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Alternative tumour-specific antigens

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Abstract

The study of tumour-specific antigens (TSA) as targets for anti-tumour therapies has accelerated within the past decade. The most commonly studied class of TSA are those derived from non-synonymous single nucleotide variants (SNVs), or SNV-neoantigens. However, to increase the repertoire of available therapeutic TSA targets, ‘alternative TSAs’, defined here as high-specificity tumour antigens arising from non-SNV genomic sources have been recently evaluated. Among these alternative TSAs include antigens derived from mutational frameshifts, splice variants, gene fusions, endogenous retroelements, and others. Unlike the patient-specific nature of SNV-neoantigens, some alternative TSAs may have the advantage of being widely shared by multiple tumours, allowing for universal off-the-shelf therapies. In this Opinion article, we will outline the biology, available computational tools, pre-clinical and/or clinical studies, and relevant cancers for

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each alternative TSA class, as well as discuss current challenges preventing the therapeutic application of alternative TSAs and potential solutions to aid in their clinical translation.

Table of Contents Summary

To date, very few actionable tumour-specific antigens (TSAs) have been identified that have successfully translated into therapeutic cancer vaccines. This Opinion article provides examples of alternative TSAs to the traditional single nucleotide variant neoantigens and the novel computational tools to identify them with the view to broaden the number of targetable antigens that can be used for cancer vaccine development.

Introduction

The role of tumour specific antigens [G] (TSAs) as targets of anti-cancer immunity was first recognized in the last century, with studies of TSA-based vaccines becoming more prevalent this past decade (Box 1)[1–3]. Neoantigens [G] are defined here as a subset of TSAs generated by nonsynonymous mutations and other genetic variations specific to the genome of a tumour, presented by major histocompatibility complex (MHC) molecules, and recognized by endogenous T cells. The most commonly studied class of neoantigens are those derived from single nucleotide variants (SNVs), which cause non-synonymous changes in a protein that subsequently may trigger antigen-specific T-cell responses against the tumour. These conventional neoantigens have the distinct advantage over other classes of tumour antigens [G] (e.g. tumour-associated antigens [G] and cancer–testis antigens [G]) in having no expression in normal tissues[4]. As a result, T cells with specificity for these neoantigens can escape negative selection [G] in the thymus, leading to generation of a TSA-specific T-cell repertoire[5].

Despite advantages of SNV-neoantigens, their applicability as vaccine targets may be limited to cancers with highly immunogenic neoantigens, likely a subset of the total neoantigen load for any given tumour. Metastatic melanoma (which contains the highest SNV burden of any cancer[6]) has been the primary focus of initial neoantigen clinical studies[2,3], and in this tumour type as in lung cancer, tumour mutational burden (which estimates neoantigen load) has been associated with response to immune checkpoint inhibition[7]. One hypothesis for this association is the increased likelihood in these tumour types of neoantigen generation and T cells bearing neoantigen-specific T cell receptors (TCRs). However, the number of neoantigens required to drive a clinical response is unknown and it has been shown that tumours with a low mutational burden can have neoantigen-specific T cell populations boosted by therapeutic personalized neoantigen vaccines[8,9].

Many investigators including our group have begun to evaluate alternative TSAs – defined as high-specificity tumour antigens arising from non-SNV-containing genomic sources. Unlike SNV-neoantigens, alternative TSAs are not necessarily restricted to protein-coding exons, allowing from a greater repertoire of available targets. Predicted tumour-antigen burden has demonstrated expression of various classes of TSAs is not always correlated, with some SNV-low cancers containing high alternative TSA expression. This is exemplified by clear cell renal cell carcinoma (ccRCC), an immune checkpoint inhibitor sensitive cancer which

contains a low predicted SNV burden but high expression of predicted frameshift-neoantigens[10] and tumour-specific endogenous retroviral antigen[11]. Thus studying these alternative TSAs may broaden the scope and increase the number of targets available to test in therapeutic vaccines and/or cellular therapies. Additionally, leukemia and sarcoma (which contain among the lowest predicted SNV burden of any cancers[12]) express gene fusion mutations[13,14] and splice variant transcripts[15,16] shared across multiple tumours, potentially allowing for universal off-the-shelf therapies. In this Opinion article, we will characterize several major classes of alternative TSAs, including those generated from mutational frameshifts, splice variants, gene fusions, endogenous retroelements [G], and other classes such as human leukocyte antigen (HLA)-somatic mutation derived antigens and post-translational TSAs (Figure 1, Table 1). One class of TSA not covered here are viral-derived cancer antigens [G] (e.g. human papillomavirus (HPV) and Epstein-Barr virus (EBV)), which have been previously reviewed[17–21]. We will begin by providing a brief overview of TSA computational prediction, and then discuss the biology, available computational tools, pre-clinical and/or clinical studies, and relevant cancers for each alternative TSA class. Last, we will discuss the current challenges impeding therapeutic application of alternative TSAs and solutions to aid their clinical translation. In addition to a review of the literature, recent studies (including several from our group) have provided estimates for antigenic burden of each TSA class among The Cancer Genome Atlas (TCGA) pan-cancer data (including selected tumour-specific viral antigens), which we have compiled here as a resource (Figure 2 **and** Supplementary Fig. 1).

Computational prediction of TSAs

Recent advancements in DNA and RNA sequencing have enabled the development of genomic and computational methods of TSA prediction (Table 2). Methods for generating TSA immunotherapies generally rely on a conserved set of steps: variant calling, HLA-typing [G], peptide enumeration, HLA binding prediction, and therapy generation (Figure 3). Variant calling is the identification of genomic regions with tumour specificity. In the case of SNVs, insertion or deletion [G] (INDEL) mutations, and gene fusions, variants are derived from mutations within the tumour exome that are not expressed by germline DNA. In contrast, endogenous retroelement-derived antigens are identified from RNA expression data, selecting for elements with higher expression in the tumour compared with matched-normal tissues. Splice variant antigens can be identified through a variety of techniques, discussed in-depth later. Subsequently, tumour HLA-typing is derived using an HLA caller (e.g. POLYSOLVER[22], OptiType[23], PHLAT[24], HLAScan[25], HLAProfiler[26]), which relies on DNA and/or RNA sequencing data, depending upon the platform. Peptide enumeration is then performed, whereby variant genomic regions are translated into peptide sequences, with removal of translation-incompatible sequences such as nonsense mutations. Following this, HLA binding prediction is performed using prediction software (e.g. NetMHCpan[27]), with higher affinity peptides characterized by either ranked percentiles or K_d [G] values ≤ 500 nM (commonly accepted binding affinity cutoff in the field)[3,27,28]. The majority of MHC binding affinity prediction tools rely on machine-learning algorithms (including artificial neural networks) trained on validated epitope [G] reference databases, where peptide binding to MHC molecules has been measured using biochemical assays[29,30]. Last,

predicted TSAs are used to generate a therapeutic product, either as a vaccine (i.e. DNA or RNA, peptide, or dendritic cell vaccine) or a cellular therapy product (i.e. adoptive T-cell therapy). Below, we will discuss the biology of each alternative TSA class, with detailed descriptions of available computational prediction tools.

Mutational frameshift neoantigens

Biology of INDEL mutations

INDEL mutations are derived from insertion or deletion of base pairs into the genome, which have the capacity to generate nonsynonymous novel open reading frames, known as mutational frameshifts. INDEL-derived neoantigens have been hypothesized (but not yet proven) to generate more robust immune responses compared with SNV-derived neoantigens, as their sequences are completely unique from germline sequences downstream of the INDEL[10,31]. Epitopes generated from these mutations could induce a T-cell response similar to SNV-neoantigens, due to decreased potential for negative selection in the thymus against the INDEL-neoantigen-specific T cell.

Cancer types particularly relevant for targeting of INDEL-neoantigens include microsatellite instability-high (MSI-H) tumours as well as all renal cell carcinomas (RCCs). Early studies examining the role of INDEL mutations for anti-tumour immunity were mainly pursued in colon cancer, where MSI caused by hereditary diseases (e.g. Lynch syndrome [G]) and in sporadic tumours (MSI-H in 15%) are common[32,33]. MSI-H tumours are also observed in other non-hereditary cancers, including gastric, endometrial, and pancreatic cancers[34]. MSH-H cancers are characterized by impaired DNA mismatch repair pathways and contain significantly greater INDEL burden compared with non-MSI-H tumours[31,35]. The association between INDEL burden and presence of tumour infiltrating T cells has been well described in the literature, providing early support for the hypothesis that MSI-H tumours would be susceptible to immunotherapies[31,36–39]. Concurrent with these findings, immune checkpoint inhibitors have demonstrated clinical activity for patients with MSI-H tumours independent of the tissue of origin[40]. As a result, MSI-H tumours are the only non-tissue restricted class of tumours with US food and drug administration (FDA) approval for immune checkpoint inhibitor therapy[41]. In MSI-H tumours, the burden of both SNV-and INDEL-neoantigens are high, making both neoantigen classes potentially useful for targeted therapy[10].

In contrast, RCC contains relatively few SNVs, despite having immune infiltrates and a high clinical response rate to immune checkpoint inhibitor therapy[42]. A potential explanation for this was explored recently by Turajlic et al.[10] whereby examining the pan-cancer INDEL profile in the cancer genome atlas (TCGA) dataset revealed that all RCC subtypes (clear cell RCC (ccRCC), renal papillary cell carcinoma and chromophobe RCC) have the highest proportion and number of INDEL mutations of any cancer types. The presence of INDELs was also associated with immune features (e.g. T-cell activation and immune checkpoint inhibitor response) in three individual cohorts of patients with melanoma. While the number of predicted INDELs across the pan-cancer cohort were orders of magnitude lower than SNV mutations, they were estimated to produce approximately 3-to-9-times more predicted neoantigens [G] per mutation than SNVs[10].

Tools for predicting INDEL-derived neoantigens

Currently, we are aware of at least six tools in peer-reviewed publications with the capacity to predict INDEL-derived neoantigens – pVAC-seq[43], Neopepsee[44], MuPeXI[45], Epidisco[46], Antigen.garnish[47], and TSNAD[48] (not included here are the custom neoantigen prediction pipelines being used in translational and clinical studies, which may contain proprietary methods for antigen prediction along with integration of a publicly available variant caller (e.g. Indelocator and Strelka[49]) and peptide–MHC binding prediction methods). Among these tools, Neopepsee, is unique in its integration of machine-learning algorithms to predict immunogenicity – as well as peptide–MHC binding – a feature not easily validated biologically in human neoantigen studies prior to induction of therapy.

Translation of INDEL-derived antigens into the clinic

A rare example of a publicly shared neoantigen has been observed from a common frameshift mutation in the gene transforming growth factor β receptor type 2 (*TGFβR2*), frequently found in Lynch syndrome and 15% of sporadic gastric and colon cancers with MSI[39]. Three independent studies published in 2001 demonstrated HLA-specific epitopes generated from mutated TGFβR2 capable of generating antigen-specific T cells, one associated with MHC class I–$CD8^+$ T cell responses[31,39] and one with MHC class II–$CD4^+$ T cell responses[50]. A more recent study from Inderberg et al.[51] isolated cytotoxic T lymphocytes (CTLs) from a patient with colon cancer who had showed greater than 10 year survival after vaccination with a TGFβR2 frameshift mutation-derived peptide, and used these CTLs to generate a TCR paired α and β chain clone, which was subsequently transfected into both $CD4^+$ and $CD8^+$ T cells. The transfected T cells demonstrated evidence of efficacy against colon cancer cell lines containing the TGFβRII mutation *in vitro* (cytotoxicity and cytokine release) and *in vivo* (an immunodeficient xenograft mouse model).

A recent publication from Ott et al.[3] studied the use of personalized neoantigen vaccines in the treatment of metastatic melanoma, with prioritization of INDEL-neoantigens in their prediction pipeline. Four unique INDEL mutations across six tumours were predicted, with T-cell cultures generated specific for two of those INDEL-neoantigens (one $CD4^+$ T cell epitope and one $CD8^+$ T cell epitope), which in turn demonstrated detectable interferon-γ (IFN-γ) secretion in response to their respective epitopes. This was compared with only 3–5 of 28 predicted SNV-neoantigens, which exhibited IFN-γ responses of a similar concentration. While INDEL-neoantigen cross-reactivity with the respective reference wild-type epitope was not measured (presumably as it was expected there would be no cross-reactivity), over half of the SNV-specific T cells demonstrated cross-reactivity with their wild-type epitope at escalating concentrations. Due to the small patient cohort and follow-up so far only at 20–32 months, clinical benefit of INDEL-neoantigens cannot yet be determined from this study.

Splice variant antigens

Splice variant antigen frequency in cancer

Splice variant antigens are post-transcriptionally derived TSAs arising from alternative splicing events, including from mRNA splice junction mutations[52–57], intron retention[58–63], or dysregulation of the spliceosome [G] machinery in the tumour cell[15,64,65]. Other types of post-transcriptionally derived TSAs include alternative ribosomal products (e.g. ribosomal frameshifting [G] [66,67], non-canonical initiation[68–71], termination codon read-through[69], reverse-stand transcription[72], and doublet decoding [G] [73]) and post-translational splicing [G] [74–76] – these two mechanisms are difficult to apply for anticancer therapies given the lack of tools for predicting such products.

The study of splice variant proteins has historically focused on haematological malignancies, with splice variant protein expression understudied in solid tumours. As such, putative splice variant antigens derived from these splice variant proteins have received less attention in solid tumours, with expression only recently validated[77]. In haematological cancers where SNV burden is relatively low[6], splice variant antigens could broaden the number of available TSA targets for therapeutic application. Splice variant proteins can arise through *cis*-acting mutations which disrupt or create splice site motifs or through *trans*-acting alterations in slicing factors which have historically been identified in haematologic malignancies[77,78]. The role of spliceosome machinery in the generation of splice variants in haematological malignancies is a current area of investigation. Mutations in spliceosome proteins (e.g. splicing factor 3b subunit 1 (SF3B1), serine-and arginine-rich splicing factor 2 (SRSF2), U2 small nuclear RNA auxiliary factor 1(U2AF1) and U2AF2) are common in myelodysplastic syndrome [G], acute myeloid leukemia (AML), chronic myelomonocytic leukemia (CMML), and chronic lymphocytic leukemia (CLL)[79–83]. Sharing of these spliceosome protein mutations across haematological cancer types has led to the hypothesis that spliceosome dysregulation may cause expression of splice variant mRNAs, which are not detectable in normal tissues, leading to translation of TSAs[84–86]. Beyond haematological malignancies, recent reanalysis of the TCGA pan-cancer dataset demonstrated strong association between somatic mutations in components of the spliceosome machinery and expression of splice variant products[77], providing evidence for the relevance of splice variant antigens in solid tumours.

Tools for predicting splicing events and splice variant antigens

Several types of splice variant callers have been described in the literature. Two of these tools, Spliceman[87] and MutPred Splice[88], predict for the capacity of exonic variants surrounding an annotated splice junction to interfere with normal splicing. Other tools provide *de novo* identification of alternative splicing events, including JuncBase[89], SpliceGrapher[90], rMATS[91], SplAdder[92], and ASGAL[93]. Many of these tools (e.g. SpliceGrapher, SplAdder and ASGAL) predict alternative splicing events through generation of splicing graphs. This splicing graph is generated through comparison of spliced alignments of RNA-seq reads against a genome reference, which consists of vertices (nodes) that represent predicted splicing sites for a given gene as well as edges that represent exons and introns between splicing sites. In addition to these splice variant callers, at least one

peer-reviewed tool has been described with the capacity to predict for splice variant antigens, Epidisco[46] (the computational pipeline for the multi-institutional PGV-001 personalized vaccine trial[94]).

Jayasinghe et al.[52] reported MiSplice, which integrates DNA-seq and RNA-seq data to discover mutation-induced splice sites, which they applied to the TCGA pan-cancer dataset. Splice variant mutations contained 2–2.5x more predicted TSA candidates than SNVs, with some tumorigenesis-related genes containing ≥40 unique predicted TSAs. Furthermore, predicted splice variant antigen burden was correlated with programmed cell death protein 1 ligand 1 (PDL1) expression, suggesting PD-L1 blockade therapy may be efficacious in tumours with a high frequency of splice variant antigens. Additionally, Kahles et al.[77] reported a comprehensive analysis of splice variants in the TCGA pan-cancer dataset, and then used mass spectrometry to identify tryptic digested polypeptides that contained splice variant antigens in 63 primary breast and ovarian cancer samples. This method found on average 1.7 predicted splice variant antigens per sample, with up to 30% more alternative splicing events in tumours compared to normal tissues. Notably, Kahles et al.[77] also reported several known (SF3B1 and U2AF1) and novel splicing quantitative trait loci [G] (transcriptional adaptor 1 (TADA1), the serine-threonine protein phosphatase PPP2R1A and isocitrate dehydrogenase 1 (IDH1)) which were associated with alternative splicing events in 385 genes, suggesting these loci are important for predicting the burden of splice variant antigens.

While these studies have demonstrated TSAs derived from cancer-specific splice junctions, further work is needed to refine the computational methods for splice variant antigen prediction. Particular emphasis is needed on identifying novel splice junctions that are likely to yield mRNA isoforms that will not undergo nonsense mediated decay [G] (NMD)[95]. To address this problem, improved full-length mRNA isoform inference procedures or hybrid (i.e. long and short read) RNA-seq algorithms will need to be developed. These procedures would identify the full-length splice variant transcript, allowing for filtering of transcripts that do not contain premature stop codons which could subsequently trigger NMD.

While tumour-specific splice variants of particular genes have been described in multiple tumour types, there are currently no reports of the use of splice variant antigens in personalized therapies. For example, the presence of tumour-associated splice variants have been described in select genes, including receptor for hyaluronan-mediated motility (*RHAMM;* two tumour-enriched variants, *RHAMM-48* and *RHAMM-147* in multiple myeloma)[96] and Wilms tumour protein 1 (*WT1;* one variant, E5+, enriched in multiple cancers)[97–99]. WT1 derived peptides have been studied as a therapeutic target in leukemias[100–104], lung[105], and kidney cancers[106]; however, these trials did not use epitopes specific for the E5+ splice variant. Additionally, an HLA-B44 restricted epitope derived from a variant of the minor histocompatibility antigen HMSD (HMSD-v) selectively expressed by primary haematological malignant cells (including those of myeloid lineage, and multiple myeloma) but also normal mature dendritic cells was observed to be targeted by $CD8^+$ cytotoxic T cell clone 2A12-CTL[107]. Co-incubation of 2A12-CTL with primary AML cells conferred tumour resistance to immunodeficient animals after injection, suggesting this HMSD-v derived antigen to be a viable target for immunotherapy. Lastly,

Vauchy et al.[108] described a CD20 splice variant (D393-CD20) whose expression is detectable in transformed B cells and upregulated in various B cell lymphomas. They subsequently demonstrated the capacity of D393-CD20 derived epitope vaccines to trigger both $CD4^+$ and $CD8^+$ T cell responses in HLA-humanized transgenic mice, supporting the use of CD20 splice variant epitopes for targeted immunotherapies in B cell malignancies.

Gene fusion neoantigens

Gene fusion occurrence in cancer

Gene fusions were originally identified in leukemia[109], with subsequent observations in bladder[110], breast[111], renal[112], colon[113], and lung cancers[114] (among others). Similar to splice variants, gene fusion proteins have been a focus of study in leukemia (particularly AML, acute lymphocytic leukemia (ALL), and chronic myeloid leukemia (CML)[115]) but also sarcomas[116] where SNV burden is limited. These cancers contain conserved gene fusions, some of which are observed in nearly 100% of cancer subtypes (e.g. t(11;22)(p13;q12) in synovial sarcoma[117]). As gene fusions are often driver mutations of certain tumours, compounds aimed to inhibit fusion protein function have been clinically successful[118]. Immunotherapies directed against driver mutation gene fusions may be especially beneficial, as they would directly target the source of oncogenesis. However, while driver mutation expression has been demonstrated to be highly clonal in early cancers[119], studies in non-small cell lung cancer have demonstrated highly heterogeneous driver alterations[119], frequent loss of HLA heterozygosity[120], and epigenetic silencing of neoantigen-containing genes occurring in later disease[121], all of which may contribute to immune escape. As such, targeting of a single driver mutation may limit long-term therapeutic efficacy, whereby therapy resistant sub-clones with differential driver mutations and HLA expression profiles may arise. While overall gene fusion frequency is relatively low compared to SNV and INDEL mutations, they can be shared within and between different tumour types[122], making them identifiable through targeted methods (e.g. fluorescence *in situ* hybridization) and potentially targetable by universal (as opposed to patient-specific) neoantigen-based strategies.

Prediction tools for gene fusion neoantigens

Using current genomic techniques, gene fusions are typically identified through alignment of fusion-containing reads from RNA-seq to more than one reference gene. In addition to general gene fusion callers[123], several personalized gene fusion neoantigen calling pipelines have been developed, including INTEGRATE-neo, which is specifically designed for prediction of gene fusion neoantigens[124]. Using INTEGRATE-neo for analysis of the TCGA prostate adenocarcinoma cohort, 1761 gene fusions were identified in 333 patient samples that generated 2707 fusion transcript isoforms. Among this set, 61 (3.5% of the total) gene fusions were identified in >1 patient. Furthermore, 1600 fusion junction peptides were identified from the 2707 transcripts, of which 240 (15%) were predicted HLA binders[124]. Notably, the binding affinity score for these 240 predicted neoantigens were skewed toward tighter affinity, suggesting that predicted fusion-derived neoantigens may have substantially better MHC binding capacity than SNV-neoantigens. In addition to INTEGRATE-neo, several other tools have been described for gene fusion neoantigen calling, including

pVACfuse (which performs neoantigen epitope calling using fusion variants reported from INTEGRATE-neo), NeoepitopePred[125], Antigen.garnish[47], and Epidisco[46].

Clinical studies with gene fusion neoantigens

Clinical trials targeting gene fusion neoantigens have been pursued in CML (targeting BCR–ABL fusion) and pediatric sarcomas. Pinilla-Ibraz et al.[126] demonstrated that three of six patients with CML receiving a high dose of a BCR–ABL fusion protein breakpoint peptide vaccine developed antigen-specific T-cell responses, although no cytotoxic response was observed. While this phase I study was designed to assess safety and not clinical efficacy, one patient demonstrated transient loss of BCR–ABL mRNA, one patient experienced transient and partial cytogenic response [G] during vaccination, and two patients progressed to an accelerated phase of disease during the study period. A follow-up phase 2 trial from the same group similarly demonstrated evidence of vaccine safety and measurable immunogenic response, but no evidence of clinical efficacy[127]. Another trial, summarized in a publication from Mackall et al.[128] studied the effects of dendritic cells pulsed with tumour-specific translocation breakpoints [G] and E7, a peptide known to bind HLA-A2 (given alongside autologous T cells +/− interleukin-2 (IL-2) and, serving as a control, influenza vaccinations) in patients with Ewing's sarcoma and alveolar rhabdomyosarcoma. Compared with 31% five-year overall survival in patients who underwent control apheresis [G], immunotherapy treated patients had 43% five-year overall survival with minimal toxicity. These studies (among others[129,130]) underscore the potential for gene fusion neoantigens as universal off-the-shelf therapeutics, although current clinical efficacy remains modest. This may be in part related to therapies only targeting a single gene fusion epitope, allowing for resistant sub-clones to arise in later disease course[119,120]. While an off-the-shelf approach has clear logistical merit, identification and application of multiple patient specific gene fusion epitopes may improve therapeutic efficacy.

Currently, few studies have applied patient-specific fusion proteins predicted through DNA and/or RNA sequencing methods for therapeutic vaccination. One recent example from Yang et al.[131] demonstrated the capacity of INTEGRATE-neo-derived fusion epitopes from head and neck cancers including fusion epitopes derived from cancers with low overall mutational burden to generate ex vivo activation of host and healthy donor T cells. Large cohort clinical studies (e.g. PGV-001[46,94]) are currently underway which will include gene fusion neoantigens among the set of targeted TSAs. Future use of this potential class of neoantigens alone or in combination will require larger clinical trials with more robust clinical and immunological endpoints.

Endogenous retroelement antigens

Retrotransposons in cancer

Retrotransposons [G] are mobile genetic elements capable of self-replication through transcription and reverse transcription from genomic DNA[132]. They can be broadly divided into long-terminal repeat (LTR, also known as retroviral-like) and non-LTR subclasses, which differ by their genomic structures and replication mechanisms[132]. Retrotransposons can be expressed in cancer through epigenetic dysregulation, either through inherently low

methylation states[11,133,134] or following pharmacological induction of demethylation[135–138], resulting in transcription (and potential translation) of retroviral TSAs[139]. Among the many classes of retrotransposons, long interspersed nuclear elements (LINEs, a class of non-LTR retrotransposon) have been best characterized in terms of their ability to impact cancer biology. LINE-1 has been shown to induce cancer cell apoptosis[140], trigger adenomatous polyposis coli (APC)-mediated tumorigenesis in colon cancer[141], associate with clinical features and changes in cellular morphology in breast cancer[142,143], among other roles.

Endogenous retroviruses (ERVs), a type of LTR retrotransposon in mammals, are remnants of exogenous retroviruses which have been incorporated into the genome throughout evolution[144]. Human ERVs (hERVs) impact pathogenesis and progression of cancers, including melanomas, lymphoma, leukemia, ovarian, prostate, urothelial, and renal carcinomas[134,145–153]. Transcription of tumour-specific or enriched hERVs arise through epigenetic dysregulation of the cancer genome (which can either be inherent to the epigenetic state of the cancer or pharmacologically induced through epigenetic modulating agents), resulting in expression of hERV-containing genomic regions otherwise not observed under physiological conditions[136,138]. These tumour-specific or enriched hERVs can impact both the innate and adaptive immune system through distinct mechanisms. With the innate immune system, hERVs signal through innate sensors, most commonly the RIG-I-like pathway recognition of viral double stranded RNAs[136,138]. This results in downstream nuclear factor-$_{K}$B (NF-KB)-mediated inflammation, with release of type I interferon which causes immune activation and expression of class I MHC on tumour cells. Additionally, hERV-derived protein antigens can induce B-and T-cell activation[154–156]. Therefore, it has been proposed that tumour-specific hERV antigens could be applied to anti-tumour adoptive cellular therapies and therapeutic vaccines.

In addition to INDEL-derived neoantigens, hERVs have been proposed as key driver of anti-tumour immunity in ccRCC[11,157]. In ccRCC, hERVs demonstrate baseline expression in the tumour without exogenous pharmacological epigenetic modulation, with expression of these hERVs showing strong association with both clinical prognosis and response to immunotherapy[11,157]. A 2015 study from Rooney et al.[158] provided an initial genomic evaluation into the interaction between hERVs and the tumour-immune microenvironment, demonstrating three of 66 hERVs (ERVH-5, ERVH48–1, ERVE-4; identified in a previous study from Mayer et al.[159]) to have tumour specific expression and correlate with a cytotoxicity signature (granzyme A and perforin-1) in several cancers. Based on this study as well as several other translational studies showing the presence of a hERV-specific T-cell response in ccRCC[155,160], our group performed comprehensive analyses into the role of hERVs in ccRCC[11,157]. From immunogenomic analysis [G] of hERVs in ccRCC, we demonstrated hERV-derived signatures to be the best predictor of patient prognosis, outperforming both clinical stage and M1–M4 molecular subtyping[11]. Additionally, expression of tumour-specific hERV 4700 in pretreatment ccRCC samples was strongly associated with post-treatment response rates to anti-PD-1 therapy. As such, hERV-derived antigens may be a viable alternative TSA target in ccRCC. Additionally, recent evidence suggests a potential role for hERVs in the modulation of low grade glioma (where SNV burden is among the lowest of any cancer)[11] and testicular cancer (particularly those with

KIT mutations) where global DNA hypomethylation is associated with high hERV expression[133].

Computational methods for quantification of retroelement expression

Several computational methods for retroelement quantification currently exist, with the majority providing quantification of ERV-like or retrotransposon-like elements (partial or full-length) rather than full-length, intact ERVs at specific genomic coordinates. This is due to the historic lack of well-annotated ERV references containing full proviral sequences and coordinates (rather than segments of ERV-like elements), which have only recently been published to allow for mapping of full-length, intact ERVs[161,162]. The most well-known tool is RepeatMasker, designed to identify interspersed repeats and low complexity sequences of any class, including simple and tandem repeats, segmental duplications [G], and interspersed repeats (including ERV-like elements, LINE and short interspersed nuclear elements (SINE), LTRs, and other classes)[163]. RepeatMasker used in its default state is not optimal for detection of ERVs. However, many ERV-specific databases (e.g. HERVd[164], HESAS[165], EnHERV[166]) have been subsequently generated using RepeatMasker. A more recent quantifier designed by our group aimed specifically for analysis of hERVs from RNA-seq data is hervQuant[11], which quantifies full-length, intact hERV proviral sequences. The hervQuant reference is derived from Vargiu et al.[161], which compiled genomic coordinates for 3,173 full-length hERV proviruses. Notably, hervQuant provided the first description of a broad genomic screening method for tumour-specific hERV antigens.

As there are currently no tools available to identify retroelement TSAs, the retroelement or ERV quantifiers described above must be paired with downstream epitope prediction software (e.g. NetMHCpan[27]) for retroelement antigen binding predictions. Additionally, as retroelements are present in the genome of both tumour and normal tissues, prediction of tumour-specific retroelements provides unique challenges. Unlike identification of neoantigens, retroelement TSAs must be derived through differential expression analysis of tumour versus normal tissue RNA-seq. While hERVs and other retroelements share common homology among their overall sequences, which might theoretically make them unsuitable targets for TSA therapeutic approaches, they also exhibit highly unique regions specific to each hERV capable of generating equally unique peptide epitopes[11]. Our analysis of hERV homology during the design of hervQuant revealed only a minority of hERVs to contain >95% sequence homology with one or more other hERVs, providing the basis for our ability to differentiate hERVs from short read RNA-seq data. hERV unique regions can be leveraged for hERV-based TSA therapies, as long as one can confirm specificity of expression of that particular hERV within a tumour. Additionally, evidence of hERV specific T cells found natively within the tumour immune microenvironment (e.g. hERV 4700[11] and CT RCC HERVE[167]) suggests a lack of thymic central tolerance against these hERV-specific epitopes.

Translational relevance of tumour-specific hERV targets

Several studies have described the translational application of tumour-specific hERV targets. A 2016 study from Cherkasova et al.[155] identified a $CD8^+$ T cell clone from a patient with regressing ccRCC and found the clone to have tumour-specific cytotoxicity *in vitro.* The

CTL recognized an antigen from a specific hERV CT-RCC HERV-E – which was the same as one of the tumour-specific hERVs (ERVE-4) described by Rooney et al.[158] and was also identified during our screen of differentially expressed hERVs in ccRCC (hERV 2256). This particular CTL clone is being studied in clinical trials for adoptive T-cell therapy in metastatic ccRCC[167]. Our analysis additionally identified a second hERV (hERV 4700) with preferential expression in ccRCC compared to normal tissues, evidence of translation, and presence of tumour infiltrating CTLs specific for hERV-4700 *gag* and *pol* derived antigens of the virus[11].

Other alternative TSAs

HLA-somatic mutation derived neoantigens

Several studies have described somatic mutations in tumour HLA allowing for altered T-cell recognition. This was first described by Brandle et al.[168] where mutated HLA-A2*0201 in a ccRCC tumour promoted an antitumour T-cell response. This study did not elucidate if the mechanism for T-cell response was a result of TCR recognition of the antigen presented by the mutated HLA or if the recognition was against the HLA molecule itself. Huang et al.[169] later demonstrated a similar finding in metastatic melanoma, with evidence that tumour-specific T cells may recognize an unknown antigen or set of antigens presented on mutated tumour HLA-A11. Together, these studies provided early evidence for potential targeting of novel antigens with specificity of binding to somatically mutated HLA on the tumour. A recent publication from Shulka et al. presented a whole exome based HLA-typing software, POLYSOLVER, able to call HLA somatic mutations with high prediction power validated by RNA-seq (estimated sensitivity 94.1%, specificity: 53.3%)[22]. More recently, HLAProfiler improved upon the breadth and accuracy of HLA somatic mutation calls and is able to work from RNA-seq data alone[26]. Combined with existing tools capable of predicting antigen binding directly from HLA sequences (e.g. NetMHCpan), it is possible to predict for sets of antigens with specificity for the mutated tumour HLA and thus specificity for anti-tumour T-cell responses. Notably, a more advanced version of NetMHCpan is theoretically able to predict MHC binding to novel MHC molecules (including those containing mutations) through machine-learning prediction of MHC binding based upon the amino acid sequence of the MHC variant[27].

Post-translational TSAs

TSAs can arise post-translationally in tumours, with the potential to be targets for therapy but are difficult to predict with current computational tools. Post-translational splicing may occur in human cancers, resulting in excision of a polypeptide segment followed by subsequent ligation of the free carboxyl terminal with an amino terminal of a new peptide[74,75]. Additionally, a second class of antigens known as T-cell epitopes associated with impaired peptide processing (TEIPP) has been described to be presented on transporter involved in antigen processing (TAP)-deficient, MHC-low tumours and recognized by a TEIPP-specific T cell population[170–174]. Interestingly, these epitopes are non-mutated and derived from housekeeping genes. Yet, they are not presented on normal cells. TEIPP-specific T cells can escape thymic selection in wild-type animals (but not in TAPI-deficient animals), making them promising candidates for anti-tumour therapeutic targets.

Challenges and future directions

Among the challenges impeding broad clinical application of alternative TSAs as therapeutics include the need to increase the sensitivity and accuracy of epitope prediction. The computational methods described above have provided avenues to predict a greater number of TSAs from a broader variety of genomic sources. However, methods both upstream and downstream of these algorithms can be generally applied to improve prediction performance for all TSA classes. Here, we highlight several strategies which may universally increase the number and accuracy of all TSA predictions: improvement of MHC epitope binding predictions, algorithms for direct prediction of TSA generation and immunogenicity, and mass spectrometry approaches to improve TSA calling accuracy.

MHC epitope calling

Most TSA therapeutic vaccine studies to date have focused on the use of predicted MHC I binding epitopes, largely due to the classical hypothesis that $CD8^+$ T cells play a greater role in anti-tumour immunity than $CD4^+$ T cells, and better performance of MHC I epitope prediction algorithms compared with MHC II epitope predictors. Despite this, further improvements are required for both MHC I and II prediction algorithms in order to identify greater numbers of accurately predicted TSAs. A recent analysis from our group demonstrated that the accuracy of MHC I binding affinity predictions by NetMHCpan varied greatly by allele type, with performance measures strongly correlated with the proportion of training data epitopes which were ‘binders’ ($K_d \leq 500$ nM – the generally accepted cutoff within the field for MHC binding) and less so with the amount of total training data per allele[175]. As such, alleles with fewer ‘binders’ in the training set suffered from poor sensitivity and specificity, suggesting more high-quality data is necessary for application of MHC I predictors for clinical TSA prediction.

Regarding MHC II predictions, recent pre-clinical and clinical studies have suggested the importance of MHC II binding neoantigens in promoting anti-tumour immunity. A study from Kreiter et al.[176] was the first to describe MHC I predicted neoantigens to in fact be presented on MHC II, subsequently triggering $CD4^+$ T cell responses. The relevance of SNV-specific $CD4^+$ T cells in anti-tumour immunity is further supported by an earlier study from Tran et al.[177] whereby infusion of an ERBB2 interacting protein (ERBB2IP) mutation-specific $CD4^+$ T cell population abrogated tumour growth for 35 months in a patient with metastatic cholangiocarcinoma. Clinical studies from Sahin et al.[2,3] confirmed the importance of $CD4^+$ T cell responses in human trials, providing evidence in support of the clinical importance of MHC II TSAs. Despite this evidence, a major hurdle faced by computational prediction methods for MHC II epitopes arises from the open binding cleft structure of the MHC II complex. This structure results in relatively promiscuous binding of epitopes compared with MHC I, whereby the binding core [G] of the longer class II epitope must be accurately predicted before binding affinity can be subsequently calculated[178].

Recent improvements have been made for computational prediction of MHC II epitope binding affinity, largely facilitated by the application of machine-learning algorithms trained on large, validated epitope datasets. Many earlier algorithms focused on the identification of the epitope binding core, with predictions based on the interactions between this peptide-

core and the MHC complex. Neilson and colleagues first described NN-align, which provided MHC II binding prediction trained on both peptide-core as well as flanking region characteristics, which significantly improved MHC II binding prediction performance[179]. While the binding affinity of an epitope is primarily determined by its peptide-core, flanking region characteristics can also influence the binding affinity. NN-align was later adapted as the core algorithm for NetMHCIIpan by Andreatta et al.[180] which further improved performance as well as leading to the description of alternative epitope–MHC interactions. Even with these improvements to MHC II binding prediction, performance characteristics of state-of-the-art algorithms still lag behind MHC I binding predictors. While the importance of MHC II epitopes in promoting anti-tumour immunity has primarily been observed with SNV-neoantigens, it is expected that alternative TSAs would similarly be applicable as MHC II epitopes. As such, increasing both the breadth of available TSAs from alternative sources as well as improvements to MHC II epitope prediction can together provide a concerted strategy to multiplicatively increase the targetable pool of tumour antigens.

Direct prediction of TSA generation and immunogenicity

In addition to MHC binding affinity prediction, new methods for direct prediction of TSA generation and immunogenicity may aid in clinical selection of therapeutic epitopes. The majority of neoantigen prediction algorithms currently rely on predicted peptide–MHC binding affinity as the primary method for epitope screening. However, pre-clinical and clinical studies demonstrate that only a minority of all neoantigen candidates are capable of producing immune responses[2,3,176,181]. One such explanation for this high false-positive rate is that current binding prediction tools do not account for other steps involved in MHC peptide processing[182]. A study from Pearson et al.[183] demonstrated MHC class-I associated peptides (MAPs; i.e. epitopes) were derived from only 10% of exomic sequences expressed in B lymphocytes, with 41% of protein-coding genes generating no MAPs. Using features of transcripts and proteins associated with efficient MAP production, they generated a logistic regression model to predict whether a gene is capable of MAP generation. Another approach to improve TSA prediction is to directly predict for the epitope immunogenicity. Briefly mentioned above, Neopepsee is a new tool which incorporates a machine-learning algorithm trained on HLA alleles that generate T-cell responses to directly predict immunogenicity of putative neoantigens[44]. Compared with conventional binding affinity metrics, Neopepsee predicted immunogenicity in two external validation datasets with significantly improved sensitivity and specificity, providing evidence in support of direct immunogenicity prediction approaches. As the algorithm of Neopepsee was trained on a broad set of HLA alleles rather than specifically using TSA epitope immunogenicity, biological differences between self-derived neoantigens and the non-self epitopes of the training set may be a limiting factor for algorithmic performance. With an increasingly growing number of clinical trials collecting neoantigen immunogenicity data, future algorithms trained specifically on TSAs may potentially provide even better predictive capabilities.

Mass spectrometry approaches

Apart from computational TSA prediction, mass spectrometry-based peptidomic approaches have been applied for identification of tumour antigens[184]. The identification of endogenously presented epitopes by mass spectrometry began in the early 1990s[185,186]. The

first peptide antigens were discovered with manual interpretation of tandem mass spectrometry [G]; however, computational methods are now the routine strategy to make comparisons between tandem mass spectrometry and peptide sequences on proteomics databases. While conceptually similar to genomic alignment and sequencing, tandem mass spectrometry sequencing is substantially more error prone and less sensitive. Standard proteomics experiments with complex peptide mixtures from well characterized biological samples are typically only able to identify ~25% of the tandem mass spectra in a proteomics database[187,188]. In addition to the computational difficulties with sequence identification, peptides can undergo rearrangements in the mass spectrometer, generating sequences that were not present in the original biological sample[189,190]. Despite these challenges, progress has been made in confirmation of predicted neoantigens using mass spectrometry. Immunogenomic methods have been used to generate virtual peptidomes from tumour sequencing data, and neoantigens have been identified[191,192]. A recent study by Laumont et al.[193] used mass spectrometry approaches and observed that approximately 90% of identified TSAs from two mouse cancer cell lines and seven human primary tumours were derived from non-coding regions, including introns, alternative reading frames, non-coding exons, untranslated region (UTR)–exon junctions, structural variants and endogenous retroelements. Notably, these non-coding regions are not identified through current exome or transcriptome-based sequencing approaches. This study underscores the potential importance of the alternative TSAs and provides strong evidence for their application in therapy design, importantly demonstrating that classical SNV-neoantigens may comprise only a minority of the total TSA repertoire. While these studies have enabled neoantigen discovery on a large scale, the limitations of tandem mass spectroscopy alignment and the possibilities of unexpected peptide rearrangements mean that suspected neoantigens should be confirmed by direct comparison of the sample’s tandem mass spectrum to that of the synthetic peptide[175,191,194].

Conclusion

Conventional SNV-neoantigens remain the most well studied class of TSA, with distinct advantages of ease of prediction, prevalence in a wide cohort of patients, and promising pre-clinical and clinical therapeutic evidence of immunogenicity. While SNV-neoantigens will continue to be a driving force for therapeutic vaccine development in the coming years, many groups have broadened the search for other alternative TSAs derived from self and non-self-antigens. While certain sources of alternative TSAs have been studied for decades (e.g. gene fusion proteins, and viral antigens), the advent of powerful computational methods for patient-specific prediction of TSAs has expanded the breadth of targets available for potential clinical application. Unlike SNV-neoantigens, which are largely patient specific in expression[12], some classes of alternative TSAs are shared among the population (e.g. splice variant antigens, gene fusion antigens, and hERV antigens), making them ideal for off-the-shelf therapies. Additionally, many of these peptide sequences are highly dissimilar from germline sequences (e.g. frameshifts), allowing for potentially greater immunogenicity than SNV-neoantigens. Thus, alternative TSAs should play a major role in the future of cancer immunotherapy.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Glossary Box

Apheresis:
Medical technique used to purify various components of whole blood. Apheresis can be performed to harvest purified T lymphocytes for subsequent immunotherapeutic application

Artificial neural network:
A class of computational modeling based on biological neural networks, able to implement change based on training input and output information to form an optimized prediction model

Binding core:
The segment of polypeptide on an antigenic peptide responsible for interaction with the major histocompatibility complex (MHC) binding groove. The binding core is recognized as an important predictor for binding affinity, but binding as also influenced by other factors of the epitope sequence

Cancer–testis antigens:
Antigens whose expression is limited to cancer cells as well as reproductive tissues but not adult somatic tissue

Cytogenic response:
A decrease in the number of cells with a particular chromosomal trait (classically associated with the *BCR–ABL* gene fusion) in response to therapy

Doublet decoding:
Translational process by which an amino acid is translated from a two base pair codon rather than the conventional three base pair codon. This process can result in −1 frameshifting during translation

Epitope:
Specific portion of the antigen specifically recognized by a T or B cell receptor

HLA-typing:
The process for identifying the human leukocyte antigen (HLA) receptor allele of a particular tissue. This can be performed through a variety of molecular or immunological techniques

Immunogenomic analysis:

Study of the combined genomics of cancer cell and immune cell components of a tumour

Insertion or deletion (INDEL):
Insertion or deletion of bases into the genome of an organism, typically in the context of a mutation or genetic variation

K_d:
Dissociation constant that measures the concentration of a ligand necessary to reversibly bind half of its corresponding molecular pair. In the context of peptide–MHC-binding, this refers to the concentration of peptide necessary to bind half of all MHC molecules

Lynch syndrome:
Also known as Hereditary nonpolyposis colorectal cancer. An autosomal dominant genetic disorder of DNA mismatch repair, resulting in increased risk of microsatellite instability driven colon cancer (among other cancer types)

Myelodysplastic syndrome:
A class of low-grade malignancies in which abnormal bone marrow stem cells fail to fully mature

Neoantigens:
Antigens specific to the genome of the cancer cell

Nonsense-mediated decay (NMD):
Checkpoint by which mRNA transcripts containing premature stop codons are eliminated in order to reduce aberrant translation

Post-translational splicing:
Post translational excision of polypeptides, with subsequent ligation of the carboxy-and amino-terminal residues

Predicted neoantigens:
Genomically predicted neoantigens with unconfirmed tumour expression and/or in vivo immunogenicity

Quantitative trait loci:
A section of DNA (locus) that is correlated with a particular qualitative trait (or phenotype) in an organismal population

Retroelements:
Genetic elements capable of self-amplification, found within the genome of eukaryotic organisms. Retrotransposon DNA can be transcribed into RNA, converted back into identical DNA via reverse transcription, then inserted into the genome at particular target sites. Retroelements include retrotransposons and endogenous retroviruses

Retrotransposons:
A subset of retroelement in eukaryotic cells that possesses some characteristics of retroviruses and transposes through an RNA intermediate

Ribosomal frameshifting:
Process by which codons are translated in an out-of-frame manner via slippage of the ribosome into a +/− 1 or 2 base pair position

Segmental duplications:
Long segments of repeated DNA (1–400kb) with highly conserved sequences (>90%) that exist in the genome as a result of duplication events

Spliceosome:
Molecular machinery responsible for removal (splicing) of introns from pre-mRNA

Tandem mass spectrometry:
Multiple step mass spectrometry (MS) whereby the sample is first ionized for separation in the first MS stage, followed by fragmentation for separation in the second MS stage

Negative selection:
Process by which self-reactive T lymphocytes are deleted during T cell education in the thymus

Translocation breakpoints:
Location where two fragments of chromosome(s) are joined subsequent to chromosomal translocation

Tumour antigen:
Any antigen produced by the tumour cell, typically in the setting of enriched or specific expression relative to normal tissue(s)

Tumour-associated antigens:
Antigens whose expression is enriched (but not specific) to cancer cells

Tumour-specific antigens (TSAs):
Antigens (molecules capable of promoting an adaptive immune response) expressed by the tumour with minimal to no expression in normal tissue

Viral-derived cancer antigens:
Antigens expressed by cancer cells derived from an oncogenic viral origin, capable of generating an adaptive immune response

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Box 1:

Historical context of neoantigen-based therapeutic vaccines.

The identification of single nucleotide variant (SNV)-neoantigens as targets of anti-tumour immunity was an important initial step for the understanding of tumour-specific antigen (TSA) vaccine therapies. This first began with the theorization that SNV-neoantigens could be leveraged to develop therapeutic vaccines and cellular modalities[5,195].

Subsequently, proof-of-concept for SNV-neoantigen therapeutic vaccines was demonstrated in preclinical tumour models, providing the framework for neoantigen clinical trials:

- Identification and description of nonsynonymous somatic point mutations in mouse models[196]
- Tumour neoantigens function as targets of T cells activated by immune checkpoint inhibitor therapy[197]
- Combined exome and mass spectrometry approach to identify neoantigens[191]
- Characterization of mouse tumour neoantigens demonstrates that the majority of recognition is provided by CD4+ T cells[176]

More recently, human neoantigen therapy trials have been pursued:

- Dendritic cell[198], peptide[3], and DNA[2] neoantigen vaccines in melanoma
- Neoantigen vaccines in low mutation containing glioblastoma[8,9]

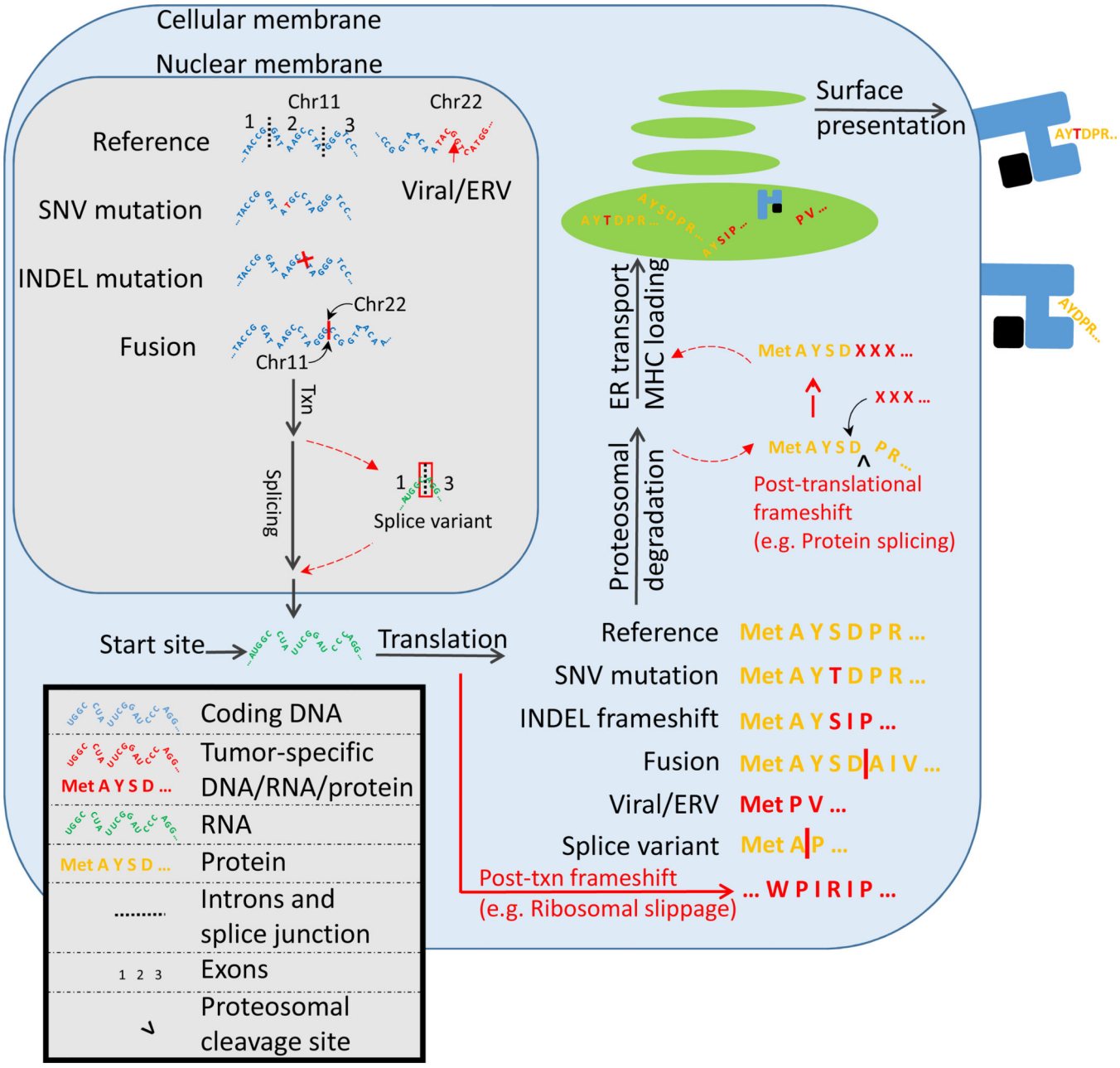

Figure 1: Summary of tumour-specific antigen production in the tumour cell.

Mutations and other tumour-specific nucleotide sequences (shown in red) can be observed at the genomic DNA level, where they undergo transcription (1) and splicing to form mRNA (2). Alternative splicing can occur at this step to form splice variant mRNA. Next, translation occurs on variant mRNA, resulting in production of variant proteins (3). Post-translational frameshifts (e.g. ribosomal slippage, among other mechanisms) can occur at this step, resulting in frameshifted protein variants. These proteins then can undergo proteasomal degradation (4) and transport to the endoplasmic reticulum (ER) to subsequently be loaded on major histocompatibility complexes (MHCs) (5). Other forms of post-translational frameshift can occur during these steps (e.g. protein splicing). Lastly,

peptides containing variant sequences can be presented at the cell surface in the context of MHC, resulting in T-cell targetable tumour-specific antigens (6).

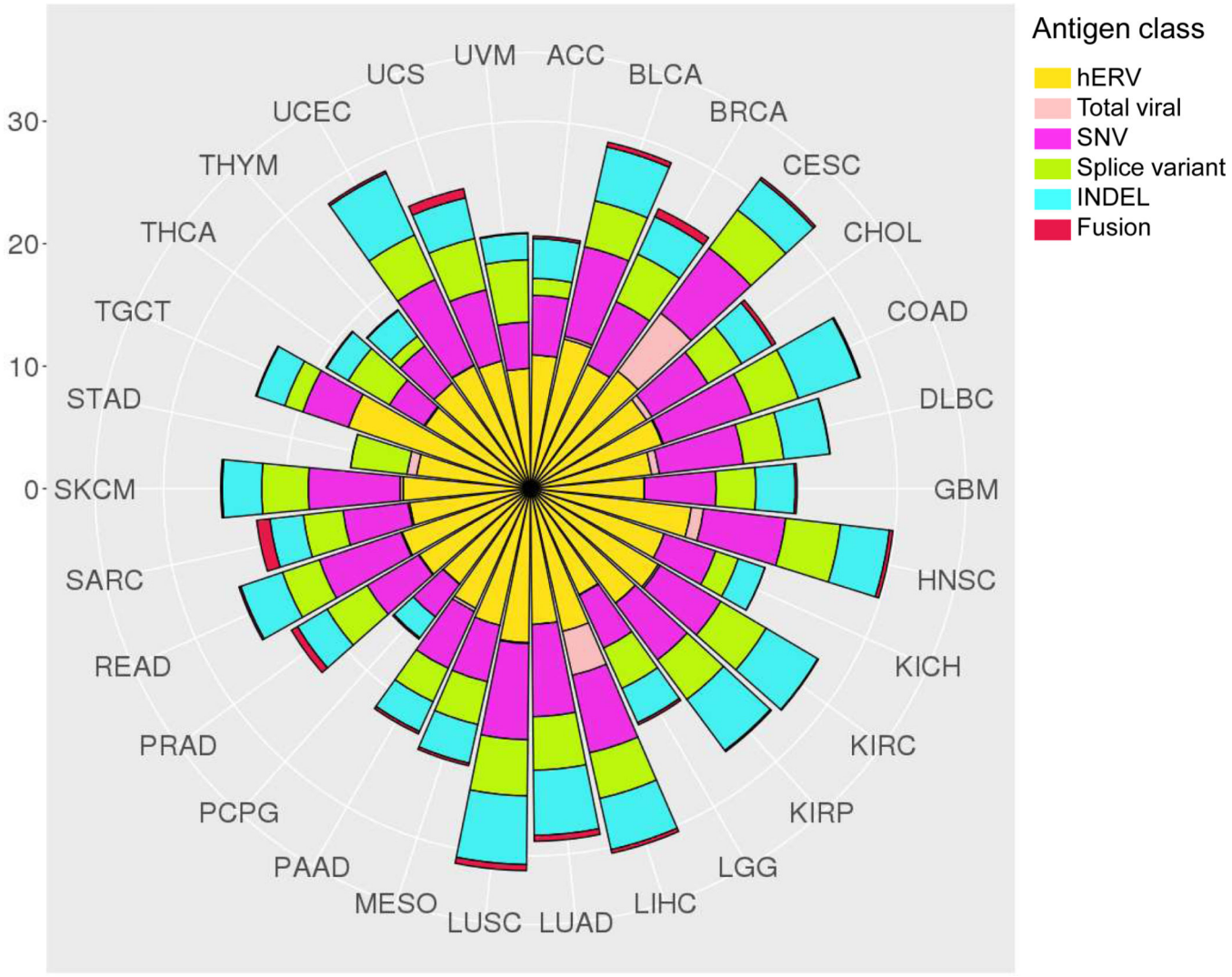

Figure 2: Average tumour-specific antigen counts by cancer type.

Plots represent number of unique identified epitopes by The Cancer Genome Atlas (TCGA) cancer type. Insertion or deletion (INDEL)-neoantigen counts demonstrated significant correlation with single nucleotide variant (SNV)-neoantigens among all cancer types (coefficient: 0.81, $p < 0.0001$). Notable outliers in this correlation were kidney renal clear cell carcinoma (KIRC; commonly known as clear cell renal cell carcinoma (ccRCC)) and kidney renal papillary cell carcinoma (KIRP; commonly known as papillary RCC), where the INDEL-to-SNV ratio was significantly higher than other cancer types (ccRCC: 0.85 and papillary RCC: 0.90; all others: 0.43 – 0.72). Analysis of splice variant antigens demonstrated similar burden to INDEL-neoantigens, with significant correlation with INDEL-and SNV-neoantigen burden.A notable outlier is thyroid cancer (thyroid carcinoma (THCA)), where the average number of splice variant antigens per sample is higher than SNV-neoantigens. Mean burden of fusion-derived neoantigens was highest in sarcomas (sarcoma (SARC): 1.1, uterine carcinosarcoma (UCS): 0.78), with carcinoma fusion burden highest in breast (breast invasive carcinoma (BRCA); 0.70) and prostate (prostate adenocarcinoma (PRAD); 0.58) cancer. Testicular cancer (testicular germ cell tumours

(TGCT)) contained substantially greater burden of human endogenous retrovirus (hERV)-derived tumour-specific antigens (TSAs) than any other TCGA cancer type. SNV and INDEL epitopes are derived from Thorsson et al.[12]. Fusion epitopes are derived from Gao et al. (Cell Reports,2018)[199]. Splice variant epitopes are derived from Jayasinghe et al. (Cell Reports, 2018)[52]. Viral epitopes are derived from Selitsky et al. (mSystems, 2018)[200]. hERV epitopes are derived from differentially expressed hERVs (>10-fold tumour-vs-mean normal expression by DESeq2) in Smith et al. (JCI, 2018)[11]. All TSA classes represent the average number of predicted class I human leukocyte antigen (HLA) binders (8–11mers, < 500 nM) predicted from NetMHCPan. Stomach adenocarcinoma (STAD) INDEL and SNV calls were absent from Thorsson et al.[12] and esophageal carcinoma (ESCA), acute myeloid leukaemia (LAML), and ovarian serous cystadenocarcinoma (OV) were not included in all original reports. Data shown represents reanalysis of the above reports, with modification of data in order to derive values comparable across TSA groups. ACC, adrenocortical carcinoma; BLCA, bladder urothelial carcinoma; CESC, cervical and endocervical cancers; CHOL, cholangiocarcinoma; COAD, colon adenocarcinoma; DLBC, lymphoid neoplasm diffuse large B-cell lymphoma; GBM, glioblastoma multiforme; HNSC, head and neck squamous cell carcinoma; KICH, kidney chromophobe; LGG, brain lower grade glioma; LIHC, liver hepatocellular carcinoma; LUAD, lung adenocarcinoma; LUSC, lung squamous cell carcinoma; MESO, mesothelioma; PAAD, pancreatic adenocarcinoma; PCPG, pheochromocytoma and paraganglioma; READ, rectum adenocarcinoma; SKCM, skin cutaneous melanoma; THYM, thymoma; UCEC, uterine corpus endometrial carcinoma; UVM, uveal melanoma. A version of these data with individual numbers of unique TSAs by cancer type is available online (Supplementary Fig. 1).

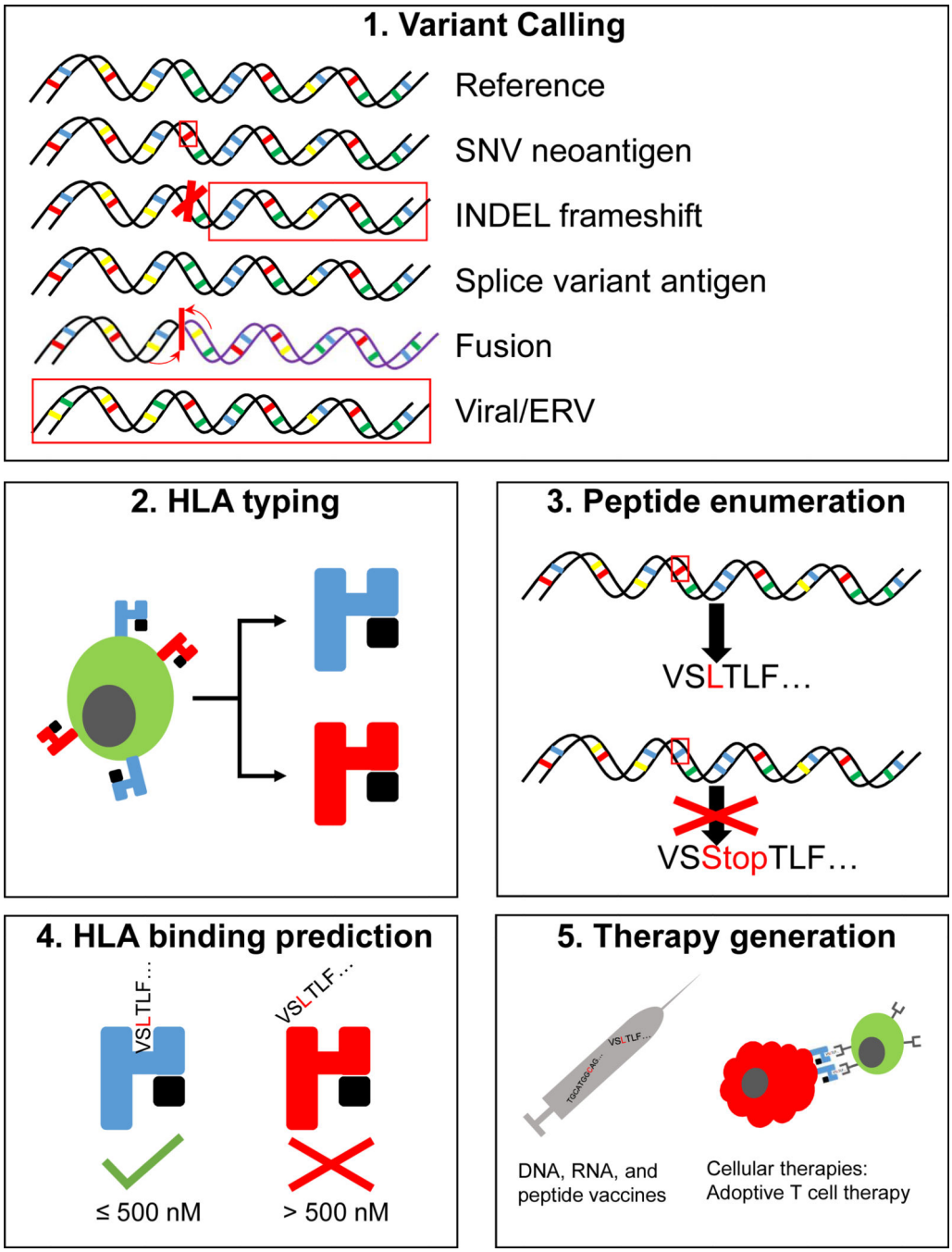

Figure 3: Computational workflow for tumour-specific antigen calling.

a) Identification of tumour-specific antigens begins with variant calling. This can be done through comparison of tumour versus normal tissue DNA sequences (single nucleotide variants (SNVs) and insertions or deletions (INDELs)) or RNA sequences (splice variants, fusions, viral sequences and retroelements) to look for tumour-specific variants in the exome or tumour-specific transcripts in the transcriptome, respectively. b) Tumour human leukocyte antigen (HLA)-typing is performed to enable downstream major histocompatibility complex (MHC) binding prediction. c) Peptide enumeration occurs through translation of variant

nucleotide sequences into their respective amino acid sequences, filtering for translation incompatible sequences such as those containing intervening stop codons or those with low evidence of RNA expression. These polypeptides are then used to derive 8–11 mer sequences (for MHC class I epitopes) or 15mer sequences (MHC class II epitopes) to allow for d) downstream MHC or HLA binding prediction of each sequence. Binders are typically defined in the literature as those with predicted binding affinity (K_d) of ≤ 500 nM or are selected from those with the highest rank percentile for predicted binding affinity. Other filtering criteria may be performed after this step, such as immunogenicity prediction or filtering away sequences with high homology to self-antigens. e) Lastly, therapies are generated using predicted tumour-specific antigens. These can be either DNA, RNA, or peptide vaccines or cellular therapies such as adoptive T-cell (ACT) therapy.

Table 1:

Advantages, disadvantages, and relevant cancers for each tumour-specific antigen class.

Antigen class	Advantages	Disadvantages	Relevant Cancers
SNV-neoantigens	• Well studied • Simple prediction • Relatively high burden	• Similar to self-antigen • Rarely shared between patients	• Melanoma • Glioblastoma • Lung cancer (adeno and squamous) • Bladder cancer
INDEL frameshift neoantigens	• Many targets per mutation • More dissimilar from self-antigen	• Relatively low burden	• Microsatellite instability-high tumours • Clear cell, papillary, and chromophobe renal cell carcinomas
Splice variant antigens	• High number of predicted targets • More dissimilar from self-antigen	• Fewer tools available • Not well validated in pre-clinical models • Current tools do not account for nonsense mediated decay	• AML • CMML • CLL • Myelodysplastic syndrome
Fusion protein neoantigens	• More dissimilar from self-antigen • Shared targets between tumours • More potential targets per mutation	• Relatively low burden	• AML • ALL • CML • Sarcomas
Endogenous retroelement antigens	• Large number of targets per retroelement • High immunogenicity • Shared between patients	• Less well studied • Potential for off-target effects • Difficult to validate protein translation	• Clear cell renal cell carcinoma • Low grade glioma • Testicular cancer

ALL, acute lymphocytic leukemia; AML, acute myeloid leukemia; CLL, chronic lymphocytic leukemia; CML, chronic myeloid leukemia; CMML, chronic myelomonocytic leukemia; ERV, endogenous retroviruses; INDEL, insertion or deletion; SNV, single nucleotide variants.

Table 2:
Computational workflows for tumour-specific antigen calling.

BAM, binary alignment map (the format for aligned sequencing data); FASTQ, a text-based unaligned sequencing format; GUI, graphical user interface; hERV, human endogenous retrovirus; INDEL, insertion or deletion; MHC, major histocompatibility class; NGS, next-generation sequencing; SNV, single nucleotide variant; TSA, tumour-specific antigen; VCF, variant call format (the format for storing gene sequence variations).

Computational prediction method	Class of TSA identified	Main features of the workflow	Advantages	Disadvantages	Ref
INTEGRATE-neo	• Gene fusion *	Full workflow gene fusion caller	• Standalone module for fusion calls • Efficient requirements	• Highly specific tool, only relevant for gene fusion calling	124
pVACtools	• SNV • INDEL • Gene fusion%	Tool suite which includes neoantigen calling and prioritization as well as optimization of DNA-based vaccine design	• pVACvector allows for easy construction of DNA-based vaccines	• %No stand-alone gene fusion calling; works downstream of INTEGRATE-neo fusion calls • Requires BAM (aligned) and VCF (somatic mutation) input	43
Neopepsee	• SNV * • INDEL *	Unique neoantigen caller that incorporates immunogenicity prediction	• Machine-learning based immunogenicity prediction for peptides • Well validated, with better results than standard MHC binding affinity ranking	• Requires VCF input (somatic mutation)	44
MuPeXI	• SNV • INDEL	Focus on providing additional information regarding prediction, including comparison against self-peptide	• Available as stand-alone or web service • Searches for similar selfpeptides, penalizing similar TSAs during prioritizing	• Requires VCF input (somatic mutation) • Requires HLA-typing input	45
TSNAD	• SNV • INDEL	Comprehensive suite, including mutation calling. Also includes analysis of membrane protein mutations, outside the context of MHC	• GUI for ease of use • Includes membrane protein mutation calling, allowing for possible antibody-based targeting	• Complex configuration for input paths, parameters, and naming conventions; however, theoretically easy to run after initial configuration	48
NeoepitopePred	• SNV • Gene fusion	Comprehensive web interface tool allowing for either FASTQ or BAM input	• Software used for the St. Jude's Pediatric Cancer Genome Project • Web-based interface	• Information regarding pipeline only indirectly published, with little information regarding the NeoepitopePred program itself	125
Epidisco	• SNV * • INDEL * • Splice variant * • Gene fusion *	Comprehensive workflow using FASTQ input, allows for calling of the broadest set of TSAs.	• Software used for the PGV-001 pipeline • Self-contained FASTQ-only input	• Information regarding pipeline only indirectly published, with no publication of the Epidisco program itself • Computationally intensive	46
Antigen.garnish	• SNV • INDEL • Gene fusion	R package that uses VCF input to call and rank TSAs	• MHC I and II calling with a wide variety of downstream analysis tools • Efficient, integrated with Bioconductor, a commonly used tool for analysis of NGS data	• Requires VCF input (somatic mutation)	47
RepeatMasker	• Retroelements	Screens DNA for interspersed repeats and low complexity RNA	• Well validated, used as the basis for multiple other	• Quantifier only, must be combined with downstream epitope prediction software	163

Computational prediction method	Class of TSA identified	Main features of the workflow	Advantages	Disadvantages	Ref
			retroelement quantification software	• Not retroelement or hERV specific	
hervQuant	• hERV	Full-length, intact hERV quantification software	• Provides quantification of 3000+ full-length hERVs using common STAR alignment and Salmon quantification workflow	• Quantifier only, must be combined with downstream epitope prediction software	11

* Class I MHC calling only. Software included in this table represents peer-reviewed, published TSA callers (that is, software encompassing the entire workflow from upstream variant identification to downstream epitope binding predictions). Therefore, stand-alone upstream variant callers, HLA-typing software, or MHC binding prediction tools are not listed with the exceptions of RepeatMasker and hervQuant, as there are currently no software packages described in the literature to predict epitope binding from retroelement calls.