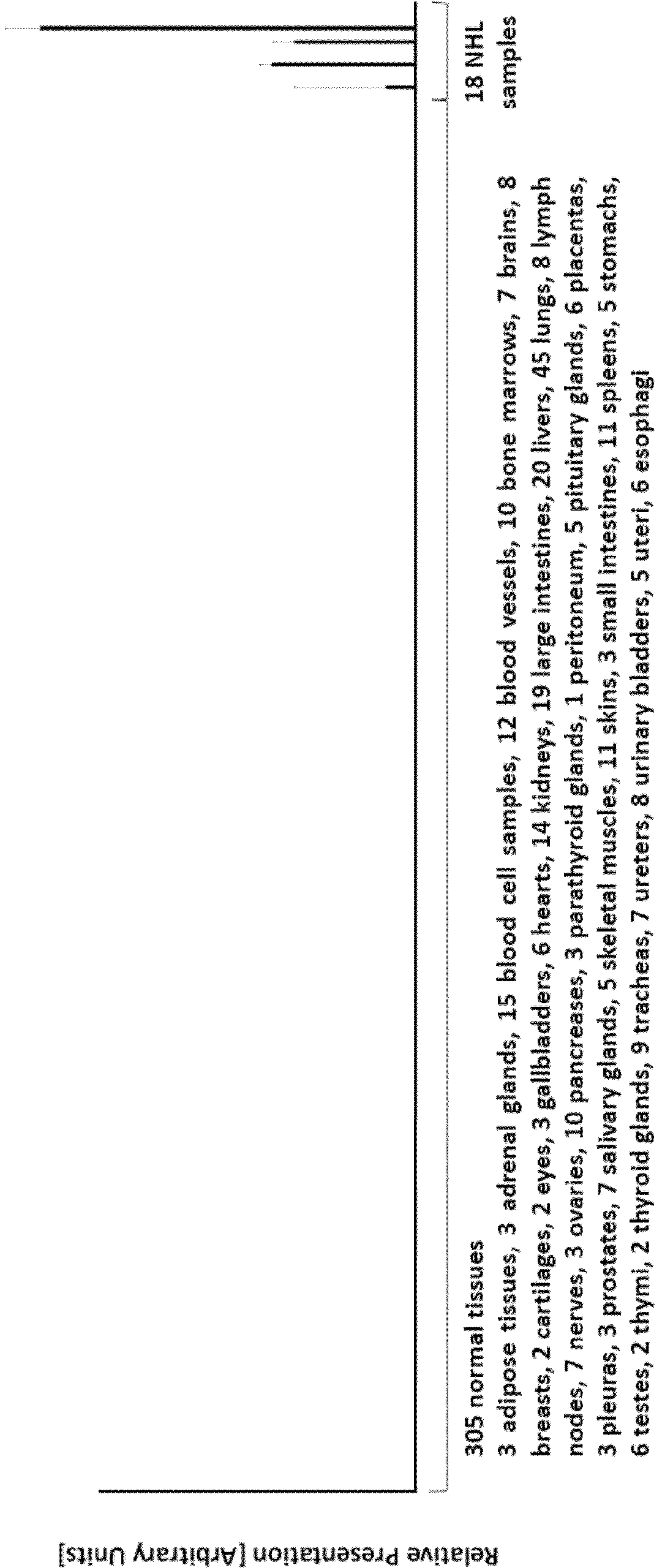


Figure 1C

Peptide: ILASIFETV (A*02)
Seq ID NO: 41

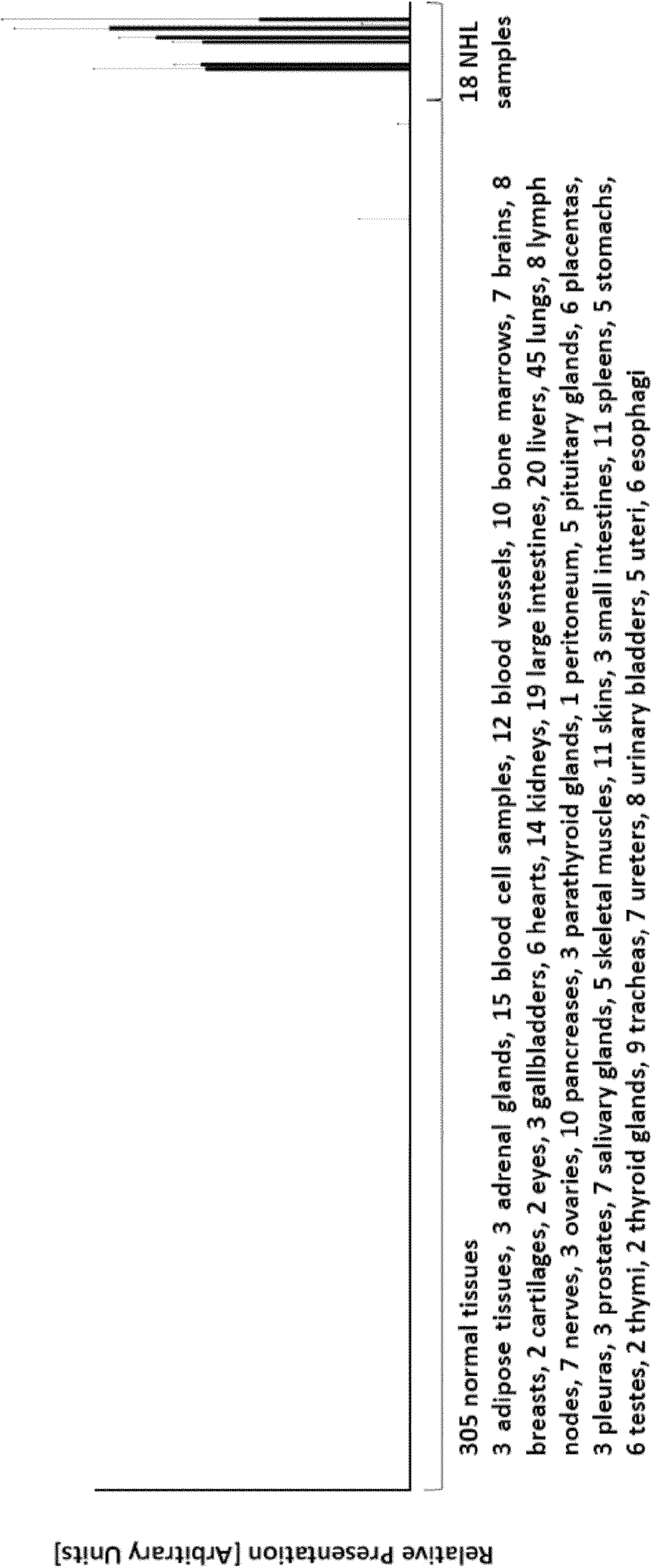


Figure 1D

Peptide: NLLEQFILL (A*02)
SEQ ID NO: 248

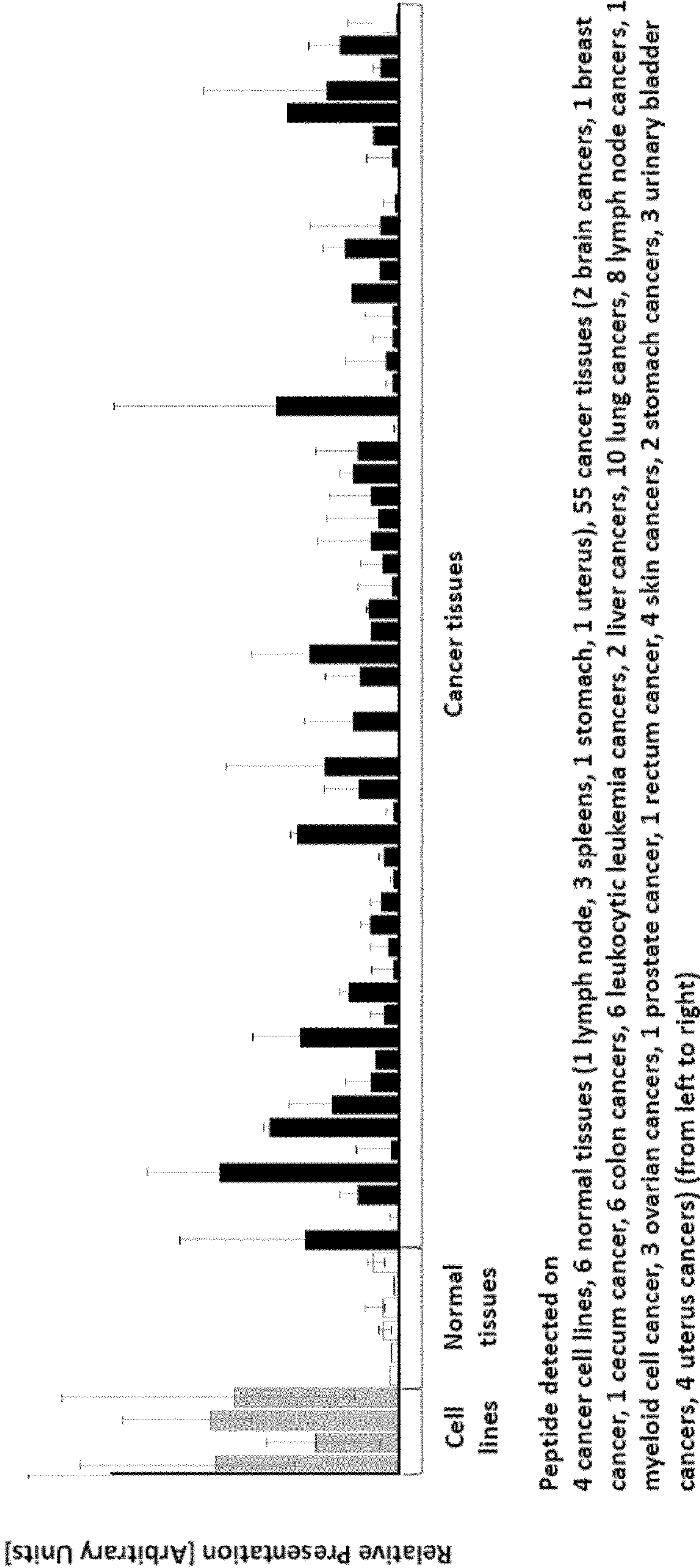
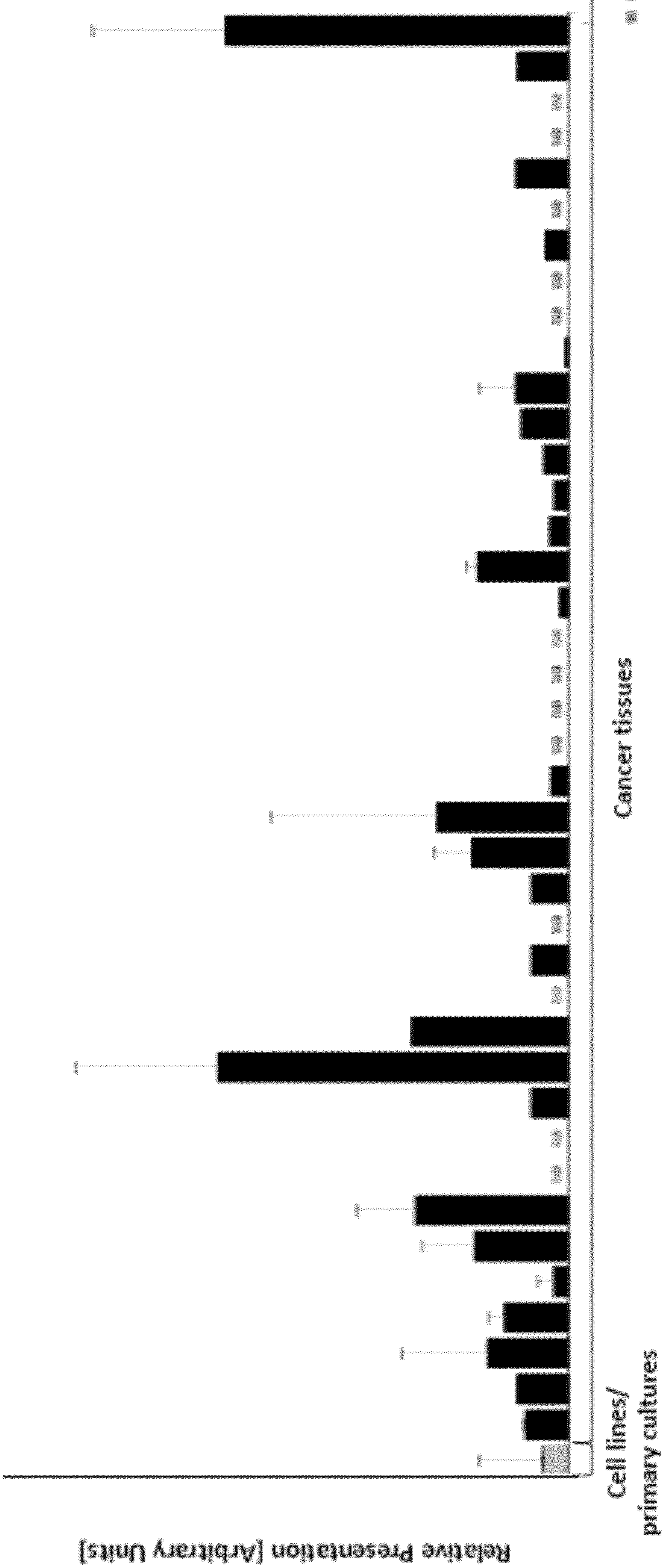
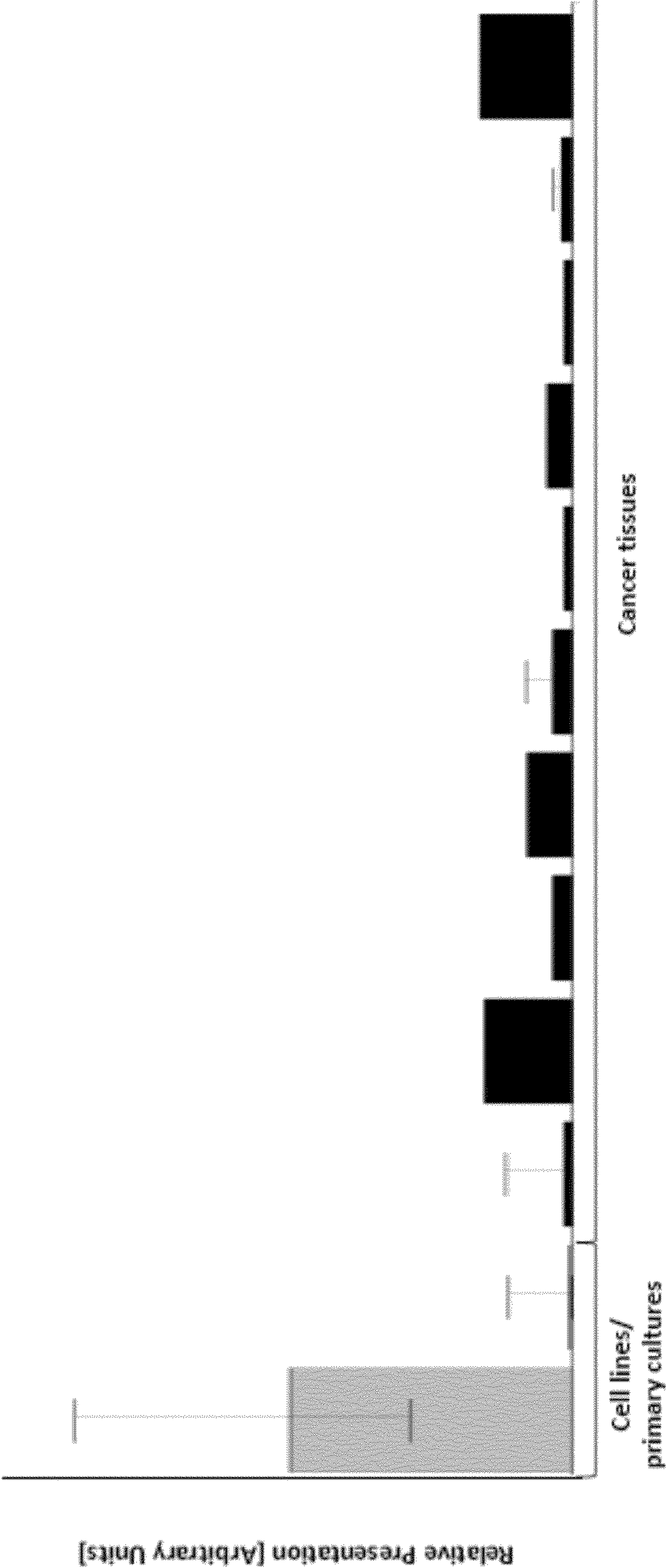


Figure 1E
Peptide: LLSEETPSA (A*02)
SEQ ID NO: 2



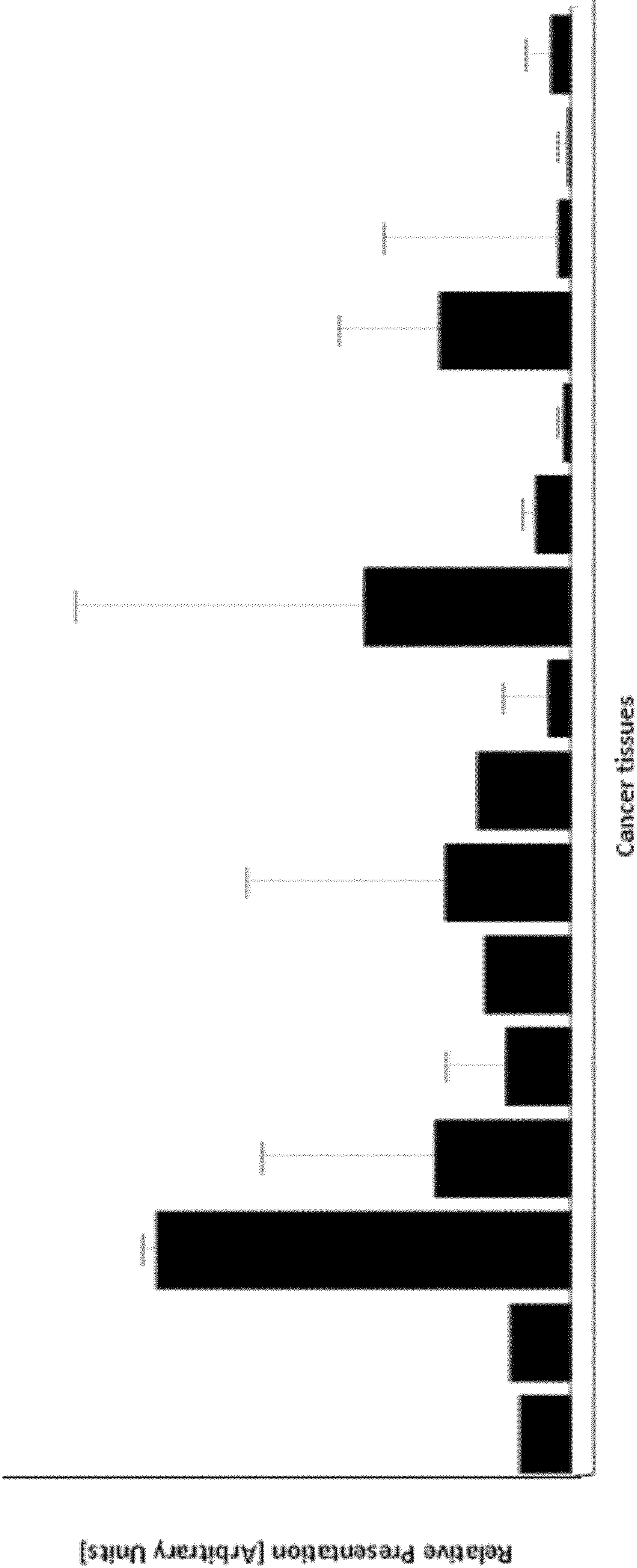
Peptide detected on
1 primary culture, 40 cancer tissues (1 bone marrow cancer, 1 brain cancer, 2 breast cancers, 8 head and neck cancers, 4 leukocytic leukemia cancers, 1 liver cancer, 7 lung cancers, 6 lymph node cancers, 2 myeloid cell cancers, 1 ovarian cancer, 3 skin cancers, 3 urinary bladder cancers, 1 uterus cancer) (from left to right)

Figure 1F
Peptide: FLLVGTQIDL (A*02)
SEQ ID NO: 10



Peptide detected on
2 cell lines, 10 cancer tissues (2 breast cancers, 1 head and neck cancer, 1 leukocytic leukemia cancer, 1 lung cancer, 4 lymph node cancers, 1 uterus cancer) (from left to right)

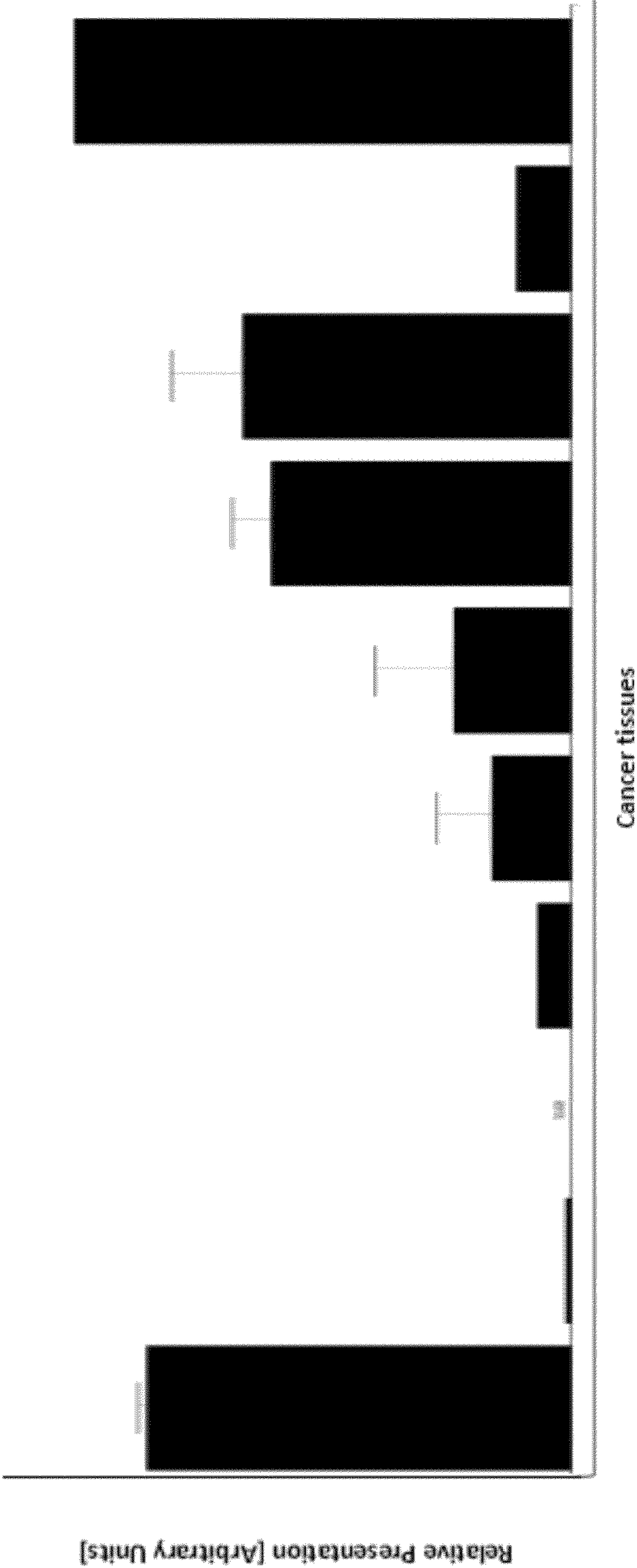
Figure 1G
Peptide: GLLLLVPLL (A*02)
SEQ ID NO: 12



Peptide detected on
16 cancer tissues (1 breast cancer, 1 colon cancer, 1 colorectal cancer, 1 esophageal cancer, 1 gallbladder cancer, 1 head and neck cancer, 2 lung cancers, 5 lymph node cancers, 2 ovarian cancers, 1 skin cancer) (from left to right)

Figure 1H

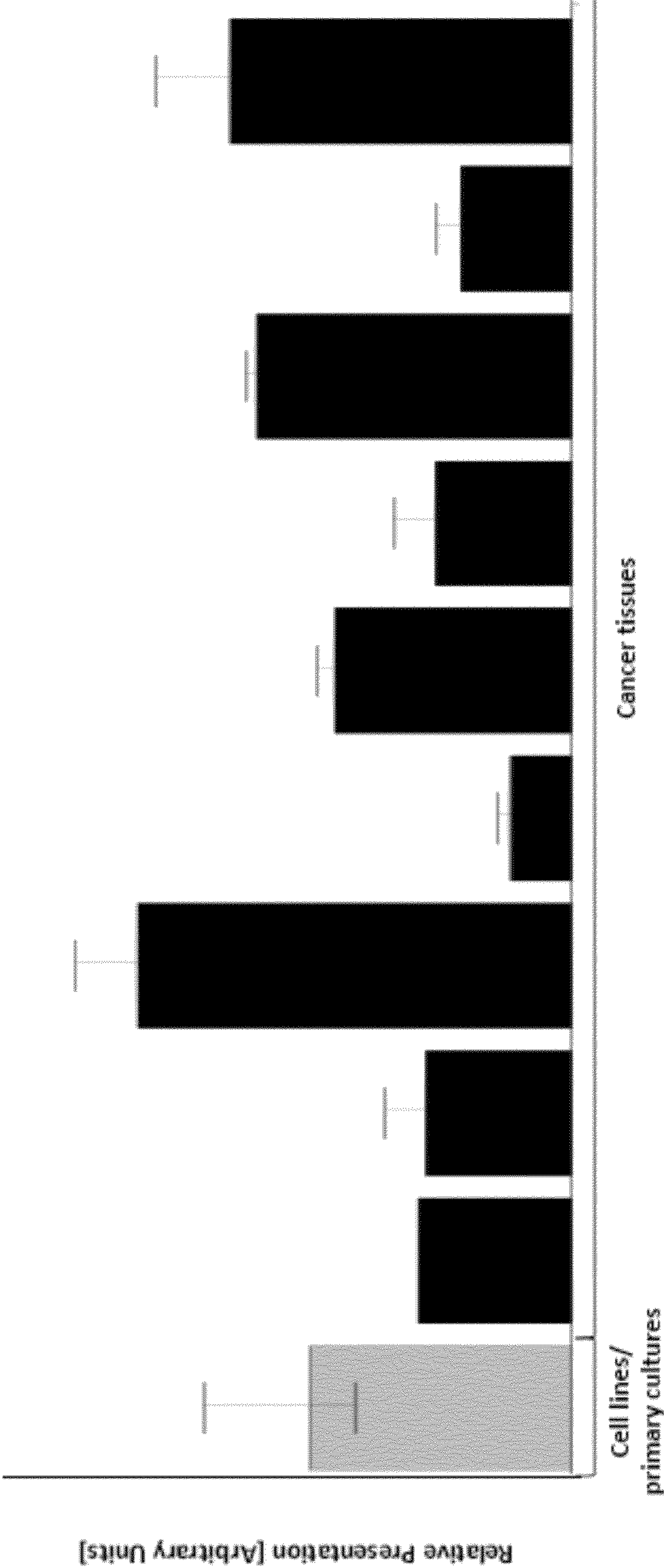
Peptide: HLVPAWKL (A*02)
SEQ ID NO: 13



Peptide detected on
10 cancer tissues (1 leukocytic leukemia cancer, 1 lung cancer, 5 lymph node cancers, 1 ovarian cancer, 1 skin cancer, 1 testis cancer) (from left to right)

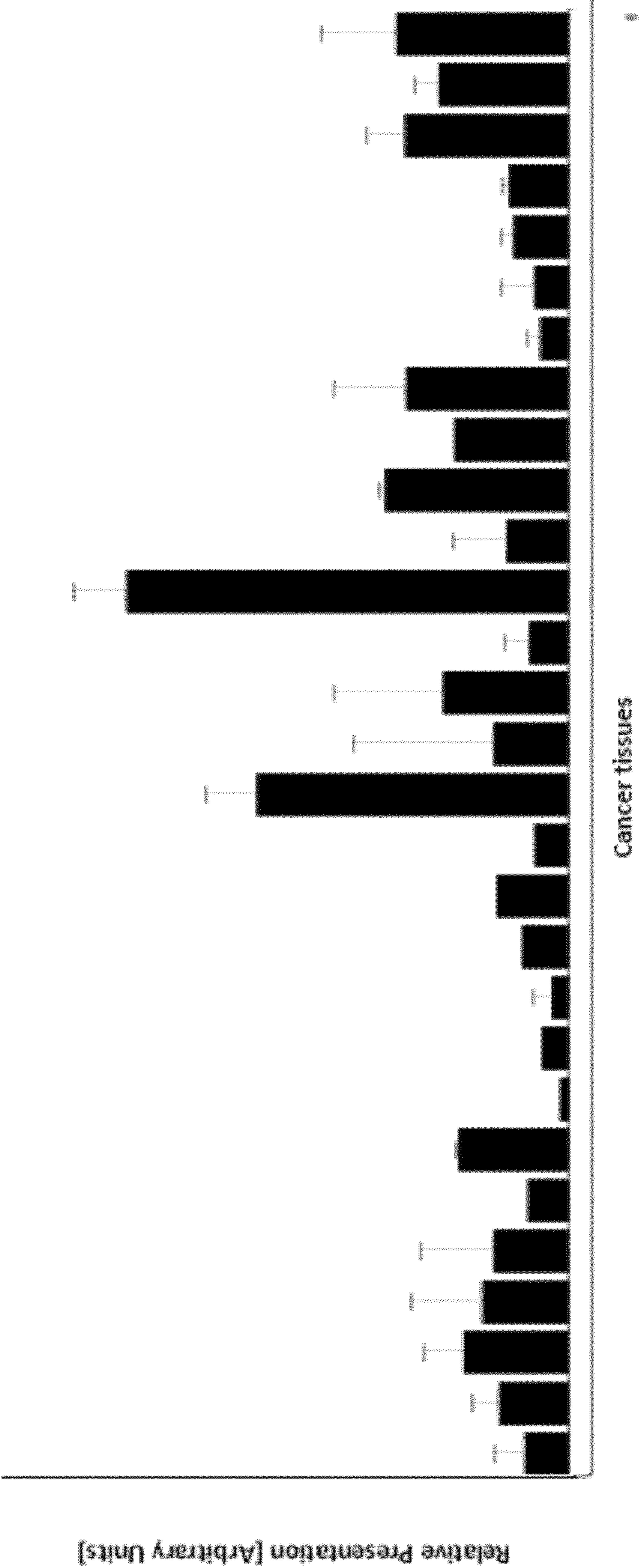
9/22

Figure 1I
Peptide: FLGSFIDHV (A*02)
SEQ ID NO: 26



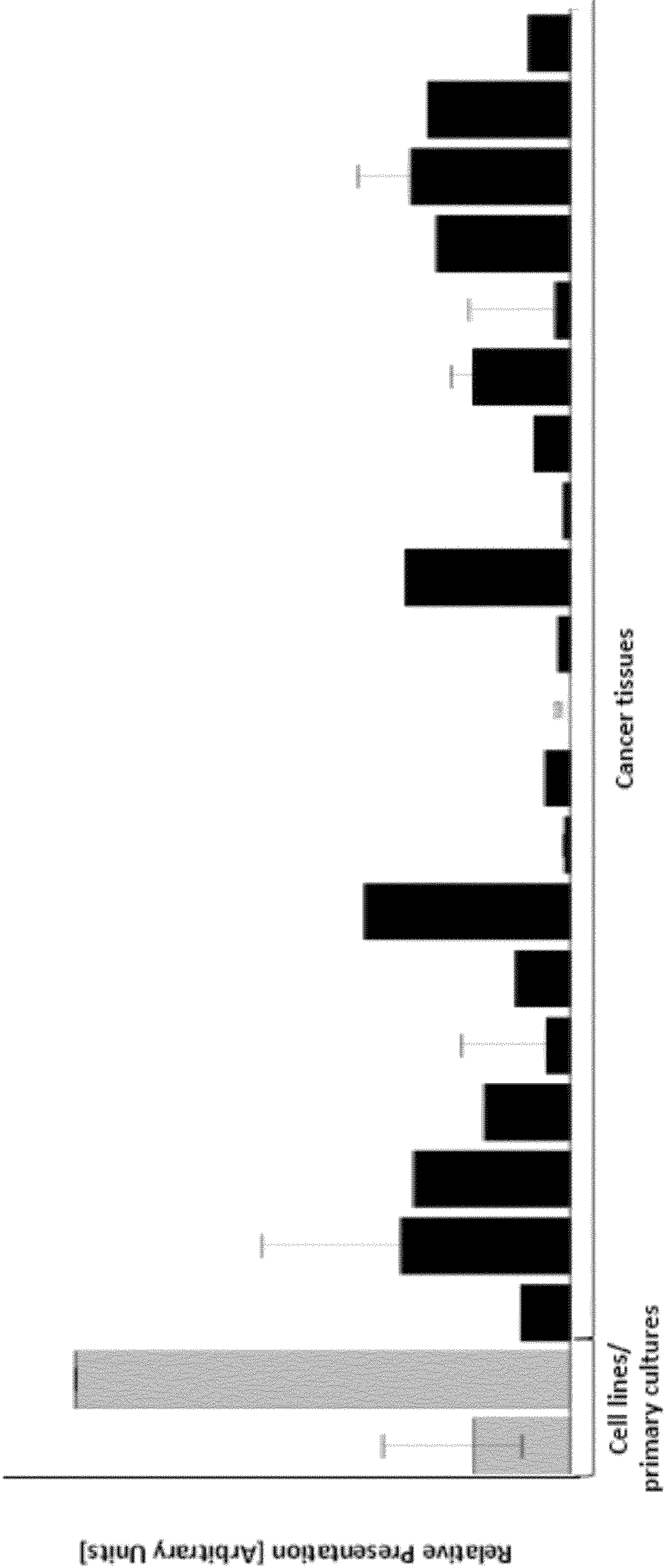
Peptide detected on
1 cell line, 9 cancer tissues (1 brain cancer, 1 lung cancer, 1 lymph node cancer, 1 myeloid cell cancer, 2 ovarian cancers, 2 skin cancers, 1 uterus cancer) (from left to right)

Figure 1J
Peptide: ILSTLDVEL (A*02)
SEQ ID NO: 30



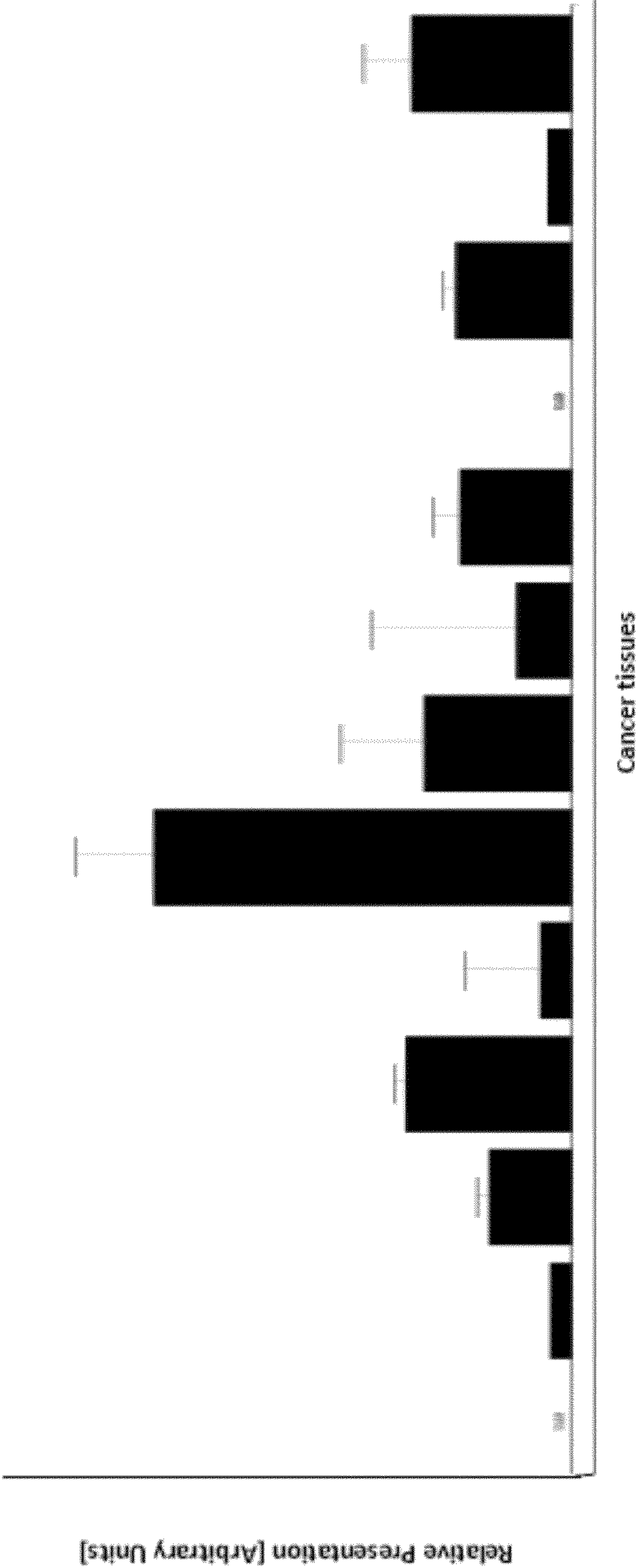
Peptide detected on
29 cancer tissues (1 bone marrow cancer, 2 colon cancers, 1 gallbladder cancer, 3 head and neck cancers, 1 kidney cancer, 5 lung cancers, 7 lymph node cancers, 1 ovarian cancer, 5 skin cancers, 2 urinary bladder cancers, 1 uterus cancer) (from left to right)

Figure 1K
Peptide: VILDIPLLLET (A*02)
SEQ ID NO: 36



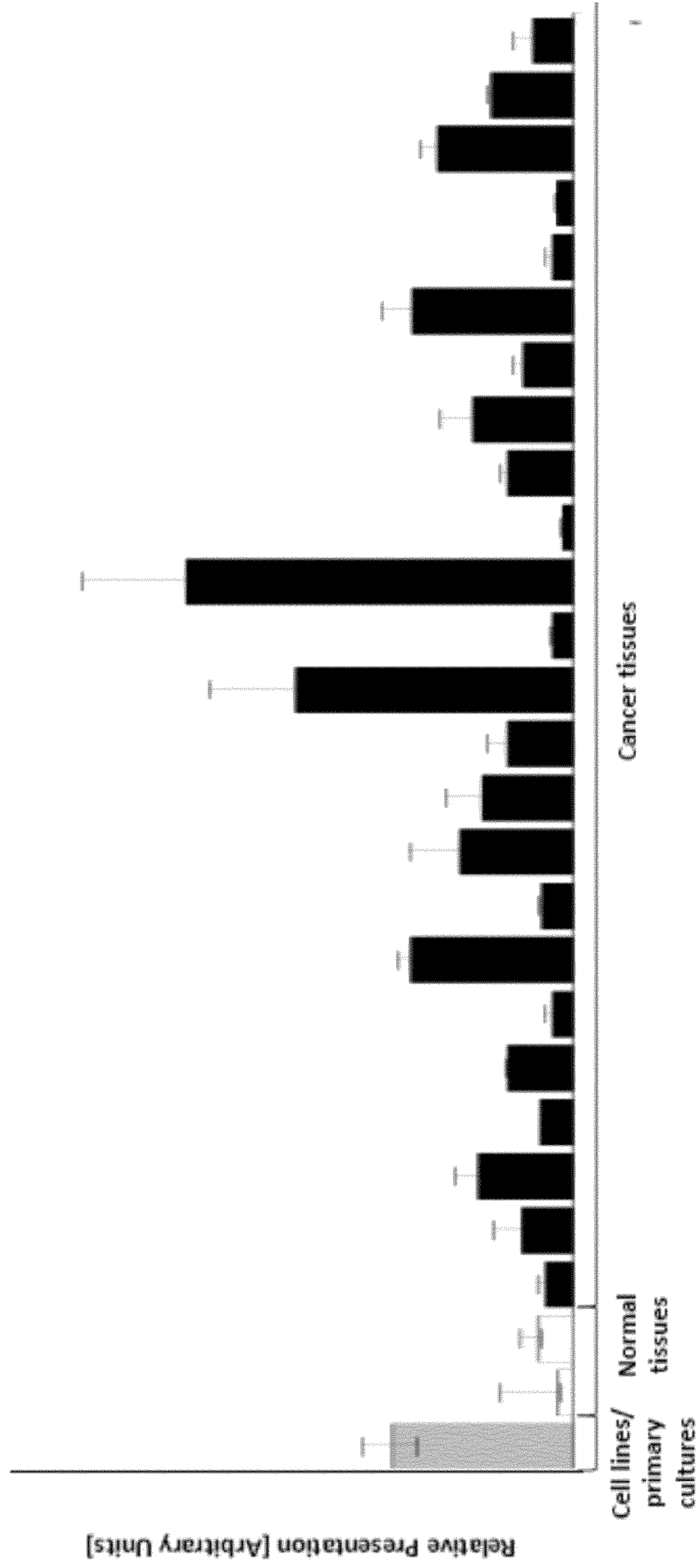
Peptide detected on
2 cell lines, 20 cancer tissues (1 brain cancer, 1 breast cancer, 1 colorectal cancer, 1 head and neck cancer, 1 leukocytic leukemia cancer, 1 liver cancer, 3 lung cancers, 4 lymph node cancers, 1 myeloid cell cancer, 1 ovarian cancer, 4 skin cancers, 1 uterus cancer) (from left to right)

Figure 1L
Peptide: ALLEGVKNV (A*02)
SEQ ID NO: 43



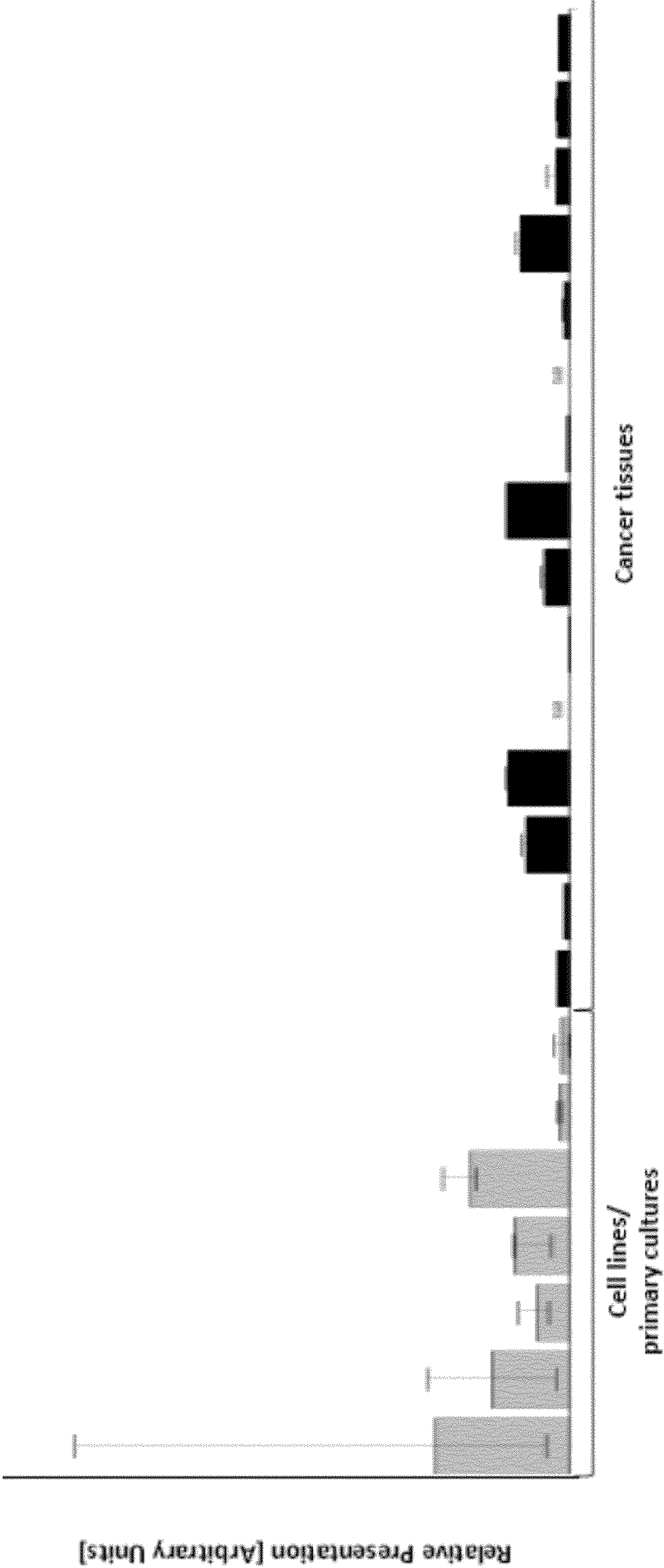
Peptide detected on
13 cancer tissues (1 breast cancer, 1 leukocytic leukemia cancer, 1 lung cancer, 6 lymph node cancers, 3 ovarian cancers, 1 rectum cancer) (from left to right)

Figure 1M
Peptide: SLDLRPLEV (A*02)
SEQ ID NO: 74



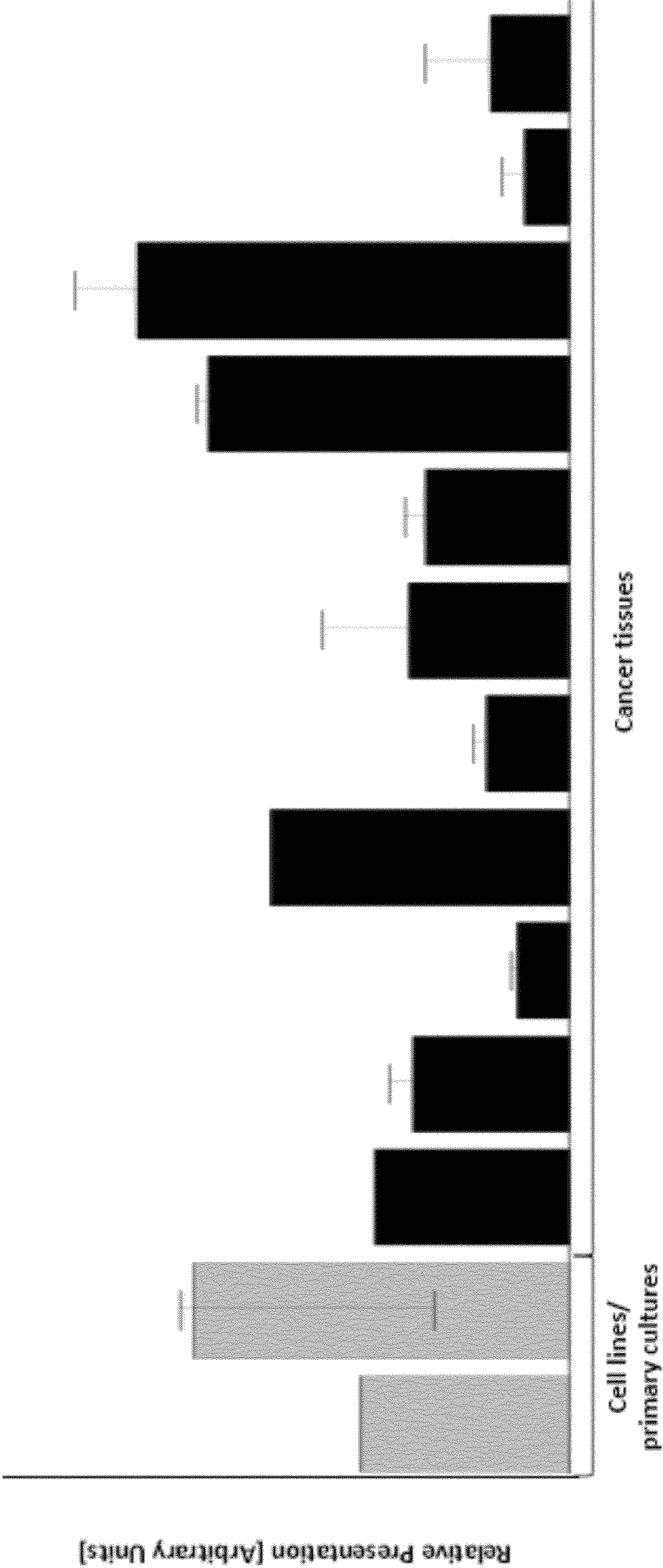
Peptide detected on
1 cell line, 2 normal tissues (1 lymph node, 1 spleen), 24 cancer tissues (3 brain cancers, 1 colon cancer, 1 gallbladder cancer, 1 kidney cancer, 1 lung cancer, 12 lymph node cancers, 1 ovarian cancer, 1 skin cancer, 2 stomach cancers, 1 testis cancer) (from left to right)

Figure 1N
Peptide: FLYSETWNI (A*02)
SEQ ID NO: 254



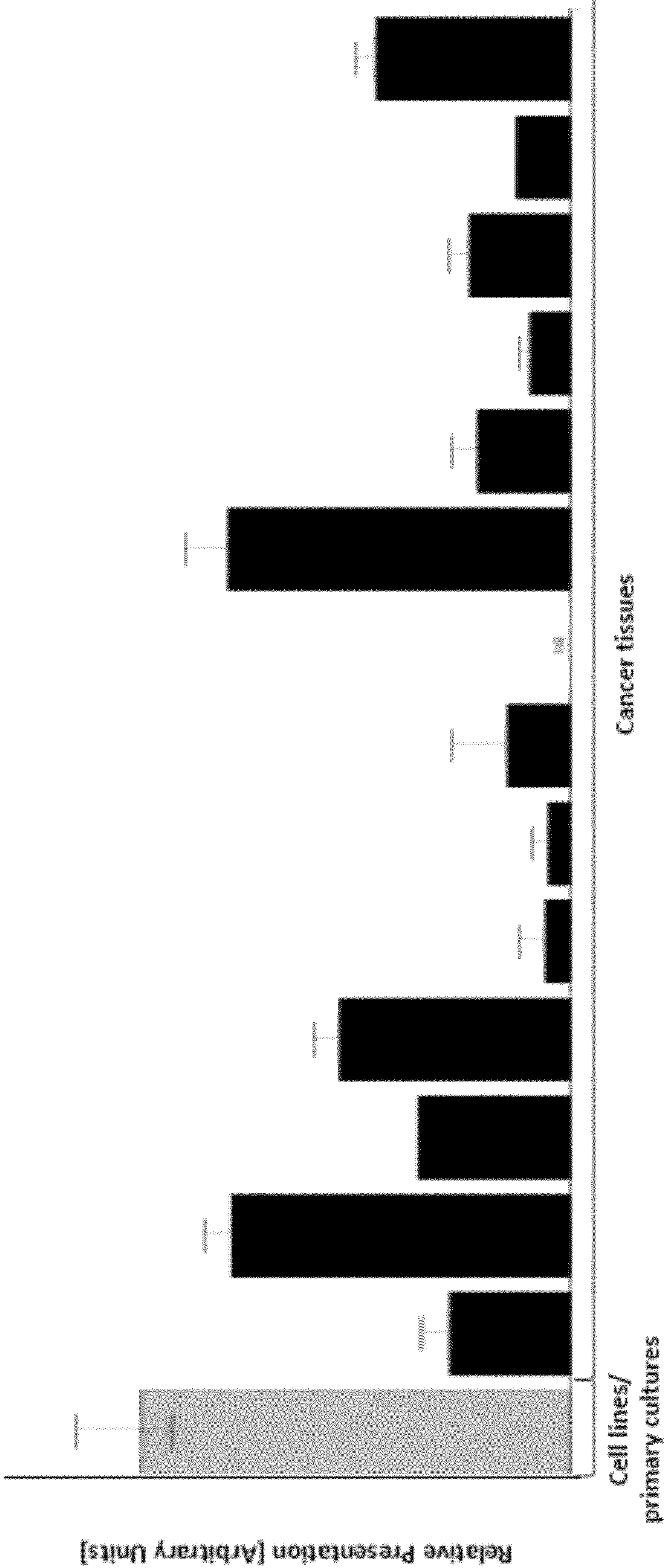
Peptide detected on
7 cell lines, 15 cancer tissues (1 colon cancer, 2 head and neck cancers, 3 leukocytic leukemia cancers, 1 liver cancer, 6 lymph node cancers, 1 myeloid cell cancer, 1 skin cancer) (from left to right)

Figure 10
Peptide: FLQWEWEVYA (A*02)
SEQ ID NO: 257



Peptide detected on
2 cell lines, 11 cancer tissues (2 leukocytic leukemia cancers, 1 liver cancer, 4 lymph node cancers, 1 myeloid cells cancer, 2 skin cancers, 1 urinary bladder cancer) (from left to right)

Figure 1P
Peptide: TVLDGLEFKV (A*02)
SEQ ID NO: 259



Peptide detected on
1 primary culture, 14 cancer tissues (1 head and neck cancer, 3 leukocytic leukemia cancers, 3 lung cancers, 3 lymph node cancers, 1 myeloid cell cancer, 1 ovarian cancer, 2 skin cancers) (from left to right)

Figure 2A

Gene: MIXL1
(Peptide: LLPPSPAA, SEQ ID NO: 160)

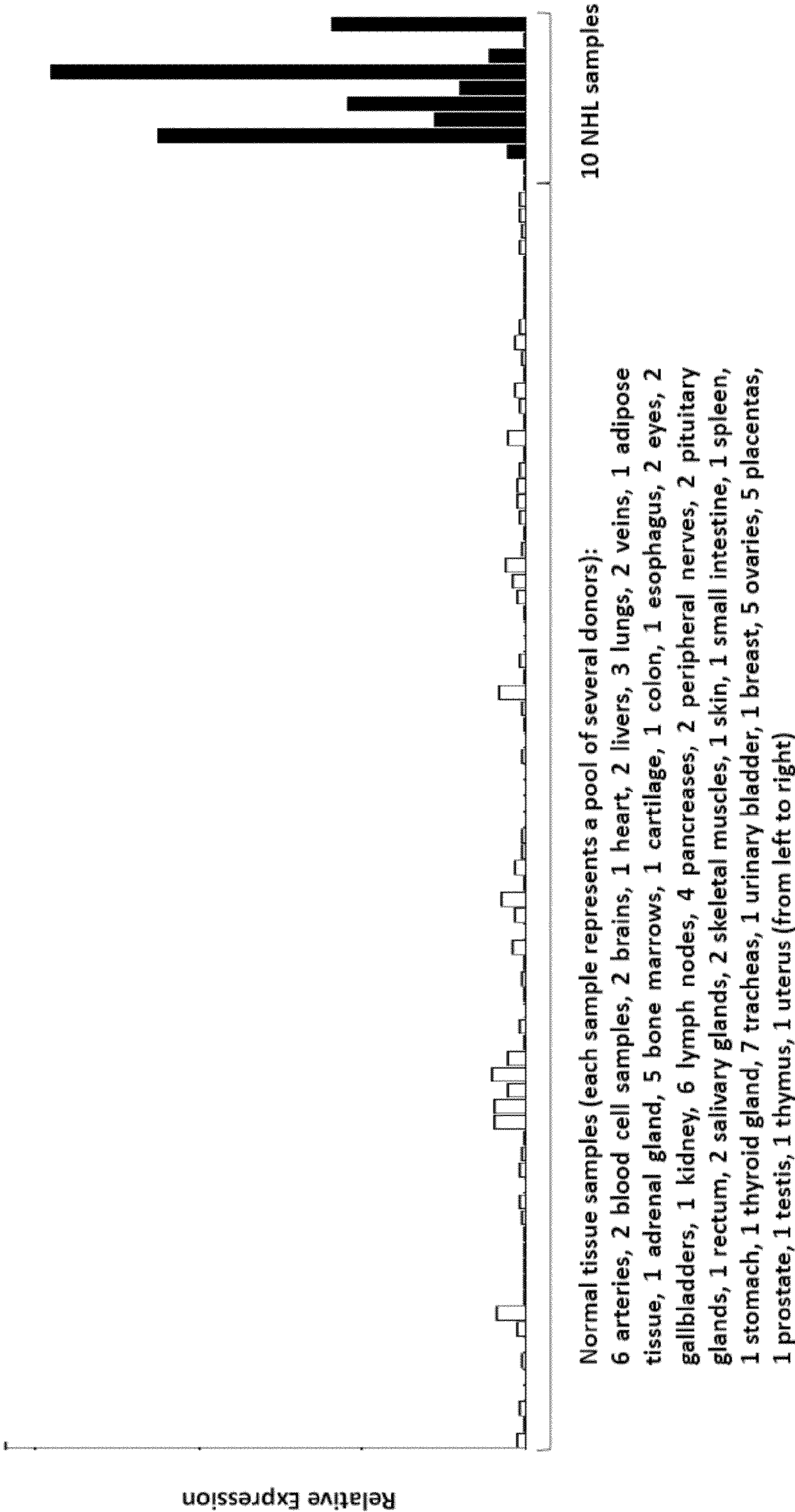


Figure 2B

Gene: CCR4
(Peptide: SLNSTTWKV, SEQ ID NO: 199)

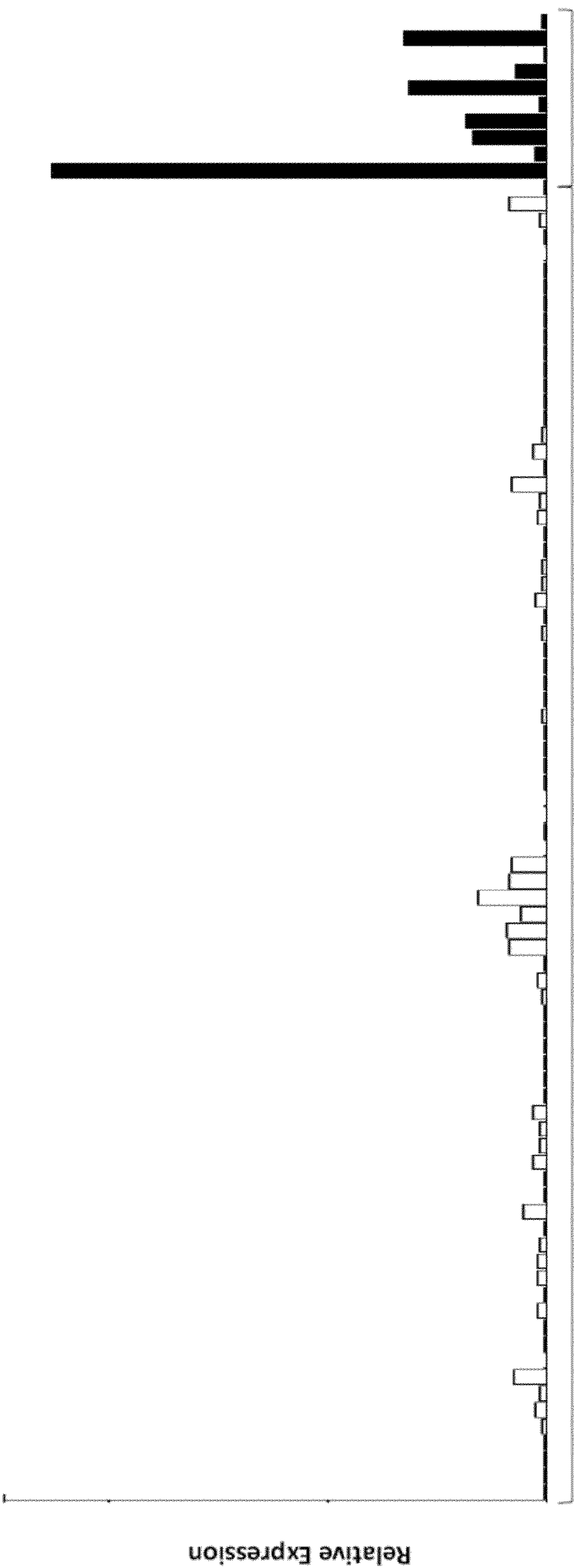
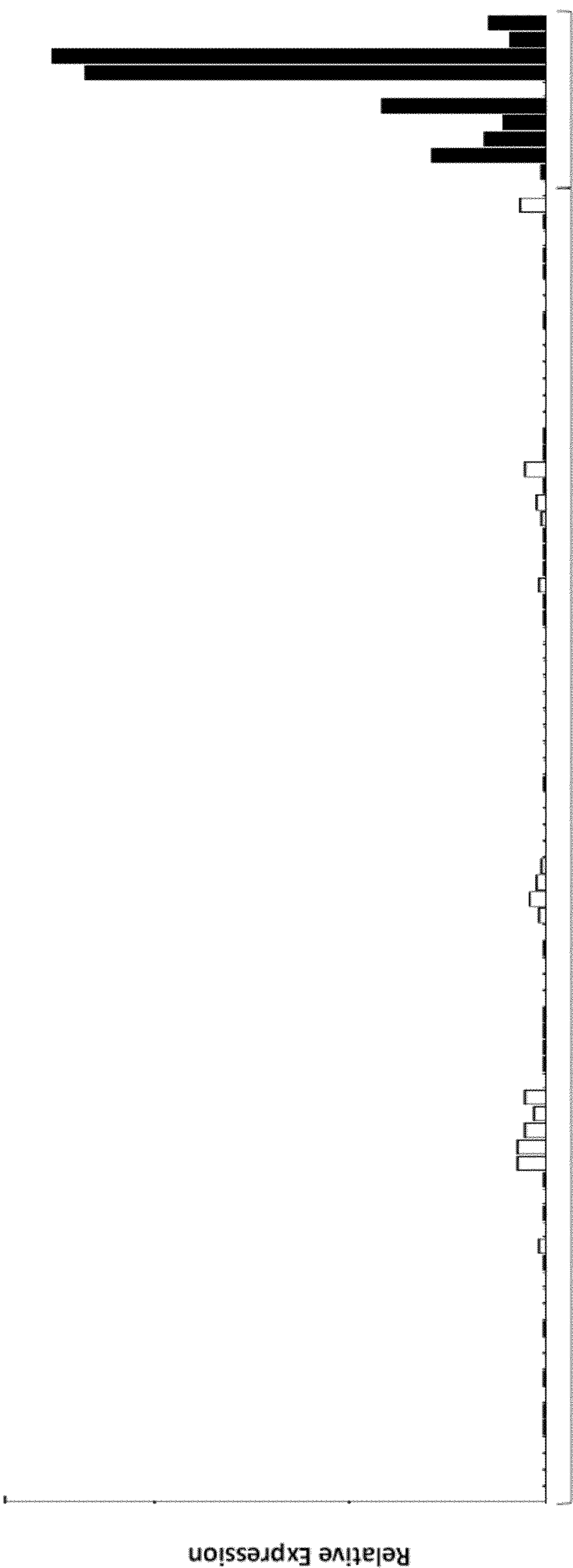


Figure 2C

Gene: HIST1H1B
(Peptide: ALAAGGYDV, SEQ ID NO: 202)



Normal tissue samples (each sample represents a pool of several donors):
6 arteries, 2 blood cell samples, 2 brains, 1 heart, 2 livers, 3 lungs, 2 veins, 1 adipose tissue, 1 adrenal gland, 5 bone marrows, 1 cartilage, 1 colon, 1 esophagus, 2 eyes, 2 gallbladders, 1 kidney, 6 lymph nodes, 4 pancreases, 2 peripheral nerves, 2 pituitary glands, 1 rectum, 2 salivary glands, 2 skeletal muscles, 1 skin, 1 small intestine, 1 spleen, 1 stomach, 1 thyroid gland, 7 tracheas, 1 urinary bladder, 1 breast, 5 ovaries, 5 placentas, 1 prostate, 1 testis, 1 thymus, 1 uterus (from left to right)

Figure 3

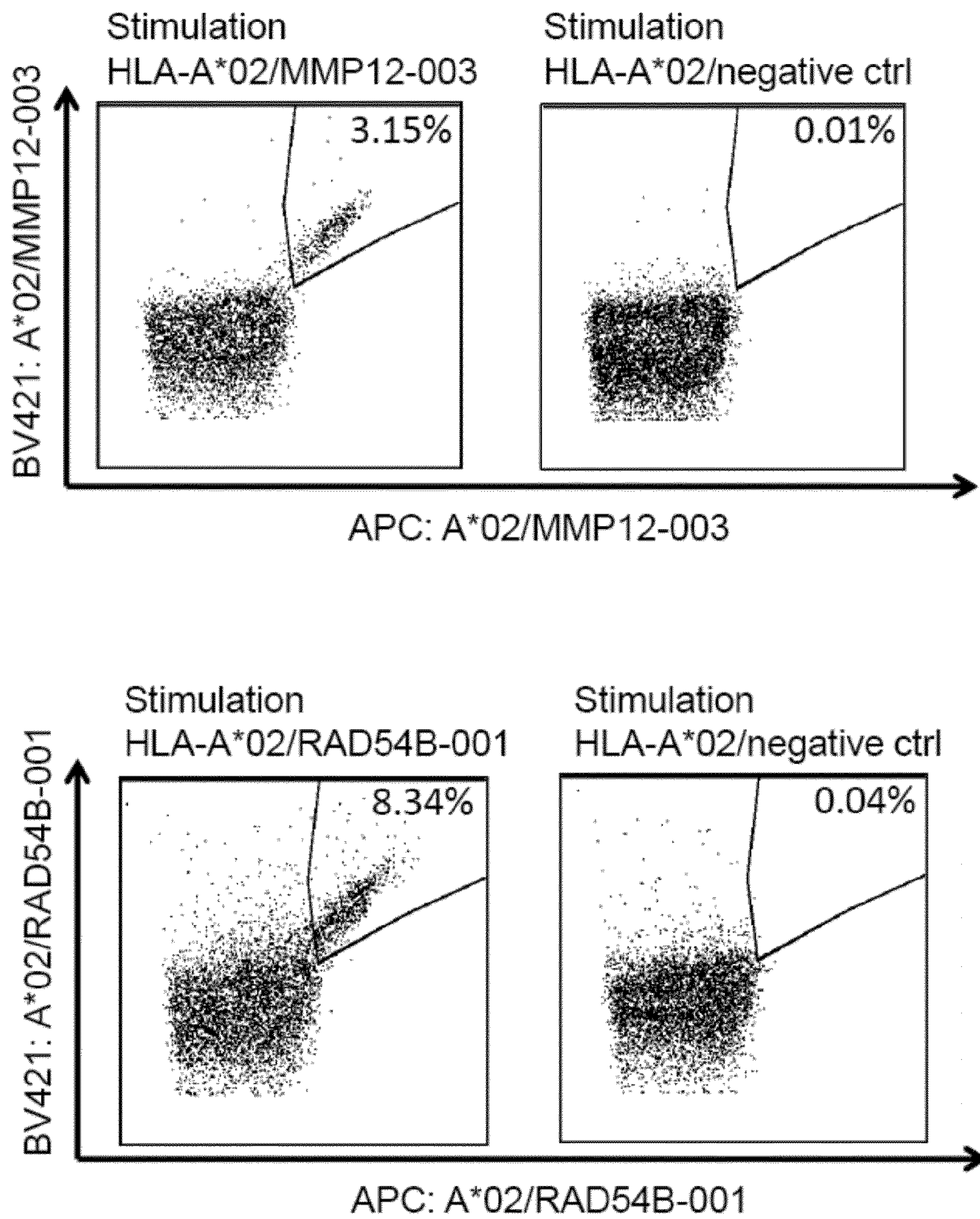


Figure 4

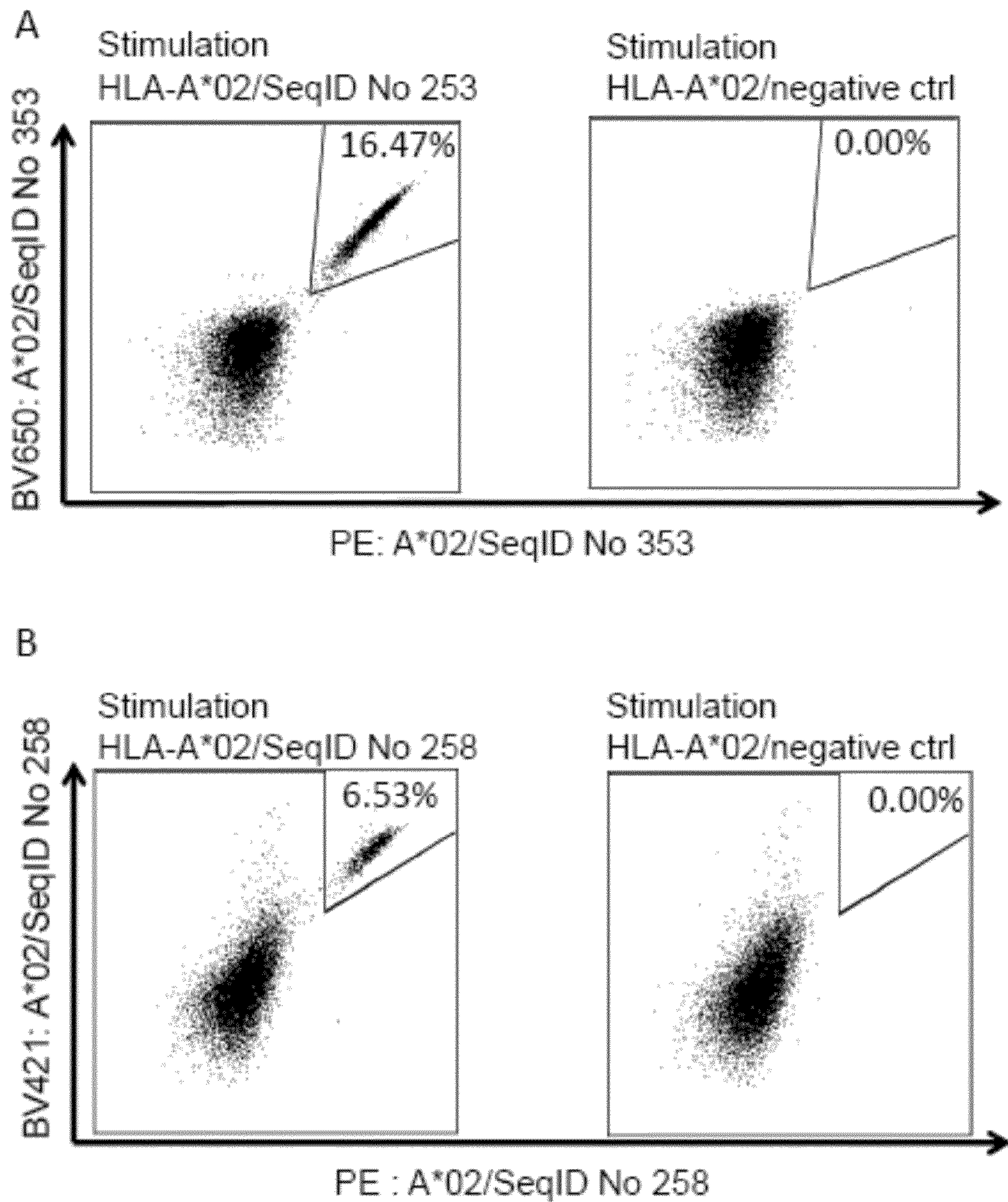


Figure 4 (continued)

