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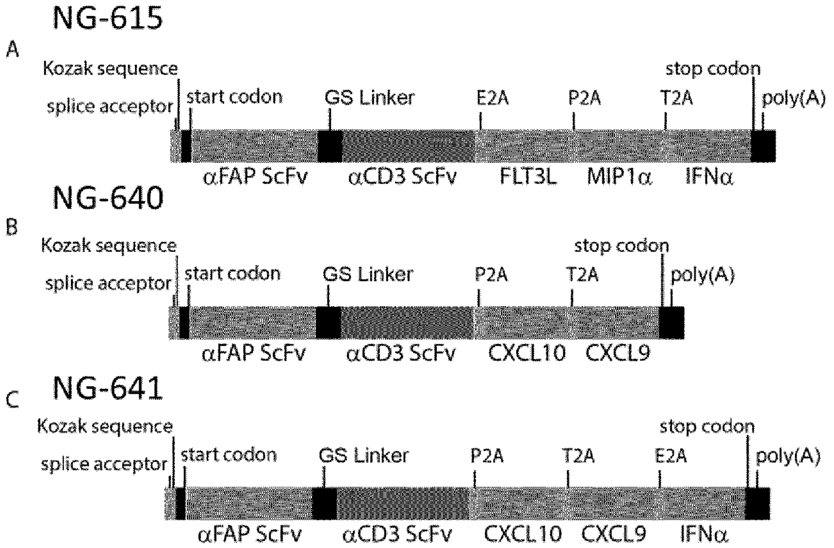
(54) Title: ADENOVIRUS ARMED WITH BISPECIFIC T CELL ENGAGER (BITE)

Figure 1



(57) Abstract: An adenovirus comprising a sequence of formula (I) $5'ITR-B_1-B_A-B_2-B_X-B_B-B_Y-B_3-3'ITR$ wherein $B\gamma$ comprises a transgene cassette containing four transgenes, said genes encoding a FAP- BITE, CXLI O, CXL9, and IFN. The disclosure also extends to pharmaceutical composition comprising the virus, and use of the virus or formulation is treatment.

[Continued on next page]

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Adenovirus armed with bispecific T cell engager (BiTE)

The present disclosure relates to a modified adenovirus, in particular Enadenotucirev (EnAd), armed with a a FAP-BITE, composition, such as a pharmaceutical formulation comprising the adenovirus, use of the virus and virus formulations, particularly in treatment, especially in the treatment of cancer. The disclosure also extends to processes for preparing the virus and DNA encoding the same. The disclosure also extends to novel sequences provide in the sequence listing in combination with the technical disclosure herein, for example wherein the virus exemplified is replaced with, for example an alternative cassette or alternative virus provided in the sequence listing.

BACKGROUND

Cancer is still a huge social burden to society in terms of the hardship and suffering of patients and their loved ones, and also in terms of the high financial cost of treating, caring for and supporting patients.

The stroma around the cancer cells is a physical protection in that it may have a function of trapping immune cells sent to fight the tumour. In addition, the stroma shields the hypoxic microenviroment of the tumour, which is permissive and optimised for the tumour's growth. There are some theories that cells in the stroma are a source of energy in the tumour.

A large component of tumour stroma are fibroblasts, which have been corrupted to serve the purpose of the cancer. Other cells that infiltrate the stroma are tumour associated macrophages (TAMs), which are type 2 (M2) macrophages that can promote tumour growth by secreting cytokines and chemokines, such as IL-10 that suppress immune responses.

It is especially difficult to target the tumour stroma because the cells that make up the environment are "native" immune or connective tissue cells, which are found throughout the body. Thus, targeting these cells with therapeutic agents can lead to serious off-target effects.

Hence, there is a need for an improved method of delivering a BiTE directly to tumour cells where it can provide maximal therapeutic benefit, in particular delivery to tumour cells surrounded by stromal fibroblasts.

WO2018/041838 and WO2018/041827 both incorporated herein by reference disclose certain adenoviruses encoding BITEs. However, it would be useful to augment the activity of the BITE enoded in the virus by incorporating activating cytokines. Incorporation of two cytokines co-located with the BITE can achieved without much difficult. However, when three cytokines are co-loated with the BITE the nature of the genes starts to impact on the expression of the BITE. The present inventors made the virus NG-615 with 4 transgenes, shown in Figure 1. However, the expression of the BITE was reduced. Surprisingly the virus NG-641 wherein two of the cytokines are changed (in comparison to NG-615), the virus has good activity, including good expression of the BITE. Thus, it appears the four transgenes together are compatible with being co-in the virus.

The presently claimed invention relates to virus accomodating said four transgenes colocated between the fibre, L5, and the E4 region.

SUMMARY OF INVENTION

The following paragraphs are a summary of the present disclosure:

1. An adenovirus comprising a sequence of formula **(I)**:

$$5'ITR\text{-}B_1\text{-}B_A\text{-}B_2\text{-}B_X\text{-}B_B\text{-}B_Y\text{-}B_3\text{-}3'ITR \quad \textbf{(I)}$$

wherein:

B_1 is a bond or comprises: E1A, E1B or E1A-E1B;

B_A comprises-E2B-L1-L2-L3-E2A-L4;

B_2 is a bond or comprises: E3;

B_X is a bond or a DNA sequence comprising: a restriction site, one or more transgenes or both;

B_B comprises L5;

B_Y comprises a transgene cassette containing four transgenes, said genes encoding a FAP-BITE, CXL10, CXL9, and IFN;

B_3 is a bond or comprises: E4.

2. An adenovirus according to paragraph 1, wherein the encoded FAB-BITE comprises an anti-CD3 shown in SEQ ID NO: 5 or a sequence at least 95% identical thereto, such as SEQ ID NO: 5.
3. An adenovirus according to paragraph 1 or 2 wherein the FAP-BITE comprises an anti-FAP shown in SEQ ID NO: 9 or a sequence at least 95% identical thereto, such as SEQ ID NO: 9
4. An adenovirus according to paragrah 1, wherein the encoded FAB-BITE comprises a sequence selected from SEQ ID NO: 75, SEQ ID NO: 76 or a sequence at least 95% identical to any one thereof.
5. An adenovirus according to any one of paragraphs 1 to 4, wherein the transgene cassette encodes CXL10 shown in SEQ ID NO: 100 or a sequence at least 95% identical thereto, such as SEQ ID NO: 100.
6. An adenovirus according to any one of paragraphs 1 to 5, wherein the transgene cassette encodes CXCL9 shown in SEQ ID NO: 99 or a sequence at least 95% identical thereto, such as SEQ ID NO: 99.
7. An adenovirus according to any one of paragraphs 1 to 6, wherein the transgene cassette encodes IFNα shown in SEQ ID NO: 98 or a sequence at least 95% identical thereto, such as SEQ ID NO: 98.
8. An adenovirus according to any one of paragraphs 1 to 7, wherein the transgenes are operably linked.
9. An adenovirus according to any one of paragraphs 1 to 8, wherein the transgenes are separated by 3 different high efficiency self-cleavage peptides.
10. An adenovirus according to paragraph 9, wherein the self-cleavage peptides are independently selected from E2A, F2A, P2A and T2A.
11. An adenovirus according to any one of paragraphs 1 to 10, wherein the relative order of the transgenes from L5 to E4 is FAP-BITE, CXL10, CXL9 and IFNα, for example as shown for NG-641 in Figure 1.
12. An adenovirus according to any one of paragraphs 1 to 11, wherein the transgene cassette has a polynucleotide sequence shown in SEQ ID NO: 95 or a polynucleotide encoding the same amino acid sequence, in particular SEQ ID NO: 95.
13. An adenovirus according to any one of paragraphs 1 to 12, wherein the adenovirus comprises SEQ ID NO: 84.

14. An adenovirus according to any one of paragraphs 1 to 13, wherein the adenovirus is replication competent.
15. An adenovirus according to any one of paragraphs 1 to14, wherein the adenovirus is oncolytic.
16. An adenovirus according to any one of paragraphs 1 to 15, wherein the virus has a hexon and fibre from Ad11.
17. A pharmaceutical composition comprising an adenovirus according to any one of paragraphs 1 to 16 and an excipient, diluent or carrier.
18. An adenovirus according to any one of paragraphs 1 to 16, or a pharmaceutical composition according to paragraph 17, for use in treatment, for example for use in the treatment of cancer.
19. A method of treating a patient comprising administering an adenovirus according to any one of paragraphs 1 to 16 or a pharmaceutical composition according to paragraph 17.
20. Use an adenovirus according to any one of paragraphs 1 to 16, or a pharmaceutical composition according to paragraph 17, for the manufacture of a medicament for the treatment of cancer.

In one embodiment the BiTE or BiTEs of according to the present disclosure do not comprise a transmembrane domain and so are not expressed on the cancer cell surface but rather comprises a signal sequence to facilitate release of the BiTE molecule from the cancer cell infected by the virus.

In one embodiment the transgene cassette is under the control of an endogenous promoter, for example the major later promoter.

Advantageously, the present inventors have discovered that arming an adenovirus with a BiTE molecule allows the bi-specific antibody fragment molecule to 'piggyback' on the ability of the adenovirus to selectively infect cancer cells, thereby enabling the targeted delivery of the BiTE to tumour cells.

Advantageously, BiTEs are small and can be made in mammalian cells. Hence once infected by the adenoviruses of the present disclosure, the BiTE molecules are synthesized by tumour cells, secreted and can act locally, spreading beyond the immediate footprint of the virus. This therefore allows the BiTE to spread beyond the immediate site of infection but at the same time limits the spread of the virus too far beyond the infected tumour cell site. This minimises the risk of undesired off-target effects.

In one embodiment, the adenovirus is EnAd. EnAd has been shown to have an enhanced oncolytic activity compared to other adenovirus platforms, for example based on Ad5. EnAd has also been shown to have a high selectivity for human epithelial-derived carcinoma cells, such as colon, lung, bladder and renal cancer cells. This makes it an ideal delivery vehicle for BiTE molecules because T-cells can be activated by the BiTE molecule to attack target cells whilst EnAd simultaneously infects and lyses cancer cells. This results in a two-pronged attack on the tumour which has a synergistic oncolytic effect.

In one embodiment the anti-CD3 component of the BITE is selective for an antigen selected from CD3ε, CD3γ and CD3δ, in particular CD3ε.

FAP is a tumour stroma antigen. Advantageously, stromal cells (non-transformed cells) expressing these antigens are not subjected to the same level of mutation-resistance-selection process as transformed cells. Therefore, these cells are easier to target for cancer therapy since they are not a 'moving target'. Furthermore, the types of receptors found in stromal cells are often common across different types of cancer. Hence, targeting FAP is likely to be effective for multiple cancer types.

Advantageously, FAP is upregulated on tumour associated fibroblasts. Fibroblasts are a vital component of solid carcinomas supporting growth, invasion and recovery from interventions. They typically comprise 40-60% of the cells in advanced carcinomas. Advantageously, fibroblasts are genetically stable cells that are less likely to escape therapy than cancers cells. Activated fibroblasts are also relatively similar across a variety of tumour types. Thus, by activating T cells to target and kill FAP expressing tumour associated fibroblasts, the adenoviruses of the present disclosure can help to diminish a spectrum of immune suppressive pathways, such as those mediated by IL-10, TGFβ and IDO.

In one embodiment B_X is not a bond.

In one embodiment the adenovirus is chimeric. In one embodiment the adenovirus is oncolytic. In one embodiment the adenovirus is chimeric and oncolytic. In one embodiment the adenovirus replication capable. In one embodiment the adenovirus is chimeric, oncolytic and replication capable. In one embodiment the adenovirus is replication competent. In another embodiment the adenovirus is chimeric, oncolytic and replication competent. In one embodiment the adenovirus is replication deficient, i.e. is a vector.

In one embodiment B_X comprises a transgene or transgene cassette, in particular a transgene cassette encoding a BiTE. In one embodiment the further transgene is under the control of an exogenous promoter, such as a CMV promoter.l

Employing an exogenous promoter may be advantageous in some embodiments because it can strongly and constitutively express the antibody or fragment, which may be particularly useful in some situations, for example where the patient has very pervasive cancer. Advantageously, the use of a constitutive exogenous promoter results in continuous transcription of the transgene which may be desirable in certain instances.

In one embodiment the transgene cassette, comprises a Kozak sequence, for example at the start of the coding sequence, in particular at the L5 end of the transgene cassette.

In one embodiment the transgene cassette further comprises a polyadenylation sequence, for example at the end of the sequence, in particular at the E4 region end of the transgene cassette.

In one embodiment the transgene cassette has the arrangement shown in Fig 1, such as virus NG-641.

In one embodiment the BiTE molecule has short half-life, for example 48 hours or less.

In one embodiment the adenovirus only contains one BiTE.

In another embodiment the adenovirus contains two BiTEs.

In one embodiment the FAP-BiTE comprises a VH domain comprising an amino acid sequence as set forth in SEQ ID NO: 11, or an amino acid sequence that is at least 95% identical thereto.

In one embodiment the FAP-BiTE comprises a VL domain comprising an amino acid sequence set forth in SEQ ID NO: 10, or an amino acid sequence that is at least 95% identical thereto.

In one embodiment the anti-CD3 portion of the FAP-BiTE comprises a VH domain comprising an amino acid sequence set forth in SEQ ID NO: 6, or an amino acid sequence that is at least 95% identical thereto.

In one embodiment the anti-CD3 portion of the FAP-BiTE comprises a VL domain comprising an amino acid sequence set forth in SEQ ID NO: 7, or an amino acid sequence that is at least 95% identical thereto.

In one embodiment the adenovirus according to the present disclosure comprises a sequence set forth in SEQ ID NO: 34 or 35, or a polynucleotide encoding the same scFv amino acid sequence, in particular SEQ ID NO: 34.

In one embodiment the adenovirus according to the present disclosure comprises a sequence set forth in SEQ ID NO: 68, SEQ ID NO: 69 or a polynucleotide sequence encoding the same amino acid sequence.

In one embodiment the adenovirus according to the present disclosure comprises a sequence set forth in SEQ ID NO: 90 or a polynucleotide encoding the same amino acid sequence.

In one embodiment the adenovirus according to the present disclosure comprises a sequence set forth in SEQ ID NO: 91 or a polynucleotide encoding the same amino acid sequence.

In one embodiment the adenovirus according to the present disclosure comprises a sequence set forth in SEQ ID NO: 92 or a polynucleotide encoding the same amino acid sequence.

The skilled person is aware that there is redundcy in the DNA code, thus the present disclosure extends to EnAd or Ad11 encoding a BiTE with an amino acid disclosed herein.

A C-terminal His affinity tag (suchas a deca or hexa-his tag) is useful for purification of the BiTE or adenovirus. However, it is optional and may be excluded for example in the end product. The skilled person is aware that other affinity tags other than deca-His can be used and likewise may be excluded without affecting the biological function of the BiTE or adenovirus.

Accordingly, in one embodiment the BiTE comprises an amino acid sequence as set forth in SEQ ID NO: 1 or 2 but excludes the His affinity tag at the C-terminal end of the sequence, such as SEQ ID NO: 61 or 62.

The exclusion of the deca-His affinity tag further extends to all other sequences disclosed herein comprising the deca-His affinity tag, i.e. the present disclosure includes the same amino acid or DNA sequences lacking the C-terminal His tag.

In one aspect there is provided a composition comprising an adenovirus as described herein and a diluent or carrier.

In one aspect, there is provided a method of treating a patient comprising administering a therapeutically effective amount of an adenovirus or a composition as described herein.

In one embodiment the method is for the treatment of cancer, for example an epithelial cancer, in particular a solid tumour.

In one embodiment there is provide a method of treatment comprising administering a virus according to the present disclosure in combination with a checkpoint inhibitor (such as a PD-1 or PDL1 inhibitor), in particular wherein the checkpoint inhibitor is encoding in the virus.

In one embodiment there is provide a method of treatment comprising administering a virus according to the present disclosure which is NOT in combination with a checkpoint inhibitor (for example as listed elsewhere herein such as a PD-1 or PDL1 inhibitor), in particular wherein the checkpoint inhibitor is not encoding in the virus.

The BiTEs encoded by the virus as per the present disclosure have the ability to potentiate the cytotoxicity of the virus.

Surprisingly the BiTes encoded by a virus as *per* the present disclosure can activate CD4+ cells and/or CD8+ cells, for example even cells in the suppressive environment of the tumor, including T cells in the fluid environment, such as ascites, of the tumor.

Advantageously the BiTes encoded by a virus as *per* the present disclosure can activate cytotoxic T cells, for example even T cells in the suppressive environment of the tumor, including T cells in the fluid environment, such as ascites, of the tumor.

Even more surprisingly the BiTEs encoded by a virus as *per* the present disclosure are capable of stimulating (activating) T cell proliferation.

The viruses encoding BiTEs according to the present disclosure seem to be able to by-pass, overcome or reverse the immune suppressive microenvironment of the tumor.

In one embodiment the activation of T cells results in upregulation of a T cell marker, for example CD25.

DETAILED DESCRIPTION

Immune cell as employed herein is a cell with a funcational role in the immune system, including (but not limited to), macrophages, neutrophils, dendritic cells, NK cells, lymphocytes, such as T lymphocytes (in particular T cells and NKT cells).

Antigen binding site as employed herein refers to a portion of the molecule, which comprises a pair of variable regions, in particular a cognate pair that interact specifically with the target antigen.

Specifically, as employed herein, is intended to refer to a binding site that only recognises the antigen to which it is specific or a binding site that has significantly higher binding affinity to the antigen to which it is specific compared to affinity to antigens to which it is non-specific, for example 5, 6, 7, 8, 9, 10 times higher binding affinity. Affinity can be measured by techniques such as BIAcore.

Bi-specific antibody molecule as employed herein refers to a molecule with two antigen binding domains, which may bind the same or different antigens. A BiTE is a subclass of bispecific antibody molecules.

BITE as employed herein refers to a bispecific T cell engager, in particular comprising an anti-CD3 binding domain and a further binding domain, in this instance an anti-FAP binding domain. Generally, the binding domains are in the form of a scFv. A diagrammatic representation of a BiTE is shown in s Fig 12.

Thus, Bispecific T cell Engager (BiTE) as used herein refers to a class of artificial bispecific monoclonal antibodies comprising 2 scFvs of different antibodies or amino acid sequences from 4 different genes on a single peptide chain of about 55 KDa. One of the scFvs is specific for an immune cell, such as a T cell antigen, such as the CD3 receptor, expressed on the surface of T cells. The other scFv, in the prior art, typically binds to a tumour cell via a tumour-specific molecule. Accordingly, BiTEs are able to form a link between T cells and tumour cells by virtue of their specificities for an antigen on the T cell and an antigen on the tumour cell. This leads to activation of the T-cells and triggers the T cells to exert their cytotoxic effects on tumour cells, independently of MHC I or co-stimulatory molecules.

In one embodiment the T cell engager is arranged is the format VL1-linker1-VH1-linker2-VH2-linker3-VL2, for example employing linkers independently selected from linker sequences disclosed herein.

In one embodiment the BITE Linker is in the range 10 to 30 amino acids in length, such as 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29 or 30, for example a linker disclosed herein.

Stroma or stromal antigen as employed herein refers to an antigen therapeutic target in the stroma, including expressed in the molecular structure of the stroma matrix, such as connective tissue molecules or molecules associated with this matrix or antigens associated with the cellular components of the stroma, for example expressed on fibroblasts, tumour-associated macrophages, dendritic cells, NK cells and/or T-cells which have infiltrated the stroma. Examples of stroma antigens include but are not limited to FAP, TGFβ, TREM1, IGFBP7, FSP-1, fibroblast associated antigen, NG2, endosialin (CD248), platelet-derived growth factor-α receptor (PDGFR-α), platelet-derived growth factor-β receptor (PDGFR-β) and vimentin. Generally stromal antigens are not expressed on cancer cells i.e. they are only expressed on stromal cells.

Fibroblasts may be targeted by employing the antigen fibroblast activation protein (FAP), in particular an antibody specific to FAP which does not bind CD26, (see US2012/0258119 incorporated herein by reference).

FAP was originally identified as a serine protease on reactive stromal fibroblasts. Subsequent molecular cloning revealed that FAP is identical to seprase, a 170 kDa membrane associated gelatinase that is expressed by melanoma cell lines. Full length cDNA encoded a type H transmembrane protease of 760 amino acids (aa) highly homologous to dipeptidyl peptidase IV (DPPIV) with a 52% aa identity over the entire sequence and almost 70% identity in the catalytic domain. US5,587,299, incorporated herein by reference, describes nucleic acid molecules encoding FAP and applications thereof.

In summary, FAP is recognized as a multifunctional protein that executes its biological functions in a cell dependent manner through a combination of its protease activity and its ability to form complexes with other cell-surface molecules. Over-expression of FAP in epithelial and fibroblastic cell lines promotes malignant behaviour, pointing to the clinical situation, where cellular expression levels of FAP are correlated with worse clinical outcome.

Through paracrine signaling molecules, cancer cells activate stromal fibroblasts and induce the expression of FAP, which in turn, affects the proliferation, invasion and migration of the cancer cells. Recent studies have demonstrated that TGF-β is the dominant factor in promoting FAP protein expression (Chen, H et al (2009) Exp and Molec Pathology, doi: 10.1016/j.yexmp. 2009.09.001). FAP is heavily expressed on reactive stromal fibroblasts in 90% of human epithelial carcinomas, including those of the breast, lung, colorectum and ovary (Garin-Chesa, P et al (1990) PNAS USA 87: 7236-7239). Chen *et al* have recently shown that FAPα influences the invasion, proliferation and migration of HO-8910PM ovarian cancer cells (Chen, H *et al* (2009) Exp and Molec Pathology, doi: 10.1016/j.yexmp. 2009.09.001).

FAP may be targeted by binding said antigen and sterically blocking its interaction with biologically relevant molecules. Alternatively, or additionally cross-linking the FAP molecule with another FAP molecule or a different molecule, for example to T cells. This cross linking raised the visibility of the cells bearing the FAP to the immune systems, which then may be activated to neutral or destroy the same.

The adenovirus of the present disclosure has the ability to infect tumour cells, and in particular is chosen to preferentially infect tumour, cells. The oncolytic virus infection causes death and lysis of the cancer cell with release of newly generated virus particles. Incorporated transgenes such as BiTEs and cytokine are synthesized in th cells and actively secreted by said tumor cells prior to their death. Some molecules will also be released upon cell lysis.

Antibody molecules, such as BiTEs, with a short half-life may be particularly suitable for use in the present disclosure because this minimises off-target effects because the body rapidly clears the molecules if they become systemically available.

Thus, the adenovirus according to the present disclosure has at least two or three mechanisms for attacking the tumour, including indirect mechanisms which undermine the tumour stroma.

Transgene as employed herein refers to a gene that has been inserted into the genome sequence, which is a gene that is unnatural to the virus (exogenous) or not normally found in that particular location in the virus. Examples of transgenes are known in the art and discussed herein. Transgene as employed herein also includes a functional fragment of the gene that is a portion of the gene which when inserted is suitable to perform the function or most of the function of the full-length gene.

Transgene and coding sequence are used interchangeably herein in the context of inserts into the viral genome, unless the context indicates otherwise. Coding sequence as employed herein means, for example a DNA sequence encoding a functional RNA, peptide, polypeptide or protein. Typically, the coding sequence is cDNA for the transgene that encodes the functional RNA, peptide, polypeptide or protein of interest. Functional RNA, peptides, polypeptide and proteins of interest are described below.

Clearly the virus genome contains coding sequences of DNA. Endogenous (naturally occurring genes) in the genomic sequence of the virus are not considered a transgene, within the context of the present specification unless then have been modified by recombinant techniques such that they are in a non-natural location or in a non-natural environment.

In one embodiment transgene, as employed herein refers to a segment of DNA containing a gene or cDNA sequence that has been isolated from one organism and is introduced into a different organism i.e. the virus of the present disclosure. In one embodiment, this non-native segment of DNA may retain the ability to produce functional RNA, peptide, polypeptide or protein.

Thus, in one embodiment the transgene inserted encodes a human or humanised protein, polypeptide or peptide.

Operably linked as employed herein refers to transgenes being associated with the necessary regulatory elements to allo the genes to be functional i.e. to allow the genes to expressed using the cellularly machinery once the virus inside the cell.

In one or more embodiments, the cassette is arranged as shown in the one or more of the Figures or the examples.

Transgene cassette as employed herein refers to a DNA sequence encoding one or more transgenes in the form of one or more coding sequences and one or more regulatory elements.

A transgene cassette may encode one or more monocistronic and/or polycistronic mRNA sequences.

In one embodiment, the transgene or transgene cassette encodes a monocistronic or polycistronic mRNA, and for example the cassette is suitable for insertion into the adenovirus genome at a location under the control of an endogenous promoter or exogenous promoter or a combination thereof.

Monocistronic mRNA as employed herein refers to an mRNA molecule encoding a single functional RNA, peptide, polypeptide or protein.

In one embodiment, the transgene cassette encodes monocistronic mRNA.

In one embodiment the transgene cassette in the context of a cassette encoding monocistronic mRNA means a segment of DNA optionally containing an exogenous promoter (which is a regulatory sequence that will determine where and when the transgene is active) or a splice site (which is a regulatory sequence determining when a mRNA molecule will be cleaved by the spliceosome) a coding sequence (i.e. the transgene), usually derived from the cDNA for the protein of interest, optionally containing a polyA signal sequence and a terminator sequence.

In one embodiment, the transgene cassette may encode one or more polycistronic mRNA sequences.

Polycistronic mRNA as employed herein refers to an mRNA molecule encoding two or more functional RNA, peptides or proteins or a combination thereof. In one embodiment the transgene cassette encodes a polycistronic mRNA.

In one embodiment transgene cassette in the context of a cassette encoding polycistronic mRNA includes a segment of DNA optionally containing an exogenous promoter (which is a regulatory sequence that will determine where and when the transgene is active) or a splice site (which is a regulatory sequence determining when a mRNA molecule will be cleaved by the spliceosome) two or more coding sequences (i.e. the transgenes), usually derived from the cDNA for the protein or peptide of interest, for example wherein each coding sequence is separated by either an IRES or a 2A peptide. Following the last coding sequence to be transcribed, the cassette may optionally contain a polyA sequence and a terminator sequence.

In one embodiment, the transgene cassette encodes a monocistronic mRNA followed by a polycistronic mRNA. In another embodiment the transgene cassette a polycistronic mRNA followed by a monocistronic mRNA.

In one embodiment, the adenovirus is a human adenovirus. “Adenovirus”, “serotype” or adenoviral serotype” as employed herein refers to any adenovirus that can be assigned to any of the over 50 currently known adenoviral serotypes, which are classified into subgroups A-F, and further extends to any, as yet, unidentified or unclassified adenoviral serotypes. See, for example, Strauss, "Adenovirus infections in humans," in The Adenoviruses, Ginsberg, ea., Plenum Press, New York, NY, pp. 451-596 (1984) and Shenk, "Adenoviridae: The Viruses and Their Replication," in Fields

Virology, Vol.2, Fourth Edition, Knipe, 35ea., Lippincott Williams & Wilkins, pp. 2265-2267 (2001), as shown in Table 1.

Table 1

SubGroup	Adenoviral Serotype
A	12,18,31
B	3,7,11,14,16,21,34,35,51
C	1,2,5,6
D	8-10,13,15,17,19,20,22-30,32,33,36-39,42-49,50
E	4
F	40,41

In one embodiment the adenoviruses of the present disclosure are subgroup B viruses, namely, Ad11, in particular Ad11p (the Slobitski strain) and derivatives thereof, such as EnAd.

Adenoviruses are allocated to their groups/serotypes based on the capsid, such as the hexon and/or fibre

In one embodiment the adenovirus of the present disclosure is not a group A, C, D, E or F virus. The viruses of the present disclosure do not comprise an adenovirus death protein.

In one embodiment, the adenovirus of the present disclosure is chimeric. When an adenovirus is chimeric then the characteristics of the outer capsid will be employed to determine the serotype. Chimeric as employed herein refers to a virus that comprises DNA from at least two different virus serotypes, including different serotypes within the same group.

In one embodiment, the oncolytic virus has a fibre, hexon and penton proteins from the same serotype, for example Ad11, in particular Ad11p, for example found at positions 30812-31789, 18254-21100 and 13682-15367 of the genomic sequence of the latter wherein the nucleotide positions are relative to genbank ID 217307399 (accession number: GC689208).

In one embodiment, the adenovirus is enadenotucirev (also known as EnAd and formerly as EnAd). Enadenotucirev as employed herein refers the chimeric adenovirus of SEQ ID NO: 28. It is a replication competent oncolytic chimeric adenovirus which has enhanced therapeutic properties compared to wild type adenoviruses (see WO2005/118825). EnAd has a chimeric E2B region, which features DNA from Ad11p and Ad3, and deletions in E3/E4. The structural changes in enadenotucirev result in a genome that is approximately 3.5kb smaller than Ad11p thereby providing additional "space" for the insertion of transgenes. Almost all of the E3 region and part of the E4 region is deleted in EnAd. Therefore, it has significant space in the genome to accommodate additional genetic material whilst remaining viable. Furthermore, because EnAd is a subgroup B adenovirus, pre-existing immunity in humans is less common than, for example, Ad5. Other examples of chimeric oncolytic viruses with Ad11 fibre, penton and hexon include OvAd1 and OvAd2 (see WO2008/080003 incorporated by reference). Thus in one embodiment the adenovirus employed in OvAd1 or OvAd2.

EnAd seems to preferentially infect tumour cells, replicates rapidly in these cells and causes cell lysis. This, in turn, can generate inflammatory immune responses thereby stimulating the body to also fight the cancer. Part of the success of EnAd is hypothesised to be related to the fast replication of the virus *in vivo*.

Advantageously arming a virus, with DNA encoding certain proteins, such as a BiTE, that can be expressed inside the cancer cell, may enable the body's own defences to be employed to combat tumour cells more effectively, for example by making the cells more visible to the immune system or by delivering a therapeutic gene/protein preferentially to target tumour cells.

It is important that expression of the transgenes does not adversely affect the replication or other advantageous properties of the virus. Thus, the gene or genes must be inserted in a location that does not compromise the replication competence and other advantageous properties of the virus. In addition, the genome of adenoviruses is tightly packed and therefore it can be difficult to find a suitable location to insert transgenes. This also limits the size of transgenes that can be accommodated.

Oncolytic adenovirus as employed herein means an adenovirus that preferentially kills cancer cells as compared with non-cancer cells. In one embodiment, the oncolytic virus is apoptotic. That is, it hastens programmed cell death.

In one embodiment, the oncolytic virus is cytolytic. The cytolytic activity of oncolytic adenoviruses of the disclosure can be determined in representative tumour cell lines and the data converted to a measurement of potency, for example with an adenovirus belonging to subgroup C, such as Ad5, being used as a standard (i.e. given a potency of 1). A suitable method for determining cytolytic activity is an MTS assay (see Example 4, Figure 2 of WO2005/118825 incorporated herein by reference).

In one embodiment the oncolytic virus is necrolytic. That is, it causes or hastens cell necrosis or immunogenic cell death. In one embodiment necrolytic cell death is advantageous because it triggers, induces the patients (host) immune responses.

Unless the context indicates otherwise, adenovirus as employed herein refers to a replication capable virus (such as a replication competent virus) and also replication deficient viral vectors.

Replication capable as employed herein refers to a replication competent virus or a virus whose replication is dependent on a factor in the cancer cells, for example an upregulated factor, such as p53 or similar.

In one embodiment the virus is replication competent. Replication competent in the context of the present specification refers to a virus that possesses all the necessary machinery to replicate in cells *in vitro* and *in vivo*, i.e. without the assistance of a packaging cell line. A viral vector, for example deleted in the E1 region, capable of replicating in a complementary packaging cell line is not a replication competent virus in the present context.

Viral vectors are replication deficient and require a packaging cell to provide a complementary gene to allow replication.

Adenovirus genome as employed herein means the DNA sequence encoding the structural proteins and elements relevant to the function/life cycle of an adenovirus.

All human adenovirus genomes examined to date have the same general organisation i.e., the genes encoding specific functions are located at the same position in the viral genome (referred to herein as structural elements). Each end of the viral genome has a short sequence known as the inverted terminal repeat (or ITR), which is required for viral replication. The viral genome contains five early transcription units (E1A, E1B, E2, E3, and E4), three delayed early units (IX, IVa2 and E2 late) and one late unit (major late) that is processed to generate five families of late mRNAs (L1-L5).

Proteins encoded by the early genes are primarily involved in replication and modulation of the host cell response to infection, whereas the late genes encode viral structural proteins. Early genes are prefixed by the letter E and the late genes are prefixed by the letter L.

The genome of adenoviruses is tightly packed, that is, there is little non-coding sequence, and therefore it can be difficult to find a suitable location to insert transgenes.

In one embodiment the oncolytic or partial oncolytic virus according to the disclosure may be as a result of deletion in the E4 and/or E3 region, for example deleted in part of the E4 region or fully deleted in the E3 region, or alternatively deleted in part of the E4 region (such as E4orf4) and fully deleted in the E3 region, for example as exemplified in the sequences disclosed herein.

In one embodiment the oncolytic virus is EnAd or an active derivate thereof which retains the essential beneficial properties of the virus. EnAd is disclosed in WO2005/118825 (incorporated herein by reference) and the full sequence for the virus is provided herein SEQ ID NO: 28. The chimeric E2B region is disclosed herein as SEQ ID NO: 60.

Advantageously, the adenoviruses of the present disclosure exhibit similar virus activity, for example replication and/or infectivity, profiles to EnAd following infection of a variety of different colon cancer cell lines *in vitro*.

STRUCTURAL ELEMENTS OF ADENOVIRUSES

As the structure of adenoviruses is, in general, similar the elements below are discussed in terms of the structural elements and the commonly used nomenclature referring thereto, which are known to the skilled person. When an element is referred to herein then we refer to the DNA sequence encoding the element or a DNA sequence encoding the same structural protein of the element in an adenovirus. The latter is relevant because of the redundancy of the DNA code. The viruses' preference for codon usage may need to be considered for optimised results.

Any structural element from an adenovirus employed in the viruses of the present disclosure may comprise or consist of the natural sequence or may have similarity over the given length of at least 95%, such as 96%, 97%, 98%, 99% or 100%. The original sequence may be modified to omit 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2% or 1% of the genetic material. The skilled person is aware that when making changes the reading frames of the virus must be not disrupted such that the expression of structural proteins is disrupted.

In one embodiment the given element is a full-length sequence i.e. the full-length gene.

In one embodiment the given element is less than a full-length and retains the same or corresponding function as the full-length sequence.

In one embodiment for a given element which is optional in the constructs of the present disclosure, the DNA sequence may be less than a full-length and have no functionality.

The structural genes encoding structural or functional proteins of the adenovirus are generally linked by non-coding regions of DNA. Thus, there is some flexibility about where to "cut" the genomic sequence of the structural element of interest (especially non-coding regions thereof) for the purpose of inserting a transgene into the viruses of the present disclosure. Thus for the purposes of the present specification, the element will be considered a structural element of reference to the extent that it is fit for purpose and does not encode extraneous material. Thus, if appropriate the gene will be associated with suitable non-coding regions, for example as found in the natural structure of the virus.

Thus, in one embodiment an insert, such as DNA encoding a restriction site and/or transgene, is inserted into a non-coding region of genomic virus DNA, such as an intron or intergenic sequence. Having said this some non-coding regions of adenovirus may have a function, for example in alternative splicing, transcription regulation or translation regulation, and this may need to be taken into consideration.

The sites identified herein, that are associated with the L5 region (for example between L5 and the E4 region), are suitable for accommodating a variety of DNA sequences encoding complex entities such as RNAi, cytokines, single chain or multimeric proteins, such as antibodies, such as a BiTE.

Gene as employed herein refers to coding and optionally any non-coding sequences associated therewith, for example introns and associated exons. In one embodiment a gene comprises or consists of only essential structural components, for example coding region.

Below follows a discussion relating to specific structural elements of adenoviruses.

The Inverted Terminal Repeat (ITR) sequences are common to all known adenoviruses and were so named because of their symmetry, and are the viral chromosome origins of replication. Another property of these sequences is their ability to form a hairpin.

The 5'ITR as employed herein refers to part or all of an ITR from the 5' end of an adenovirus, which retains the function of the ITR when incorporated into an adenovirus in an appropriate location. In one embodiment the 5'ITR comprises or consists of the sequence from about 1bp to 138bp of SEQ ID NO: 28 or a sequence 90, 95, 96, 97, 98 or 99% identical thereto along the whole length, in particular the sequence consisting of from about 1bp to 138bp of SEQ ID NO: 28.

The 3'ITR as employed herein refers to part or all of an ITR from 3' end of an adenovirus which retains the function of the ITR when incorporated into an adenovirus in an appropriate location. In one embodiment the 3'ITR comprises or consists of the sequence from about 32189bp to 32326bp of SEQ ID NO: 28 or a sequence 90, 95, 96, 97, 98 or 99% identical thereto along the whole length, in particular the sequence consisting of from about 32189bp to 32326bp of SEQ ID NO: 28.

B_1 as employed herein refers to the DNA sequence encoding: part or all of an E1A from an adenovirus, part or all of the E1B region of an adenovirus, and independently part or all of E1A and E1B region of an adenovirus.

When B_1 is a bond then E1A and E1B sequences will be omitted from the virus. In one embodiment B_1 is a bond and thus the virus is a vector.

In one embodiment B_1 further comprises a transgene. It is known in the art that the E1 region can accommodate a transgene which may be inserted in a disruptive way into the E1 region (i.e. in the "middle" of the sequence) or part or all of the E1 region may be deleted to provide more room to accommodate genetic material.

E1A as employed herein refers to the DNA sequence encoding part or all of an adenovirus E1A region. The latter here is referring to the polypeptide/protein E1A. It may be mutated such that the protein encoded by the E1A gene has conservative or non-conservative amino acid changes, such that it has: the same function as wild-type (i.e. the corresponding non-mutated protein); increased function in comparison to wild-type protein; decreased function, such as no function in comparison to wild-type protein; or has a new function in comparison to wild-type protein or a combination of the same as appropriate.

E1B as employed herein refers to the DNA sequence encoding part or all of an adenovirus E1B region (i.e. polypeptide or protein), it may be mutated such that the protein encoded by the E1B gene/region has conservative or non-conservative amino acid changes, such that it has: the same function as wild-type (i.e. the corresponding non-mutated protein); increased function in comparison to wild-type protein; decreased function, such as no function in comparison to wild-type protein; or has a new function in comparison to wild-type protein or a combination of the same as appropriate.

Thus, B_1 can be modified or unmodified relative to a wild-type E1 region, such as a wild-type E1A and/or E1B. The skilled person can easily identify whether E1A and/or E1B are present or (part) deleted or mutated.

Wild-type as employed herein refers to a known adenovirus. A known adenovirus is one that has been identified and named, regardless of whether the sequence is available.

In one embodiment B_1 has the sequence from 139bp to 3932bp of SEQ ID NO: 28.

B_A as employed herein refers to the DNA sequence encoding the E2B-L1-L2-L3-E2A-L4 regions including any non-coding sequences, as appropriate. Generally, this sequence will not comprise a transgene. In one embodiment the sequence is substantially similar or identical to a contiguous sequence from a known adenovirus, for example a serotype shown in Table 1, in particular a group B virus, for example Ad3, Ad7, Ad11, Ad14, Ad16, Ad21, Ad34, Ad35, Ad51 or a combination thereof, such as Ad3, Ad11 or a combination thereof. In one embodiment is E2B-L1-L2-L3-E2A-L4 refers to comprising these elements and other structural elements associated with the region, for example B_A will generally include the sequence encoding the protein IV2a, for example as follows: IV2A IV2a-E2B-L1-L2-L3-E2A-L4.

In one embodiment the E2B region is chimeric. That is, comprises DNA sequences from two or more different adenoviral serotypes, for example from Ad3 and Ad11, such as Ad11p. In one embodiment the E2B region has the sequence from 5068bp to 10355bp of SEQ ID NO: 28 or a sequence 95%, 96%, 97%, 98% or 99% identical thereto over the whole length.

In one embodiment the E2B in component B_A comprises the sequences shown in SEQ ID NO: 60 (which corresponds to SEQ ID NO: 3 disclosed in WO2005/118825).

In one embodiment B_A has the sequence from 3933bp to 27184bp of SEQ ID NO: 28.

E3 as employed herein refers to the DNA sequence encoding part or all of an adenovirus E3 region (i.e. protein/polypeptide), it may be mutated such that the protein encoded by the E3 gene has conservative or non-conservative amino acid changes, such that it has the same function as wild-type (the corresponding unmutated protein); increased function in comparison to wild-type protein; decreased function, such as no function in comparison to wild-type protein or has a new function in comparison to wild-type protein or a combination of the same, as appropriate.

In one embodiment the E3 region is form an adenovirus serotype given in Table 1 or a combination thereof, in particular a group B serotype, for example Ad3, Ad7, Ad11 (in particular Ad11p), Ad14, Ad16, Ad21, Ad34, Ad35, Ad51 or a combination thereof, such as Ad3, Ad11 (in particular Ad11p) or a combination thereof.

In one embodiment the E3 region is partially deleted, for example is 95%, 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10%, 5% deleted.
In one embodiment B_2 is a bond, wherein the DNA encoding the E3 region is absent.

In one embodiment the DNA encoding the E3 region can be replaced or interrupted by a transgene. As employed herein "E3 region replaced by a transgene as employed herein includes part or all of the E3 region is replaced with a transgene.

In one embodiment the B_2 region comprises the sequence from 27185bp to 28165bp of SEQ ID NO: 28.

In one embodiment B_2 consists of the sequence from 27185bp to 28165bp of SEQ ID NO: 28.

B_X as employed herein refers to the DNA sequence in the vicinity of the 5' end of the L5 gene in B_B. In the vicinity of or proximal to the 5' end of the L5 gene as employed herein refers to: adjacent (contiguous) to the 5' end of the L5 gene or a non-coding region inherently associated herewith i.e. abutting or contiguous to the 5' prime end of the L5 gene or a non-coding region inherently associated therewith. Alternatively, in the vicinity of or proximal to may refer to being close the L5 gene, such that there are no coding sequences between the B_X region and the 5' end of L5 gene.

Thus, in one embodiment B_X is joined directly to a base of L5 which represents, for example the start of a coding sequence of the L5 gene.

Thus, in one embodiment B_X is joined directly to a base of L5 which represents, for example the start of a non-coding sequence, or joined directly to a non-coding region naturally associated with L5. A non-coding region naturally associated L5 as employed herein refers to part of all of a non-coding regions which is part of the L5 gene or contiguous therewith but not part of another gene.

In one embodiment B_X comprises the sequence of SEQ ID NO: 29. This sequence is an artificial non-coding sequence wherein a DNA sequence, for example comprising a transgene (or transgene cassette), a restriction site or a combination thereof may be inserted therein. This sequence is advantageous because it acts as a buffer in that allows some flexibility on the exact location of the transgene whilst minimising the disruptive effects on virus stability and viability.

The insert(s) can occur anywhere within SEQ ID NO: 29 from the 5' end, the 3' end or at any point between bp 1 to 201. In one embodiment B_X comprises SEQ ID NO: 29 with a DNA sequence inserted between bp 27 and bp 28 or a place corresponding to between positions 28192bp and 28193bp of SEQ ID NO: 28.

In one embodiment the insert is a restriction site insert. In one embodiment the restriction site insert comprises one or two restriction sites. In one embodiment the restriction site is a 19bp restriction site insert comprising 2 restriction sites. In one embodiment the restriction site insert is a 9bp restriction site insert comprising 1 restriction site. In one embodiment the restriction site insert comprises one or two restriction sites and at least one transgene, for example one or two transgenes. In one embodiment the restriction site is a 19bp restriction site insert comprising 2 restriction sites and at least one transgene, for example one or two transgenes. In one embodiment the restriction site insert is a 9bp restriction site insert comprising 1 restriction site and at least one transgene, for example one, two or three transgenes, such as one or two. In one embodiment two restriction sites sandwich one or more, such as two transgenes (for example in a transgene cassette). In one embodiment when B_X comprises two restrictions sites the said restriction sites are different from each other. In one embodiment said one or more restrictions sites in B_X are non-naturally occurring in the particular adenovirus genome into which they have been inserted. In one embodiment said one or more restrictions sites in B_X are different to other restrictions sites located elsewhere in the adenovirus genome, for example different to naturally occurring restrictions sites and/or restriction sites introduced into other parts of the genome, such as a restriction site introduced into B_Y. Thus in one embodiment the restriction site or sites allow the DNA in the section to be cut specifically.

DNA sequence in relation to B_Y as employed herein refers to the DNA sequence in the vicinity of the 3' end of the L5 gene of B_B. In the vicinity of or proximal to the 3' end of the L5 gene as employed herein refers to: adjacent (contiguous) to the 3' end of the L5 gene or a non-coding region inherently associated therewith i.e. abutting or contiguous to the 3' prime end of the L5 gene or a non-coding region inherently associated therewith (i.e. all or part of an non-coding sequence endogenous to L5). Alternatively, in the vicinity of or proximal to may refer to being close the L5 gene, such that there are no coding sequences between the B_Y region and the 3' end of the L5 gene.

Thus, in one embodiment B_Y is joined directly to a base of L5 which represents the “end” of a coding sequence.

Thus, in one embodiment B_Y is joined directly to a base of L5 which represents the “end” of a non-coding sequence, or joined directly to a non-coding region naturally associated with L5.

Inherently and naturally are used interchangeably herein. In one embodiment B_Y comprises the sequence of SEQ ID NO: 30. This sequence is a non-coding sequence wherein a DNA sequence, for example comprising a transgene (or transgene cassette), a restriction site or a combination thereof may be inserted. This sequence is advantageous because it acts a buffer in that allows some flexibility on the exact location of the transgene whilst minimising the disruptive effects on virus stability and viability.

The insert(s) can occur anywhere within SEQ ID NO: 30 from the 5' end, the 3' end or at any point between bp 1 to 35, for example between base pairs 1/2, 2/3, 3/4, 4/5, 5/6, 6/7, 7/8, 8/9, 9/10, 10/11, 11/12, 12/13, 13/14, 14/15, 15/16, 16/17, 17/18, 18/19, 19/20, 20/21, 21/22, 22/23, 23/24, 24/25, 25/26, 26/27, 27/28, 28/29, 29/30, 30/31, 31/32, 32/33, 33/34, or 34/35.

E4 as employed herein refers to the DNA sequence encoding part or all of an adenovirus E4 region (i.e. polypeptide/protein region), which may be mutated such that the protein encoded by the E4 gene has conservative or non-conservative amino acid changes, and has the same function as wild-type (the corresponding non-mutated protein); increased function in comparison to wild-type protein; decreased function, such as no function in comparison to wild-type protein or has a new function in comparison to wild-type protein or a combination of the same as appropriate. In one embodiment the E4 region has E4orf4 deleted.

In one embodiment the E4 region is partially deleted, for example is 95%, 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, 15%, 10% or 5% deleted. In one embodiment the E4 region has the sequence from 32188bp to 29380bp of SEQ ID NO: 28.

In one embodiment B_3 is a bond, i.e. wherein E4 is absent.

In one embodiment B_3 has the sequence consisting of from 32188bp to 29380bp of SEQ ID NO: 28.

As employed herein number ranges are inclusive of the end points.

The skilled person will appreciate that the elements in the formulas herein, such as formula (I) are contiguous and may embody non-coding DNA sequences as well as the genes and coding DNA sequences (structural features) mentioned herein. In one or more embodiments, the formulas of the present disclosure are attempting to describe a naturally occurring sequence in the adenovirus genome. In this context, it will be clear to the skilled person that the formula is referring to the major elements characterising the relevant section of genome and is not intended to be an exhaustive description of the genomic stretch of DNA.

E1A, E1B, E3 and E4 as employed herein each independently refer to the wild-type and equivalents thereof, mutated or partially deleted forms of each region as described herein, in particular a wild-type sequence from a known adenovirus.

"Insert" as employed herein refers to a DNA sequence that is incorporated either at the 5' end, the 3' end or within a given DNA sequence reference segment such that it interrupts the reference sequence. The latter is a reference sequence employed as a reference point relative to which the insert is located. In the context of the present disclosure inserts generally occur within either SEQ ID NO: 29 or SEQ ID NO: 30. An insert can be either a restriction site insert, a transgene cassette or both. When the sequence is interrupted the virus will still comprise the original sequence, but generally it will be as two fragments sandwiching the insert.

In one embodiment the transgene or transgene cassette does not comprise a non-biased inserting transposon, such as a TN7 transposon or part thereof. Tn7 transposon as employed herein refers to a non-biased insertion transposon as described in WO2006/060314.

In one embodiment one or more restrictions sites in B_X and B_Y are independently selected from a restriction site specific to an enzyme described herein, for example *Not*I, *Fse*I, *AsiS*I, *Sgf*I and *Sbf*I, in particular the restriction sites inserted are all different, such as sites specific for *Not*I and sites specific for *Fse*I located in B_X and *Sgf*I and *Sbf*I located in B_Y.

As discussed above in one embodiment the region B_X and/or B_Y do not comprise a restriction site. Advantageously, the viruses and constructs of the present disclosure can be prepared without restriction sites, for example using synthetic techniques. These techniques allow a great flexibility in the creation of the viruses and constructs. Furthermore, the present inventors have established that the properties of the viruses and constructs are not diminished when they are prepared by synthetic techniques.

Other Regulatory Sequences

"Regulator of gene expression" (or regulator/regulatory element) as employed herein refers to a genetic feature, such as a promoter, enhancer or a splice acceptor sequence that plays a role in gene expression, typically by initiating or enhancing transcription or translation.

"Splice acceptor sequence", "splice acceptor" or "splice site" as employed herein refers to a regulatory sequence determining when an mRNA molecule will be recognised by small nuclear ribonucleoproteins of the spliceosome complex. Once assembled the spliceosome catalyses splicing between the splice acceptor site of the mRNA molecule to an upstream splice donor site producing a mature mRNA molecule that can be translated to produce a single polypeptide or protein.

Different sized splice acceptor sequences may be employed in the present invention and these can be described as short splice acceptor (small), splice acceptor (medium) and branched splice acceptor (large).

SSA as employed herein means a short splice acceptor, typically comprising just the splice site, for example 4 base pairs. SA as employed herein means a splice acceptor, typically comprising the short splice acceptor and the polypyrimidine tract, for example 16 bp. bSA as employed herein means a branched splice acceptor, typically comprising the short splice acceptor, polypyrimidine tract and the branch point, for example 26 base pairs.

In one embodiment, the SA and bSA splice acceptor employed in the constructs of the disclosure are shown in SEQ ID NO: 45 and 46 respectivley. In one embodiment, the SSA is employed in a cassette according to the present disclosure and has the nucleotide sequence CAGG.

In one embodiment the SA is employed in the cassette. In one embodiment the bSA is employed in the cassette.

In one embodiment the splice site is immediately proceeded (i.e. followed in a 5' to 3' direction) by a consensus Kozak sequence. In one embodiment the splice site and the Kozak sequence are separated by up to 100 or less base pairs. In one embodiment the Kozak sequence has the nucleotide sequence of SEQ ID NO: 47.

Typically, when under the control of an endogenous or exogenous promoter (such as an endogenous promoter), the coding sequence will be immediately preceded by a Kozak sequence. The start of the coding region is indicated by the initiation codon (AUG), for example is in the context of the sequence (gcc)gccRcc**AUG**g [SEQ ID NO: 48] the start of the “start” of the coding sequences is indicated by the bases in bold. A lower case letter denotes common bases at this position (which can nevertheless vary) and upper case letters indicate highly-conserved bases, *i.e.* the 'AUGG' sequence is constant or rarely, if ever, changes; 'R' indicates that a purine (adenine or guanine) is usually observed at this position and the sequence in brackets (gcc) is of uncertain significance. Thus, in one embodiment the initiation codon AUG is incorporated into a Kozak sequence.

Internal Ribosome Entry DNA Sequence as employed herein refers to a DNA sequence encoding an Internal Ribosome Entry Sequence (IRES). IRES as employed herein means a nucleotide sequence that allows for initiation of translation a messenger RNA (mRNA) sequence, including initiation starting within an mRNA sequence. This is particularly useful when the cassette encodes polycistronic mRNA. Using an IRES results in a polycistronic mRNA that is translated into multiple individual proteins or peptides. In one embodiment the Internal Ribosome Entry DNA sequence has the nucleotide sequence of SEQ ID NO: 49. In one embodiment a particular IRES is only used once in the genome. This may have benefits with respect to stability of the genome.

“High self-cleavage efficiency 2A peptide” or “2A peptide” as employed herein refers to a peptide which is efficiently cleaved following translation. Suitable 2A peptides include P2A, F2A, E2A and T2A. The present inventors have noted that once a specific DNA sequence encoding a given 2A peptide is used once, the same specific DNA sequence may not be used a second time. However, redundancy in the DNA code may be utilised to generate a DNA sequence that is translated into the same 2A peptide. Using 2A peptides is particularly useful when the cassette encodes polycistronic mRNA. Using 2A peptides results in a single polypeptide chain being translated which is modified post-translation to generate multiple individual proteins or peptides.

In one embodiment the encoded P2A peptide employed has the amino acid sequence of SEQ ID NO: 50. In one embodiment the encoded F2A peptide employed has the amino acid sequence of SEQ ID NO: 51. In one embodiment the encoded E2A peptide employed has the amino acid sequence of SEQ ID NO: 52. In one embodiment the encoded T2A peptide employed has the amino acid sequence of SEQ ID NO: 53.

In one embodiment an mRNA or each mRNA encoded by a transgene(s) comprise a polyadenylation signal sequence, such as typically at the end of an mRNA sequence, for example as shown in SEQ ID NO: 54. Thus one embodiment the transgene or the transgene cassette comprises at least one sequence encoding a polyadenylation signal sequence.

"PolyA", "Polyadenylation signal" or "polyadenylation sequence" as employed herein means a DNA sequence, usually containing an AATAAA site, that once transcribed can be recognised by a multiprotein complex that cleaves and polyadenylates the nascent mRNA molecule.

In one embodiment the polyadenylation sequence has the nucleotide sequence of SEQ ID NO: 54.

In one embodiment the construct does not include a polyadenylation sequence. In one embodiment the regulator of gene expression is a splice acceptor sequence.

Advantageously adenoviruses of the present disclosure express and release antibody forms (such as a BiTE) and other proteins, such as cytokines, encoded by a transgene therein into the culture supernatant *in vitro* or into tumour tissue stroma *in vivo*. Leader sequences may assist the encoded proteins/polypeptide or peptide exiting the cancer cell. Therefore, in one embodiment the encoded "protein" comprises a leader sequence. Leader sequence as employed herein refers to a polynucleotide sequence located between the promoter sequence and the coding region which can regulate gene expression at the level of transcription or translation.

In one embodiment, the adenovirus according to the present disclosure comprise a transgene which is a reporter gene encoding, for example an imaging agent including bioluminescent, fluorescent imaging agents (including activatable fluorescent imaging agents), such as luciferase, GFP or eGFP or red fluorescent protein.

Reporter gene or reporter sequence as employed herein means a gene or DNA sequence that produces a product easily detected in eukaryotic cells and may be used as a marker to determine the activity of another gene with which its DNA has been closely linked or combined. Reporter genes confer characteristics on cells or organisms expressing them that are easily identified and measured, or are selectable markers. Reporter genes are often used as an indication of whether a certain gene has been taken up by or expressed in the cell or organism population. Examples of common reporter genes include, but are not limited to, LacZ, luciferase, GFP, eGFP, neomycin phosphotransferase, chloramphenicol acetyltransferase, sodium iodide symporter (NIS), nitroreductase (e.g. NfsA, NfsB) intracellular metalloproteins, HSV1-tk or oestrogen receptor.

In one embodiment the genetic material (in particular the transgene) does not encode or express a reporter gene such as an imaging agent, luciferase, GFP or eGFP.

Viruses according to the present disclosure can be investigated for their preference for a specific tumour type by examination of its lytic potential in a panel of tumour cells, for example colon tumour cell lines include HT-29, DLD-1, LS174T, LS1034, SW403, HCT116, SW48, and Colo320DM. Any available colon tumour cell lines would be equally useful for such an evaluation.

Prostate cell lines include DU145 and PC-3 cells. Pancreatic cell lines include Panc-1 cells. Breast tumour cell lines include MDA231 cell line and ovarian cell lines include the OVCAR-3 cell line. Hemopoietic cell lines include, but are not limited to, the Raji and Daudi B-lymphoid cells, K562 erythroblastoid cells, U937 myeloid cells, and HSB2 T-lymphoid cells. Other available tumour cell lines are equally useful.

The present disclosure also extends to novel sequences disclosed herein. In one embodiment the virus is shown in any one of sequences disclosed herein.

Formulations

The present disclosure relates also extends to a pharmaceutical formulation of a virus as described herein.

In one embodiment there is provided a liquid parenteral formulation, for example for infusion or injection, of a replication capable oncolytic according to the present disclosure wherein the formulation provides a dose in the range of 1×10^{10} to 1×10^{14} viral particles per volume of dose.

Parenteral formulation means a formulation designed not to be delivered through the GI tract. Typical parenteral delivery routes include injection, implantation or infusion. In one embodiment the formulation is provided in a form for bolus delivery.

In one embodiment the parenteral formulation is in the form of an injection. Injection includes intravenous, subcutaneous, intra-tumoural or intramuscular injection. Injection as employed herein means the insertion of liquid into the body via a syringe. In one embodiment, the method of the present disclosure does not involve intra-tumoural injection.

In one embodiment the parenteral formulation is in the form of an infusion.

Infusion as employed herein means the administration of fluids at a slower rate by drip, infusion pump, syringe driver or equivalent device. In one embodiment, the infusion is administered over a period in the range of 1.5 minutes to 120 minutes, such as about 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14 15, 16, 17, 18, 19 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 65, 80, 85, 90, 95, 100, 105, 110 or 115 minutes.

In one embodiment one dose of the formulation less than 100mls, for example 30mls, such as administered by a syringe driver. In one embodiment one dose of the formulation is less than 10 mls, for example 9, 8, 7, 6, 5, 4, 3, 2 or 1 mls. In one embodiment one dose of the formulation is less than 1 ml, such as 0.9, 0.8, 0.7, 0.6, 0.5, 0.4, 0.3, 0.2 or 0.1 mls.

In one embodiment, the injection is administered as a slow injection, for example over a period of 1.5 to 30 minutes.

In one embodiment, the formulation is for intravenous (i.v.) administration. This route is particularly effective for delivery of oncolytic virus because it allows rapid access to the majority of the organs and tissue and is particular useful for the treatment of metastases, for example established metastases especially those located in highly vascularised regions such as the liver and lungs.

Therapeutic formulations typically will be sterile and stable under the conditions of manufacture and storage. The composition can be formulated as a solution, microemulsion, liposome, or other parenteral formulation suitable for administration to a human and may be formulated as a pre-filled device such as a syringe or vial, particular as a single dose.

The formulation will generally comprise a pharmaceutically acceptable diluent or carrier, for example a non-toxic, isotonic carrier that is compatible with the virus, and in which the virus is stable for the requisite period of time.

The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a dispersant or surfactant such as lecithin or a non-ionic surfactant such as polysorbate 80 or 40. In dispersions the maintenance of the required particle size may be assisted by the presence of a surfactant. Examples of isotonic agents include sugars, polyalcohols such as mannitol, sorbitol, or sodium chloride in the composition.

In one embodiment, parenteral formulations employed may comprise one or more of the following a buffer, for example 4-(2-hydroxyethyl)-1-piperazineethanesulfonic acid, a phosphate buffer and/or a Tris buffer, a sugar for example dextrose, mannose, sucrose or similar, a salt such as sodium chloride, magnesium chloride or potassium chloride, a detergent such as a non-ionic surfactant such as briji, PS-80, PS-40 or similar. The formulation may also comprise a preservative such as EDTA or ethanol or a combination of EDTA and ethanol, which are thought to prevent one or more pathways of possible degradation.

In one embodiment, the formulation will comprise purified oncolytic virus according to the present disclosure, for example $1x10^{10}$ to $1x10^{14}$ viral particles per dose, such as $1x10^{10}$ to $1x10^{12}$ viral particles per dose. In one embodiment the concentration of virus in the formulation is in the range 2×10^8 to 2×10^{14} vp/mL, such as 2×10^{12} vp/ml.

In one embodiment, the parenteral formulation comprises glycerol.

In one embodiment, the formulation comprises oncolytic adenovirus as described herein, HEPES (N-2-hydroxyethylpiperazine-N′-2-ethanesulfonic acid), glycerol and buffer.

In one embodiment, the parenteral formulation consists of virus of the disclosure, HEPES for example 5mM, glycerol for example 5-20% (v/v), hydrochloric acid, for example to adjust the pH into the range 7-8 and water for injection.

In one embodiment 0.7 mL of virus of the disclosue at a concentration of 2×10^{12} vp/mL is formulated in 5 mM HEPES, 20% glycerol with a final pH of 7.8.

A thorough discussion of pharmaceutically acceptable carriers is available in Remington's Pharmaceutical Sciences (Mack Publishing Company, N.J. 1991).

In one embodiment, the formulation is provided as a formulation for topical administrations including inhalation.

Suitable inhalable preparations include inhalable powders, metering aerosols containing propellant gases or inhalable solutions free from propellant gases. Inhalable powders according to the disclosure will generally contain a virus as described herein with a physiologically acceptable excipient.

These inhalable powders may include monosaccharides (e.g. glucose or arabinose), disaccharides (e.g. lactose, saccharose, maltose), oligo- and polysaccharides (e.g. dextranes), polyalcohols (e.g. sorbitol, mannitol, xylitol), salts (e.g. sodium chloride, calcium carbonate) or mixtures of these with one another. Mono- or disaccharides are suitably used, the use of lactose or glucose, particularly but not exclusively in the form of their hydrates.

Particles for deposition in the lung require a particle size less than 10 microns, such as 1-9 microns for example from 0.1 to 5 µm, in particular from 1 to 5 µm. The particle size of the carrying the virus is of primary importance and thus in one embodiment the virus according to the present disclosure may be adsorbed or absorbed onto a particle, such as a lactose particle of the given size.

The propellant gases which can be used to prepare the inhalable aerosols are known in the art. Suitable propellant gases are selected from among hydrocarbons such as n-propane, n-butane or isobutane and halohydrocarbons such as chlorinated and/or fluorinated derivatives of methane, ethane, propane, butane, cyclopropane or cyclobutane. The above-mentioned propellant gases may be used on their own or in mixtures thereof.

Particularly suitable propellant gases are halogenated alkane derivatives selected from among TG 11, TG 12, TG 134a and TG227. Of the abovementioned halogenated hydrocarbons, TG134a (1,1,1,2-tetrafluoroethane) and TG227 (1,1,1,2,3,3,3-heptafluoropropane) and mixtures thereof are particularly suitable.

The propellant gas-containing inhalable aerosols may also contain other ingredients, such as cosolvents, stabilisers, surface-active agents (surfactants), antioxidants, lubricants and means for adjusting the pH. All these ingredients are known in the art.

The propellant gas-containing inhalable aerosols according to the invention may contain up to 5 % by weight of active substance. Aerosols according to the invention contain, for example, 0.002 to 5 % by weight, 0.01 to 3 % by weight, 0.015 to 2 % by weight, 0.1 to 2 % by weight, 0.5 to 2 % by weight or 0.5 to 1 % by weight of active ingredient.

Alternatively, topical administrations to the lung may also be by administration of a liquid solution or suspension formulation, for example employing a device such as a nebulizer, for example, a nebulizer connected to a compressor (e.g., the Pari LC-Jet Plus(R) nebulizer connected to a Pari Master(R) compressor manufactured by Pari Respiratory Equipment, Inc., Richmond, Va.).

The virus of the invention can be delivered dispersed in a solvent, e.g. in the form of a solution or a suspension, for example as already described above for parenteral formulations. It can be suspended in an appropriate physiological solution, e.g., saline or other pharmacologically acceptable solvent or a buffered solution. Buffered solutions known in the art may contain 0.05 mg to 0.15 mg disodium edetate, 8.0 mg to 9.0 mg NaCl, 0.15 mg to 0.25 mg polysorbate, 0.25 mg to 0.30 mg anhydrous citric acid, and 0.45 mg to 0.55 mg sodium citrate per 1 ml of water so as to achieve a pH of about 4.0 to 5.0.

The therapeutic suspensions or solution formulations can also contain one or more excipients. Excipients are well known in the art and include buffers (e.g., citrate buffer, phosphate buffer, acetate buffer and bicarbonate buffer), amino acids, urea, alcohols, ascorbic acid, phospholipids, proteins (e.g., serum albumin), EDTA, sodium chloride, liposomes, mannitol, sorbitol, and glycerol. Solutions or suspensions can be encapsulated in liposomes or biodegradable microspheres. The formulation will generally be provided in a substantially sterile form employing sterile manufacture processes.

This may include production and sterilization by filtration of the buffered solvent/solution used for the formulation, aseptic suspension of the antibody in the sterile buffered solvent solution and dispensing of the formulation into sterile receptacles by methods familiar to those of ordinary skill in the art.

Nebulisable formulation according to the present disclosure may be provided, for example, as single dose units (e.g., sealed plastic containers or vials) packed in foil envelopes. Each vial contains a unit dose in a volume, e.g., 2 mL, of solvent/solution buffer.

Treatment

In a further aspect, the present disclosure extends to a virus or a formulation thereof as described herein for use in treatment, in particular for the treatment of cancer.

In one embodiment, the method of treatment is for use in the treatment of a tumour, in particular a solid tumour.

Tumour as employed herein is intended to refer to an abnormal mass of tissue that results from excessive cell division that is uncontrolled and progressive, also called a neoplasm. Tumours may be either benign (not cancerous) or malignant. Tumour encompasses all forms of cancer and metastases.

In one embodiment, the tumour is a solid tumour. The solid tumour may be localised or metastasised.

In one embodiment, the tumour is of epithelial origin.

In one embodiment, the tumour is a malignancy, such as colorectal cancer, hepatoma, prostate cancer, pancreatic cancer, breast cancer, ovarian cancer, thyroid cancer, renal cancer, bladder cancer, head and neck cancer or lung cancer.

In one embodiment, the tumour is a colorectal malignancy.

Malignancy as employed herein means cancerous cells.

In one embodiment, the oncolytic adenovirus is employed in the treatment or prevention of metastasis.

In one embodiment, the method or formulation herein is employed in the treatment of drug resistant cancers.

In one embodiment, the virus is administered in combination with the administration of a further cancer treatment or therapy.

In one embodiment, there is provided a virus or formulation according to the present disclosure for use in the manufacture of a medicament for the treatment of cancer, for example a cancer described above.

In a further aspect, there is provide a method of treating cancer comprising administering a therapeutically effective amount of a virus or formulation according to the present disclosure to a patient in need thereof, for example a human patient.

In one embodiment, the oncolytic virus or formulation herein is administered in combination with another therapy.

“In combination” as employed herein is intended to encompass where the oncolytic virus is administered before, concurrently and/or post cancer treatment or therapy.

Cancer therapy includes surgery, radiation therapy, targeted therapy and/or chemotherapy. Cancer treatment as employed herein refers to treatment with a therapeutic compound or biological agent, for example an antibody intended to treat the cancer and/or maintenance therapy thereof.

In one embodiment, the cancer treatment is selected from any other anti-cancer therapy including a chemotherapeutic agent, a targeted anticancer agent, radiotherapy, radio-isotope therapy or any combination thereof.

In one embodiment, the virus of the present disclosure such as an oncolytic adenovirus may be used as a pre-treatment to the therapy, such as a surgery (neoadjuvant therapy), to shrink the tumour, to treat metastasis and/or prevent metastasis or further metastasis. The oncolytic adenovirus may be used after the therapy, such as a surgery (adjuvant therapy), to treat metastasis and/or prevent metastasis or further metastasis.

Concurrently as employed herein is the administration of the additional cancer treatment at the same time or approximately the same time as the oncolytic adenovirus formulation. The treatment may be contained within the same formulation or administered as a separate formulation.

In one embodiment, the virus is administered in combination with the administration of a chemotherapeutic agent.

Chemotherapeutic agent as employed herein is intended to refer to specific antineoplastic chemical agents or drugs that are selectively destructive to malignant cells and tissues. For example, alkylating agents, antimetabolites, anthracyclines, plant alkaloids, topoisomerase inhibitors, and other antitumour agents. Other examples of chemotherapy include doxorubicin, 5-fluorouracil (5-FU), paclitaxel, capecitabine, irinotecan, and platins such as cisplatin and oxaliplatin. The preferred dose may be chosen by the practitioner based on the nature of the cancer being treated.

In one embodiment the therapeutic agent is ganciclovir, which may assist in controlling immune responses and/or tumour vascularisation.

In one embodiment one or more therapies employed in the method herein are metronomic, that is a continuous or frequent treatment with low doses of anticancer drugs, often given concomitant with other methods of therapy.

Subgroup B oncolytic adenoviruses, in particular Ad11 and those derived therefrom such as EnAd may be particularly synergistic with chemotherapeutics because they seem to have a mechanism of action that is largely independent of apoptosis, killing cancer cells by a predominantly necrolytic mechanism. Moreover, the immunosuppression that occurs during chemotherapy may allow the oncolytic virus to function with greater efficiency.

Therapeutic dose as employed herein refers to the amount of virus, such as oncolytic adenovirus that is suitable for achieving the intended therapeutic effect when employed in a suitable treatment regimen, for example ameliorates symptoms or conditions of a disease. A dose may be considered a therapeutic dose in the treatment of cancer or metastases when the number of viral particles may be sufficient to result in the following: tumour or metastatic growth is slowed or stopped, or the tumour or metastasis is found to shrink in size, and/or the life span of the patient is extended. Suitable therapeutic doses are generally a balance between therapeutic effect and tolerable toxicity, for example where the side-effect and toxicity are tolerable given the benefit achieved by the therapy.

In one embodiment, a virus or therapeutic construct according to the present disclosure (including a formulation comprising same) is administered weekly, for example one week 1 the dose is administered on day 1, 3, 5, followed by one dose each subsequent week.

In one embodiment, a virus or therapeutic construct according to the present disclosure (including a formulation comprising same) is administered bi-weekly or tri-weekly, for example is administered in week 1 one on days 1, 3 and 5, and on week 2 or 3 is also administered on days 1, 3 and 5 thereof. This dosing regimen may be repeated as many times as appropriate.

In one embodiment, a virus or therapeutic construct according to the present disclosure (including a formulation comprising same) is administered monthly.

In one embodiment, the viruses and constructs of the present disclosure are prepared by recombinant techniques. The skilled person will appreciate that the armed adenovirus genome can be manufactured by other technical means, including entirely synthesising the genome or a plasmid comprising part of all of the genome. The skilled person will appreciate that in the event of synthesising the genome the region of insertion may not comprise the restriction site nucleotides as the latter are artefacts following insertion of genes using cloning methods.

The disclosure herein further extends to an adenovirus of formula (I) or a subformula thereof, obtained or obtainable from inserting a transgene or transgene cassette.

"Is" as employed herein means comprising.

In the context of this specification "comprising" is to be interpreted as "including".

Embodiments of the invention comprising certain features/elements are also intended to extend to alternative embodiments "consisting" or "consisting essentially" of the relevant elements/features.

Where technically appropriate, embodiments of the invention may be combined.

Technical references such as patents and applications are incorporated herein by reference.

Any embodiments specifically and explicitly recited herein may form the basis of a disclaimer either alone or in combination with one or more further embodiments.

The present application claims priority from GB1713765.4, WO2018/041838 and WO2018/041827 incorporated herein by reference. These documents may be employed to correct errors in the present specification, in particular an error in the sequence listing.

The present invention is further described by way of illustration only in the following examples, which refer to the accompanying Figures, in which:

DESCRIPTION OF THE FIGURES

Figure 1	Shows schematics of the NG-615, NG-640 and NG-641 transgene cassettes
Figure 2:	**Virus genome replication in lung, breast and bladder carcinoma cell lines.** A549 (A), MDA-MB-453 (B) and RT4 (C) cell lines were treated with NG-617, NG-615, NG-640, NG-641 or enadenotucirev virus particles for up to 7 days. The amount of virus genome detected by qPCR was assessed at days 2, 3, 4 and 7 post treatment.
Figure 3:	**Virus mediated oncolysis of lung carcinoma cells.** A549 cells were treated with NG-617, NG-615, NG-640, NG-641 or enadenotucirev virus particles for up to 4 days. Cell viability was assessed throughout the culture using an xCelligence system (A). The time at which 50% killing was observed (KT50) was determined for each virus treatment (B).

Figure 4: **NG-615 transgene expression in lung and bladder carcinoma cells.** A549 (left panels) and RT4 cells (right panels) were treated with NG-615 or enadenotucirev virus particles or left uninfected for up to 7 days. The secretion of the Flt3 Ligand (A), MIP1α (B) and IFNα (C) was assessed in the cellular supernatants by ELISA. No transgene expression was detected in enadenotucirev treated or untreated control cells (data not shown).

Figure 5: **NG-641 transgene expression in lung and bladder carcinoma cells.** A549 (left panels) and RT4 cells (right panels) were treated with NG-641 or enadenotucirev virus particles or left uninfected for up to 7 days. The secretion of the CXCL9 (A), CXCL10 (B) or IFNα (C) was assessed in the cellular supernatants by ELISA. No transgene expression was detected in enadenotucirev treated or untreated control cells (data not shown)

Figure 6: **Expression of functional transgenes in lung carcinoma cells.** A549 cells were treated with NG-615, NG-641 or enadenotucirev virus particles for up to 4 days. At day 4 post-treatment the level of functional IFNα (A) or MIP1α (B) transgenes being produced was assessed using cell-based reporter assays.

Figure 7: **Expression of functional FAP-BiTE in lung carcinoma cells.** A549 cells were treated with NG-615, NG-641 or enadenotucirev virus particles for up to 4 days. At days 2 (A), 3 (B) and 4 (C) post-treatment the expression level of functional FAP-BiTE in the cell supernatants was assessed by measuring activation of a Jurkat T cell line co-cultured with FAP expressing fibroblast cell line, MRC-5.

Figure 8A: **Transgene encoded IFNα in supernatant from NG-641 infected A549 cells induces SEAP production by Jurkat Dual reporter cells**. Jurkat-Dual reporter cells were treated with supernatant from an A549 cancer cell line either uninfected (UIC) or infected with enadenotucirev (EnAd) or NG-641 and the level of the secreted embryonic alkaline phosphatase (SEAP) reporter measured.

Figure 8B: **Transgene encoded CXCL9/10 in supernatant from NG-641 infected A549 cells activates the GPCR pathway in PathHunter β-Arrestin cells.** PathHunter β-Arrestin cells were treated with supernatant from an A549 cancer cell line either uninfected (UIC) or infected with enadenotucirev (EnAd) or NG-641 and CXCL9/10 specific induction of the G-protein coupled receptor (GPCR) pathway detected via luminescence.

Figure 9: **Transgene encoded CXCL9/10 in supernatant from NG-641 infected A549 cells induces the downregulation of CXCR3 on the surface of activated T cells.** Anti-CD3/CD28 activated human T cells were treated with supernatant from an A549 cancer cell line either uninfected (UIC) or infected with enadenotucirev (EnAd) or NG-641 and transgene CXCL9/10 induced downregulation of CXCR3 was measured by flow cytometry.

Figure 10: **Activation of endogenous tumour infiltrating T-cells in ex vivo cultures of primary human tumour samples inoculated with EnAd, NG-615, NG-617, NG-640 or NG-641, anti-CD3/28 or left uninfected (UIC)**

	Levels of the virus transgene products IFNa and Flt3L are shown in A) and levels of IFNγ, TNFα, IL-17A, granzyme B and IL-13 are shown in B)
Figure 11:	**Activation of surface marker expression and intracellular cytokines in endogenous tumour infiltrating T-cells in ex vivo cultures of a primary NSCLC tumour sample treated with EnAd, NG-617, NG-640 or NG-641 or left uninfected (UIC).** Levels of CD4 and CD8 T-cells expressing CD25, CD69 and CD107a are shown in A & B, respectively. Levels of intracellular IFNγ and TNFα expressed by CD4 and CD8 T-cells are shown in C & D, respectively.
Figure 12	Schematic representation of a BiTE antibody of the present disclosure comprising or lacking an optional decahistidine affinity tag. Ig SP: signal peptide; 10His: decahistidine affinity tag; L: GS linker; V_L: variable light domain; V_H variable heavy domain.
Figure 13	**(A)** dot blot showing the quantification of the recombinant BiTEs. **(B)** shows a graph showing the ELISA results for FAP.
Figure 14	shows a graph showing the expression levels of CD69 **(A)** and CD25 **(B)** for T cells co-cultured alone or with NHDF cells in the presence of FAP BiTE and control BiTE measured using flow cytometry. **(C)** graph shows the levels of IFN γ expression for T cells co-cultured alone or with NHDF cells in the presence of FAP BiTE and control BiTE measured by intracellular cytokine staining
Figure 15	**(A)** graph showing the results of a LDH assay showing the cytoxicity of NHDF cells which have been co-cultured with T cells and FAP BiTE or control BiTE. **(B)** graph showing the results of a LDH assay showing the cytoxicity of BTC100 cells which have been co-cultured with T cells and FAP BiTE or control BiTE. **(C)** Images of NHDF cells after co-culture with T cells and FAP BiTE vs control BiTE.
Figure 16	Is a graph showing the % of cells expressing EpCAM and FAP across multiple cells and cell lines.
Figure 17	**(A)** graph showing the NHDF dose response for FAP BiTE with increasing BiTE concentration. Graph **(B)** & **(C)** showing the results of a LDH assay showing the cytoxicity of DLD cells which have been co-cultured with T cells and EpCAM BiTE or control BiTE.
Figure 18	**(A)** graph showing FAP expression in CHO cells determined by FAP or isotope control antibody and analysed by flow cytometry. **(B)** shows a graph showing the results of a LDH assay showing the cytoxicity of CHO or CHO-FAP cells which have been co-cultured with T cells and FAP BiTE or control BiTE.
Figure 19	shows a graph showing T-cell activation (based onCD69 and CD25 expression levels) by CHO vs CHO-FAP cells, analysed using flow cytometry.
Figure 20	**(A)** graph showing the ability of FAP BiTE to activate CD4+ or CD8+ T-cells (based on CD69 and CD25 expression levels), analysed using flow cytometry. **(B)** graph showing the results of a LDH assay showing the cytoxicity of NHDF cells which have been co-cultured with CD4+ or CD8+ T cells and FAP BiTE or control BiTE.
Figure 21	**(A)** graph showing the number of CD3+ T cells from ascites cultured with control or FAP BiTE. **(B)** graph showing the CD25 expression levels of T cells from ascites

	cultured with control or FAP BiTE. **(C)** graph showing the number of FAP+ cells from ascites cultured with control or FAP BiTE.
Figure 22	**(A)** graph showing the quantification of the number of detected virus genomes per cell for NG-601, NG-602, NG-603, NG-604, NG-605, NG-606 and EnAd. **(B)** graphs showing the oncolytic activity of NG-601, NG-602, NG-603, NG-604, NG-605, NG-606 or EnAd assessed by infection of A549 cells.
Figure 23	Graphs showing T-cell activation (based on CD69 and CD25 expression levels) by NG-601, NG-602, NG-605 and NG-606 when co-cultured with CHO-FAP, analysed using flow cytometry.
Figure 24	shows graphs showing the results of experiments to determine the quantity of FAP BiTE produced from NG-605 and NG-606.
Figure 25	shows microscopy images of Ad293 cells infected with NG-607, NG-608, NG-609 and NG-610.
Figure 26	**(A)** graph indicating the ability of NG-603, NG-604, NG-605, NG-606 and EnAd to kill NHDF cells, analysed using XCELLigence. **(B)** graph indicating the ability of NG-603, NG-604, NG-605, NG-606 and EnAd to kill NHDF cells, analysed using an LDH assay.
Figure 27	shows graphs showing T-cell activation (based on CD69 and CD25 expression levels) by NG-603, NG-604, NG-605, NG-606 co-cultured with NHDF cells, SKOV and T cells, analysed using flow cytometry.
Figure 28	**(A)** graph showing T-cell activation (based on CD69 and CD25 expression levels) by NG-603, NG-604, NG-605, NG-606 co-cultured with NHDF and SKOV cells vs. SKOV alone, analysed using flow cytometry. **(B)** graph indicating the cytotoxicity of NHDF cells infected with NG-605 and NG-606, analysed using an LDH assay
Figure 29	shows still frame images from timelapse videos of lysis of NHDF cells by recombinant FAP BiTE, EnAd, NG-603 or NG-605.
Figure 30	shows still frame images from timelapse videos of lysis of NHDF cells by NG-607, NG-608, NG-609 or NG-610.
Figure 31	shows a graph indicating the cytotoxicity of DLD cells infected with EnAd, NG-601, NG-602, NG-603 and NG-604 in the presence of T cells or absence of T cells, analysed using an LDH assay.
Figure 32	**(A)** graph indicating the expression levels of CD25 on CD3+ T cells in ascites samples which were infected with viruses of the present disclosure. **(B)** graph indicating the number of FAP+ cells in ascites samples which were infected with viruses of the present disclosure.
Figure 33	shows a graph indicating the number of CD3+ T cells in ascites samples obtained from a cancer patient and infected with viruses of the present disclosure.
Figure 34	shows a graph indicating the CD25 expression levels on CD3+ T cells in ascites samples obtained from a cancer patient and infected with viruses of the present disclosure.

Figure 35 shows a graph indicating the number of FAP+ cells in ascites samples obtained from a cancer patient and infected with viruses of the present disclosure.

Figure 36 shows a comparison of activation of T-cell cytokine production by recombinant FAP BiTE protein in the presence of human fibroblasts and by polyclonal activation with anti-CD3/CD28 beads. **(A)** IFNγ levels measured by ELISA. **(B)** Cytokine levels measured by cytokine bead array.

Figure 37 **FAP-targeted BiTE induces T-cell degranulation and specific cytotoxicity of FAP+ cells**

(A) Degranulation of T-cells in culture with NHDF cells (5:1) and **(B)** BiTE-containing supernatants. Degranulation was assessed by externalisation of CD107a following 6 h culture with a CD107a-specific antibody and measured by flow cytometry. CD3/CD28 Dynabeads were used as a positive control. **(C)** Cytotoxicity of NHDF cells after 24 h in co-culture with T-cells (1:5) and 10-fold serial dilutions of BiTE-containing supernantants. Cytotoxicity was assessed by release of LDH into culture supernatants. **(D)** Lysis of NHDF by LDH release (left) and CD25 induction on T-cells (right) was assessed after 24 h co-culture with PBMC-derived T-cells (1:5) from six healthy donors and BiTE-containing supernatants.

Figure 38 **EnAd expressing FAP BiTE selectively kills FAP$^+$ fibroblasts and decreases TGFb in peritoneal ascites samples**

(A,B) Number of of FAP$^+$ fibroblasts **(A)** and EpCAM$^+$ tumour cells **(B)** after 72 h culture with PBMC-derived T-cells and EnAd or recombinant viruses. Ascites cells were first isolated from three patients ascites and expanded *ex vivo*. Cell number was measured at 72 h post-infection by flow cytometry. **(C)** Induction of activation marker CD25 on PBMC-derived CD3 cells from **(A)** was measured at 72 h post-infection. **(D)** Levels of TGFb were measured by ELISA using supernatants harvested from **(A).**

Figure 39 shows the activation of endogenous tumor associated T-cells and associated killing of FAP+ cells in patient malignant ascites biopsy samples by FAP BiTE protein and EnAd-FAPBiTE viruses. **(A)** T cell activation measured by CD25 expression. **(B)** residual number of FAP+ cells measured by flow cytometry.

Figure 40 **Effect of PD-L1 blocking antibodies on BiTE-mediated T cell activation in patient sample**

(A) Expression of PD1 by endogenous T cells and PD-L1 on FAP+ cells following their initial isolation from peritoneal ascites was assessed by flow cytometry. **(B)** Unpurified total cells from peritoneal ascites were incubated in 50% fluid from the same exudate in the presence of free BiTE, EnAd or recombinant virus, with or without anti-PD-L1 blocking antibody. After 2 days, the total cell population was harvested, and the number of CD25+ T-cells was quantified by flow cytometry. **(C)** Quantity of interferon gamma in culture supernatants from **(B, D)** measured by ELISA. **(D)** The number of residual FAP+ cells in (B) was measured using flow cytometry.

Figure 41	**EnAd expressing BiTEs activate and redirect T-cells from patient biopsy samples to lyse NHDF fibroblasts** **(A)** The expression of PD-1 by endogenous T cells following isolation from healthy donors or malignant exudate cancer biopsy samples. PD-1 expression was measured by flow cytometry. **(B)** The proportion of CD3$^+$ cells within the unpurified cell population of PBMC and cancer biopsy samples as measured by flow cytometry. **(C)** Levels of interferon gamma measured by ELISA in culture supernatants harvested from **(B)** at 120 h post-treatment. **(D)** Viability of NHDF fibroblasts were monitored in real time over 130 h by xCELLigence cytotoxicity assay in co-culture with PBMC or total cancer biopsy cells (1:5) and BiTE-containing supernatant.
Figure 42	shows the effect of immunosuppressive ascites fluid samples on FAP BiTE- and anti-CD3/CD28 bead-mediated activation of PBMC T-cells. **(A)** PBMC T cells activated with anti-CD3/Cd28 Dynabeads. **(B)** PBMC T cells activated with control or FAP BITEs in the presence of NHDF cells. NS: normal serum, A: peritoneal ascites.
Figure 43	**FAP BiTE expressing EnAd polarises CD11b$^+$ macrophage in patient ascites to a more inflammatory phenotype** **(A)** Unpurified total cells from ascites sample were incubated in 50% ascites fluid in the presence of free BiTE or BiTE expressing virus. Interferon gamma treatment was used as a positive control. After 3 days, the total cell population was harvested and the induction of activation marker CD25 on CD3$^+$ cells was measured by flow cytometry. **(B)** Levels of interferon gamma in culture supernatants from **(A)** were measured by ELISA. **(C)** At 3 days, the expression levels of CD68, CD86, CD206 and CD163 on CD11b+ cells from **(A)** were measured by flow cytometry. Representative flow cytometry spectra from triplicates is shown alongside the complete data set.
Figure 44	**Characterisation of architecture and cellular composition of solid prostate tumour** Shows levels of IFNg in tissue slice culture medium measured by ELISA. Supernatants were harvested from slices cultures of malignant and benign tissue at the specified time-point; and Levels of IL-2 in tissue culture medium of malignant and benign tissue measured by ELISA.
Figure 45	shows a schematic representation of the transgene cassette.
Figure 46	shows a graph indicating the number of viral genomes detected per cell in NG-611, NG-612 and NG-617 treated tumour cells.
Figure 47	shows the percentage of T cells expressing CD69 **(a)**, CD25 **(b)** HLA-DR **(c)**, CD40L **(d)** or cell surface CD107a **(e)** following co-culture with EpCam expressing SKOV cells and supernantants harvested from A549 cells at 24, 48 or 72hrs post-treatment with NG-611 viurs particles compared to NG-612, enadenotucirev or untreated control supernatants.

Figure 48	shows the percentage of T cells expressing CD69 **(a)**, CD25 **(b)** HLA-DR **(c)**, CD40L **(d)** or cell surface CD107a **(e)** following co-culture with FAP expressing MRC-5 cells and supernatants harvested from A549 cells at 24, 48, or 72hrs post-treatment with NG-612 virus particles compared to NG-611, enadenotucirev or untreated control supernatants.
Figure 49	shows the percentage of MRC-5 cells that express EpCAM and FAP
Figure 50	shows IFNγ expression in the supernatants of T cell co-cultures with SKOV cells (A) or MRC-5 cells (B) incubated with supernatants harvested from A549 cells at 24, 48 or 72hrs post-treatment with NG-611, NG-612 or enadenotucirev virus particles, or untreated control supernatants.
Figure 51	shows anti-tumour efficacy and immune activation of BiTE expressing viruses in vivo. **(a)** tumour volume in mice treated with saline, enadenotucirev or NG-611. **(b)** Ratio of CD8 to CD4 T cells in NG-611 treated tumours compared to enadenotucirev treated or untreated controls.
Figure 52	shows a graph indicating the number of viral genomes detected per cell in NG-612 and NG-615 treated tumour cells
Figure 53	shows the expression of IFNα, MIP1α and Flt3 L in the cellular supernatant of NG-615 vs the supernatant of enadenotucirev and untreated control tumour cells.
Figure 54	shows the number of T cells expressing CD69 **(a)**, CD25 **(b)** HLA-DR **(c)**, CD40L **(d)** or cell surface CD107a **(e)**) following co-culture with FAP expressing MRC-5 cells and supernantants harvested from A549 cells at 24, 48 or 72hrs post-treatment with NG-615 viurs particles compared to NG-612, enadenotucirev or untreated control supernatants.
Figure 55	shows IFNγ expression in the supernatants of T cell co-cultures with MRC-5 cells incubated with supernatants harvested from A549 cells at 24, 48 or 72hrs post-treatment with NG-612, NG-615 or enadenotucirev virus particles, or untreated control supernatants.

SEQUENCES

SEQ ID NO: 1	Anti-FAP BiTE DNA coding sequence, with N-terminal signal sequence and C-terminal deca-His affinity tag
SEQ ID NO: 2	Anti-FAP BiTE amino acid sequence, with N-terminal signal sequence and C-terminal deca-His affinity tag
SEQ ID NO: 3:	Control (Anti-FHA) BiTE DNA coding sequence, with N-terminal signal sequence and C-terminal deca-His affinity tag
SEQ ID NO: 4:	Control (Anti-FHA) BiTE amino acid sequence with N-terminal signal sequence and C-terminal deca-His affinity tag
SEQ ID NO: 5:	Anti-CD3 ScFv amino acid sequence
SEQ ID NO: 6:	Anti-CD3 VH
SEQ ID NO: 7:	Anti-CD3 VL
SEQ ID NO: 8:	Anti-CD3 ScFv linker sequence
SEQ ID NO: 9:	Anti-FAP ScFv
SEQ ID NO: 10:	Anti-FAP VL domain

SEQ ID NO: 11:	Anti-FAP VH domain
SEQ ID NO: 12:	Anti-FAP and Anti-EpCAM linker sequence
SEQ ID NO: 13:	BiTE leader sequence
SEQ ID NO: 14:	Control BiTE (Anti-FHA)
SEQ ID NO: 15:	Control (Anti-FHA) ScFv
SEQ ID NO: 16:	Control (Anti-FHA) VL
SEQ ID NO: 17:	Control (Anti-FHA) VH
SEQ ID NO: 18:	Control (Anti-FHA) ScFv linker sequence
SEQ ID NO: 19:	Deca-His Tag sequence
SEQ ID NO: 20:	FAP BiTE-P2A-RFP (*ITALICS* = leader, **BOLD** = furin cleavage site, UNDERLINE = P2A sequence, lower case = RFP)
SEQ ID NO: 21:	Control (Anti-FHA) BiTE-P2A-RFP (*ITALICS* = leader, **BOLD** = furin cleavage site, UNDERLINE = P2A sequence, lower case = RFP)
SEQ ID NO: 22:	Human FAP DNA coding sequence
SEQ ID NO: 23:	Human FAP amino acid sequence
SEQ ID NO: 24:	CMV promoter sequence
SEQ ID NO: 25:	SV40 late polyadenylation sequence
SEQ ID NO: 26:	NG-605 (EnAd-CMV-FAPBiTE)
SEQ ID NO: 27:	NG-606 (EnAd-SA-FAPBiTE)
SEQ ID NO: 28	EnAd genome
SEQ ID NO: 29	B_X DNA sequence corresponding to and including bp 28166-28366 of the EnAd genome
SEQ ID NO: 30	B_Y DNA sequence corresponding to and including bp 29345-29379 of the EnAd genome
SEQ ID NO: 31	HIS-Tag
SEQ ID NO: 32	Splice acceptor sequence.
SEQ ID NO: 33	SV40 poly Adenylation sequence
SEQ ID NO: 34	FAP BiTE nucleic acid sequence (OKT3)
SEQ ID NO: 35	FAP BiTE nucleic acid sequence (aCD3)
SEQ ID NO: 36	NG-611 Transgene cassette
SEQ ID NO: 37	NG-612 Transgene cassette
SEQ ID NO: 38	NG-613 Transgene cassette
SEQ ID NO: 39	Restriction site insert (B_X)
SEQ ID NO: 40	Restriction site insert (B_Y)
SEQ ID NO: 41	CMV promoter sequence
SEQ ID NO: 42	PGK promoter sequence
SEQ ID NO: 43	CBA promoter sequence
SEQ ID NO: 44	short splice acceptor (SSA) DNA sequence
SEQ ID NO: 45	splice acceptor (SA) DNA sequence
SEQ ID NO: 46	branched splice acceptor (bSA) DNA sequence
SEQ ID NO: 47	Kozak sequence (null sequence)
SEQ ID NO: 48	Example of start codon

SEQ ID NO: 49	Internal Ribosome Entry Sequence (IRES)
SEQ ID NO: 50	P2A peptide
SEQ ID NO: 51	F2A peptide
SEQ ID NO: 52	E2A peptide
SEQ ID NO: 53	T2A peptide
SEQ ID NO: 54	polyadenylation (polyA) sequence
SEQ ID NO: 55	Leader sequence
SEQ ID NO: 56	Leader sequence
SEQ ID NO: 57	IFNγ amino acid sequence
SEQ ID NO: 58	IFNα amino acid sequence
SEQ ID NO: 59	TNFα amino acid sequence
SEQ ID NO: 60	DNA sequence corresponding to E2B region of the EnAd genome (bp 10355-5068)
SEQ ID NO: 61:	Anti-FAP BiTE DNA coding sequence, with N-terminal signal sequence without C-terminal deca-His affinity tag
SEQ ID NO: 62:	Anti-FAP BiTE amino acid sequence, with N-terminal signal sequence without C-terminal deca-His affinity tag
SEQ ID NO: 63:	Control (Anti-FHA) BiTE DNA coding sequence, with N-terminal signal sequence without C-terminal deca-His affinity tag
SEQ ID NO: 64:	Control (Anti-FHA) BiTE amino acid sequence with N-terminal signal sequence without C-terminal deca-His affinity tag
SEQ ID NO: 65:	Control BiTe (Anti-FHA) without C-terminal deca-His affinity tag
Q ID NO: 66:	NG-605 (EnAd-CMV-FAPBiTE) without deca-His affinity tag
SEQ ID NO: 67:	NG-606 (EnAd-SA-FAPBiTE) without deca-His affinity tag
SEQ ID NO: 68:	FAP BiTE nucleic acid sequence (OKT3)
SEQ ID NO: 69:	FAP BiTE nucleic acid sequence (aCD3)
SEQ ID NO: 70:	NG-611 Transgene cassette
SEQ ID NO: 71:	NG-612 Transgene cassette
SEQ ID NO: 72:	NG-613 Transgene cassette
SEQ ID NO: 73:	NG-614 Transgene cassette
SEQ ID NO: 74:	NG-617 Transgene cassette
SEQ ID NO: 75:	FAP BiTE amino acid sequence (OKT3)
SEQ ID NO: 76:	FAP BiTE amino acid sequence (aCD3)
SEQ ID NO: 77:	NG-611 Genome
SEQ ID NO: 78:	NG-612 Genome
SEQ ID NO: 79:	NG-613 Genome
SEQ ID NO: 80:	NG-614 Genome
SEQ ID NO: 81:	NG-617 Genome
SEQ ID NO: 82:	NG-615 Genome
SEQ ID NO: 83:	NG-640 Genome
SEQ ID NO: 84:	NG-641 Genome
SEQ ID NO: 85:	Null sequence

SEQ ID NO: 86:	Flt3L nucleic acid sequence
SEQ ID NO: 87:	Null sequence
SEQ ID NO: 88:	MIP1α nucleic acid sequence
SEQ ID NO: 89:	Flexible linker sequence
SEQ ID NO: 90:	IFNα nucleic acid sequence
SEQ ID NO: 91:	CXCL10 nucleic acid sequence
SEQ ID NO: 92:	CXCL9 nucleic acid sequence
SEQ ID NO: 93:	NG-615 Transgene cassette
SEQ ID NO: 94:	NG-640 Transgene cassette
SEQ ID NO: 95:	NG-641 Transgene cassette
SEQ ID NO: 96:	FLT3L amino acid sequence
SEQ ID NO: 97:	MIP1α amino acid sequence
SEQ ID NO: 98:	IFNα amino acid sequence
SEQ ID NO: 99:	CXCL9 amino acid sequence
SEQ ID NO: 100:	CXCL10 amino acid sequence
SEQ ID NO: 101:	NG-618 Genome
SEQ ID NO: 102:	NG-618 FAP BiTE nucleic acid sequence
SEQ ID NO: 103:	NG-618 Transgene cassette
SEQ ID NO: 104 to 277 are linker sequences	
SEQ ID NO: 278	NG-616 Genome
SEQ ID NO: 279 to 281 are primers	

EXAMPLES

EXAMPLE 1

Recombinant BiTEs were designed and proteins produced as described in this example.

1.1 BiTE engineering

BiTEs are generated by joining two single chain antibody fragments (ScFv) of different specificities with a flexible Gly$_4$Ser linker. ScFv's are created by the joining of V$_H$ and V$_L$ domains from parental monoclonal antibodies by a linker. Each BiTE was designed with an N-terminal signal sequence for mammalian secretion and a C-terminal decahistidine affinity tag for detection and purification. BiTEs were engineered by standard DNA cloning techniques and inserted into protein expression vectors (Figure 1).

The anti-FAP BiTE was created de novo using the anti-FAP ScFv from patent WO2010037835A2 and the anti-CD3 ScFv from patent WO 2005040220 (SEQ ID 63 therein), with a signal sequence and affinity tag added.

A control BiTE used the anti-FHA (filamentous haemagglutinin from *Bordetella pertussis*) ScFv from Hussein et al, 2007 (Hussein AH et al (2007) "Construction and characterization of single-chain variable fragment antibodies directed against the Bordetella pertussis surface adhesins filamentous hemagglutinin and pertactin". Infect Immunity **75**, 5476-5482) and the anti-CD3 ScFv from patent WO 2005040220 (SEQ ID NO: 63 therein), with a signal sequence and affinity tag added.

1.2 Recombinant BiTE production

Recombinant BiTE proteins were produced by cloning the respective sequences into the pSF-CMV vector using a CMV promoter (SEQ ID NO: 24) to drive protein expression (Figure 1). The concentration of plasmid DNA for plasmids, pSF-CMV-FAPBiTE and pSF-CMV-ControlBiTE (Table 2), were measured via NanoDrop. Empty pSF-CMV vector is included as a negative control. 54.7 µg of each was diluted with 4 mL OptiMEM. 109.2 ug PEI (linear, MW 25000, Polysciences, USA) were diluted in 4 mL OptiMEM medium and mixed with the 4ml of diluted DNA to generate DNA-PEI complexes (DNA:PEI ratio of 1:2 (w/w)). After incubation at room temperature for 20 minutes, the complex mixture was topped up to 18 mL with OptiMEM and this transfection mixture was added to a T175 flask containing Ad293 cells at 90% confluency. After incubation of the cells with the transfection mix for 4 hrs at 37^{0}C, 5% CO_2, 30 mL of cell media (DMEM high glucose with glutamine supplemented, phenol red-free) was added to the cells and the flasks was incubated 37^{0}C, 5% CO_2 for 48 hours. Another flask of cells was transfected in parallel with pSF-CMV-GFP to ensure efficient transfection efficiency. In order to harvest secreted protein, the supernatant of transfected cells was collected and centrifuged at 350g at 4 °C for 5 minutes to remove cell components (Allegra X-15R, Beckman Coulter). Supernatants were transferred to 10k MWCO Amicon Ultra-15 Centrifugal Filter Units (Millipore). After spinning at 4750 rpm and 4 °C, the volume of the retentate was adjusted with the flow through to obtain a 50-fold higher concentration. Aliquots of concentrated protein were stored at -80°C.

Table 2

"p" employed as a prefix in naming constructs indicates that the construct is a plasmid.

Plasmid ID	[plasmid DNA] ng/ml
pSF-CMV-FAPBiTE	6700
pSF-CMV-ControlBiTE	5300
pSF-Lenti-FAP	659.6

1.3 Production of viruses expressing FAP-BiTEs in combination with immunomodulatory proteins

Three viruses (NG-640, NG-641 and NG-615) were generated encoding a FAP targeting BiTE molecule and 2 or 3 immunomodulatory proteins (Table 1). NG-640 encodes three transgene proteins, the FAP-BiTE molecule and chemokines CXCL9 and CXCL10. NG-641 and NG-615 both encode four transgene proteins. NG-641 encodes the FAP-BiTE, chemokines CXCL9 and CXCL10 and the cytokine IFNα and NG-615 encodes the FAP-BiTE, the chemokine MIP1α and the cytokines FLT3 Ligand and IFNα. A virus was also generated encoding just the FAP-BiTE molecule (NG-617)

Table 1

Virus ID	Transgene Cassette
NG-615 (SEQ ID NO: 1)	SSA^{1}-FAPBiTE^{2}-E2A^{3}-Flt3L^{4}-P2A^{5}-MIP1α^{6}-T2A^{7}-IFNα^{8}-PA^{9}
NG-640 (SEQ ID NO: 2)	SSA^{1}-FAPBiTE^{2}-P2A^{5}-CXCL10^{10}-T2A^{7}-CXCL9^{11}-PA^{9}
NG-641 (SEQ ID NO: 3)	SSA^{1}-FAPBiTE^{2}-P2A^{5}-CXCL10^{10}-T2A^{7}-CXCL9^{11}-E2A^{3}-IFNα^{8}-PA^{9}
NG-617 (SEQ ID NO: 4)	SSA^{1}-FAPBiTE^{2}-PA^{9}

In each transgene cassette, the cDNA encoding the BiTE and other immune modulatory proteins was flanked at the 5' end with a short splice acceptor sequence (SSA, CAGG) and at the 3' end with a SV40 late poly(A) sequence (PA, SEQUENCE ID NO: 25). cDNA sequences for each transgene were separated using 2A high efficiency self-cleavable peptide sequences (P2A, T2A, E2A, SEQUENCE ID NO: 50, 53 and 52).

Virus Production

The plasmid pEnAd2.4 was used to generate the plasmids pNG-615, pNG-640 and pNG-641 by direct insertion of synthesised transgene cassettes (SEQ ID NOs: 93, 94 and 95, respectively). NG-615 contains four transgenes encoding for a FAP-targeting BiTE (SEQ ID NO: 102), Flt3L (SEQ ID NO. 86), MIP1α (SEQ ID NO. 88) and IFNα (SEQ ID NO. 90). NG-640 and NG-641 encode for a FAP targeting BiTe (SEQ ID NO. 102), CXCL9 (SEQ ID NO. 92) and CXCL10 (SEQ ID NO. 91), NG-641 also contains a fourth transgene encoding IFNα (SEQ ID NO. 90). Schematics of the transgene cassettes are shown in Figure 1. Construction of plasmid DNA was confirmed by restriction analysis and DNA sequencing.

The plasmids, pNG-615, pNG-640 and pNG-641, were linearized by restriction digest with the enzyme AscI to produce the virus genomes. The viruses were amplified and purified according to the methods given below.

Digested DNA was purified by phenol/chloroform extraction and precipitated for 16hrs, -20^{0}C in 300μl >95% molecular biology grade ethanol and 10μl 3M Sodium Acetate. The precipitated DNA was pelleted by centrifuging at 14000rpm, 5 mins and was washed in 500μl 70% ethanol, before centrifuging again, 14000rpm, 5mins. The clean DNA pellet was air dried, resuspended in 500μl OptiMEM containing 15μl lipofectamine transfection reagent and incubated for 30 mins, RT. The transfection mixture was then added drop wise to a T-25 flask containing 293 cells grown to 70% confluency. After incubation of the cells with the transfection mix for 2hrs at 37^{0}C, 5% CO_2 4mls of cell media (DMEM high glucose with glutamine supplemented with 2% FBS) was added to the cells and the flasks was incubated 37^{0}C, 5% CO_2.

The transfected 293 cells were monitored every 24hrs and were supplemented with additional media every 48-72hrs. The production of virus was monitored by observation of a significant cytopathic effect (CPE) in the cell monolayer. Once extensive CPE was observed the virus was harvested from 293 cells by three freeze-thaw cycles. The harvested viruses were used to re-infect 293 cells in order to amplify the virus stocks. Viable virus production during amplification was confirmed by observation of significant CPE in the cell monolayer. Once CPE was observed the virus was harvested from 293 cells by three freeze-thaw cycles. The amplified stocks of viruses were used for further amplification before the viruses were purified by double caesium chloride banding to produce purified virus stocks.

Example 2: Analysis of virus replication and oncolytic activity

Virus replication

Lung (A549), breast (MDA-MB-453) or bladder (RT4) carcinoma cell lines inoculated for 72 hrs with 1ppc NG-615, NG-640, NG-641, NG-617, enadenotucirev (EnAd) or left uninfected were used for quantification of viral DNA by qPCR. Cell supernatants were collected and clarified by centrifuging for 5 mins, 1200rpm. 50µL of supernatant was used for DNA analysis.

DNA was extracted from the supernatant sample using the Qiagen DNeasy kit, according to the manufacturer's protocol. A standard curve using EnAd virus particles (2.5e10-2.5e5vp) was also prepared and extracted using the DNeasy kit. Each extracted sample or standard was analysed by qPCR using a virus gene specific primer-probe set to the early gene E3. Quantification of the number of detected virus genomes per cell demonstrated viral replication in A549, MDA-MB-453 and RT4 for all viruses tested (NG-617, NG-615, NG-640 and NG-641) (Figure 2). Viral replication was similar for all viruses and was equivalent to that of the parental EnAd virus. No virus genomes could be detected in uninfected cells.

Oncolytic activity

Lung (A549) carcinoma cells inoculated with 100ppc NG-615, NG-640, NG-641, NG-617, EnAd or left uninfected were monitored using a xCELLigence Real Time Cell Analyzer (RTCA). Cell proliferation was monitored every 60 minutes for up to 96 hours. Oncolysis of the cells was assessed by calculating the Killing Time 50 (KT50) which is the time point when 50% lysis is reached (Figure 3). These data showed an equivalent KT50 across all viruses tested including the parental EnAd virus. No oncolytic effect was observed on untreated cells.

Collectively these data indicate that inclusion of a BiTE and either two or three immunomodulatory transgenes does not significantly impact the replicative or oncolytic activity of the EnAd virus.

Example 3: Analysis of virus mediated transgene expressionRecombinant BiTE detection

To detect the BiTE, the C-terminal decahistidine affinity tag can be probed with an anti-His antibody using the technique of western blotting. Protein samples were adjusted with lysis buffer to a final volume of 15 µL including 2,5 µL 6x Laemmli SDS Sample Buffer which contains β-mercaptoethanol and SDS. Samples were incubated for 5 minutes at 95 °C to denature proteins and loaded onto 15-well 10% precast polyacrylamide gels (Mini-PROTEAN TGX Precast Gels, BioRad, UK). Gels were run at 180 V for 45 minutes in 1 x running buffer within a Mini-PROTEAN Tetra System (BioRad, UK). Proteins from the SDS gels were transferred onto nitrocellulose membranes by wet electroblotting at 300 mA and 4 °C for 90 minutes in 1 x transfer buffer within a Mini Trans-Blot Cell (BioRad, UK). Transfer was performed in presence of an ice pack to limit heat. The nitrocellulose membrane was then blocked with 5% milk in PBS-T on a shaker for 1 hour at room temperature, and probed with anti-His (C-term) antibody (mouse α-6xHis, clone 3D5, Invitrogen, UK, #46-0693), diluted 1:5000 in PBS/5% milk. After incubation on a shaker overnight at 4°C, the membrane was washed and probed with HRP-labelled polyclonal secondary α-mouse-immunoglobulin-antibody (1:10.000 in PBS/5% milk, Dako, #P0161) for 1 hour at room temperature. For visualization, SuperSignal West Dura Extended Duration Substrate (Thermo Fisher Scientific, UK) was applied, following manufacturer's instructions and exposed to X-ray film and developed in an automatic film processor. The results demonstrated the expression and secretion of BiTE protein from Ad293 cells transfected with the BiTE expression plasmids, but not the parental vector.

Recombinant BiTE quantification

To measure the quantity of recombinant BiTE protein, the technique of dot blot was used to compare the BiTE signal to a His-tagged (C-term 10His) protein standard (10 x His-tagged human Cathepsin

D, Biolegend, #556704). Two-fold serial dilutions of BiTE samples and protein standard were prepared, and 1.5 uL of each directly applied to a nitrocellulose membrane and air-dried for 20 minutes. The blocking and staining protocol described above for western blotting was then performed. The molar concentration of the protein standard was adjusted to represent a BiTE concentration of 250μg/mL. The results (Figure 13A) demonstrated the expression and secretion of BiTE protein from Ad293 cells transfected with the BiTE expression plasmids.

FAP binding ELISA

The FAP-binding activity of the FAP BiTE and control (anti-FHA) BiTE (SEQ ID NOs: 2 and 4) secreted from cells transfected with pSF-CMV-FAPBiTE or pSF-CMV-ControlBiTE was assessed by enzyme-linked immunosorbent assay (ELISA). Empty pSF-CMV vector supernatants were included as a negative control. ELISA plates (Nunc Immuno MaxiSorp 96 well microplate) were prepared by coating overnight at 4^0C with human FAP/seprase protein (100ng/well, Sino Biological Inc, 10464-H07H-10) in PBS buffer. Plates were washed between all subsequent binding steps with PBS 0.05% Tween 20. The plates were blocked for 1 hour at room temperature with 5% BSA in PBS 0.05% Tween 20. Aliquots of BiTE protein, or protein harvested from empty pSF-CMV vector-transfected wells, were diluted 10-fold into PBS/5% BSA/0.05% Tween 20. All samples were added to the FAP coated plates and incubated for 2 hr at room temperature. The detection antibody, anti-His (C-term) antibody (mouse anti-6xHis, clone 3D5, Invitrogen, UK, #46-0693), was diluted 1:1000 and applied for 1 hour at room temperature. HRP conjugated anti-mouse-Fc (1:1000 in PBS/5% milk, Dako) was then applied for 1 hr at room temperature before HRP detection was performed with HRP substrate solution 3.3.5.5'-teramethylethylenediamine (TMB, Thermo-Fisher). Stop solution was used for terminating the reaction and the developed colour was measured at 450nm on a plate reader. Absorbance at 450nm was plotted for FAP BiTE, control BiTE and empty vector supernatants, demonstrating specific binding of the FAP BiTE to FAP protein. The results (Figure 13B) show the specific binding of the FAP BiTE and not control BiTE to recombinant FAP protein.

Transgene expression assessed by ELISA

Expression of the chemokine or cytokine transgenes, IFNα, MIP1α, FLT3L, CXCL10 and CXCL9 were assessed using ELISAs. A549 and RT4 carcinoma cell lines were inoculated with 1ppc NG-615, NG-640, NG-641, NG-617, EnAd or left uninfected for up to 7 days. At 4 days and 7 days post inoculation cellular supernatants were clarified and assessed for transgene expression by ELISA.

IFNα ELISA was carried out using the Verikine Human IFN alpha Kit (Pbl assay science), MIP1α ELISA was carried out using the Human CCL3 Quantikine ELISA kit (R & D systems), Flt3L ELISA was carried out using the Flt3L human ELISA kit (Abcam), CXCL9 ELISA was carried out using the CXCL9 human ELISA kit (Abcam) and CXCL10 ELISA was carried out using the CXCL10 human ELISA kit (Abcam). All assays were carried out according to the manufacturers' protocol.

The concentrations of secreted IFNα, MIPα, FLt3L, CXCL9 and CXCL10 were determined by interpolating from the standard curves. IFNα, MIP1α and Flt3L expression could be detected in the cellular supernatant of NG-615 treated cells, IFNα, CXCL9 and CXCL10 could be detected in supernatants of NG-641 treated cells and CXCL9 and CXCL10 could be detected in the supernatants of NG-640 treated cells (Figures 4 and 5). No chemokine or cytokine transgene expression was detected in EnAd treated or untreated control cells.

Functional Transgene expression assessed by cell-based reporter assay

The expression of functional FAP-BiTE and IFNα transgenes were assessed in assays using a Jurkat-Dual reporter cell line (Invivogen). This is a human immortalized T lymphocyte cell line (Jurkat) transformed by the stable integration of two inducible reporter constructs. One of the inducible reporter constructs enables IFN- activation of the interferon regulatory factor (IRF) pathway to be studied through the secretion and activity of secreted embryonic alkaline phosphatase (SEAP, while the second is an NF-kB responsive secreted luciferase reporter that is active by signalling through the T-cell receptor. Activity of SEAP is proportional to the level of IFN- present in the supernatant and can be measured by detecting the SEAP induced degradation of the substrate Quanti-Blue™. The expression of functional MIP1α was assessed using a CCR5 reporter cell line (CHO-K1 CCR5 β-arrestin, Invivogen). A549 carcinoma cell lines were inoculated with 1ppc NG-615, NG-640, NG-641, NG-617, EnAd or left uninfected. At 2, 3, or 4 days post-inoculation cellular supernatants were collected and clarified for analysis.

To assess IFNα function 20μL of each supernatant, diluted 1:10, 1:50 or 1:250 in culture media, was added to Jurkat Dual cells ($2x10^{5}$ cells/well) and incubated for 16-20 hours. The supernatants were then harvested from the plates and treated with 200μL Quanti-Blue™ reagent for 1 hour. The plates were analysed using a microplate reader measuring absorbance (Abs) at 640nm. Responses demonstrating the presence of functional IFNα could be detected in supernatants from NG-615 and NG-641 treated carcinoma cells but not NG-640, NG-617, EnAd treated or uninfected controls (Figure 6A). The level of functional IFNα detected was at similar levels in NG-615 and NG-641 treated supernatants.

To assess MIP1α function CCR5 reporter cells were seeded ($5x10^{3}$ cells/well) and incubated for 20-24 hours. 5μL of supernatant from the treated tumour cells was then added to each well and incubated for 90 minutes. Luciferase reporter activity was then detected using a detection solution and quantification on a luminescence plate reader. Responses demonstrating the presence of functional MIP1α were detected in supernatants from NG-615 treated carcinoma cells and supernatants from cells treated with a positive control virus known to express MIP1a, NG-347 (Figure 6B).

To assess FAP-BiTE function MRC-5 lung fibroblast cells (which express FAP on their cell membrane) were seeded ($2x10^{4}$ cells/well) and incubated for 4 hours to allow cells to adhere to the plates. Jurkat-Dual cells ($2x10^{5}$ cells/well) were then added to the wells along with 20μL of supernatant from the treated tumour cells. The plates were incubated for 16-20 hours. Supernatants were then harvested and treated with 50μL Quanti-Luc reagent before immediately reading the plates on a plate reader to detect luciferase activity. Responses demonstrating the presence of functional FAP-BiTE were detected in the supernatants of NG-617, NG-615, NG-640 and NG-641 treated carcinoma cells but not EnAd treated or untreated control supernatants (Figure 7). Surprisingly, given the similar levels of IFNα produced by NG-615 and NG-641, supernatants from NG-615 treated cells had significantly lower levels of functional FAP-BiTE expression when compared to all other BiTE expressing viruses tested, including the other virus containing 4 transgenes, NG-641.

Example 2

The functional activities of recombinant BiTE proteins were assessed in a number of different assays prior to constructing BiTE transgene-bearing EnAd viruses.

Isolation of human peripheral blood mononuclear cells (PBMCs)

Human PBMCs were isolated by density gradient centrifugation either from fresh human blood samples of healthy donors or from whole blood leukocyte cones, obtained from the NHS Blood and Transplant UK in Oxford. In either case, the samples were diluted 1:2 with PBS and 25 mL of this mixture was layered onto 13 mL Ficoll (1.079g/mL, Ficoll-Paque Plus, GE Healthcare) in a 50 mL Falcon tube. Samples were centrifuged (Allegra X-15R, Beckman Coulter) at 1600 rpm for 30 minutes at 22 °C with the lowest deceleration setting to preserve phase separation. After centrifugation, 4 layers could be observed which included a plasma layer at the top, followed by an interface containing PBMCs, a Ficoll layer and a layer of red blood cells and granulocytes at the bottom. The PBMCs were collected using a Pasteur pipette and washed twice with PBS (1200 rpm for 10 minutes at room temperature) and re-suspended in RPMI medium supplemented with 10% FBS.

Isolation of CD3-positive T-cells

CD3-positive ($CD3^+$) T-cells were extracted from PBMCs by depletion of non-CD3 cells using a Pan T Cell Isolation Kit (Miltenyi Biotec, #130-096-535), according to the manufacturer's protocol.

Processing primary ascites samples

Primary human ascites samples were received from the oncology ward of the Churchill Hospital (Oxford University Hospitals) from patients with multiple indications, including but not limited to ovarian, pancreatic, breast and gastric cancer. Upon receipt, cellular and fluid fractions were separated, with aliquots of fluid frozen at -20°C for storage and future analysis. The cellular fraction was treated with red blood cell lysis buffer (Roche, #11814389001) to remove red blood cells, following the manufacturer's instructions. Cell types present in each sample was determined by staining for EpCAM, EGFR, FAP, CD45, CD11b, CD56, CD3, CD4, CD8, PD1 and CTLA4 and analysed by flow cytometry. Cells were then used fresh for *ex vivo* T-cell activation and target cell lysis experiments. In some cases, the cells were passaged in DMEM supplemented with 10% FBS for use in later experiments.

Cell line maintenance

All cell lines were maintained in DMEM (Sigma-Aldrich, UK) or RPMI medium (Sigma-Aldrich, UK) as specified in Table 3, supplemented with 10% (v/v) foetal bovine serum (FBS, Gibco™) and 1% (v/v) Penicillin/Streptomycin (10 mg/mL, Sigma-Aldrich, UK), in a humidified incubator (MCO-17AIC, Sanyo) at 37°C and 5% CO_2, unless otherwise specified. Cells were split every 2 to 3 days before reaching confluency by enzymatic dissociation with Trypsin/EDTA (0.05% trypsin 0,02% EDTA, Sigma-Aldrich, UK). In this process, culture medium was aspirated and cells were washed with 15 ml of PBS and subsequently cells were treated with 2 mL of Trypsin/EDTA for 2-10 minutes at 37 °C. Trypsin was neutralized with 10 mL of DMEM containing 10% FBS and a portion of the cells was transferred into new flasks containing fresh medium. For routine cell culture, media was supplemented with 10% FBS, for infections and virus plasmid transfections with 2% FBS and for recombinant BiTE plasmid transfections with no FBS supplement.

Table 3

Cell line	Origin of cells	Culturing Media	Source
Ascites-derived cell lines	Human primary ascites	DMEM	NHS Blood & Transplant UK
BTC100	Human primary lung cancer-associated fibroblasts (CAF)	DMEM	University of Oxford
CHO-K1	Chinese hamster ovary, adherent	RPMI	ATCC
CHO-K1 stable cell lines	Chinese hamster ovary, adherent	RPMI	-
DLD1	Human colorectal adenocarcinoma	RPMI	ATCC
HEK 293A	Human embryonic kidney, adherent	DMEM	ATCC
HEK 293A stable cell lines	Human embryonic kidney, adherent	DMEM	-
HEK 293T	Human embryonic kidney, adherent	DMEM	ATCC
MCF-7	Human, mammary gland, breast, adherent	DMEM	ATCC
Normal human dermal fibroblasts (NHDF)	Normal adult human primary dermal fibroblasts	DMEM	ATCC
SKOV3	Human ovarian adenocarcinoma	DMEM	ATCC

Statistics

In cases where two conditions were being compared, statistical analyses were performed using a t-test. In all other cases, statistical analyses were performed by using a One-way ANOVA.

Characterisation of human T-cell activation by recombinant FAP BiTE

The ability of the FAP BiTE to induce T-cell activation in the presence or absence of normal human dermal fibroblast (NHDF) cells was compared. Human CD3$^+$ T-cells (70,000 cells per well in 96-well U-bottom plates) were co-cultured alone or with NHDF cells (10:1 T:NHDF) in the presence of media alone or 300 ng/mL FAP or control BiTE. Cells were co-cultured for 24 hours at 37°C and subsequently harvested with enzyme-free cell dissociation buffer (Thermo, #13151014). The expression levels of CD69 (Figure 14A) and CD25 (Figure 14B) on CD45$^+$ T-cells were then analysed by antibody staining and flow cytometry and represented as geometric mean fluorescence (gMFI) values. Plate-immobilised anti-CD3 antibody (7.5 μg/mL) was used as positive control for T cell activation. The FAP BiTE selectively induced the expression of activation markers CD69 and CD25 on T-cells, indicating that it was able to activate T cells.

In a second similar experiment, T-cells were assessed by intracellular cytokine staining 6 hr after co-culture with NHDF cells (200,000 CD3$^+$ cells plus 40,000 NHDF in wells of a 96-well plate) and

300ng/mL FAP or control BiTE. CD45 $^+$ T-cells were intracellularly stained for IFNγ expression with Brefeldin A added into the culture medium 5 hours before harvest. As a positive control, T-cells were stimulated with soluble PMA (10ng/mL) and ionomycin (1μg/mL). The results shown in Figure 14C indicate that the FAP BiTE in the presence of NHDF resulted in a significantly higher number of IFNγ expressing T-cells compared to the control BiTE.

Example 4:

To further evaluate the functionality of the IFNα produced from the transgene in NG-641, Jurkat-Dual™ cells were treated with supernatants from A549 tumor cells either uninfected or infected with 10 particles per cell (ppc) of enadenotucirev (EnAd) or NG-641 for 3 days. To demonstrate the secretion of SEAP was IFNα specific, IFNα was blocked by incubating IFNα specific antibodies with the A549 supernatants for 30 mins prior to the treatment of the Jurkat-Dual reporter cell line – an isotype control antibody was included as a negative control. The data (Figure 8A) show that the activity of the NG-641 treated tumour cell supernatant in the Jurkat Dual reporter assay is inhibited by the anti-IFNα antibody and not the isotype control and is thus mediated by IFNα. A different reporter assay system was used to evaluate the functionality of the CXCL9 and CXL10 chemokine transgenes in NG-641. This assay used a PathHunter β-arrestin reporter cell line expressing CXCR3, the receptor for both chemokines (Eurofins). GPCR activation following CXCL9/10 binding to CXCR3 expressed by these cells leads to β-arrestin recruitment to the receptor that is measured using a gain-of-signal assay based on Enzyme Fragment Complementation (EFC) technology. PathHunter β-arrestin CXCR3 reporter cells were treated with supernatants from A549 tumor cells either uninfected or infected with 10 particles per cell (ppc) of EnAd or NG-641 for 3 days. The concentration of CXCL9/10 in the supernatant is proportional to the luminescence in the assay. To demonstrate that the GPCR activation was CXCL9/10 specific, CXCL9 and CXCL10 were blocked by incubating CXCL9/10 specific antibodies with the A549 supernatants for 30 mins prior to the treatment of the PathHunter β-arrestin cells. The data shown in Figure 8B show increased activity of the CXCR3 reporter cells in the presence of supernatants from NG-641 treated tumour cells compared to EnAd or uninfected controls, and that this increase is blocked by the antibodies to CXCL9/10.

As an alternative measure of chemokine functionality, the ability of chemokines to down-regulate the cell surface expression of their specific receptors was used as the basis of an assay, evaluating levels of CXCR3 receptor on anti-CD3/CD28 activated human T cells. A549 tumor cells were either uninfected or infected with 1 viral particles per cell (ppc) of enadenotucirev (EnAd) or NG-641 for 7 days and supernatants collected. Activated T cells were then treated with the supernatants for 30 minutes and levels of CXCR3 measured via flow cytometry, with data plotted as mean fluorescent intensity (MFI). To demonstrate that the downregulation of cell surface CXCR3 was CXCL9/10 specific, CXCL9 and CXCL10 were blocked by incubating CXCL9/10 specific antibodies with the A549 tumor cell supernatants for 30 mins prior to the treatment of the activated T cells. The data shown in Figure 9 show a selective down-regulation of CXCR3 expression on both CD4 and CD8 T-cells induced by supernatants from NG-641 infected A549 tumour cells, and this effect was abolished by pre-treatment with anti-CXCL9/10 antibodies.

Example 5: Functional activity of FAP-BiTE expressing viruses in *ex vivo* human tumor cell cultures

Samples of freshly excised human tumours, from planned surgical excisions, provided via a biobank under full ethical approval, were initially minced with scissors and a scalpel and then single cell suspensions were generated using a GentleMACs tissue dissociator (Miltenyi Biotec). These unseparated cell preparations were found to comprise tumour cells, fibroblasts and different immune cells, including T-cells, and were used to evaluate the ability of viruses to infect the primary tumour cells, produce their encoded transgenes and activate the tumour infiltrating T-cells also present in the cultures. Cells were resuspended in culture media consisting of Ham's F-12 Nutrient Mix, GlutaMAX™ Supplement (Gibco), 1x Insulin-Transferrin-Selenium-Ethanolamine (ITS -X) (Gibco), Amphotericin B 2.5 mg/mL (Gibco™), Penicillin 100 units/mL, Streptomycin 100 mg/mL, Sodium Pyruvate and 10% FBS, and plated at ~1 x 10^6cells/ml in either 96 well plates (0.25ml final volume) or 24 well plates (0.5ml final volume). They were inoculated with EnAd, NG-615, NG-617, NG-640 or NG-641 at 1000ppc, or left untreated (UIC). As a positive T-cell activation control, some wells were also stimulated with anti-CD3 and anti-CD28 antibodies each at 2μg/ml. Cells were cultured in duplicate wells for 72h, then supernatants were collected and levels of different cytokines produced were measured using multi-cytokine fluorescent bead-based kits (LEGENDplex™) and a flow cytometer. Three non-small cell lung carcinoma (NSCLC) samples (T016, T017, T024), one renal cell carcinoma (RCC) and one colorectal (CRC) liver metastasis sample were tested. In line with the transgene expression data in Figures 4-6, IFNα was produced selectively in cultures treated with NG-615 and NG-641 (Figure 10A). Flt3 ligand (FLT3L) was readily detected following NG-615 treatment but only very low levels were detected with other viruses, and these levels were similar to those induced by activating T-cells with anti-CD3/28 indicating that the Flt3L in NG-615 cultures was the transgene product. The results for other cytokines showed that, as with the tumour cell line inoculation study described in Example 3 (Figure 7), NG-615 inoculation lead to much lower levels of T-cell activation than the other FAP-BiTE encoding viruses NG-617, NG-640 and the other 4-transgene-bearing virus NG-641, as shown for IFNγ, TNFα, IL-17, Granzyme B and IL-13 in Figure 10B.

Activation of the endogenous tumour T-cells in an excised NSCLC tumour cell culture was also measured by flow cytometry, assessing levels of the T-cell activation markers CD25, CD69 and CD107a as well as intracellular cytokine (IFNγ and TNFα) expression by both CD4 and CD8 T-cells after 3 days of culture. As shown in Figure 11A-D, EnAd had little effect on either activation markers or cytokine expression, whereas NG-617, NG-640 and NG-641 treatments all led to upregulation of all these measured of T-cell activation. The similar levels of activation seen with the FAP-BiTE-bearing viruses is in line with the cytokine data described above (Figure 10B)

Example 6

In this example, the ability of recombinant FAP BiTE-activated T-cells to induce death of the fibroblast target cells was evaluated.

FAP BiTE induces T cell-mediated lysis of FAP-positive cell lines and primary cells

NHDF (7,000 cells) were co-cultured with 70,000 T-cells in wells of a U-bottom 96 well plate in the presence of media alone or 300 ng/mL of control or FAP BiTE. After 24 hours of co-culture, supernatants were harvested and cytotoxicity determined by LDH assay following the manufacturer's instructions. The results are in Figure 15A show that the FAP BiTE significantly increased lysis of NHDF cells.

In a similar experiment, 7,000 primary lung fibroblast cells (BTC100) were co-cultured with 70,000 $CD3^+$ T-cells with or without 300 ng/mL of control or FAP BiTE. After 24 hours of co-culture, supernatants were harvested and cytotoxicity determined by LDH assay. The results in Figure 15B & C show that the FAP BiTE significantly increased lysis of primary human cancer associated fibroblast (CAF) cells. Expression of FAP by these and other patient-derived cell lines is shown in Figure 16.

The dose-response relationship for FAP BiTE-mediated cell lysis was evaluated by co-culturing 8,000 NHDF cells with 40,000 T-cells and BiTE concentrations ranging from 2×10^3 to 2×10^{-2} ng/mL. After co-culture for 24 hours at 37°C, an LDH assay was performed on supernatants to determine target cell cytotoxicity. Dose response curves were fitted using a four parameter non-linear fit model integrated into GraphPad Prism, generating an EC50 value for the FAP BiTE of 3.2ng/mL. The results (Figure 17A) show a dose-dependent relationship between FAP BiTE concentration and cytotoxicity as measured by LDH assay (shown as Abs_{490}).

Example 7

Stable FAP expressing CHO and Ad293 cell lines were generated as a means to demonstrate the FAP antigen specificity of the FAP BiTE by comparing to parental untransfected cells.

Generation of FAP-expressing stable-transfected cell lines

The protein sequence of the FAP gene was obtained from the NCBI database (SEQ ID 23), reverse transcribed to generate a DNA coding sequence that was synthesised by Oxford Genetics Ltd (Oxford, UK). The FAP gene was cloned into pSF-Lenti vector by standard cloning techniques producing the pSF-Lenti-FAP vector. HEK293T cells were transfected with the lentivirus FAP expression vector alongside pSF-CMV-HIV-Gag-Pol, pSF-CMV-VSV-G, pSF-CMV-HIV-Rev. Lipofectamine 2000 was used as a transfection reagent and was added to the vector DNA at a DNA:lipofectamine ratio of 1:2, and incubated with the cells at 37°C. Supernatant containing lentivirus was harvested 48 hours later and mixed with polybrene (final concentration, 8μg/mL). The Lentivirus/polybrene mixture was added to seeded Ad293 or CHO cells and incubated at 37°C. On day 4, the supernatant was exchanged for media containing puromycin (2μg/mL for Ad293 and 7.5μg/mL for CHO). Stable variants were then clonally selected and FAP expression of the parental cell lines or stable-transfected variant was determined by staining with FAP or isotope control antibody and analysed by flow cytometry (Figure 18A).

FAP BiTE-mediated target cell lysis is specific to FAP-expressing cells

CHO or CHO-FAP cells (7,000 cells) were co-cultured alone or with human T-cells (70,000) in the presence of media alone or 2μg/mL control or FAP BiTE in wells of a U-bottom 96-well plate. After 24 hours incubation, supernatants were harvested and target cell cytotoxicity measured by LDH cytotoxicity assay as described in example 4 (Figure 18B). T-cell activation was also determined by analysing the expression levels of CD69 and CD25 via flow cytometry (Figure 19). Cytotoxicity was only observed when CHO-FAP cells were cultured with T-cells and FAP BiTE. This indicates that FAP

BiTE mediated T-cell activation and target cell lysis is highly specific and limited to FAP-expressing cells, and not the FAP-negative parental cell line.

Example 8

In a further experiment, the ability of the recombinant FAP BiTE protein to activate CD4 or CD8 T-cells and the ability of each of these T-cell subsets to lyse NHDF cells was assessed. $CD3^+$ T-cells (35,000) were co-cultured with 7,000 NHDF cells in the presence of 300ng/mL control or FAP BiTE in wells of a U-bottom 96 well plate, and incubated at 37°C for 24 hours. Cells were harvested and stained with antibodies to CD4 or CD8 and CD69 and CD25, and analysed by flow cytometry. The results (Figure 20A) demonstrated that the FAP BiTE induced an increase in activation markers CD69 and CD25 in both $CD4^+$ and $CD8^+$ T-cells.

In a similar experiment, the ability of each T-cell subset (CD4 and CD8) to kill target cells was assessed. $CD4^+$ T-cells were extracted from CD3-purified cells by positive selection using a CD4 T Cell Isolation Kit (Miltenyi Biotec, #130-045-101), according to the manufacturer's protocol, with the CD8 cells within non-isolated flow-through. In wells of a U-bottom 96-well plate, 7,000 NHDF were co-cultured with 35,000 $CD4^+$ or $CD8^+$ T-cells together with 300ng/mL of control or FAP BiTE and incubated at 37°C. After 24 hours, supernatants were harvested and target cell cytotoxicity measured by LDH cytotoxicity assay. The results (Figure 20B) show that the FAP BiTE induced both $CD4^+$ and $CD8^+$ T-cells to kill NHDF cells.

Example 9

Characterising FAP BiTE-mediated activation of autologous tumour-associated lymphocytes from primary malignant ascites

To evaluate the activity of BiTE proteins using cancer patient derived cells, samples of primary malignant ascetic fluids containing both $CD3^+$ T-cells and FAP^+ cells were obtained for testing. Unpurified ascites cells (therefore unchanged from when received) were seeded at 250,000 cells per well of a U-bottom 96-well plate in either 100% ascites fluid or medium supplemented with 1% human serum in the presence of 500 ng/mL control or FAP BiTE. Untreated wells served as negative controls. After incubation at 37°C for 5 days, the total cell population was harvested and the numbers of $CD3^+$ T-cells (Figure 21A) and expression levels of CD25 on $CD3^+$ T-cells were determined (Figure 21B). Total cell numbers per well were determined using precision counting beads. The results demonstrate that the FAP BiTE resulted in significant increase in T-cell activation of the tumour-associated T-cells from cancer patients.

As an extension of the experiment above, replicate wells were harvested and the number of FAP^+ cells determined by flow cytometry (Figure 21C). Total cell numbers per well were determined using precision counting beads. The results show that the FAP BiTE resulted in a significant decrease in numbers of autologous FAP-expressing cells in the ascites sample.

Example 10

Recombinant BiTE-expressing EnAd viruses were engineered, produced and purified using the methods described below.

Generation of BiTE-expressing Enadenotucirev

EnAd is a replication competent chimeric group B adenovirus that contains frequent non-homologous nucleotide substitutions of Ad3 for Ad11p in the E2B region, a nearly complete E3 deletion and a smaller E4 deletion mapped to E4orf4 (Kuhn et al, Directed evolution generates a novel oncolytic virus for the treatment of colon cancer, PLoS One, 2008 Jun 18; 3(6): e2409).

The plasmid pEnAd2.4 was used to generate the plasmids ppEnAd2.4-CMV-FAPBiTE, pEnAd2.4-SA-FAPBiTE, pEnAd2.4-CMV-ControlBiTE, pEnAd2.4-SA-ControlBiTE (Table 4) by direct insertion of a cassette encoding the FAP BiTE (SEQ ID NO: 1) or Control BiTE (SEQ ID NO: 3). The transgene cassette contained a 5' short splice acceptor sequence CAGG or an exogenous CMV promoter (SEQ ID NO: 24), the EpCAM, FAP or control BiTE cDNA sequence and a 3' polyadenylation sequence (SEQ ID NO: 25). Construction of the plasmid was confirmed by DNA sequencing. The exogenous CMV promoter is constitutively active and thus leads to early expression of transgenes. The splice acceptor sequence drives expression under the control of the viral major late promoter and leads to later transgene expression following initiation of virus genome replication.

Table 4

Plasmid ID	**[plasmid DNA] ng/ml**
pEnAd2.4-CMV-FAPBiTE	1322.8
pEnAd2.4-SA-FAPBiTE	3918.3
pEnAd2.4-CMV-ControlBiTE	189.1
pEnAd2.4-SA-ControlBiTE	236.2
pEnAd2.4-CMV-FAPBiTE-RFP	1599
pEnAd2.4-SA-FAPBiTE-RFP	1872
pEnAd2.4-CMV-ControlBiTE-RFP	1294
pEnAd2.4-SA-ControlBiTE-RFP	2082

Virus Production and characterisation

The plasmids EnAd2.4-CMV-EpCAMBiTE, pEnAd2.4-SA-EpCAMBiTE, pEnAd2.4-CMV-FAPBiTE, pEnAd2.4-SA-FAPBiTE, pEnAd2.4-CMV-ControlBiTE, pEnAd2.4-SA-ControlBiTE were linearised by restriction digestion with the enzyme AscI to produce the liner virus genome. Digested DNA was purified by isopropanol extraction and precipitated for 16hrs, -20^{0}C in 300µl >95% molecular biology grade ethanol and 10µl 3M Sodium Acetate. The precipitated DNA was pelleted by centrifuging at 14000rpm, 5 mins and was washed in 500µl 70% ethanol, before centrifuging again, 14000rpm, 5mins. The clean DNA pellet was air dried and resuspended in 100µL water. 6.25 µg DNA was mixed with 15.6µL lipofectamine transfection reagent in OptiMEM and incubated for 20 mins, RT. The transfection mixture was then added to a T-25 flask containing Ad293 cells grown to 80% confluency. After incubation of the cells with the transfection mix for 4hrs at 37^{0}C, 5% CO_2 4mls of cell media (DMEM high glucose with glutamine supplemented with 10% FBS) was added to the cells and the flasks was incubated 37^{0}C, 5% CO_2. The transfected Ad293 cells were monitored every 24hrs and were supplemented with additional media every 48-72hrs. The production of virus was monitored by observation of a significant cytopathic effect (CPE) in the cell monolayer. Once extensive CPE was observed the virus was harvested from Ad293 cells by three freeze-thaw cycles. Single virus clones were selected by serial diluting harvested lysate and re-infecting Ad293 cells, and harvesting wells containing single plaques. Serial infections of Ad293 cells were performed once an infection had reached full CPE in order to amplify the virus stocks. Viable virus production during amplification was confirmed by observation of significant CPE in the cell monolayer.

Virus Purification

Once potent virus stocks were amplified the viruses were purified by double caesium chloride density gradient centrifugation (banding) to produce, NG-603, NG-604, NG-605 and NG-606 virus stocks. These stocks were titred by micoBCA assay (Life Technologies), following manufacturer's instructions (Table 5).

Table 5

EnAd ID	NG ID NO:	Virus Genome SEQ ID	vp/mL	TCID50/ mL
EnAd-CMV-ControlBiTE	NG-603		$1.42607\text{x}10^{12}$	$5.01\text{x}10^{10}$
EnAd-SA-ControlBiTE	NG-604		$3.31073\text{x}10^{12}$	$2.00\text{x}10^{11}$
EnAd-CMV-FAPBiTE	NG-605	SEQ ID NO: 26	$1.64653\text{x}10^{12}$	$1.58\text{x}10^{11}$
EnAd-SA-FAPBiTE	NG-606	SEQ ID NO: 27	$1.28148\text{x}10^{12}$	$3.98\text{x}10^{10}$
EnAd-CMV-ControlBiTE-P2A-RFP	NG-607		$5.963\text{x}10^{12}$	$1.26\text{x}10^{9}$
EnAd-SA-ControlBiTE-P2A-RFP	NG-608		$1.51848\text{x}10^{12}$	$6.31\text{x}10^{9}$
EnAd-CMV-FAPBiTE-P2A-RFP	NG-609		$1.57517\text{x}10^{12}$	$7.94\text{x}10^{9}$
EnAd-SA-FAPBiTE-P2A-RFP	NG-610		$7.74881\text{x}10^{11}$	$5.01\text{x}10^{10}$

Example 11

The activities of NG-601, NG-602, NG-603, NG-604, NG-605 and NG-606 viruses were characterised using the methods described below.

Characterisation of BiTE encoding EnAd activity compared to EnAd in carcinoma cell lines

The ability NG-601, NG-602, NG-603, NG-604, NG-605, NG-606 or EnAd to replicate was analysed by infection of A549 lung carcinoma cells and assessed by qPCR. A549 cells were seeded in wells of a 24-well plate at a cell density of $2\text{x}10^5$ cells/well. Plates were incubated for 18 hrs, 37^0C, 5% CO_2, before cells were either infected with 100 virus particles per cell (ppc) or were left uninfected. Wells were harvested 24, 48 or 72 hrs post infection and DNA purified using PureLink genomic DNA mini kit (Invitrogen) according to the manufacturer's protocol. Total viral genomes were quantified by qPCR with each extracted sample or standard using an EnAd hexon gene specific primer-probe set in the reaction mix detailed in Table 6. qPCR was performed as per the programme in Table 7.

Table 6

Reagent	**Volume/well (µl)**
2 × qPCRBIO Probe Mix (PCRBiosystems)	10
EnAd Forward primer	0.08
EnAd Reverse primer	0.08
EnAd Probe	0.8
NFW	4.04
Sample	5
Well Volume	20

Table 7

No. Cycles	Temperature (^{0}C)	Duration (secs)
1	95	120
40	95 60-65	5 20-30

Quantification of the number of detected virus genomes per cell demonstrated that NG-601, NG-602, NG-603, NG-604, NG-605, NG-606 and EnAd virus replication were comparable in the A549 cell line (Figure 22A).

Oncolytic activity of NG-601, NG-602, NG-603, NG-604, NG-605, NG-606 or EnAd was assessed by infection of A549 (Figure 22B). A549 cells were seeded in 96-well plate at a cell density of 1.5x10^4 cells/well. Plates were incubated for 18 hrs, 37^{0}C, 5% CO_2, before cells were infected with increasing ppc of virus (5-fold serial dilution, 4.1x10^{-7} to 5000 virus ppc) or were left uninfected. A549 cytotoxicity was measured on day 5 by CellTiter 96® AQueous One Solution Cell Proliferation Assay (MTS) (Promega, # G3582). Dose response curves were fitted using a four parameter non-linear fit model integrated into GraphPad Prism. IC50 values generated for each virus demonstrated that the oncolytic activities of NG-601, NG-602, NG-603, NG-604, NG-605, NG-606 and EnAd was comparable for each virus.

Confirmation of functional BiTE transgene expression from NG-603, NG-604, NG-605, NG-606

To determine whether the viruses NG-601, NG-602, NG-605, NG-606 produced functional BiTEs, T-cell activation assays using CHO, CHO-EpCAM and CHO-FAP cell lines as target cells were performed. 10,000 target cells were co-cultured with 50,000 CD3$^+$ T-cells in wells of a U-bottom 96-well plate with Ad293 viral supernatants diluted 100-fold in culture medium and incubated for 24 hrs, 37^{0}C, 5% CO_2. T-cells were harvested and stained with antibodies specific for CD25 and CD69 and analysed by flow cytometry. The results (Figures 23A and 23B) indicated that the viruses NG-601 and NG-602 expressed a functional BiTE transgene that activated T cells when co-cultured with CHO-EpCAM cells, and NG-605 and NG-606 expressed a functional BiTE transgene that activated T cells when co-cultured with CHO-FAP cells, but not when co-cultured with CHO cells.

Quantification of BiTE expression in a colon carcinoma cell line

The quantity of BiTE expression by NG-601, NG-602, NG-605, NG-606 infection of the human colon carcinoma cell line DLD was assessed. DLD cells were seeded in 6 well culture plates at a density of 1.2x10^6 cells per well. 18 hrs post-seeding, DLD cells were infected with EnAd, NG-601, NG-602, NG-603, NG-604, NG-605, NG-606 at 100 ppc. Cells were cultured for 72 hrs before the supernatants were collected from the wells and centrifuged for 5 mins, 1200rpm to remove cell debris. The clarified supernatants were then used for a killing assay, with cytotoxicity compared to a standard curve generated with a recombinant BiTE of known concentration, allowing determination of quantity of BiTE in viral supernatants.

To determine the quantity of FAP BiTE produced from NG-605 and NG-606, a cytotoxicity assay was performed in which 8,000 NHDF were co-cultured with 40,000 CD3$^+$ T-cells and DLD viral supernatants diluted 1 in10^3, 1 in 10^4 and 1 in 10^5. A standard curve was generated by incubating NHDF and CD3$^+$ T-cells with FAP or control BiTE at 10-fold serial dilutions from 3333 to 3.33x10^{-4} ng/μL. Supernatants were harvested 24 hour post-treatment and cytotoxicity measured by LDH assay. Quantity of BiTE expressed was determined by comparing cytotoxicity of viral supernatants to that of the recombinant BiTE standard curve. The results (Figure 24) indicated that the viruses NG-605 and NG-606 produced 9.8 and 49.2 µg FAP BiTE per million DLD cells, respectively.

Example 12

In addition to encoding a FAP or Control BiTE, the NG-607, NG-608, NG-609, NG-610 viruses also carry a red fluorescent protein (RFP) transgene for visualization of infected cells using fluorescent microscopy methods (SEQ ID NOS: 20 & 21 Table 4). The functional activities of these viruses were characterised using the methods described below.

Confirmation of transgene expression from NG-607, NG-608, NG-609, NG-610

The ability of viruses NG-607, NG-608, NG-609 and NG-610 to produce their BiTE transgene was assessed by infection of Ad293 cells. Ad293 cells were plated in a 6-well plate at $1x10^6$ cells/well. Plates were incubated for 24 hrs, 37^0C, 5% CO_2, before cells were infected with viruses at 100 ppc or were left uninfected. At 48 hours post-infection, plaques were irradiated with a fluorescent mercury lamp and photographed (Figure 18). The results suggested that the viruses NG-607, NG-608, NG-609 and NG-610 express the RFP transgene.

Example 13

In the next series of experiments, the ability of EnAd and FAP or control BiTE viruses NG-603, NG-604, NG-605, NG-606, NG-607, NG-608, NG-609, NG-610 to kill target cells, including tumour cells and fibroblasts, was evaluated.

In the first study, the ability of EnAd to kill DLD cells was assessed using xCELLigence technology. DLD cells were plated in a 48-well E-plate at $1.2x10^4$ cells/well and incubated for 18 hrs, 37^0C, 5% CO_2, before cells were either infected with 100 EnAd ppc or were left uninfected. XCELLigence was used to measure target cell cytotoxicity every 15 minutes over an 8 day incubation period.

In a similar experiment, the ability of NG-603, NG-604, NG-605, NG-606 and EnAd to kill NHDF cells was assessed in co-culture with SKOV tumour cells and $CD3^+$ T-cells using xCELLigence. NHDF cells and SKOV cells were seeded in a 48-well E-plate at $4x10^3$ and $1x10^3$ cells/well, respectively. Plates were incubated for 18 hrs, 37^0C, 5% CO_2, before cells were either infected with 100 ppc of EnAd, of NG-603, NG-604, NG-605 or NG-606 or were left uninfected. After 2 hour incubation, 37,500 $CD3^+$ T-cells were added to each well. xCELLigence was used to measure target cell cytotoxicity every 15 minutes. The results (Figure 26A) demonstrate that the FAP BiTE-expressing viruses NG-605 and NG606, but not EnAd or control BiTE-expressing viruses NG-603 and NG-604, were able to induce lysis of NHDF cells, with kinetics dependent on the promoter used for BiTE expression (faster with CMV promoter).

In a similar experiment, the ability of NG-603, NG-604, NG-605, NG-606 and EnAd to kill NHDF cells, was assessed in co-culture with SKOV and $CD3^+$ T-cells using LDH cytotoxicity assay. NHDF cells and SKOV cells were seeded in a 96-well U-bottom plate at $8x10^3$ and $2x10^3$ cells/well, respectively, and either infected with 100 ppc of EnAd, of NG-603, NG-604, NG-605 or NG-606 or were left uninfected. After 2 hour incubation, 75,000 $CD3^+$ T-cells were added to each well and plates were incubated at 37^0C, 5% CO_2. Supernatants were harvested at 0, 24, 48 and 96 hours post-treatment and cytotoxicity measured by LDH cytotoxicity assay. The results (Figure 26B) demonstrate that the FAP BiTE-expressing viruses NG-605 and NG606, but not EnAd or control BiTE-expressing viruses NG-

603 and NG-604, were able to induce lysis of NHDF cells, with kinetics dependent on the promoter used for BiTE expression.

As an extension of the LDH experiment above, the cells were also harvested at 0, 24, 48 and 96 hours post-treatment, stained with antibodies for CD45, CD69 and CD25 and analysed by flow cytometry. The results (Figure 27) demonstrate that the FAP BiTE-expressing viruses NG-605 and NG-606, but not EnAd or control BiTE-expressing viruses NG-603 and NG-604, were able to induce T-cell activation, with kinetics dependent on the promoter used for BiTE expression.

In a similar experiment, the dependence on FAP to induce FAP BiTE-mediated T-cell activation was evaluated. In a 96-well U-bottom plate, SKOV cells were seeded at $2x10^3$ cells/well alone or in combination with NHDF cells at $8x10^3$ cells/well. Viral particles were added to each well at 100 ppc, and plates incubated at 37^0C, 5% CO_2. After two hours, 75,000 $CD3^+$ T-cells were added and plates incubated further. At 96-hours post-infection, cells were harvested and stained for CD45 and CD25 and analysed by flow cytometry (Figure 28A). The results demonstrate that the FAP BiTE-expressing viruses NG-605 and NG-606, only induced T-cell activation in the presence of FAP-positive NHDF cells.

In a similar experiment, the specificity of promoter (CMV or virus MLP/SA)-driven BiTE expression in NG-605 and NG-606 was investigated further. In a 96-well U-bottom plate, NHDF cells were seeded at $4x10^3$ cells/well. 100 viral particles per cell were added to each well, and plates incubated at 37^0C, 5% CO_2. After two hours, 40,000 CD3 cells were added and plates incubated further. At 72-hours post-infection, supernatants were harvested and cytotoxicity measured by LDH cytotoxicity assay. The results (Figure 28B) demonstrate that the CMV-driven virus NG-605, but not SA-driven NG-606, was able to mediate killing of NHDF cells upon infection of NHDF cells alone.

The results indicate that NG-605 and NG-606 were both able to induce T cell activation and target cell lysis, although the kinetic profile was slightly different depending on the promoter used.

Timelapse videos were obtained to observe viral or T cell-mediated lysis of target cells by recombinant FAP BiTE, EnAd, NG-603 or NG-605. NHDF cells were stained with CellTracker Orange CMTMR Dye (Life Tech, #C2927) and $CD3^+$ T-cells were stained with CellTrace Violet Cell Proliferation Kit (Life Tech, #C34557) following manufacturer's protocols. Dyed NHDF were plated in a 24-well plate at $7.5x10^3$ cells/well in co-culture with $1.35x10^4$ DLD or SKOV tumour cells. Plates were incubated for 18 hrs, 37^0C, 5% CO_2. Cells were then treated with 300 ng/mL FAP BiTE or infected with 100 ppc of EnAd, NG-603, and NG-605 or left untreated. After two hours incubation, 100,000 dyed $CD3^+$ T-cells were added to necessary wells, in addition to 1.5 µM CellEvent Caspase 3-7 reagent (Life Tech, #C10423). Videos were obtained on a Nikon TE 2000-E Eclipse inverted microscope, with images captured every 15 minutes for 96 hours. Frames from the videos are shown in Figure 29. The results show that the recombinant FAP BiTE and NG-605, but not EnAd or NG-603, were able to induce rapid lysis of NHDF cells.

In a similar experiment, NHDF cells were stained with CellTracker Green CMFDA Dye (Life Tech, #C2925) and $CD3^+$ T-cells were stained with CellTrace Violet Cell Proliferation Kit (Life Tech, #C34557) following manufacturer's protocols. Dyed NHDF were plated in a 24-well plate at $7.5x10^3$ cells/well in co-culture with $1.35x10^4$ DLD or SKOV tumour cells. Plates were incubated for 18 hrs, 37^0C, 5% CO_2. Cells were then infected with 100 ppc of NG-607, NG-608, NG-609 or NG-610 or left uninfected. After two hours incubation, 100,000 dyed $CD3^+$ T-cells were added to necessary wells.

Videos were obtained on a Nikon TE 2000-E Eclipse inverted microscope, with images captured every 15 minutes for 96 hours. Frames from the videos are shown in Figure 30. The results show that all viruses lead to tumour cell infection (RFP, red fluorescence, positive), but only NG-609 and NG-610 were able to induce rapid lysis of the co-cultured NHDF cells.

Example 14

In this example, the activation of autologous tumour-associated lymphocytes from FAP$^+$ primary malignant ascites from cancer patients by EnAd, NG-603, NG-604, NG-605 and NG-606 was evaluated. Patient samples considered suitable for further analysis were those containing CD3$^+$ T-cells and FAP$^+$ cells.

In the first experiment, unpurified (therefore unchanged from when received) ascites cells from a patient were seeded at 250,000 cells per well of a U-bottom 96-well plate in 100% ascites fluid. Cells were infected with viruses at 100 ppc, with untreated wells serving as negative controls. EnAd-CMV-GFP and EnAd-SA-GFP were also included in the experiment as a reporter to determine infection and late stage viral gene expression, respectively, with micrographs. After incubation at 37^{o}C for 5 days, the total cell population was harvested and the expression level of CD25 on CD3$^+$ T-cells (Figure 32A) was determined. Total cell numbers per well were determined using precision counting beads. The results demonstrate that the FAP BiTE viruses NG-605 and NG-606 resulted in significant increases in T-cell activation of tumour-associated lymphocytes.

As an extension of the experiment above, replicate wells were harvested and the number of endogenous FAP$^+$ cells determined by flow cytometry. Total cell numbers per well were determined using precision counting beads. The results (Figure 40B) show that NG-605 and NG-606 resulted in a significant decrease in numbers of autologous FAP-expressing cells in the ascites samples, suggesting some FAP$^+$ cells had been killed by the activated T-cells.

In a second experiment, unpurified (therefore unchanged from when received) ascites cells from a cancer patient were seeded at 250,000 cells per well of a U-bottom 96-well plate in either 100% ascites fluid or medium supplemented with 1% human serum. Cells were infected with viruses at 100 ppc, with untreated wells serving as negative controls. EnAd-CMV-GFP and EnAd-SA-GFP were also included as a reporter to determine infection and late stage viral gene expression, respectively, with micrographs. After incubation at 37^{o}C for 5 days, the total cell population was harvested and the number of CD3$^+$ T-cells (Figure 33) and expression level of CD25 on CD3$^+$ T-cells (Figure 34) was determined. Total cell numbers per well were determined using precision counting beads. The results demonstrate that for this patient recombinant FAP BiTE and NG-605, but not NG-606, resulted in significant increase in T-cell activation of tumour-associated lymphocytes in media. Neither virus led to activation in ascites fluid.

As an extension of the experiment above, replicate wells were harvested and the number of FAP$^+$ cells was determined by flow cytometry (Figure 35). Total cell numbers per well were determined using precision counting beads. The results demonstrate that recombinant FAP BiTE and NG-605, but not NG-606, resulted in a significant decrease in numbers of autologous FAP-expressing cells in media. Neither virus led to a reduction in FAP$^+$ cells in ascites fluid.

Example 15 - Discussion

Oncolytic viruses offer an intriguing new strategy to combine several therapeutic modalities within a single targeted, self-amplifying, agent (Keller & Bell, 2016; Seymour & Fisher, 2016). As they replicate selectively within cancer cells and spread from cell to cell, some oncolytic viruses are thought to mediate cell death by non-apoptotic death pathways (Ingemarsdotter et al, 2010; Li et al, 2013), as part of the process allowing virus particles to escape from dying cells. EnAd, in particular, kills cells by a pro-inflammatory process known as oncosis or ischemic cell death (Dyer, 2017). This non-apoptotic death mechanism causes release of several pro-inflammatory cellular components, such as ATP, HMGB1 and exposure of calreticulin (known as damage-associated molecular patterns, DAMPs)(Weerasinghe & Buja, 2012), and is likely pivotal to the ability of the virus to promote an effective anticancer immune response. In addition to the consequences of direct lysis, however, viruses offer the potential to encode and express other anticancer biologics, obviating delivery challenges and ensuring the biologic achieves its highest concentration within the tumour microenvironment. Imlygic encodes GM-CSF, however the potential for arming viruses is virtually limitless and provides many exciting opportunities to design multimodal therapeutic strategies with additive or synergistic anticancer effects (de Gruijl et al, 2015; Hermiston & Kuhn, 2002).

Encoding BiTEs within oncolytic viruses provides a powerful means to activate tumour infiltrating lymphocytes to become cytotoxic and lyse antigen-positive target cells, providing a completely separate therapeutic modality from the effects of direct viral lysis. In this study we have shown that BiTE-targeted cytotoxicity is fully antigen-specific, can be mediated by both CD4 and CD8 T cells (Brischwein et al, 2006) and can be incorporated into an oncolytic adenovirus and expressed only in cells that allow virus replication. In addition, the current study shows, for the first time, that endogenous T cells within liquid cancer biopsies can be activated by BiTEs and virus-encoded BiTEs and can kill endogenous tumour cells without any additional stimulation or reversal of immune suppression. Importantly, this can happen even in the primary fluids that comprise the microenvironment of peritoneal ascites or pleural effusions, as surrogates for the immune suppressive microenvironment of solid tumours.

Arming oncolytic viruses to express BiTEs combines two quite distinct therapeutic mechanisms, with the former providing lytic death of tumour cells that are permissive for virus infection, and the latter targeting T cell cytotoxicity via a specific, chosen, antigen. This provides considerable flexibility in the design of a therapeutic approach, perhaps using the BiTEs to deliver cytotoxicity to tumour-associated cells that are relatively resistant to kill by the virus directly. For example, while we have exemplified the technology here using a BiTE that recognises a carcinoma-associated antigen (EpCAM), it is also possible to use the BiTE approach to target cytotoxicity to tumour-associated fibroblasts or other stromal cells. Indeed, even when the targets for BiTE-recognition are not restricted to expression in the tumour microenvironment, by linking BiTE production to virus replication allows expression of the BiTE to be spatially restricted to the tumour, minimising systemic toxicities. This is important, as BiTEs administered intravenously show relatively short circulation kinetics (Klinger et al, 2012) and are often associated with considerable on-target off-tumour toxicities (Teachey et al, 2013).

The possibility to encode BiTEs within oncolytic viruses has been previously explored using an oncolytic vaccinia virus with an Ephrin A2-targeting BiTE. This agent showed that the Ephrin BiTE could mediate activation of PBMCs and antigen-targeted killing of tumour cells both *in vitro* and *in vivo*. Intriguingly, although the BiTE could activate T cells it did not lead to T cell proliferation without the addition of exogenous IL-2, whereas the BiTE used in the current study led to extensive proliferation both of PBMC *in vitro* and of tumour-associated lymphocytes using the clinical biopsy samples *ex vivo*.

We believe that the differences observed may reflect the different BiTE design, the different oncolytic virus used or perhaps depend on the antigen density giving sufficient crosslinking of CD3 on the T cells.

One central aim of oncolytic virus therapy is to create an anticancer T cell response that recognises patient specific neoantigens as well as "public" tumour associated antigens. Lytic viruses may do this by stimulating improved antigen presentation by lysing tumour cells in the context of DAMPs alongside virus-related pathogen-associated molecular patterns (PAMPs). Immunohistochemical staining of resected colon tumours, following intravenous delivery of EnAd, suggest the virus promotes a strong influx of CD8+ T cells into tumour tissue (Garcia-Carbonero, 2017). However, while this is potentially a very powerful approach, adaptive T cell responses are ultimately dependent on the expression of MHC class I antigens by tumour cells, to allow targeted killing. Loss of MHC expression is a well documented immune evasion strategy for tumours (Garrido et al, 2016). It is noteworthy that both cytotoxic strategies that are immediately engaged by BiTE-armed oncolytic viruses operate independently of MHC class I by the tumour cells, and therefore can be employed to kill cancer cells even when tumour cells have lost MHC expression.

The present study thus demonstrates that encoding BiTEs within EnAd provides a particularly promising strategy to achieve targeted expression in disseminated tumours, exploiting the known blood-stability and systemic bioavailability of the virus, which has now been studied in several early phase clinical trials. Notably, in a study where the virus is given intravenously a few days prior to resection of primary colon cancer, subsequent immunohistological assessment of tumour sections showed that the virus had reached to regions through the tumours and gave strong intranuclear hexon signals, indicating successful infection and virus replication selectively in tumour cells. This confirms preclinical data (Di et al, 2014; Illingworth, 2017) indicating that this virus is stable in 100% human blood and should be capable of tumourtargeted infection of disseminated and metastatic malignancies in human patients.

BiTEs could be encoded by EnAd without any loss of oncolytic virulence , reflecting the considerable transgene packaging capacity of the virus. The presence of the transgene will not affect the physicochemical properties of the virus particles, hence the modified viruses should exhibit exactly the same clinical pharmacokinetics as the parental agent, and should be capable of expressing the encoded BiTE selectively within tumours throughout the body. This provides an exciting and potentially very effective new approach to systemically targeted cancer immunotherapy that should now be prioritised for clinical assessment.

Example 16

Immunosuppression of human T-cell activation and target cell cytotoxicity by patient malignant exudate fluids

Malignant exudates represent an environment of potential immune tolerance with suppressed immune responses commonly observed in patients with late-stage metastatic cancer. The quantity of IL-10, considered to be an anti-inflammatory cytokine, was measured in normal serum or patient malignant exudate fluids (A, peritoneal ascites; P, pleural effusion) using Human IL-10 ELISA MAX kit (Biolegend, 430604). IL-10 levels in the exudates (88.1 – 633.4 pg/mL) were far in excess of those measured in normal serum (7.2 – 10 pg/mL)..

The ability of CD3/CD28 beads (Gibco, 11161D) to activate PBMC T-cells in the presence of normal serum, ascites or pleural fluid was investigated. Human PBMC T-cells (100,000 cells per well in 96 well plate) were treated with CD3/CD28 beads (following manufacturers instructions) in normal serum or patient exudate fluid (50%). T-cells were left untreated in each fluid as negative control. After 24 hours of culture, cells were harvested and the expression levels of CD69 and CD25 on CD3+ T-cells were then analysed by antibody staining and flow cytometry represented as percentage of dual positive (CD69+CD25+ cells). In normal serum the anti-CD3/CD28 beads gave approximately 60% of T cells dual positive for both CD25 and CD69, whereas the presence of ascites fluid attenuated T cell activation in 6/12 fluids.

In a similar experiment, 100,000 T-cells were treated with CD3/CD28 beads in the presence of normal serum, ascites or pleural fluid (50%). Anti-CD107a or isotype control antibody were added directly to culture medium. After 1 hour, monensin was added (BD Golgistop, BD Biosciences) according to manufacturers instructions. After 5 further hours, cells were harvested and analysed by flow cytometry to determine degranulation. In normal serum the anti-CD3/CD28 beads gave approximately 22.5% of T cells degranulated, whereas the presence of ascites fluid attenuated T cell activation in 10/12 fluids. The level of degranulation was significantly correlative (Pearson co-efficient, $r = -0.7645$; $p = 0.0038$) with quantity of IL-10 in each fluid.

In a similar experiment, 75,000 T-cells were co-cultured with 15,000 SKOV3 and EpCAM in the presence of normal serum, ascites or pleural fluid (50%). T-cells were treated with control BiTE in each fluid as negative control. After 24 hours of culture, cells were harvested and the expression levels of CD69 and CD25 on CD3+ T-cells were then analysed by antibody staining and flow cytometry represented as percentage of dual positive (CD69+CD25+ cells). In normal serum the EpCAM BiTE gave approximately 67.6% of T cells dual positive for both CD25 and CD69, whereas the presence of ascites fluid attenuated T cell activation in 0/12 fluids, and slightly induced activation in 4/10 fluids.

In a similar experiment, 75,000 T-cells were co-cultured with 15,000 SKOV3 and EpCAM in the presence of normal serum, ascites or pleural fluid (50%). T-cells were treated with control BiTE in each fluid as negative control. Anti-CD107a or isotype control antibody were added directly to culture medium. After 1 hour, monensin was added (BD Golgistop, BD Biosciences) according to manufacturers instructions. After 5 further hours, cells were harvested and analysed by flow cytometry to determine degranulation. In normal serum the EpCAM BiTE beads gave approximately 41.4% of T cells degranulated, whereas the presence of ascites fluid attenuated T cell activation in 2/12 fluids.

The ability of EnAd-SA-EpCAMBiTE and EnAd-SA-ControlBiTE to induce T cell-mediated target cell lysis in malignant exudate fluids was assessed using xCELLigence technology. SKOV cells were plated in 48-well E-plate at 1e4 cells/well respectively. Plates were incubated for 18 hrs, 37^0C, 5% $CO2$, before cells were either infected with 100 virus particles per cell (ppc) or were left uninfected. After two hours, PBMC T-cells (5:1) in normal serum or patient exudate fluid (final, 50%) were added. xCELLigence was used to measure target cell cytotoxicity every 10 minutes. The results suggest that BiTE-mediated SKOV3 lysis by T-cells is independent of fluid used.

Unpurified ascites cells (therefore unchanged from when received) are seeded at 100,000 cells per well of a flat-bottom 96-well plate in RPMI media or ascites fluid. Cells were treated with EpCAM or control BiTE, with untreated wells serving as a negative control. After incubation at 37C for 24 hours, cells were harvested, and the expression level of CD25 and CD69 on CD3 cells determined. The results demonstrate that EpCAM BiTE resulted in significant increase in T-cell activation (CD69/CD25 dual positive) of tumour-associated lymphocytes, slightly increased by ascites fluid.

In a similar experiment, unpurified ascites cells (therefore unchanged from when received) are seeded at 100,000 cells per well of a flat-bottom 96-well plate in RPMI media or ascites fluid. Cells were treated with EpCAM, control BiTE or recombinant BiTE viruses (100 vp/cell), with untreated wells serving as a negative control. After incubation at 37C for 5 days, the total cell population was harvested, and the number of CD3+ cells and expression level of CD25 on CD3 cells determined and the number of endogenous EpCaM + cells determined by flow cytometry. Total cell numbers per well were determined using precision counting beads. The results demonstrate that EpCAM BiTE and EnAd expressing EpCAM BiTE resulted in significant increase in T-cell activation (CD3 number, CD25) of tumour-associated lymphocytes and cytotoxicity of EpCAM+ cells in both RPMI media and ascites fluid.

As an extension of the experiment above, six more patient exudate samples (for a total of 7) were treated identically in ascites fluid and number of CD3+, CD25 expression of T-cells and number of EpCAM+ cells determined by flow cytometry. The results show that EpCAM BiTE and EnAd expressing EpCAM BiTE resulted in significant increase in T-cell activation (CD3 number, CD25) of tumour-associated lymphocytes and cytotoxicity of EpCAM+ cells reproducibly in a range of exudate biopsy samples.

Example 17

FAP BiTE mediate activation of T-cells and killing of FAP+ cells by diferent donor T-cells

In other experiments, methods described in Example 2 were used to further evaluate the T-cell activating properties of recombinant FAP BiTE protein tested in co-cultures of NHDF and T-cells, comparing to control BiTE and polyclonal T-cell activation using anti-CD3/CD28 Dynabeads.

Supernatants taken after 24 hours of culture were tested by ELISA for IFNγ (Figure 36A) and by cytokine bead array (LEGENDplex human T helper cytokine panel, BioLegend #74001) for a panel of cytokines (Figure 36B). The control BiTE induced no significant change in any cytokine, however the FAP-BiTE led to strong increases in gamma interferon, IL-2, TNFα, IL-17 and IL-10, consistent with different subsets of T-cells being stimulated, and production of IFNγ was far greater than that triggered by anti-CD3/CD28.

Stimulation with the FAP BiTE, but not control BiTE, in the presence of NHDF cells also induced rapid degranulation (within 6 hr) of T-cells, both CD4+ and CD8+ subsets, as determined by the externalisation of CD107a/LAMP1 on the T-cell surface (as assessed by flow cytometry), which is strongly correlative with their ability to kill target cells (Figure 36A&B). This induction of degranulation by the FAP BiTE translated to potent fibroblast lysis (Figure 69C), as measured by LDH release after 24 h co-culture with PBMC T-cells (EC_{50} of ~2.5 ng/mL) with induced T-cell activation and cytotoxicity observed using 6/6 donor T-cells (Figure 69D). No cytotoxicity was induced by the control BiTE, consistent with T-cells remaining in an inactivated state.

Example 18

Effect of FAP BiTE and EnAd-FAP BiTE viruses on cells in primary malignant ascites samples from different ancer patients

As a follow-on to studies described in Example 16, fresh primary malignant peritoneal ascites from further cancer patients were obtained for study of EnAd FAP BiTE virus activities. Three patient samples containing both EpCAM$^+$ tumour cells and FAP$^+$ fibroblasts were expanded *ex vivo*, and the mixed (adherent) cell populations were cultured with PBMC-derived T-cells and unmodified or BiTE expressing EnAd viruses. After 72 h, total cells were harvested and the number of FAP$^+$ (Figure 38A) and EpCAM$^+$ cells (Figure 38B) determined by flow cytometry. Additionally, the activation status of T-cells (by CD25 expression) was measured (Figure 38C). Infection with both EnAd-CMV-FAPBiTE and EnAd-SA-FAPBiTE induced T-cell activation and FAP$^+$ cell depletion in all patient samples, with no significant change in levels of EpCAM+ tumour cells. Parental EnAd or the control viruses induced no observable T cell activation, with FAP$^+$ cell numbers remaining similar to the uninfected control. Importantly, this depletion in FAP+ fibroblasts consistenly led to a strong reduction in levels of the immunosuppressive cytokine TGFβ detected in supernatants (Figure 38D).

In a second series of experiments, total (and unpurified) cells from five patient biopsy samples were evaluated to assess the activity of endogenous tumour-associated T-cells in the samples. Cells were plated in 50% ascites fluid and treated with recombinant control or FAP BiTE proteins, or 100 vp/cell of EnAd or EnAd-BiTE viruses. After 5 days incubation, T-cell activation (by CD25 expression) and residual number of FAP$^+$ cells was measured by flow cytometry (Figure 39A&B). In all 3 patient samples, recombinant FAP-BiTE and EnAd-CMV-FAP BiTE induced strong T-cell activation, with up to ~80% of patient-derived T-cells activated, which caused a marked depletion FAP$^+$ fibroblasts. Interestingly, EnAd-SA-FAP-BiTE induced CD25 expression in 2/3 samples, with no observable activation or FAP$^+$ cell depletion in patient 1. This is probably due to insufficient tumour cells being present for infection by the virus and production of BiTE protein (no EpCAM$^+$ tumour cells were detected in this sample by flow cytometry), consistent with the requirement for tumour cells for MLP (SA)-driven transgene expression (this likely also explains the lack of T-cell activation and FAP+ cell depletion by EnAd-SA-FAP-BiTE virus with the patient ascites sample illustrated in Figs 42-44). Collectively, the data shows that EnAd expressing FAP-BiTE can, following infection of tumor cells, reproducibly lead to activation of tumour-associated T-cells to kill endogenous fibroblasts.

Another experiment investigated whether FAP-BiTE activity could be improved by blocking the PD-1 checkpoint, using a patient biopsy sample in which T-cells were 73.6% PD-1 positive and FAP$^+$ cells were 62.9% PDL1-positive (Figure 40A). Co-cultures similar to those described above were set up in the presence or absence of a purified blocking mouse IgG2b antibody to human PDL1 (BioLegend, clone 29E.2A3) at a final concentration of 2.5 μg/mL. After 2 days of culture, total cells were harvested and residual FAP+ cells and T-cell activation was measured. The inclusion of the blocking anti-PDL1 antibody led to a modest increase in CD25 induction (Figure 40B) and a two-fold higher IFNγ production (Figure 40C), without altering the depletion of FAP+ cells (Figure 40D) with near complete lysis by day 2 in either setting.

Tumour-associated lymphocytes (TALs) isolated from ovarian cancer patient ascites are reported to have enriched expression of PD-1 and impaired effector functions – including cytotoxicity and IFNg production. Consistent with this, PD-1 expression was 2-fold higher on $CD3^+$ cells from six cancer patient ascites biopsies than on those in peripheral blood mononuclear cells (PBMCs) from three healthy donors (Figure 41A). To evaluate the functionality of the T-cells within these cancer biopsy samples, NHDF cells and unpurified PBMC or ascites cells (the % CD3+ cells for each of the samples is shown in Figure 41B) were co-cultured with control or FAP BiTE-containing supernatants, and supernatants were harvested 5 days later and tested for IFNγ by ELISA (Figure 41C). No IFNγ was induced by the control BiTE. Three of the ascites cell samples produced IFNγ at a similar level to that of the PBMC samples, while the other three had an attenuated response to the FAP BiTE. We next investigate the ability of these T-cells to induce BiTE-mediated lysis of the NHDF cells. NHDF were plated, and PBMC or ascites cells added along with BiTE-containing supernatants and the viability of cells in the culture monitored in real-time using the xCELLigence cytotoxicity assay system. Despite the variability in IFNγ production, all ascites samples induced full cytotoxicity of NHDF cells when added with the FAP BiTE, with an overall similar rate of BiTE-mediated NHDF lysis to that seen with when effected by PBMCs (Figure 41D).

To investigate whether the FAP BiTE can mediate T-cell activation in the presence patient malignant exudate samples (all at 50%), PBMC T-cells were activated with control or FAP BiTEs in the presence of NHDF cells, or activated with anti-CD3/CD28 Dynabeads, either in 50% normal human serum (NS) or different (cell-free) malignant exudate samples. Whereas in normal serum 74% of T-cells were activated (dual-positive for both CD25 and CD69) at 24 h following stimulation with the anti-CD3/CD28 beads, 3/5 tested ascites fluid significantly attenuated T-cell activation compared to the response in NS (Figure 42A). However, when PBMCs were cultured with NHDF and stimulated with the FAP BiTE, there was no observable suppression of T-cell activation in the presence of any of the exudate fluids (Figure 42B), demonstrating that the FAP BiTE can overcome immunosuppressive mechanisms to activate T-cells.

Example 19

EnAd-FAPBiTE-mediated oncolysis and T cell stimulation polarise CD11b+ TAMs in patient ascites to a more activated phenotype

To investigate whether the production of Th1 cytokines, including IFNγ, TNFα and IL-2, by FAP BiTE-mediated activation of T-cells, and the subsequent elimination of FAP^+ fibroblasts (and associated reduction in TGFβ1 was associated other shifts in the tumour microenvironment from immunosuppressive and pro-oncogenic towards anti-tumour activity, the effect on tumour-associated macrophages (TAMs) in an unseparated ascites cell sample was evaluated. Total unpurified patient ascites cells were plated in 50% ascites fluid and treated with free control or FAP BiTE or infected with EnAd-SA-control BiTE or EnAd-SA-FAPBiTE virus (at 100 vp/cell). In parallel, some cells were treated in with IFNγ to induce an activated CD11b myeloid cell phenotype. After 3 days incubation, the activation status of T-cells was first measured; CD25+ cells measured by flow cytometry and IFNγ secretion by ELISA.

Treatment with FAP BiTE and EnAd-SA-FAPBiTE led to approximately 60% of $CD3^+$ T-cells becoming CD25+ (Figure 43A) and large quantities of IFNγ in culture supernatants (Figure 43B). No increase above background by the control BiTE or control virus was observed for CD25 expression or IFNγ. To evaluate TAM polarisation, the expression levels of CD64 and CD86 (M1 or 'activated' macrophage markers) and CD206 and CD163 (M2 or TAM markers) were measured on CD11b+ cells by flow cytometry (Figure 43C). Treatment with free FAP BiTE or EnAd expressing FAP BiTE induce a more activated phenotype, manifested by significant increases in CD64 expression, and strong decreases CD206 and CD163 – similar to that observed when IFNγ was spiked into the cultures.

While treatment with free FAP BiTE or control virus induced no clear change in CD86 above background in this experiment, the EnAd expressing FAP BiTE induced a large increase in CD86 expression, indicating that EnAd virus infection and FAP BiTE activity may synergize to activate primary myeloid cells within a suppressive tumour microenvironment such as the malignant ascetic fluid samples tested here. In this study, IFNγ treatment induced a modest decrease in CD86, indicating that the strong increase in CD86 observed by EnAd-SA-FAPBiTE may be via an IFNγ-independent mechanism.

Example 20

EnAd-FAPBiTE activates tumour-infiltrating lymphocytes and induces cytotoxicity in solid prostate tumour biopsies ex vivo

Tissue slice cultures provide one of the most realistic preclinical models of diverse tissues, organs and tumours. To evaluate the activity of the FAP BiTE expressing viruses in this highly clinically-relevant setting, several paired punch biopsies of malignant and benign prostate tissue from resected human prostates were studies. At initial screening, prostate tissue was reproducibly shown to have circular rings of EpCAM+ tumour cells (Figure 44A) interspersed between large regions of stroma containing scattered CD8 T-cells (Figure 44B). FAP staining was found on fibroblasts adjacent to tumour regions (Figure 44C).

Cores were sliced by a vibratome to 300μm thickness and slice cultures established in the presence of virus (1.5e9 vp/slice), or left uninfected. After 7 days, slices were fixed, paraffin-embedded, sectioned and T-cell activation status was assessed by immunohistochemistry (IHC) by staining for CD25 expression (Figure 44D). Only samples receiving EnAd-CMV-FAPBiTE or EnAd-SA-FAPBiTE showed activation of tumour-infiltrating T-cells, manifest by strong CD25 staining. Neither untreated or control virus-treated had detectable CD25-positive cells. Supernatants from these slice cultures taken at 4 and 7 days post-infection were tested for IFNγ and IL-2 by ELISA, with increases in IFNγ detected from malignant, but not benign, prostate slice cultures infected with either FAP BiTE virus (Figure 44E) and IL-2 detected in cultures with EnAd-SA-FAPBiTE virus (Figure 44F). The EnAd-SA-FAPBiTE induced higher quantities of IFNγ, which were detectable earlier, than the CMV-driven FAPBiTE virus.

Example 21 – Further EnAd viurses expressing FAP BiTEs

Five viruses (NG-611, NG-612, NG-613, NG-614, NG-617) were generated that encode a single BiTE (Table 8).

Table 8

Virus ID	Transgene Cassette
NG-612 (SEQ ID NO: 78	SSA^1-FAPBiTE^5-His^3-PA^4
NG-613 (SEQ ID NO: 79)	SA^6-FAPBiTE^5-His^3-PA^4
NG-614 (SEQ ID NO: 73)	SA^6-FAPBiTE^7-His^3-PA^4
NG-617 (SEQ ID NO: 81)	SSA^1-FAPBiTE^5-PA^4

In each transgene cassette, the cDNA encoding the BiTE was flanked at the 5' end with either a short splice acceptor sequence (SSA, CAGG) or a longer splice acceptor sequence (SA, SEQUENCE ID NO: 45). At the 3' end of the BiTE, a SV40 late poly(A) sequence (PA, SEQUENCE ID NO: 54) was encoded preceded by either a Histidine tag (HIS)or no tag. In viurses NG-611, NG-612, NG-613 and NG-617 the anti-CD3 portion of the BiTE molecule used a single chain variant of the mouse anti-human CD3ε monoclonal antibody OKT3.

Virus Production

The plasmid pEnAd2.4 was used to gerneate the plasmids pNG-611, pNG-612, pNG-613, pNG-614 and pNG-617 by direct insertion of synthesised transgene cassettes (SEQ ID NOs: 70-74, respectively). The pNG-612, pNG-613 and pNG-617 transgene cassettes encode a FAP targeting BiTE of SEQ ID NO. 75 and the pNG-614 transgene cassette encodes a FAP targeting BiTE of SEQ ID NO. 76. Schematics of the transgene cassettes are shown in Figure 45A to C. Construction of plasmid DNA was confirmed by restriction analysis and DNA sequencing.

The plasmids, pNG-611, pNG-612, pNG-613, pNG-614 and pNG-617, were linearised by restriction digest with the enzyme AscI to produce the virus genomes. The viruses were amplified and purified according to methods given below.

Digested DNA was purified by phenol/chloroform extraction and precipitated for 16hrs, -20^{0}C in 300µl >95% molecular biology grade ethanol and 10µl 3M Sodium Acetate. The precipitated DNA was pelleted by centrifuging at 14000rpm, 5 mins and was washed in 500µl 70% ethanol, before centrifuging again, 14000rpm, 5mins. The clean DNA pellet was air dried, resuspended in 500µl OptiMEM containing 15µl lipofectamine transfection reagent and incubated for 30 mins, RT. The transfection mixture was then added drop wise to a T-25 flask containing 293 cells grown to 70% confluency. After incubation of the cells with the transfection mix for 2hrs at 37^{0}C, 5% CO_2 4mls of cell media (DMEM high glucose with glutamine supplemented with 2% FBS) was added to the cells and the flasks was incubated 37^{0}C, 5% CO_2.

The transfected 293 cells were monitored every 24hrs and were supplemented with additional media every 48-72hrs. The production of virus was monitored by observation of a significant cytopathic effect (CPE) in the cell monolayer. Once extensive CPE was observed the virus was harvested from 293 cells by three freeze-thaw cycles. The harvested viruses were used to re-infect 293 cells in order to amplify the virus stocks. Viable virus production during amplification was confirmed by observation of significant CPE in the cell monolayer. Once CPE was observed the virus was harvested from 293 cells by three freeze-thaw cycles. The amplified stocks of viruses were used for further amplification before the viruses were purified by double caesium chloride banding to produce purified virus stocks.

Virus activity assessed by qPCR

A549 cells, either infected for 72 hrs with 1ppc NG-611, NG-612, NG-617, enadenotucirev or left uninfected, were used for quantification of viral DNA by qPCR. Cell supernatants were collected and clarified by centrifuging for 5 mins, 1200rpm. DNA was extracted from 45µL of supernatant using the Qiagen DNeasy kit, according to the manufacturer's protocol. A standard curve using enadenotucirev virus particles (2.5e10-2.5e5vp) was also prepared and extracted using the DNeasy kit. Each extracted sample or standard was analysed by qPCR using a virus gene specific primer-probe set to the early gene E3.

Quantification of the number of detected virus genomes per cell demonstrated that NG-611, NG-612, and NG-617 showed significant genome replication in A549 cell lines (Figure 45D). This was similar for all viruses tested including the parental virus enadenotucirev, indicating that inclusion of the BiTE transgene does not impact virus replicative activity. No virus genomes could be detected in uninfected cells (data not shown).

T cell activation and degranulation mediated by BiTE expressing viruses.

Carcinoma cell infection

A549 cells were seeded into 24 well plates at a density of 2.5e5 cells/well. Plates were incubated for 4 hrs, 37^{0}C, 5% CO$_2$, before cells were either infected with 1ppc of NG-611, NG-612, enadenotucirev or were left uninfected. At 24, 48 or 72hrs post-infection supernatants were harvested from the cells, clarified by centrifuging for 5 mins, 1200rpm and snap frozen.

T cell Assay

FAP expressing lung fibroblast cell lines MRC-5, or EpCam expressing ovarian carcinoma cells, SKOV3 were seeded into 48 well plates at densities of 5.7e4 cells/well and 1.2e5 cells/well, respectively. Plates were incubated for 4 hrs, 37^{0}C, 5% CO$_2$, before media was replaced with 150µL/well of thawed supernatant harvested from the A549 plates. Purified CD3 T cells isolated form human PBMC donors were then also added to the plates to give a ratio of T cells to MRC-5 or SKOV3 of 2 to 1. The co-cultures were incubated for 16hrs, 37^{0}C, 5% CO$_2$ before cellular supernatants were collected for ELISA analysis and T cells harvested for flow cytometry analysis. Culture media containing non-adherent cells was removed from co-culture wells and centrifuged (300xg). The supernatant was carefully removed, diluted 1 in 2 with PBS 5% BSA and stored for ELISA analysis. The adherent cell monolayers were washed once with PBS and then detached using trypsin. The trypsin was inactivated using 10% FBS RPMI media and the cells were added to the cell pellets that had been collected from the culture supernatants. The cells were centrifuged (300xg), the supernatant discarded and the cell pellet washed in 200µL of PBS. The cells were centrifuged again then resuspended in 50µL of PBS containing Live/Dead Aqua (Life tech) for 15 minutes at RT. The cells were washed once in FACs buffer before staining with panels of directly conjugated antibodies: anti-CD3 conjugated to AF700; anti-CD25 conjugated to BV421; anti-HLA-DR conjugated to PE/CY5; anti-CD40L conjugated to BV605; anti-CD69 conjugated to PE and anti-CD107a conjugated to FITC. A sample of cells from each co-culture condition was also stained with relevant isotype control antibodies. All staining was carried out in FACs buffer in a total volume of 50µL/well for 15 minutes, 4°C. Cells were then washed twice with FACs buffer (200µL) before resuspension in 200µL of FACs buffer and analysis by Flow cytometry (Attune).

Upregulation of T cell activation markers

Flow cytometry analysis of T cell activation was assessed by expression of the T cell activation markers CD25, CD69, HLA-DR and CD40L or the T cell degranulation marker, CD107a on live, single cells. These data showed that when co-cultured with EpCam^{+} SKOV3 cells the number of T cells expressing CD25, CD69, HLA-DR, CD40L or cell surface CD107a was significantly increased when

NG-611 supernantants were added to the cells compared to NG-612, enadenotucirev or untreated control supernatants (Figure 47). For all these markers little T cell activation was stimulated by supernatants from A549 cells infected for 24hrs however, by 48 hrs post-infection, supernatants stimulated significant T cell activation across all markers. This was also the case at 72hrs post-infection.

When co-cultured with FAP$^+$ MRC-5 cells the number of T cells expressing CD25, CD69, HLA-DR, CD40L or cell surface CD107a was significantly increased when NG-612 supernantants were added to the cells compared to NG-611, enadenotucirev or untreated control supernatants (Figure 48). Some T cell activation could also be observed with the NG-611 virus, which was likely due to low but detectable expression of EpCam (~5%) on the MRC-5 cell lines engaging the EpCam BiTE expressed by the NG-611 virus (Figure 49). For all these markers, little T cell activation was stimulated by supernatants from A549 cells infected for 24hrs however, by 48 hrs post-infection, supernatants stimulated significant T cell activation across all markers. CD25 and CD69 markers were also upregulated following incubation with supernatants harvested 72hrs post-infection, however, activation markers, HLA-DR, CD40L and CD107a were detected at lower levels with supernatants harvested 72hrs post-infection than 48hrs post-infection. This could be due to high levels of BiTE present at this later stage of infection leading to rapid and potent T cell activation that means the effector functions need to measured at timepoints earlier than 16 hrs post-incbuation with the supernatants.

For detection of IFNγ expression, co-culture supernatants were diluted into 5% BSA/PBS assay buffer (in a range of 1:10 to 1:1000) and ELISA was carried out using the Human IFN gamma Quantikine ELISA kit (R&D systems) according to the manufacturer's protocol. The concentration of secreted IFNγ was determined by interpolating from the standard curve. Expression of IFNγ could only be detected in the supernatants of co-cultures using NG-611 on SKOV3 cells Figure 50A) or NG-611, NG-612 on MRC-5 cells (Figure 50B).

Example 22 Immune activation and anti-tumour efficacy of BiTE expressing viruses in vivo

NSG mice humanised CD34+ haematopoietic stem cells (from Jackson Labs) were implanted with HCT116 tumour cells subcutaneously on both flanks at 18 weeks post engraftment. Once tumours reached 80-400mm^3 mice were grouped such that each treatment arm had an equivalent distribution of tumour volumes, 7 mice per group. Mice were injected intratumourally with either saline, enadenotucirev or NG-611 at 5x10^9 particles per injection, 2 injections per tumour. Tumours on both flanks were treated. Tumour volume was measured 3-4 times per week and demonstrated that NG-611 treatment resulted in a significant anti-tumour response out to 20 days post-dosing compared to enadenotucirev or untreated controls (Figure 51a). After the 20 days post-dosing one tumour from 4 mice in each group was processed for flow cytometry while remaining tumours were frozen on dry ice.

Flow cytometry

Tumour samples were mechanically disaggregated immediately following resection in a small volume of RPMI media. Disaggregated tumours were then passed through a 70μm cell strainer and centrifuged at 300g for10 minutes. Cell pellets were resuspended in 100μL of PBS containing

Live/Dead Aqua (Life tech) for 15 minutes on ice. The cells were washed once in FACs buffer (5% BSA PBS) before staining with a panel of directly conjugated antibodies: anti-CD8 (RPA-T8, AF700); anti-CD4 (RPA-T4, PE); anti-CD45 (2D1, APC-Fire 750); anti-CD3 (OKT3, PerCP-Cy5.5); anti-CD25 (M-A251, PE-Dazzle 594); anti-CD69 (FN50, APC); anti-HLA-DR (L243, BV605); anti-CD107a (H4A3, FITC). A pool of tumour cell suspensions was also stained with relevant isotype control antibodies. All staining was carried out in FACs buffer in a total volume of 50μL/well for 20 minutes at 4°C. Cells were washed three times with FACs buffer (200μL) before resuspension in 200μL of FACs buffer and analysis by Flow cytometry (Attune). FACs analysis demonstrated that the ratio of CD8 to CD4 T cells in the tumour was significantly increased in NG-611 treated tumours compared to enadenotucirev treated or untreated controls (Figure 51b).

Example 23– EnAd viruses co-expressing FAP BiTEs and immune-modulatory cytokines and chemokines

Three viruses (NG-615, NG-640 and NG-641) were generated that encoded a FAP BiTE and immunomodulatory proteins (Table 9).

Table 9

Virus ID	Transgene Cassette
NG-615 (SEQ ID NO: 82)	SSA^{1}-FAPBiTE^{2}-E2A^{3}-Flt3L^{4}-P2A^{5}-MIP1α^{6}-T2A^{7}-IFNα^{8}-PA^{9}
NG-640 (SEQ ID NO: 83)	SSA^{1}-FAPBiTE^{2}-P2A^{5}-CXCL10^{10}-T2A^{7}-CXCL9^{11}-PA^{6}
NG-641 (SEQ ID NO: 84)	SSA^{1}-FAPBiTE^{5}-P2A^{5}-CXCL10^{10}-T2A^{7}-CXCL9^{11}-E2A^{3}-IFNα^{8}-PA^{6}
NG-615 (SEQ ID NO: 278)	SA^{12}-FAPBiTE^{2}-E2A^{3}-Flt3L^{4}-P2A^{5}-MIP1α^{6}-T2A^{7}-IFNα^{8}-PA^{9}

Virus Production

The plasmid pEnAd2.4 was used to gerneate the plasmids pNG-615, pNG-616, pNG-640 and pNG-641 by direct insertion of synthesised transgene cassettes (SEQ ID NOs: 93-95, respectively). NG-615 and NG-616 contain four transgenes encoding for a FAP-targeting BiTE (SEQ ID NO: 75), Flt3L (SEQ ID NO. 96), MIP1α SEQ ID NO. 97) and IFNα (SEQ ID NO. 98). NG-640 and NG-641 encode for a FAP targeting BiTe (SEQ ID NO. 75), CXCL9 (SEQ ID NO. 99) and CXCL10 (SEQ ID NO. 100), NG-641 also contains a fourth transgene encoding IFNα (SEQ ID NO. 98). Construction of plasmid DNA was confirmed by restriction analysis and DNA sequencing.

The plasmids, pNG-615, pNG-616, pNG-640 and pNG-641, were linearised by restriction digest with the enzyme AscI to produce the virus genomes. The viruses were amplified and purified according to methods detailed in Example 33.

Virus activity assessed by qPCR and transgene ELISA

Carcinoma cell infection

A549 cells either infected for 72 hrs with 1ppc NG-615, enadenotucirev or left uninfected were used for quantification of viral DNA by qPCR and analysis of transgene expression by ELISA. Cell supernatants were collected and clarified by centrifuging for 5 mins, 1200rpm. 45μL of supernatant was used for DNA analysis and the remaining supernatant was used for ELISA.

qPCR

DNA was extracted from the supernatant sample using the Qiagen DNeasy kit, according to the manufacturer's protocol. A standard curve using enadenotucirev virus particles (2.5e10-2.5e5vp) was also prepared and extracted using the DNeasy kit. Each extracted sample or standard was analysed by qPCR using a virus gene specific primer-probe set to the early gene E3. Quantification of the number of detected virus genomes per cell demonstrated that NG-615 showed significant genome replication in A549 cell lines at a level similar to that of the parental virus enadenotucirev (Figure 52). These data indicated that inclusion of the BiTE and three immunomodulatory transgenes does not significantly impact virus replicative activity. No virus genomes could be detected in uninfected cells.

ELISA

IFNα ELISA was carried out using the Verikine Human IFN alpha Kit (Pbl assay science), MIP1α ELISA was carried out using the Human CCL3 Quantikine ELISA kit (R & D systems) and Flt3L ELISA was carried out using the Flt3L human ELISA kit (Abcam). All assays were carried out according to the manufacturers' protocol.

The concentrations of secreted IFNα, MIPα or FLt3L were determined by interpolating from the standard curves. IFNα, MIP1α and Flt3 L expression could be detected in the cellular supernatant of NG-615 but not enadenotucirev or untreated control cells (Figure 53).

T cell activation and degranulation mediated by BiTE expressing viruses.

Carcinoma cell infection

A549 cells were seeded into 24 well plates at a density of 2.5e5 cells/well. Plates were incubated for 4 hrs, 37^{0}C, 5% CO_2, before cells were either infected with 1ppc of NG-612, NG-615, enadenotucirev or were left uninfected. At 24, 48 or 72hrs post-infection supernatants were harvested from the cells, clarified by centrifuging for 5 mins, 1200rpm and snap frozen.

T cell Assay

FAP expressing lung fibroblast cell lines MRC-5 were seeded into 48 well plates at a density of 5.7e4 cells/well. Plates were incubated for 4 hrs, 37^{0}C, 5% CO_2, before media was replaced with 150μL/well of thawed supernatant harvested from the A549 plates. Purified CD3 T cells isolated form human PBMC donors were then also added to the plates to give a ratio of T cells to MRC-5 of 2 to 1. The co-cultures were incubated for 16hrs, 37^{0}C, 5% CO_2 before cellular supernatants were collected for ELISA analysis and T cells harvested for flow cytometry analysis according to the methods detailed in Example 29.

Upregulation of T cell activation markers

Flow cytometry analysis of T cell activation was assessed by expression of the T cell activation markers CD25, CD69, HLA-DR and CD40L or the T cell degranulation marker, CD107a on live, $CD3^+$, single cells. These data showed that when co-cultured with FAP^+ MRC-5 cells the number of T cells expressing CD25, CD69, HLA-DR, CD40L or CD107a was significantly increased when NG-615 or 612 supernantants were added to the cells compared to enadenotucirev or untreated control supernatants (Figure 54).

Secretion of the stimulatory cytokine IFNγ

For detection of IFNγ expression, co-culture supernatants were diluted into 5% BSA/PBS assay buffer (in a range of 1:10 to 1:1000) and ELISA was carried out using the Human IFN gamma Quantikine kit (RandD Systems) according to the manufacturer's protocol. The concentration of secreted IFNγ was determined by interpolating from the standard curve. Expression of IFNγ could only be detected in the supernatants of co-cultures using NG-612 or NG-615 infected A549 supernatants (Figure 55).

SEQ ID NO: 95 Transgene cassette for NG-641

CAGGCCCACCATGGGCTGGAGCTGCATCATCTTGTTCCTGGTCGCAACTGCTACCGGAGTCCATTCGGACATC
GTCATGACCCAAAGCCCTGACTCGCTCGCTGTGTCACTGGGAGAGCGGGCGACTATCAACTGCAAATCATCCC
AGAGCCTGCTGTATTCACGCAATCAGAAAAACTACCTGGCCTGGTATCAGCAGAAGCCGGGCCAGCCTCCCAA
GCTGCTGATCTTCTGGGCCTCCACCCGCGAAAGCGGCGTGCCGGACCGCTTCAGCGGAAGCGGATTCGGAACT
GACTTTACTCTGACCATTAGCTCCTTGCAGGCGGAGGACGTGGCCGTCTACTACTGCCAGCAGTATTTCTCCT
ATCCGCTCACCTTTGGGCAAGGCACCAAGGTGGAGATTAAGGGAGGGGGCGGCAGCGGGGGAGGCGGCAGCGG
CGGCGGGGGATCGCAGGTCCAGCTCGTCCAATCCGGAGCCGAAGTCAAGAAGCCGGGAGCGTCGGTCAAGGTC
AGCTGCAAAACTTCGCGCTACACCTTCACTGAGTACACGATCCACTGGGTCCGCCAGGCGCCCGGCCAGCGGC
TGGAGTGGATCGGCGGGATCAACCCAAACAACGGAATCCCAAATTACAATCAGAAATTTAAAGGGCGGGTGAC
TATCACCGTGGATACCTCGGCCTCCACGGCGTACATGGAGCTCTCATCACTCAGATCGGAGGACACCGCGGTC
TATTACTGCGCCCGCCGCCGGATCGCTTATGGATACGATGAAGGACATGCGATGGATTACTGGGGCCAGGGCA
CCCTCGTCACGGTGTCGTCAGGAGGCGGCGGTTCACAGGTGCAGCTGCAGCAGTCTGGGGCTGAACTGGCAAG
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CTCGGGGACAAAGTTGGAAATAAACCGGGGAAGCGGAGCTACTAACTTCAGCCTGCTGAAGCAGGCTGGAGAC
GTGGAGGAGAACCCTGGACCTAATCAAACTGCCATTCTGATTTGCTGCCTTATCTTTCTGACTCTAAGTGGCA
TTCAAGGAGTACCTCTCTCTAGAACTGTACGCTGTACCTGCATCAGCATTAGTAATCAACCTGTTAATCCAAG
GTCTTTAGAAAAACTTGAAATTATTCCTGCAAGCCAATTTTGTCCACGTGTTGAGATCATTGCTACAATGAAA
AAGAAGGGTGAGAAGAGATGTCTGAATCCAGAATCGAAGGCCATCAAGAATTTACTGAAAGCAGTTAGCAAGG
AAAGGTCTAAAAGATCTCCTGGAAGCGGAGAGGGCAGAGGAAGTCTGCTAACATGCGGTGACGTCGAGGAGAA
TCCTGGACCTAAGAAAAGTGGTGTTCTTTTCCTCTTGGGCATCATCTTGCTGGTTCTGATTGGAGTGCAAGGA
ACCCCAGTAGTGAGAAAGGGTCGCTGTTCCTGCATCAGCACCAACCAAGGGACTATCCACCTACAATCCTTGA
AAGACCTTAAACAATTTGCCCCAAGCCCTTCCTGCGAGAAAATTGAAATCATTGCTACACTGAAGAATGGAGT
TCAAACATGTCTAAACCCAGATTCAGCAGATGTGAAGGAACTGATTAAAAAGTGGGAGAAACAGGTCAGCCAA
AAGAAAAAGCAAAAGAATGGGAAAAAACATCAAAAAAAGAAAGTTCTGAAAGTTCGAAAATCTCAACGTTCTC
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AACTAGAATGCAGTGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATA
AGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGG
TTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTAGTCGTCAGCTAT

CLAIMS:

1. An adenovirus comprising a sequence of formula **(I)**:

$$5'\text{ITR-}B_1\text{-}B_A\text{-}B_2\text{-}B_X\text{-}B_B\text{-}B_Y\text{-}B_3\text{-}3'\text{ITR} \quad \textbf{(I)}$$

wherein:

B_1 is a bond or comprises: E1A, E1B or E1A-E1B;

B_A comprises-E2B-L1-L2-L3-E2A-L4;

B_2 is a bond or comprises: E3;

B_X is a bond or a DNA sequence comprising: a restriction site, one or more transgenes or both;

B_B comprises L5;

B_Y comprises a transgene cassette containing four transgenes, said genes encoding a FAP-BITE, CXL10, CXL9, and IFN;

B_3 is a bond or comprises: E4.

2. An adenovirus according to claim 1, wherein the encoded FAB-BITE comprises an anti-CD3 shown in SEQ ID NO: 5 or a sequence at least 95% identical thereto, such as SEQ ID NO: 5.

3. An adenovirus according to claim 1 or 2 wherein the FAP-BITE comprises an anti-FAP shown in SEQ ID NO: 9 or a sequence at least 95% identical thereto, such as SEQ ID NO: 9.

4. An adenovirus according to claim 1, wherein the encoded FAB-BITE comprises a sequence selected from SEQ ID NO: 75, 76 or a sequence at least 95% identical to any one thereof.

5. An adenovirus according to any one of claims 1 to 4, wherein the transgene cassette encodes CXL10 shown in SEQ ID NO: 100 or a sequence at least 95% identical thereto, such as SEQ ID NO: 100.

6. An adenovirus according to any one of claims 1 to 5, wherein the transgene cassette encodes CXCL9 shown in SEQ ID NO: 99 or a sequence at least 95% identical thereto, such as SEQ ID NO: 99.

7. An adenovirus according to any one of claims 1 to 6, wherein the transgene cassette encodes IFNα shown in SEQ ID NO: 98 or a sequence at least 95% identical thereto, such as SEQ ID NO: 98.

8. An adenovirus according to any one of claims 1 to 7, wherein the transgenes are operably linked.

9. An adenovirus according to any one of claims 1 to 8, wherein the transgenes are separated by 3 different high efficiency self-cleavage peptides.

10. An adenovirus according to claim 9, wherein the self-cleavage peptides are independently selected from E2A, F2A, P2A and T2A.

11. An adenovirus according to any one of claims 1 to 10, wherein the relative order of the transgenes from L5 to E4 is FAP-BITE, CXL10, CXL9 and IFNα, for example as shown in Figure XC.

12. An adenovirus according to any one of claims 1 to 11, wherein the transgene cassette has a polynucleotide sequence shown in SEQ ID NO: 95 or a polynucleotide encoding the same amino acid sequence, in particular SEQ ID NO: 95.

13. An adenovirus according to any one of claims 1 to 12, wherein the adenovirus comprises SEQ ID NO: 84.

14. An adenovirus according to any one of claims 1 to 13, wherein the adenovirus is replication competent.

15. An adenovirus according to any one of claims 1 to14, wherein the adenovirus is oncolytic.

16. An adenovirus according to any one of claims 1 to 15, wherein the virus has a hexon and fibre from Ad11.

17. A pharmaceutical composition comprising an adenovirus according to any one of claims 1 to 16 and an excipient, diluent or carrier.

18. An adenovirus according to any one of claims 1 to 16, or a pharmaceutical composition according to claim 17, for use in treatment, for example for use in the treatment of cancer.

19. A method of treating a patient comprising administering an adenovirus according to any one of claims 1 to 16 or a pharmaceutical composition according to claim 17.

20. Use an adenovirus according to any one of claims 1 to 16, or a pharmaceutical composition according to claim 17, for the manufacture of a medicament for the treatment of cancer.

Figure 1

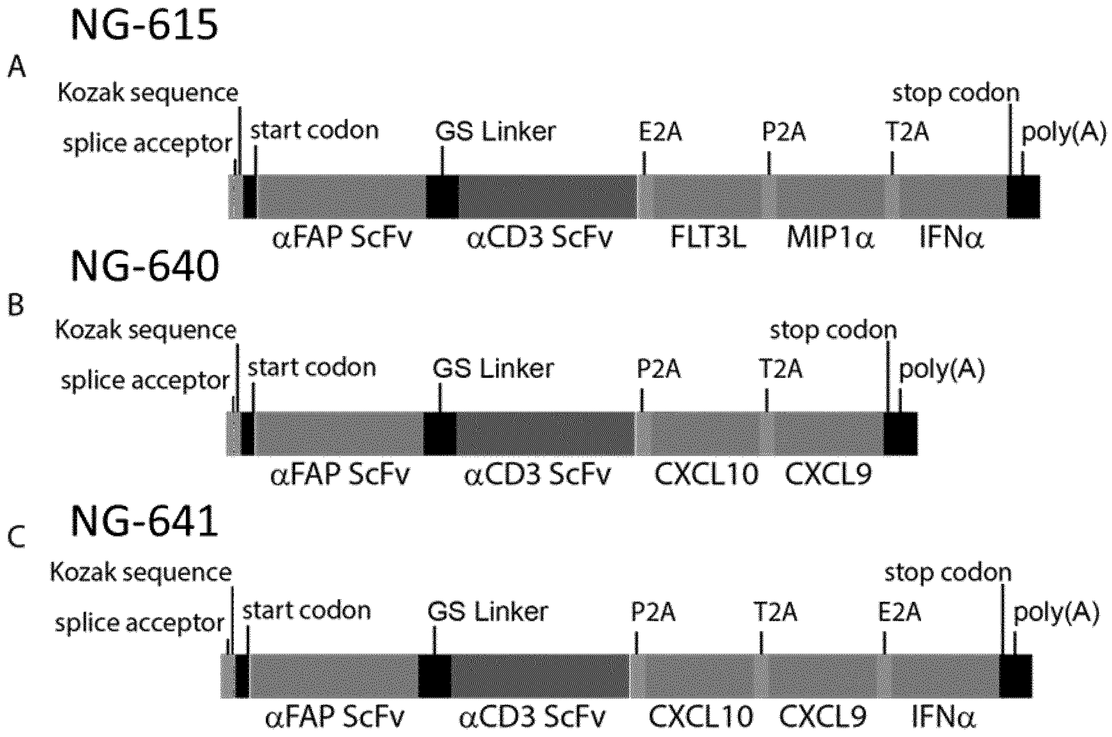


Figure 2A

Virus Replication in A549 Cells

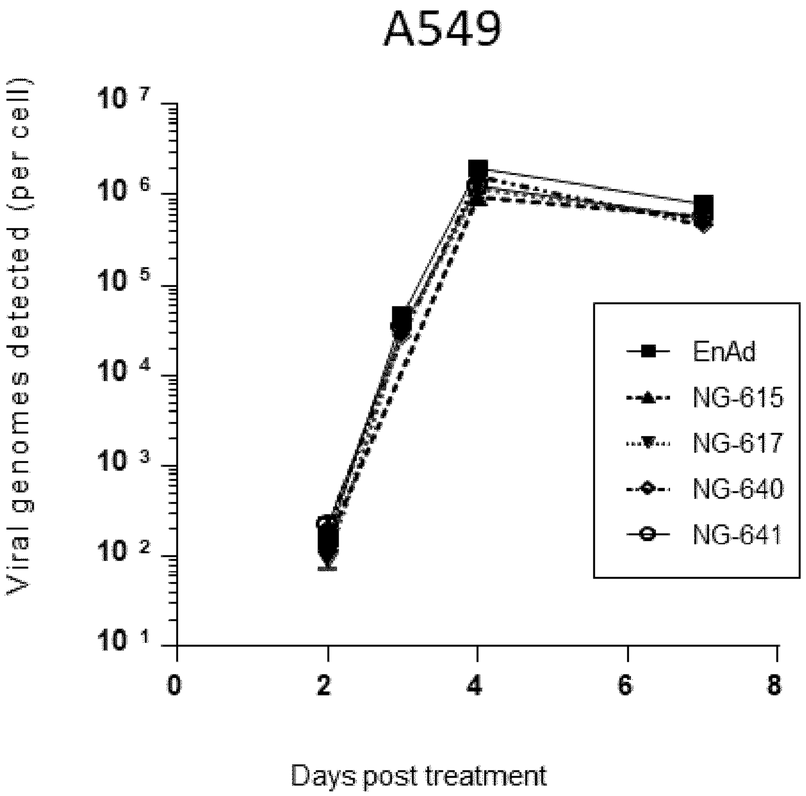


Figure 2B **Virus Replication in MDA-MB-453 Cells**

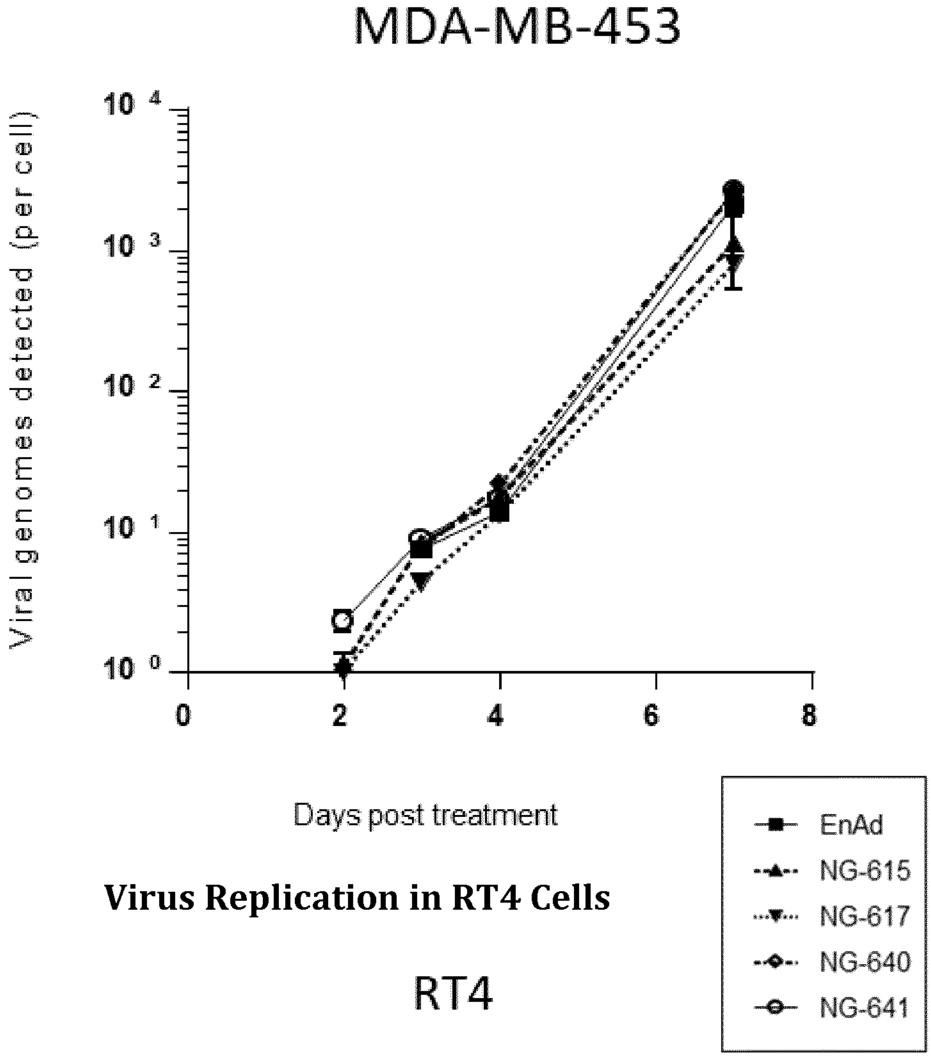


Figure 2C **Virus Replication in RT4 Cells**

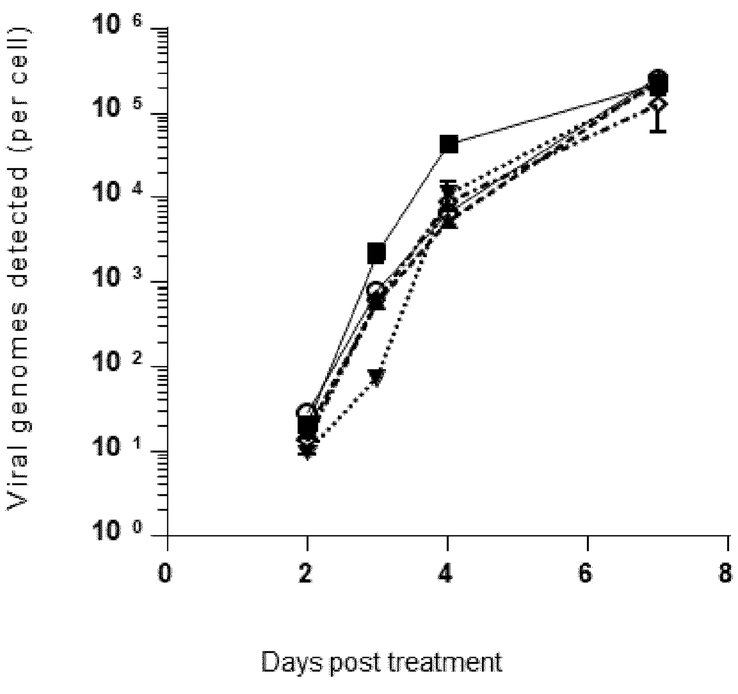


Figure 3A

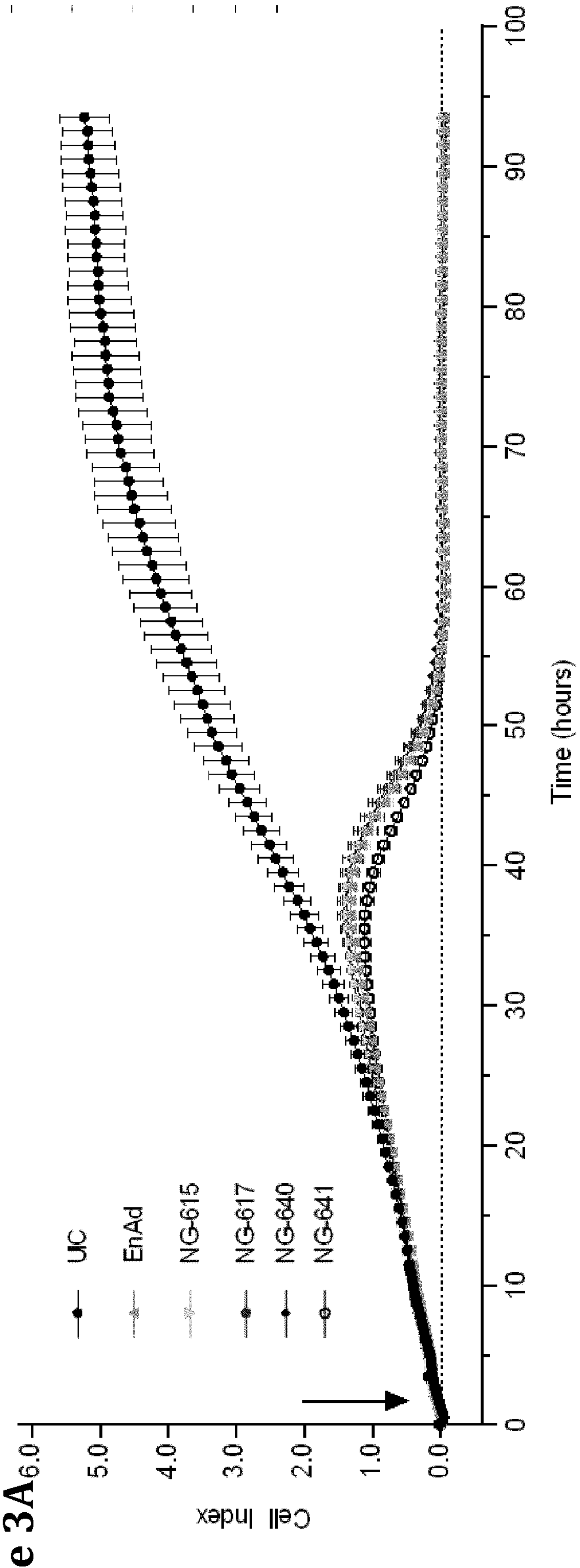


Figure 3B

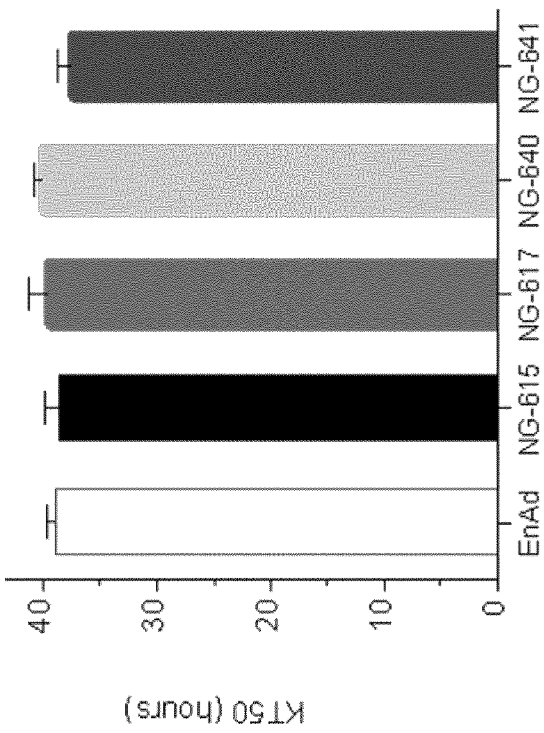


Figure 4 Cytokine Transgene Expression for NG-615 in Lung and Carcinoma Cells

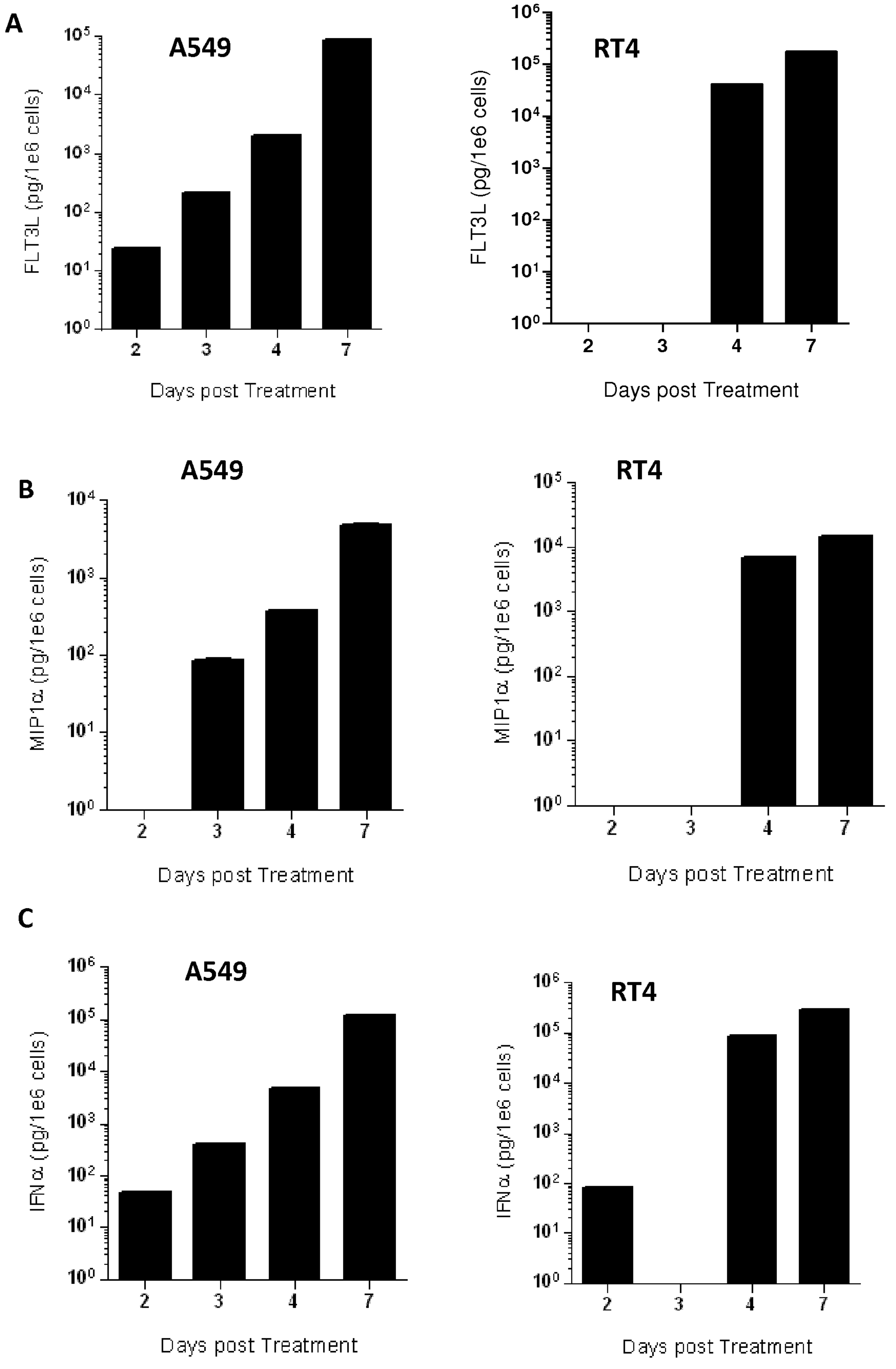


Figure 5 Cytokine Transgene Expression for NG-641 in Lung and Carcinoma Cells

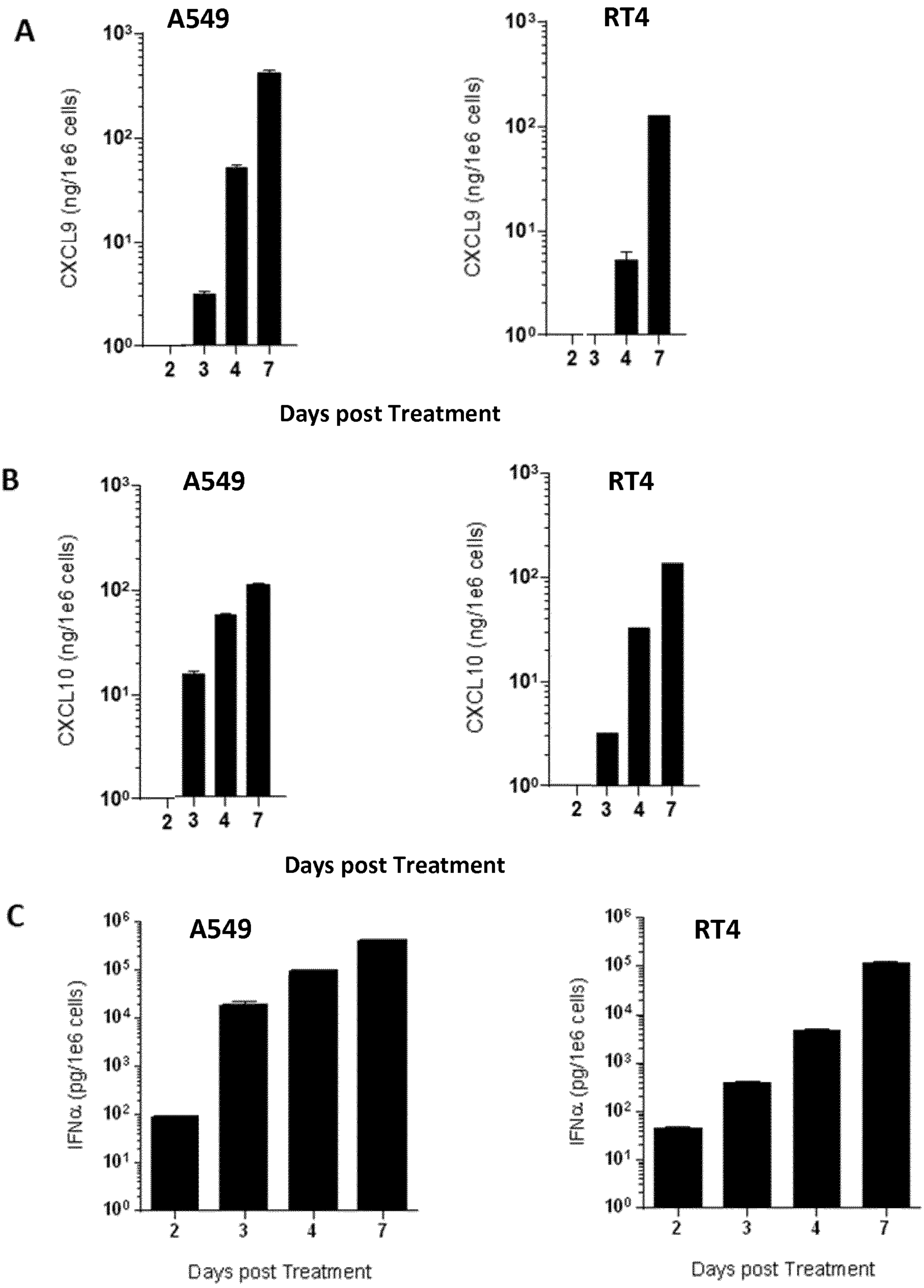


Figure 6A

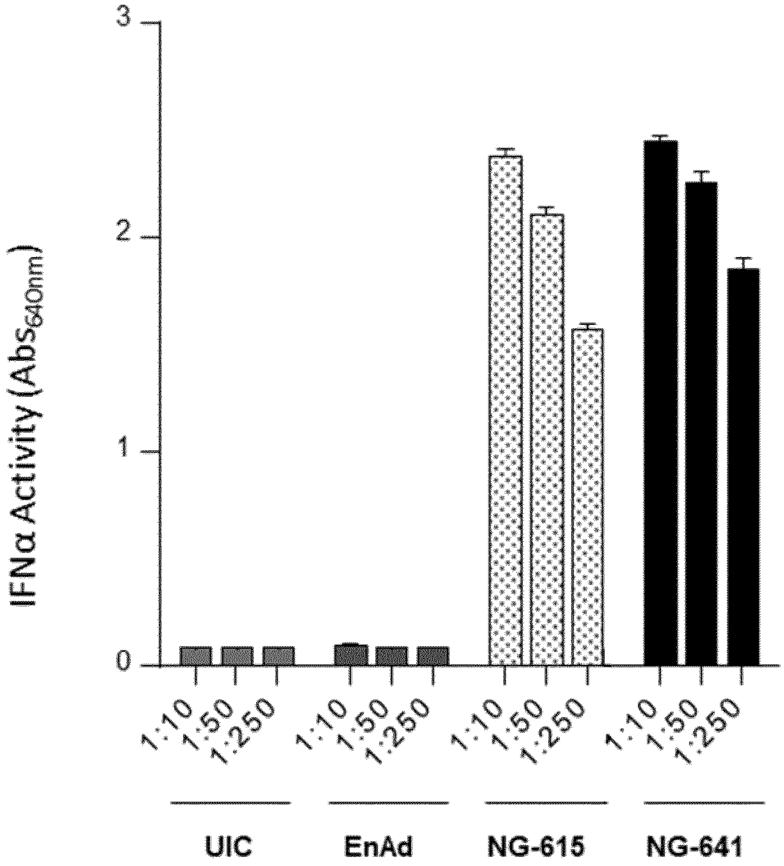


Figure 6B

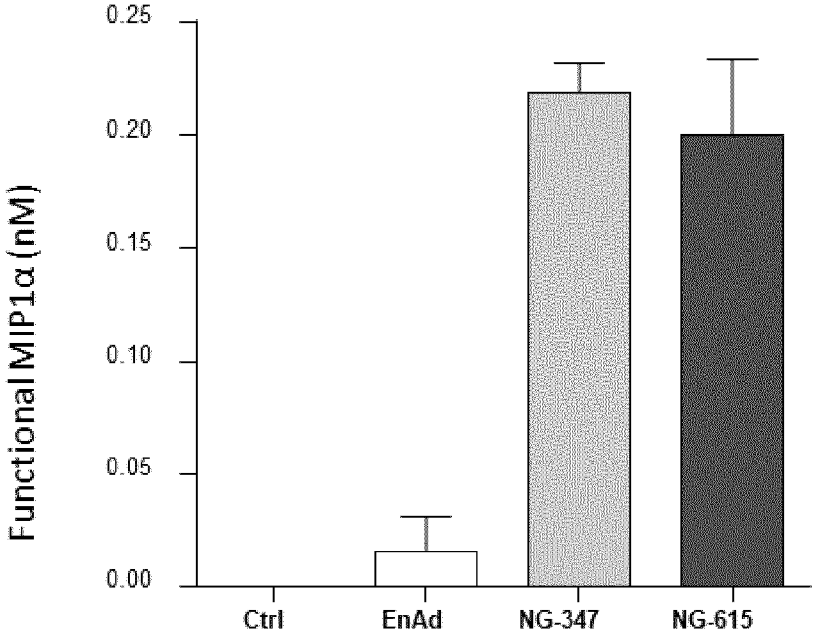
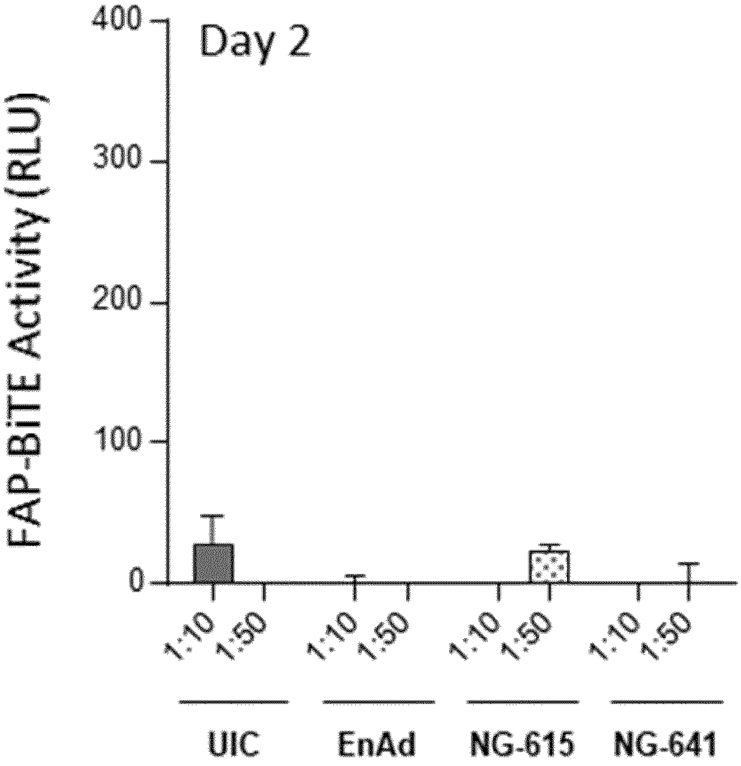


Figure 7

A


Day 2
FAP-BiTE Activity (RLU)
400
300
200
100
0
1:10
1:50
UIC
EnAd
NG-615
NG-641

B

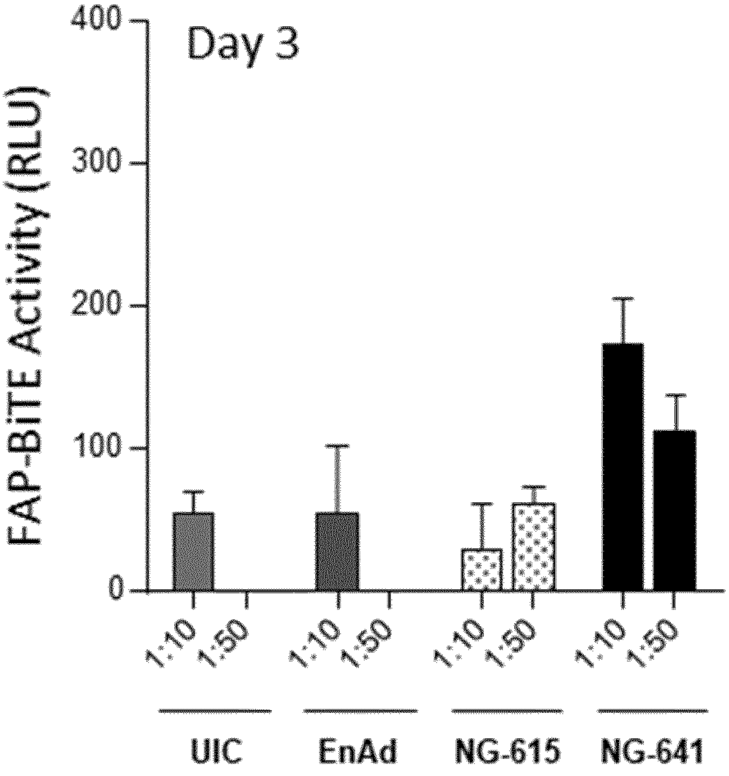

Day 3
FAP-BiTE Activity (RLU)
400
300
200
100
0
1:10
1:50
UIC
EnAd
NG-615
NG-641

Figure 7C

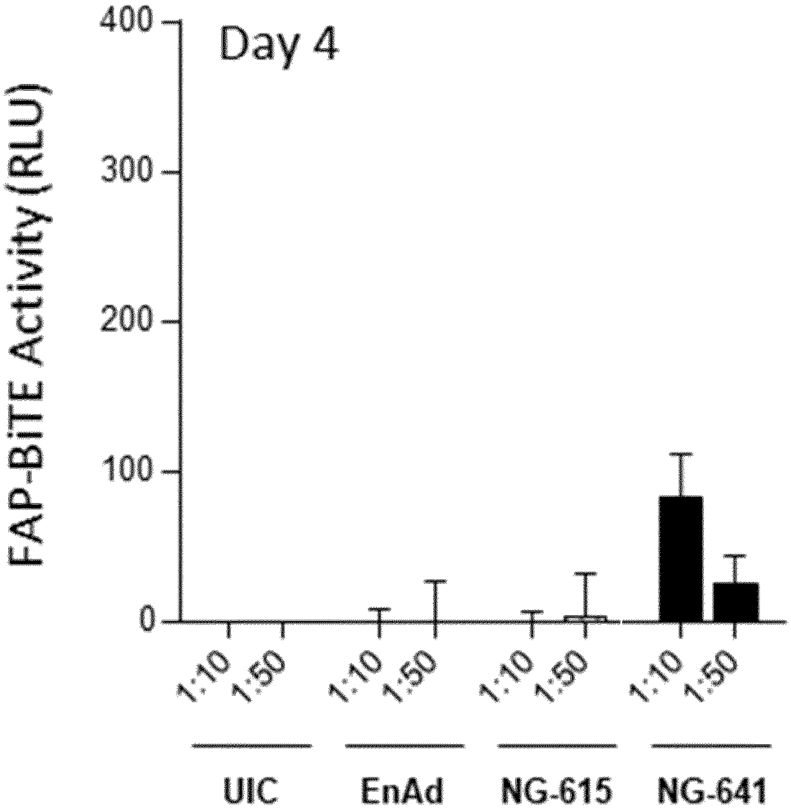


Figure 8A

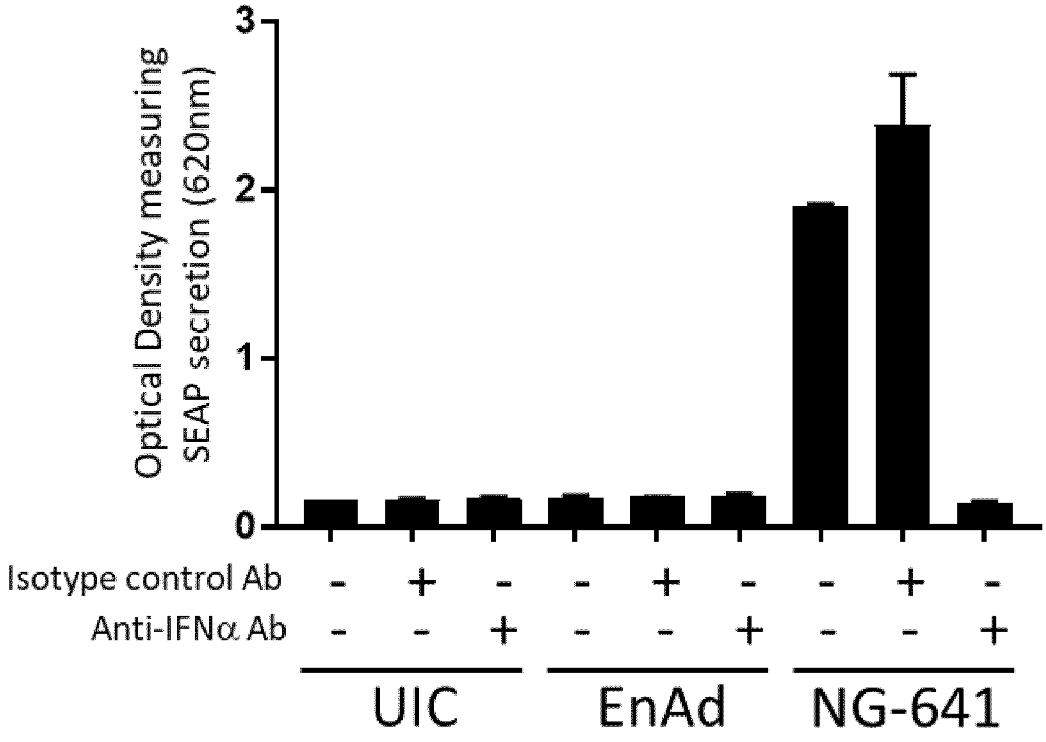


Figure 8B

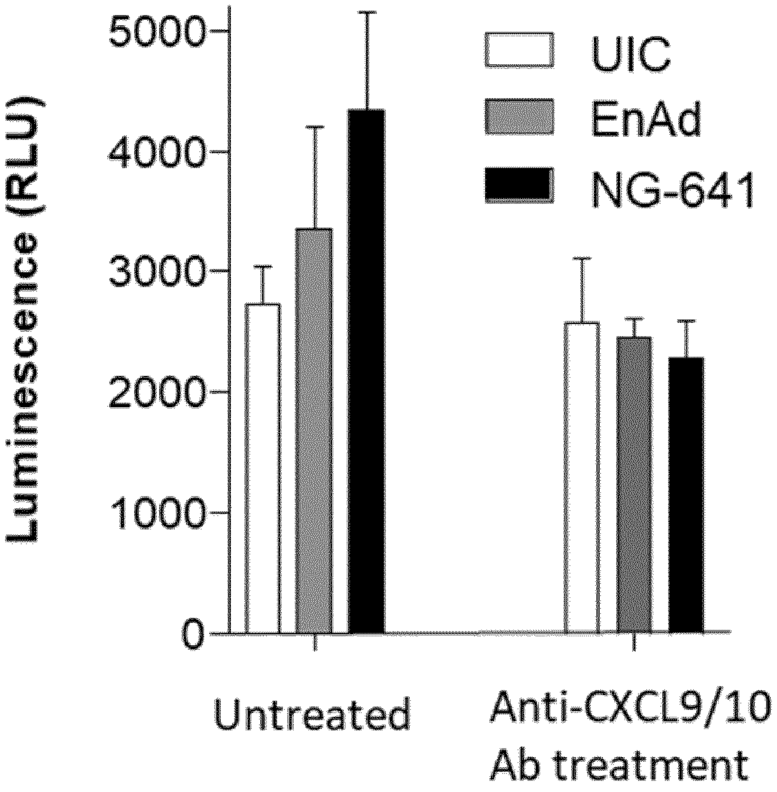

5000
4000
3000
2000
1000
0
Luminescence (RLU)
UIC
EnAd
NG-641
Untreated
Anti-CXCL9/10
Ab treatment

Figure 9

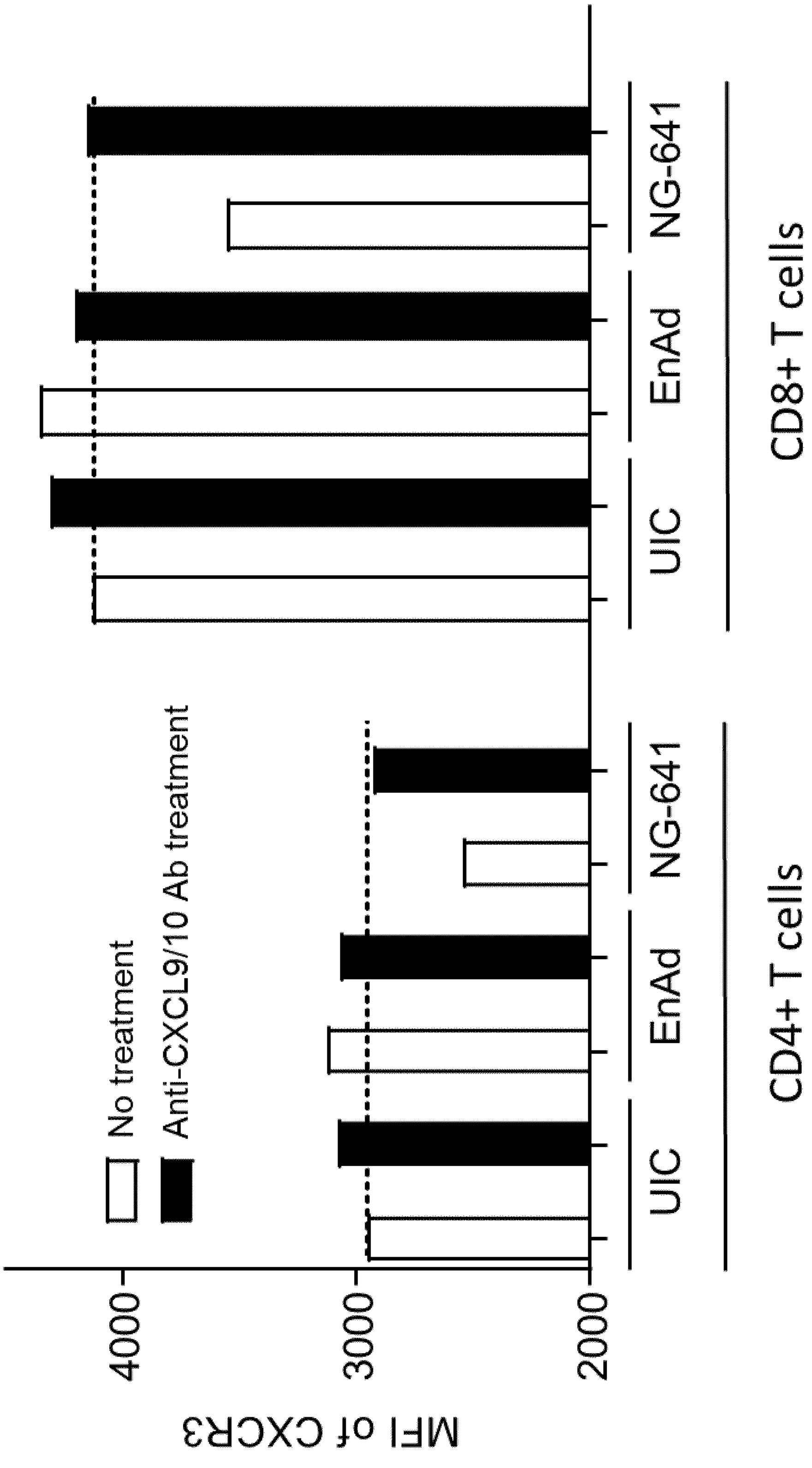
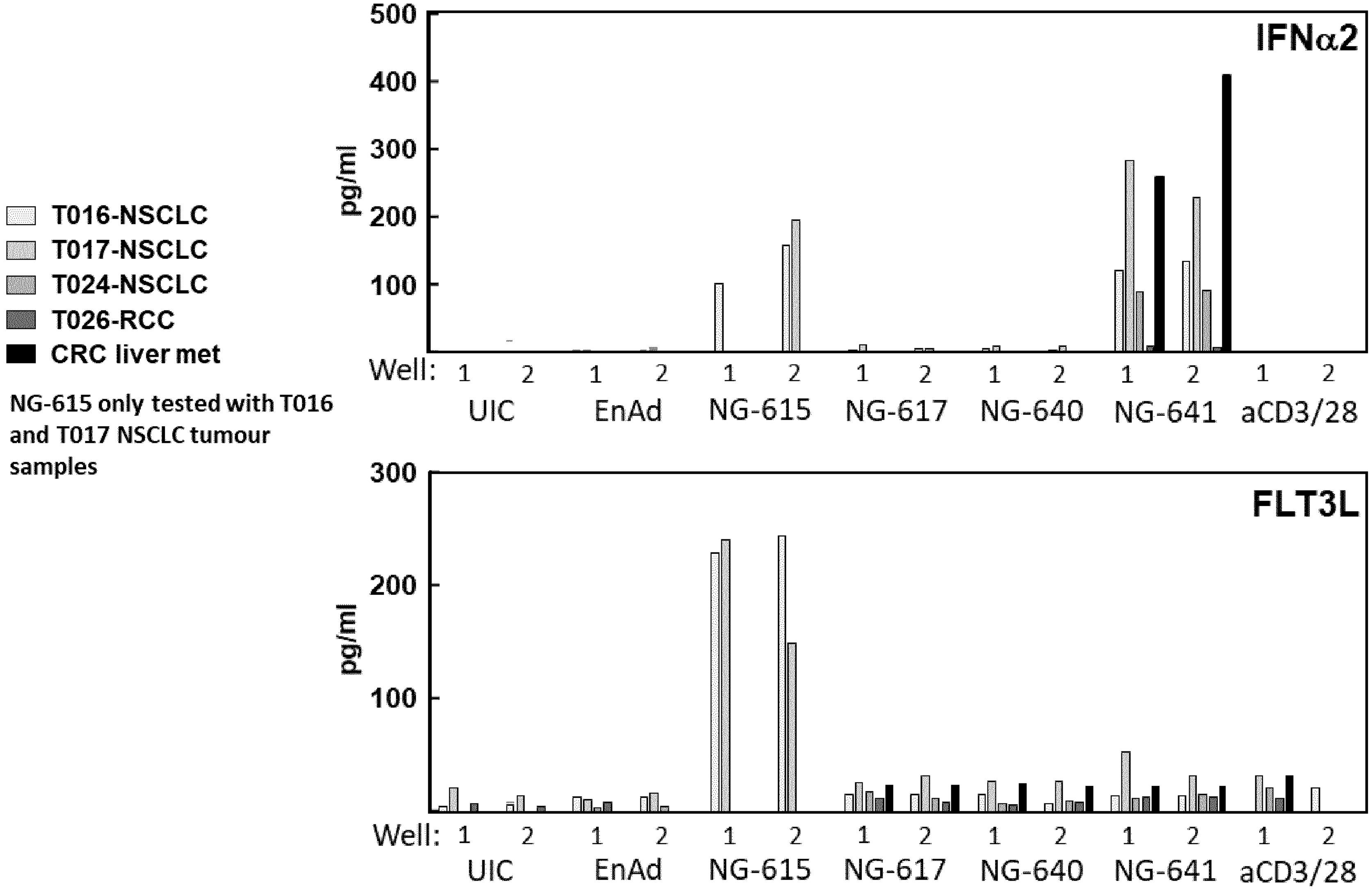

MFI of CXCR3
4000
3000
2000
No treatment
Anti-CXCL9/10 Ab treatment
UIC
EnAd
NG-641
CD4+ T cells
UIC
EnAd
NG-641
CD8+ T cells

Figure 10A



NG-615 only tested with T016 and T017 NSCLC tumour samples

Figure 10B

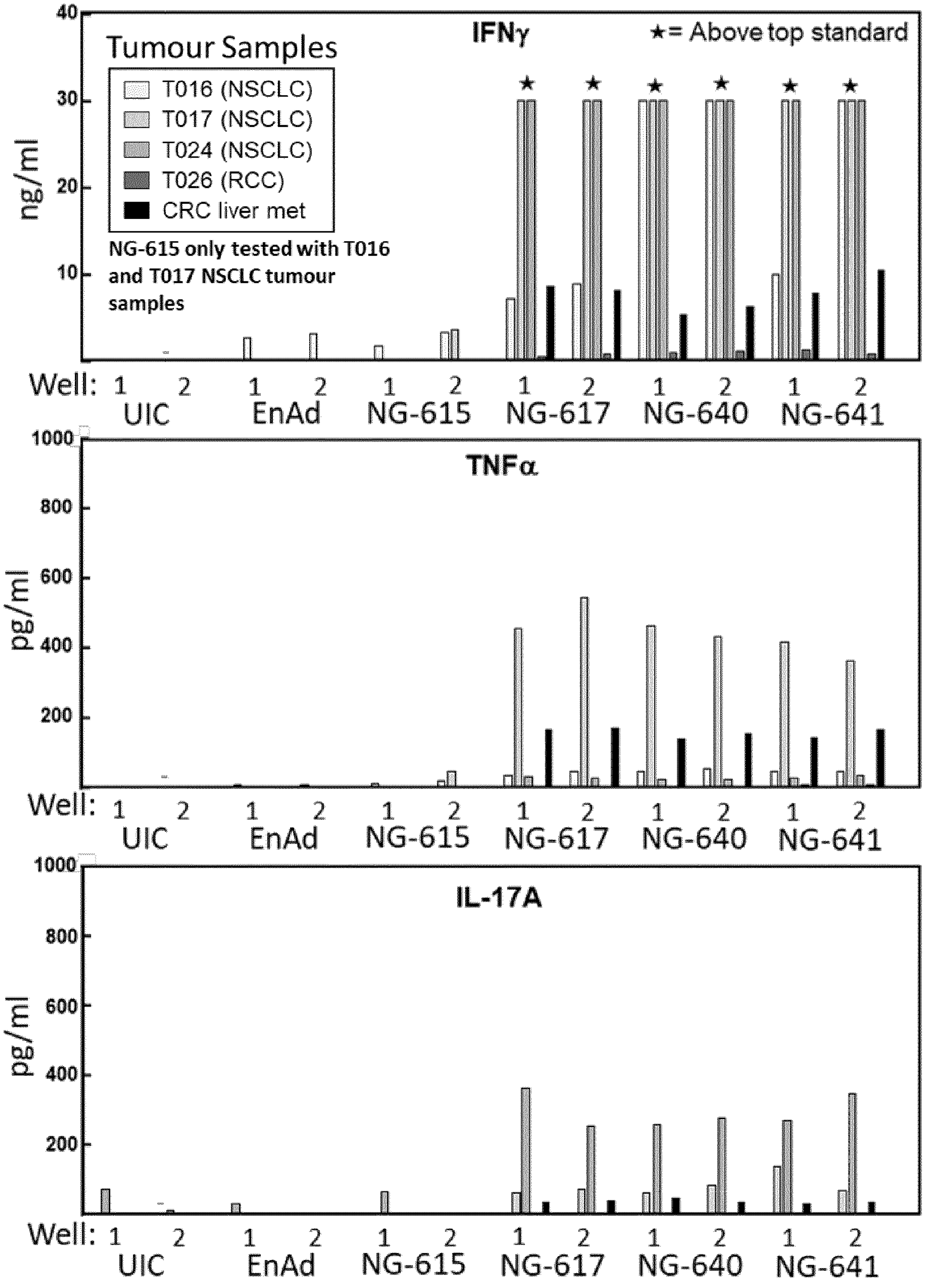
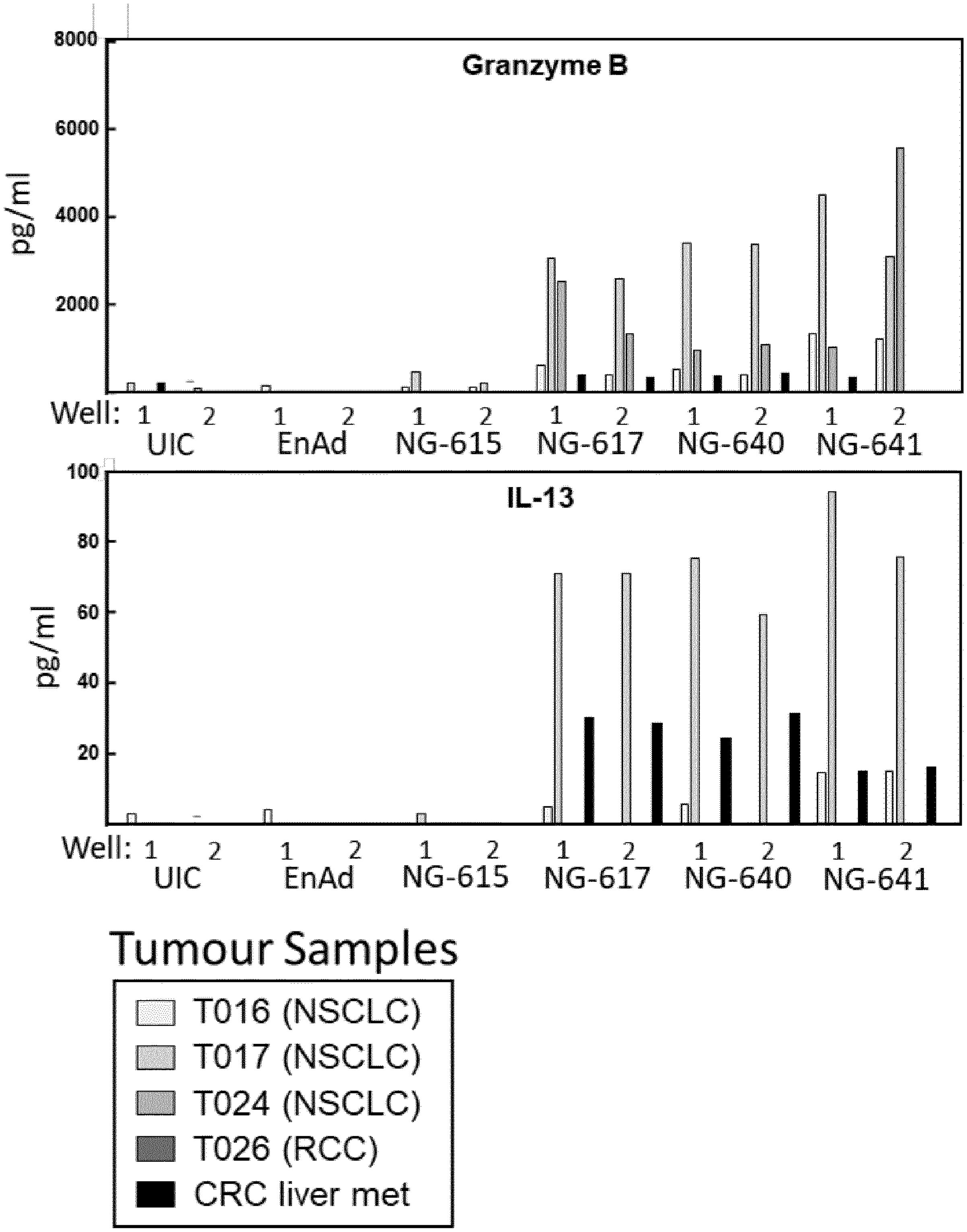

IFNγ
★= Above top standard
Tumour Samples
T016 (NSCLC)
T017 (NSCLC)
T024 (NSCLC)
T026 (RCC)
CRC liver met
NG-615 only tested with T016 and T017 NSCLC tumour samples
ng/ml
40
30
20
10
Well: 1 2 1 2 1 2 1 2 1 2 1 2
UIC
EnAd
NG-615
NG-617
NG-640
NG-641
TNFα
pg/ml
1000
800
600
400
200
IL-17A

Figure 10B cont.



NG-615 only tested with T016 and T017 NSCLC tumour samples

Figure 11A (X-axis Comp-RL1-A:CD69-A, Y-axis Comp-YL4-A: CD25-A)

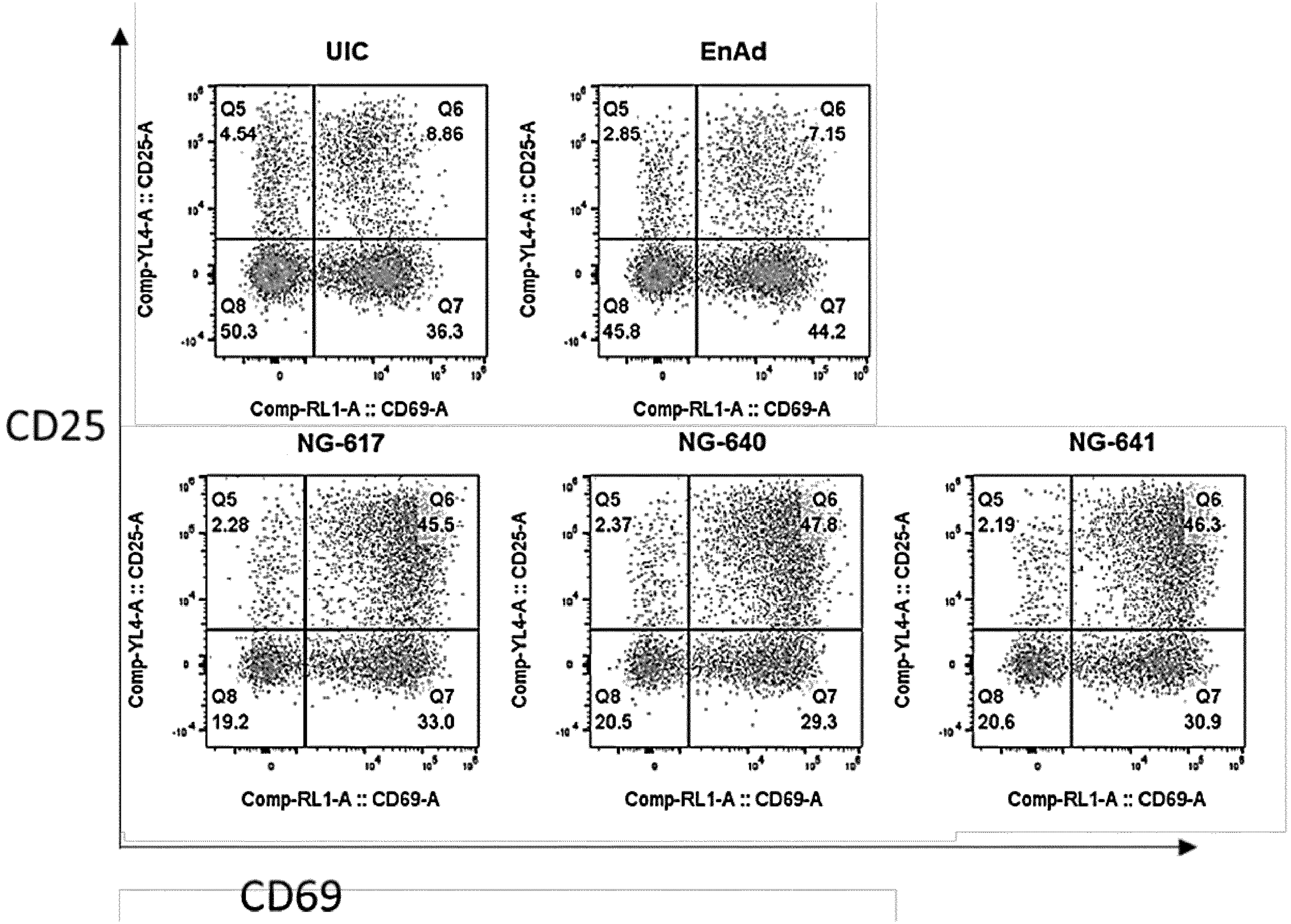


Figure 11A Cont. (X-axis Comp- YL1A:107a-A, Y-axis Comp-YL4-A: CD25-A)

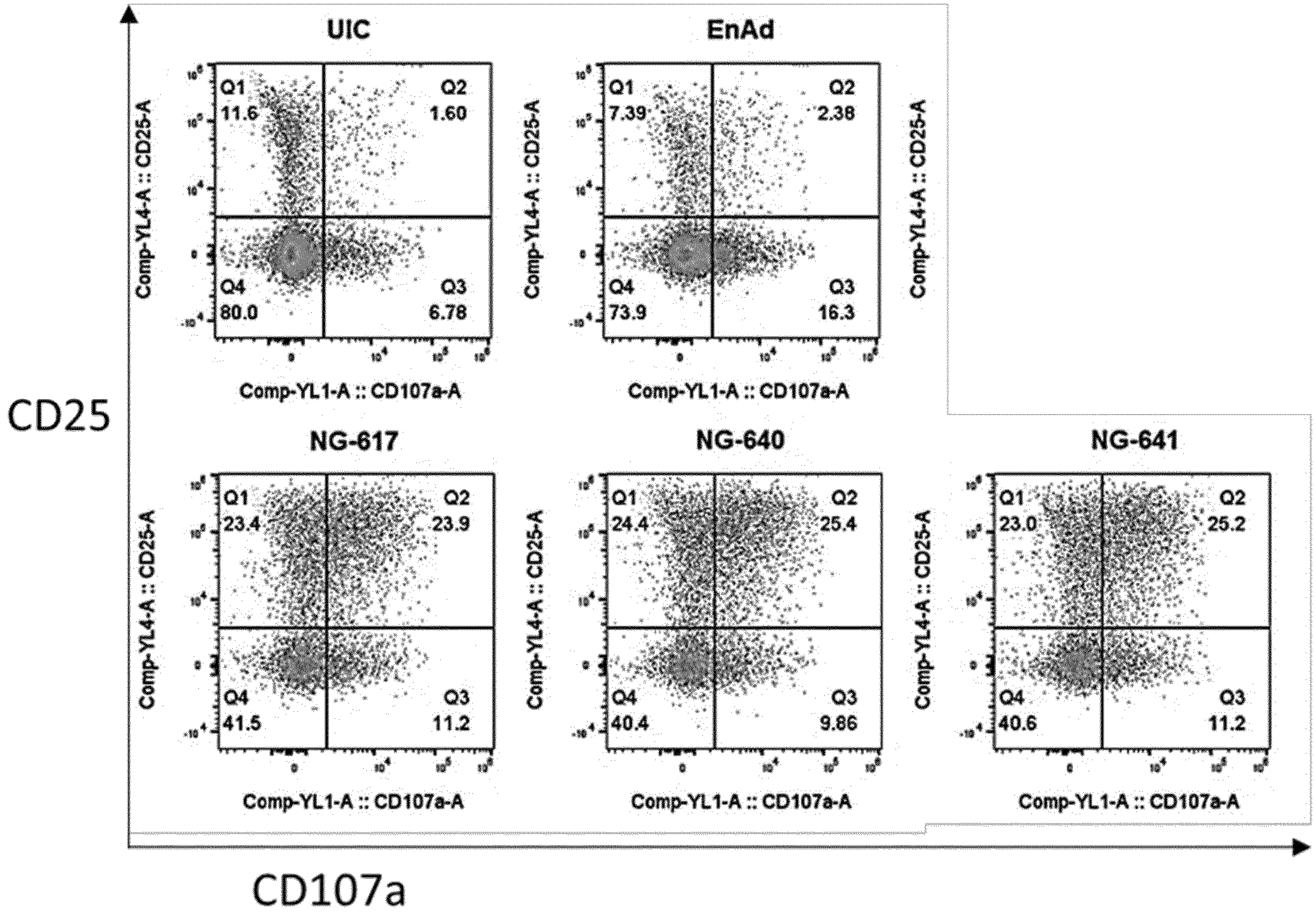


Figure 11B (X-axis Comp-RL-A:CD69-A, Y-axis Comp-YL4-A: CD25-A)

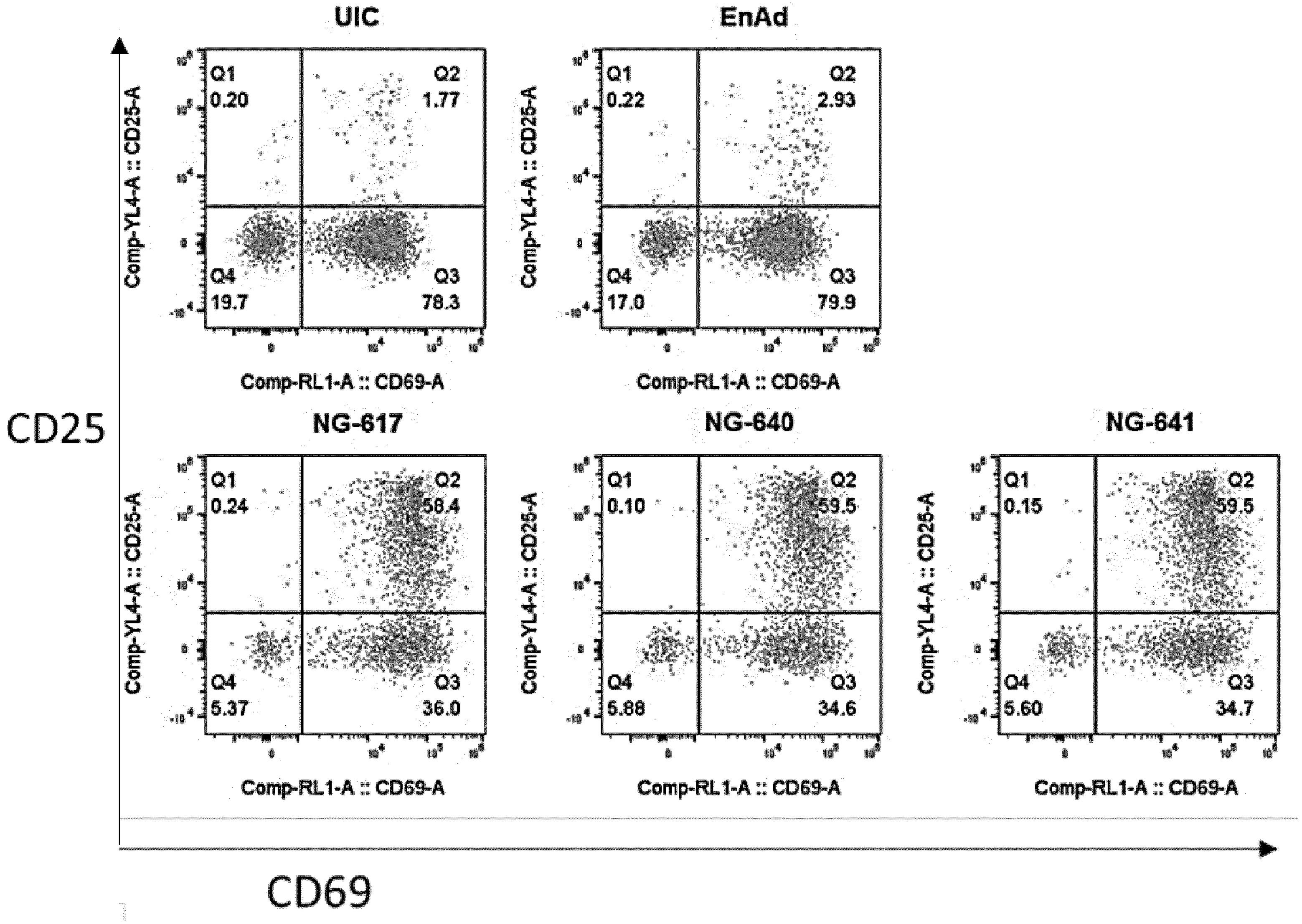


Figure 11B Cont. (X-axis Comp-YL1-1:CD107-a-A, Y-axis Comp-YL4-A: CD25-A)

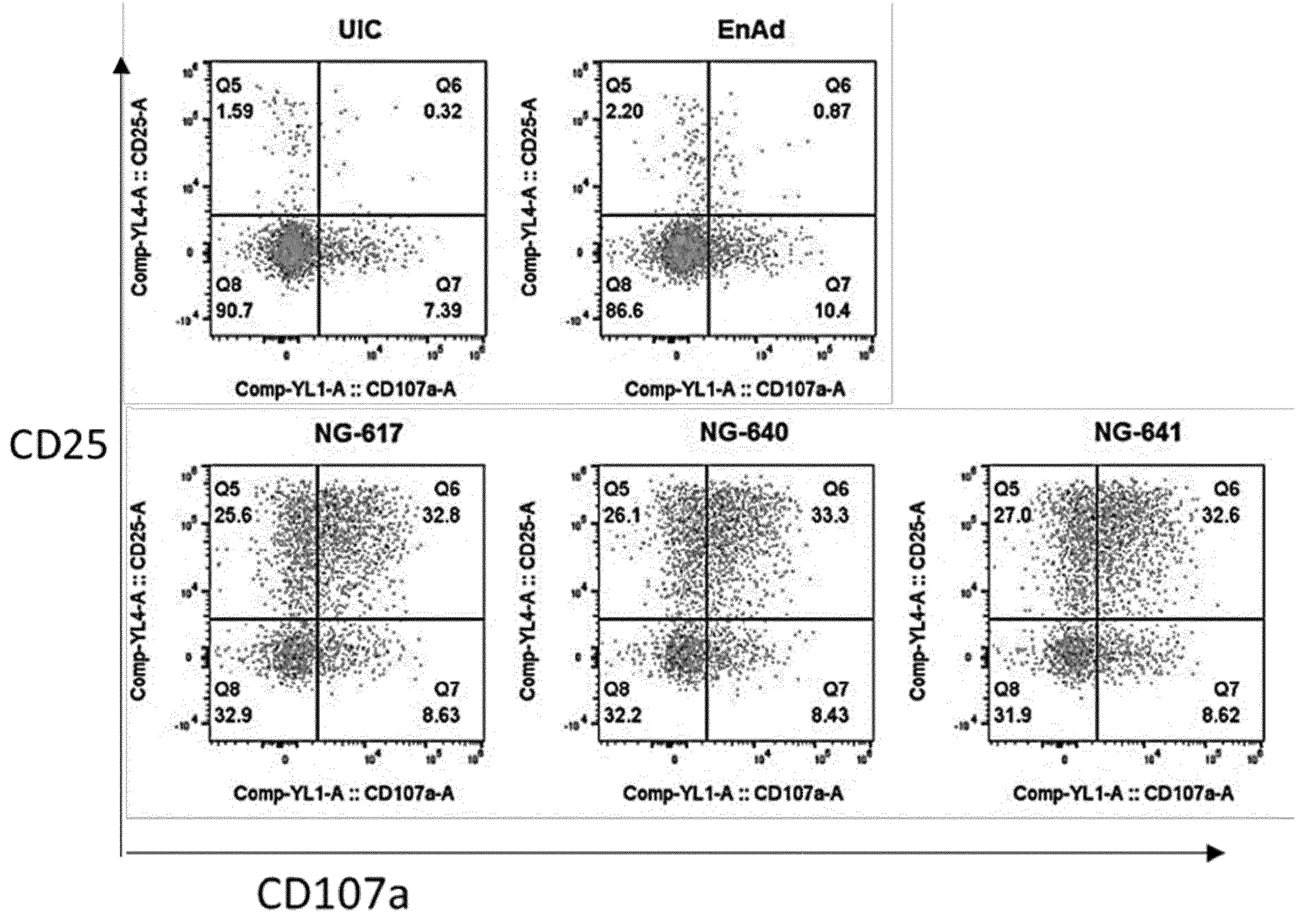


Figure 11C (X-axis Comp-VL-A: IFN-g-A, Y-axis Comp-YL4-A: CD25-A)

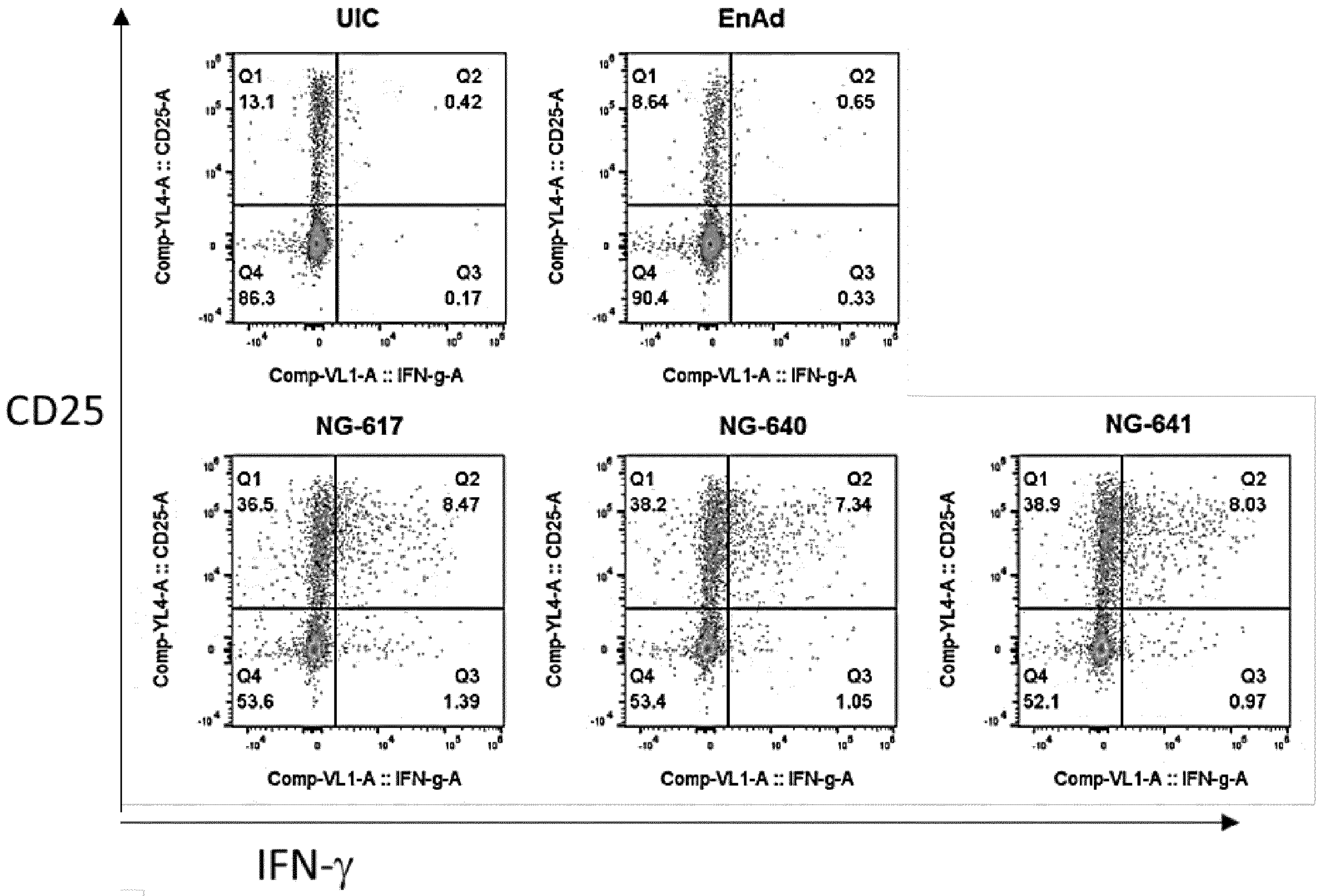


Figure 11C Cont. (X-axis Comp-RL1-A:TNF-a-A, Y-axis Comp-YL4-A: CD25-A)

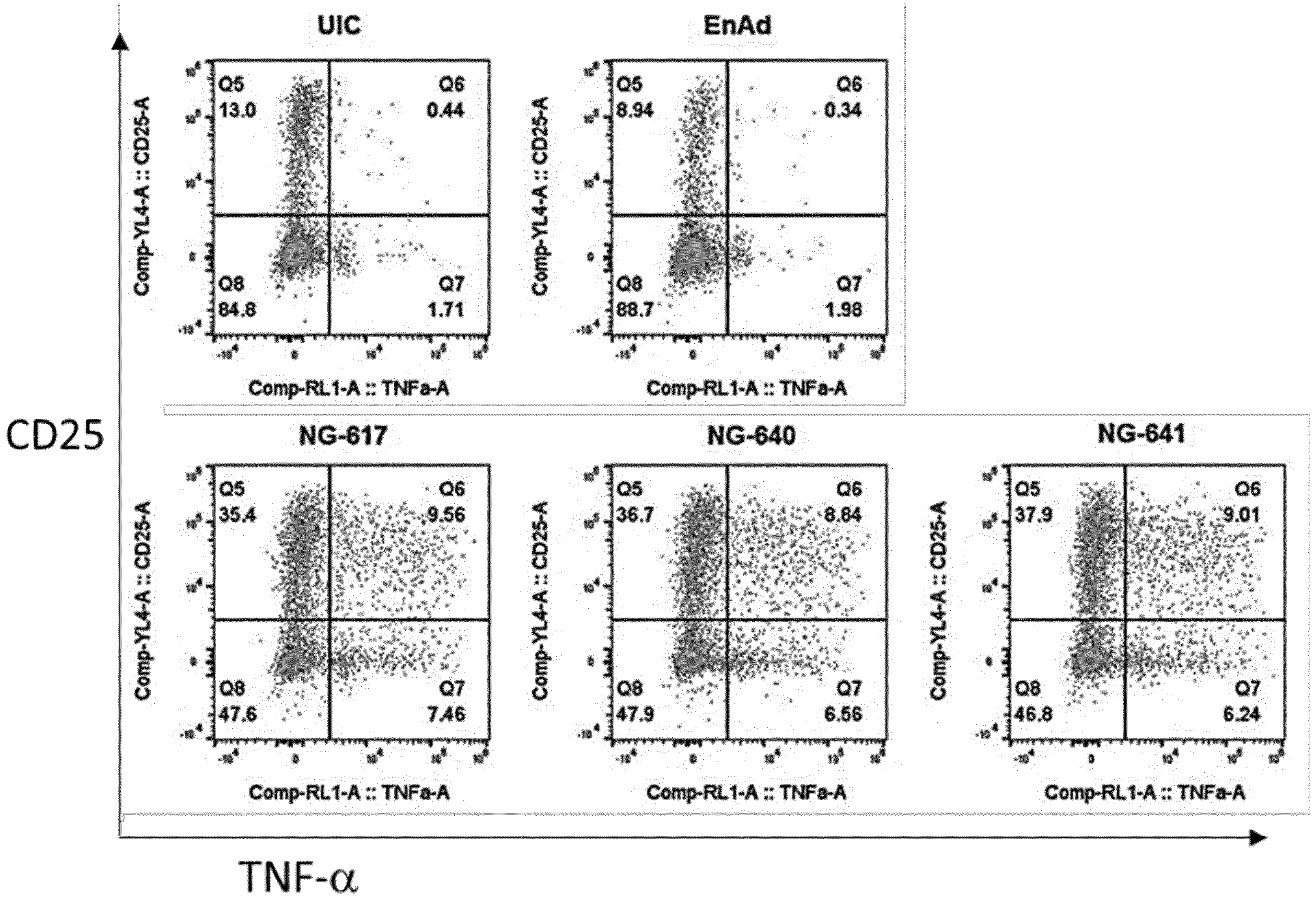


FIGURE 11D (X-axis Comp-VL-A: IFN-g-A, Y-axis Comp-YL4-A: CD25-A)

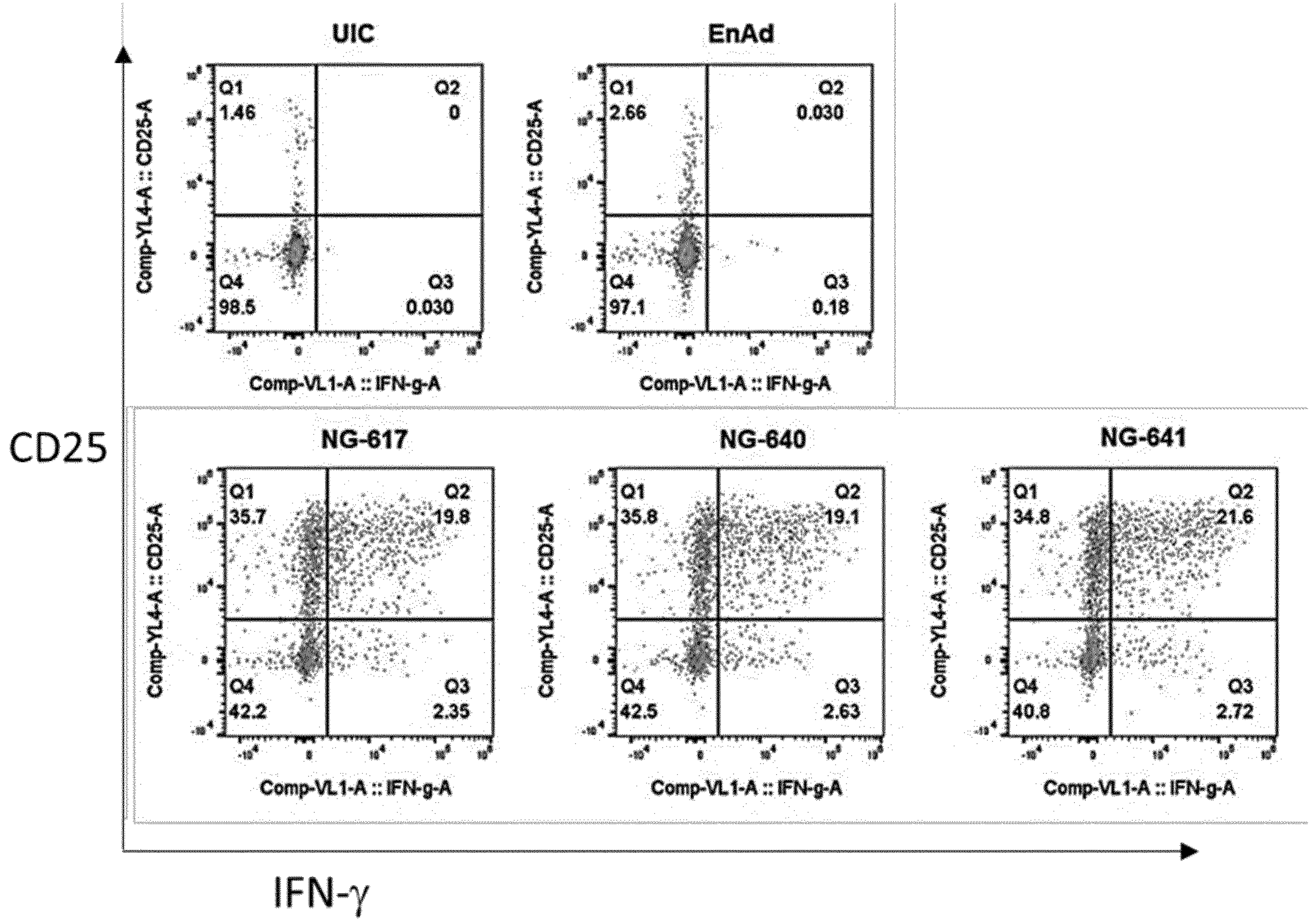


FIGURE 11D Cont. (X-axis Comp-RL1-A:TNF-a-A, Y-axis Comp-YL4-A: CD25-A)

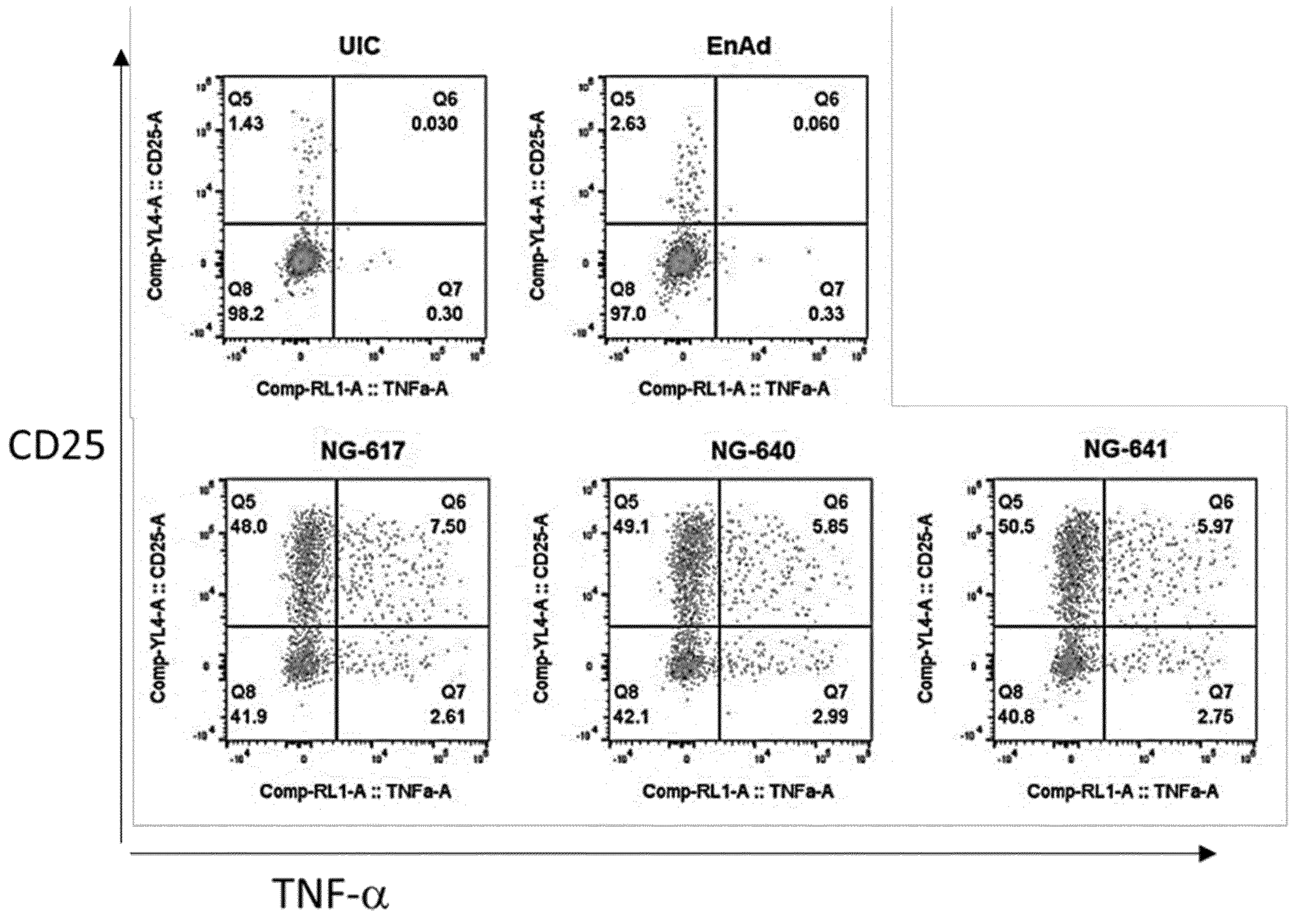


Figure 12

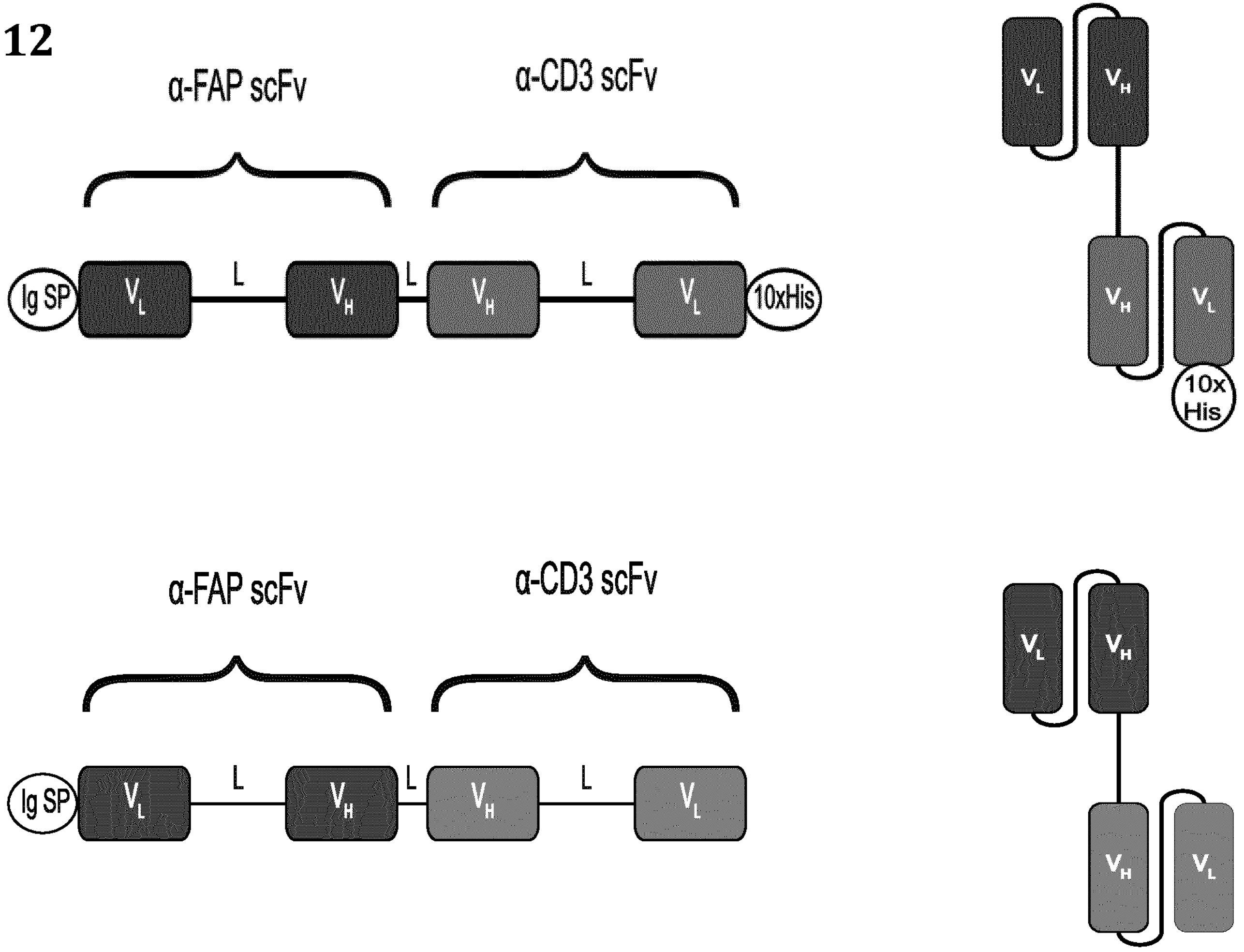
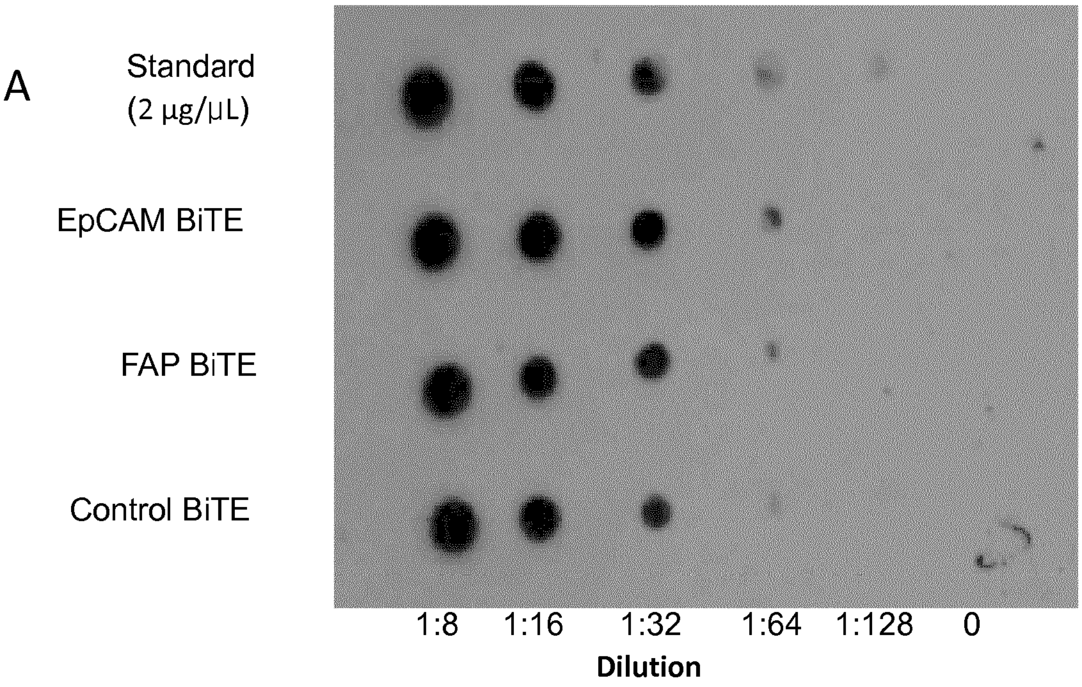

α-FAP scFv
α-CD3 scFv
Ig SP
V_L
L
V_H
L
V_H
L
V_L
10xHis
V_L
V_H
V_H
V_L
10x His
α-FAP scFv
α-CD3 scFv
Ig SP
V_L
L
V_H
L
V_H
L
V_L
V_L
V_H
V_H
V_L

Figure 13


A
Standard
(2 µg/µL)
EpCAM BiTE
FAP BiTE
Control BiTE
1:8
1:16
1:32
1:64
1:128
0
Dilution

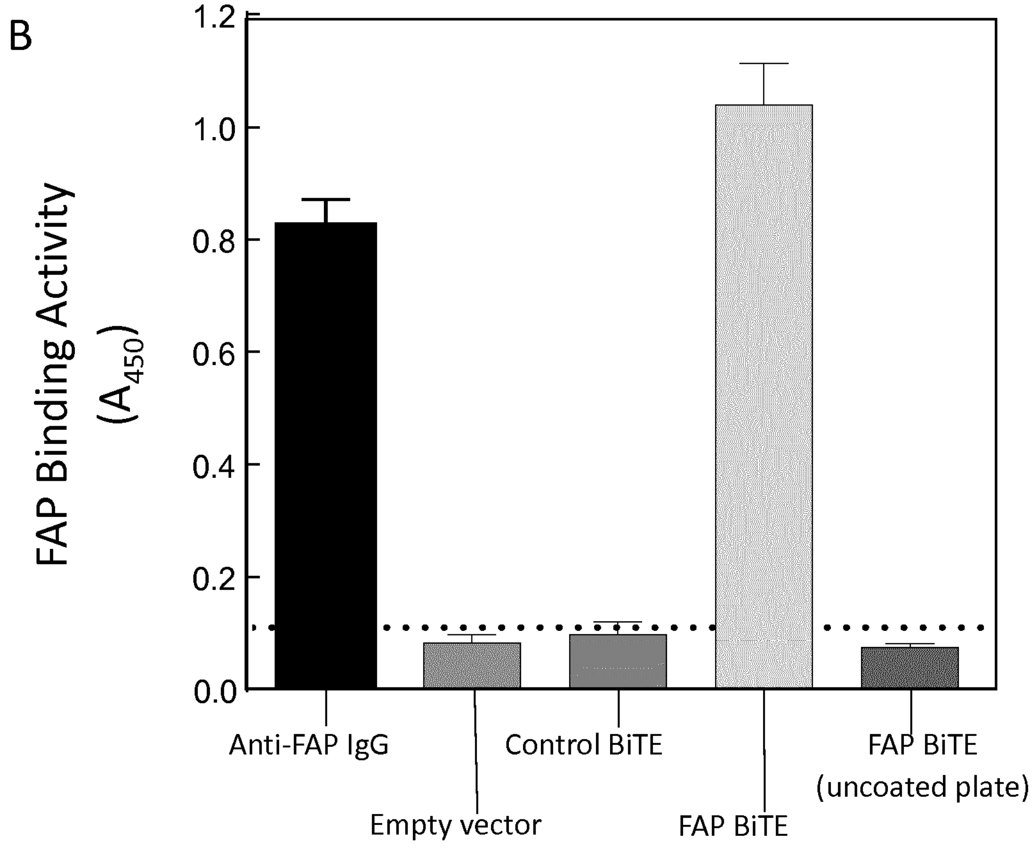
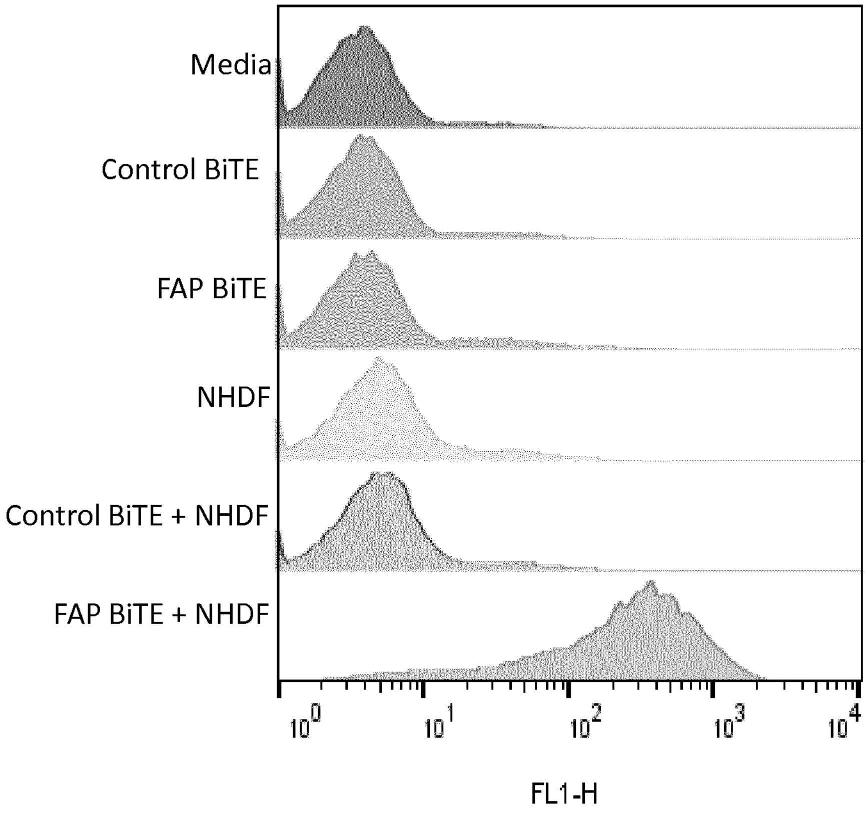

B
FAP Binding Activity
(A_{450})
1.2
1.0
0.8
0.6
0.4
0.2
0.0
Anti-FAP IgG
Empty vector
Control BiTE
FAP BiTE
FAP BiTE
(uncoated plate)

Figure 14A


Media
Control BiTE
FAP BiTE
NHDF
Control BiTE + NHDF
FAP BiTE + NHDF
10^0
10^1
10^2
10^3
10^4
FL1-H

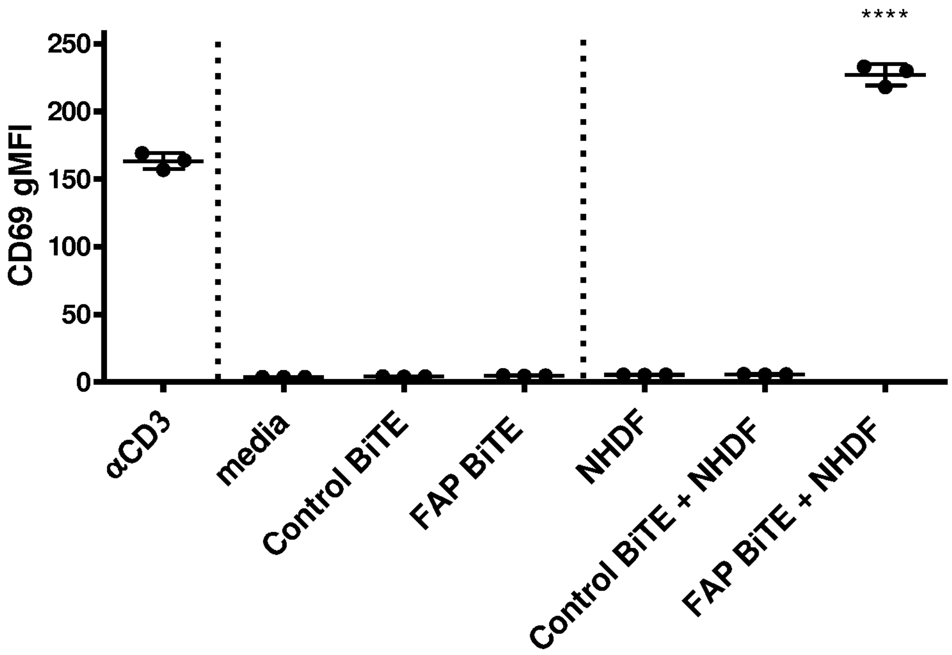
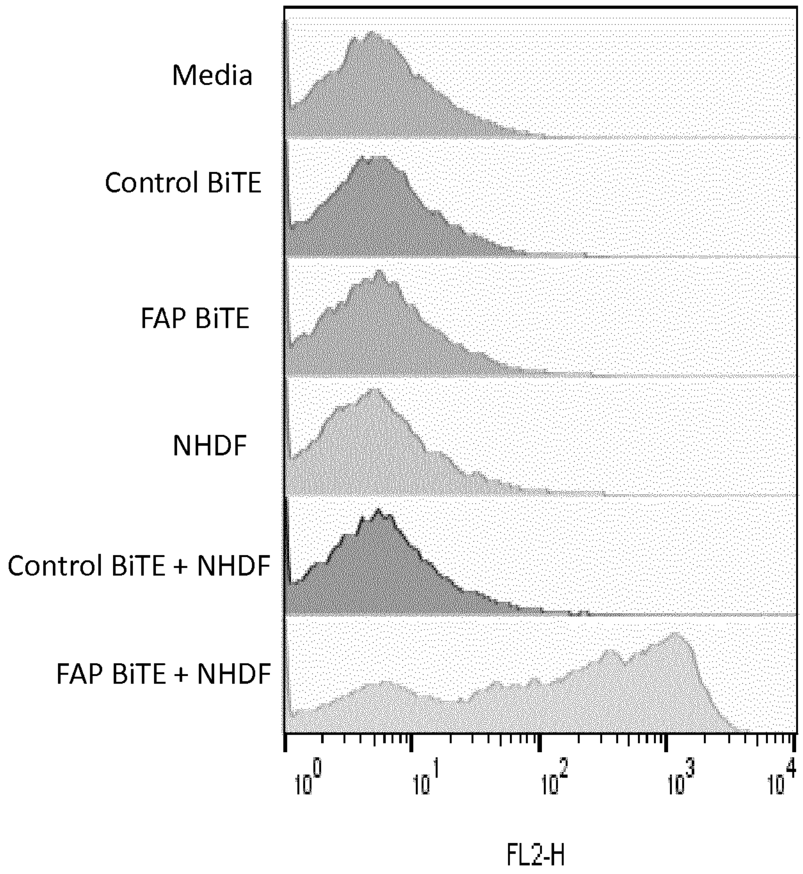

****
CD69 gMFI
250
200
150
100
50
0
αCD3
media
Control BiTE
FAP BiTE
NHDF
Control BiTE + NHDF
FAP BiTE + NHDF

Figure 14B


Media
Control BiTE
FAP BiTE
NHDF
Control BiTE + NHDF
FAP BiTE + NHDF
10^0
10^1
10^2
10^3
10^4
FL2-H

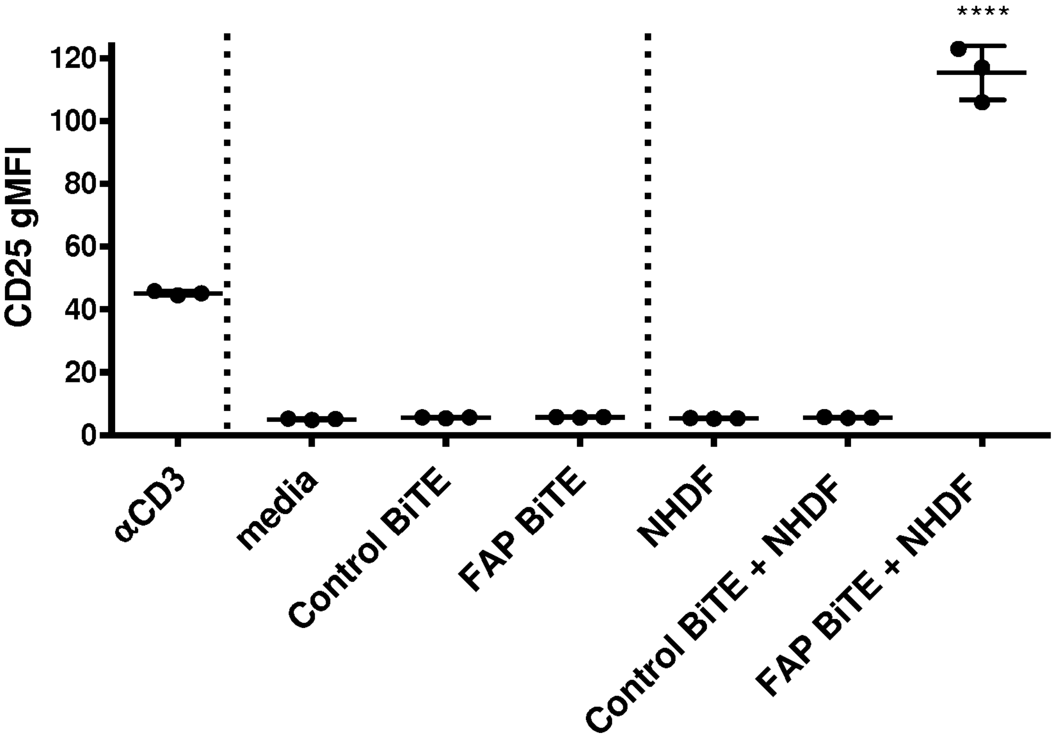

****
CD25 gMFI
0
20
40
60
80
100
120
αCD3
media
Control BiTE
FAP BiTE
NHDF
Control BiTE + NHDF
FAP BiTE + NHDF

Figure 14C

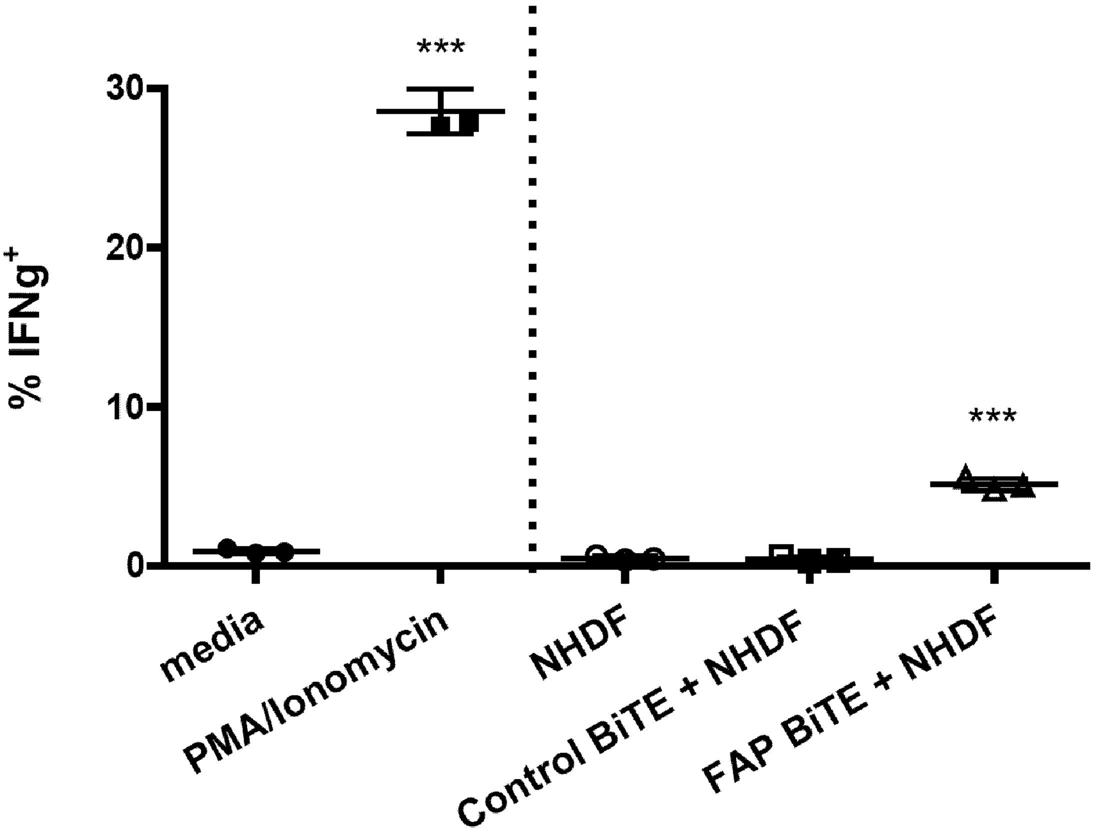

***
***
30
20
10
0
% IFNg+
media
PMA/Ionomycin
NHDF
Control BiTE + NHDF
FAP BiTE + NHDF

Figure 15

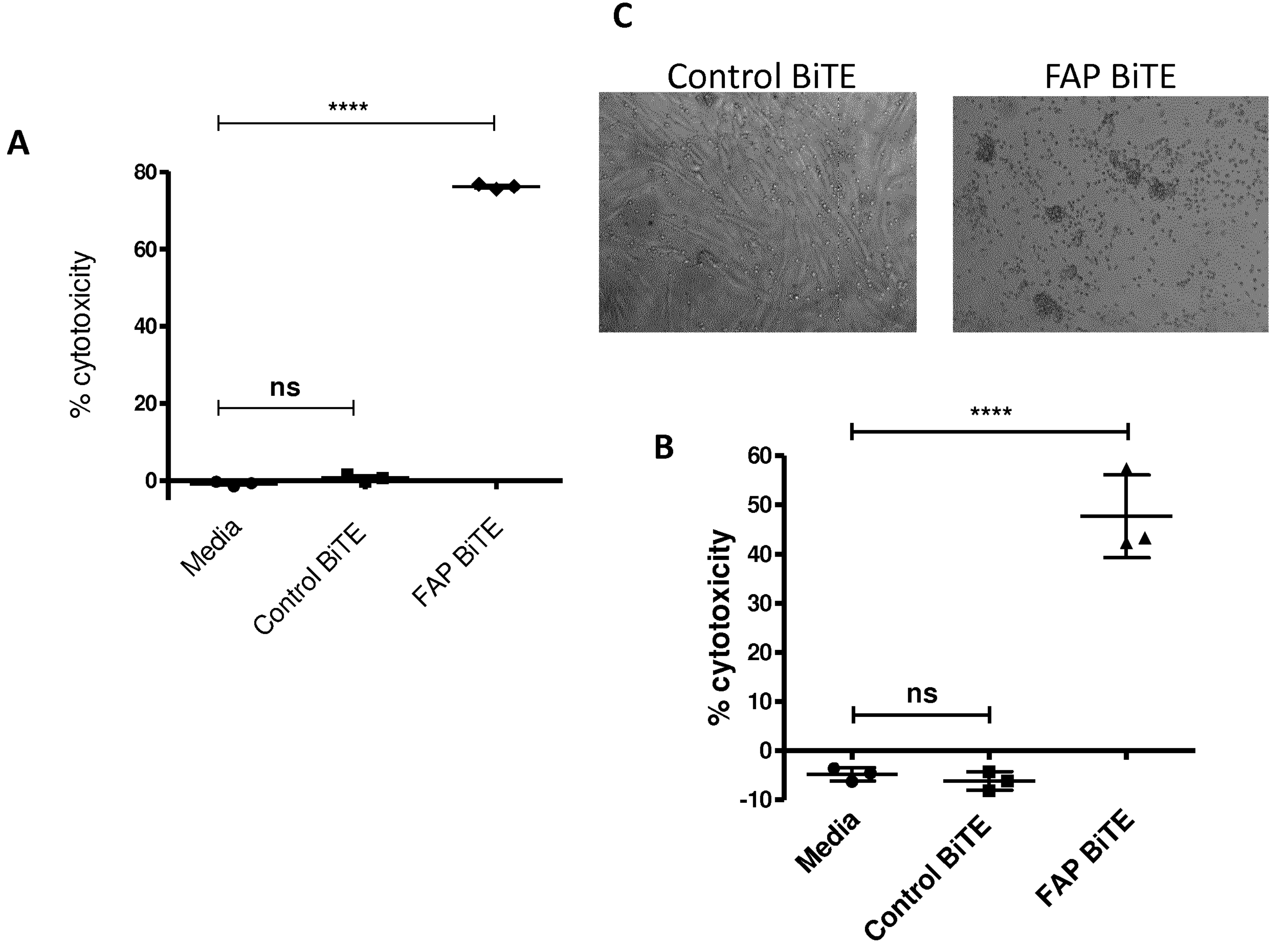

A
% cytotoxicity
80
60
40
20
0
****
ns
Media
Control BiTE
FAP BiTE
C
Control BiTE
FAP BiTE
B
% cytotoxicity
60
50
40
30
20
10
0
-10
****
ns
Media
Control BiTE
FAP BiTE

Figure 16

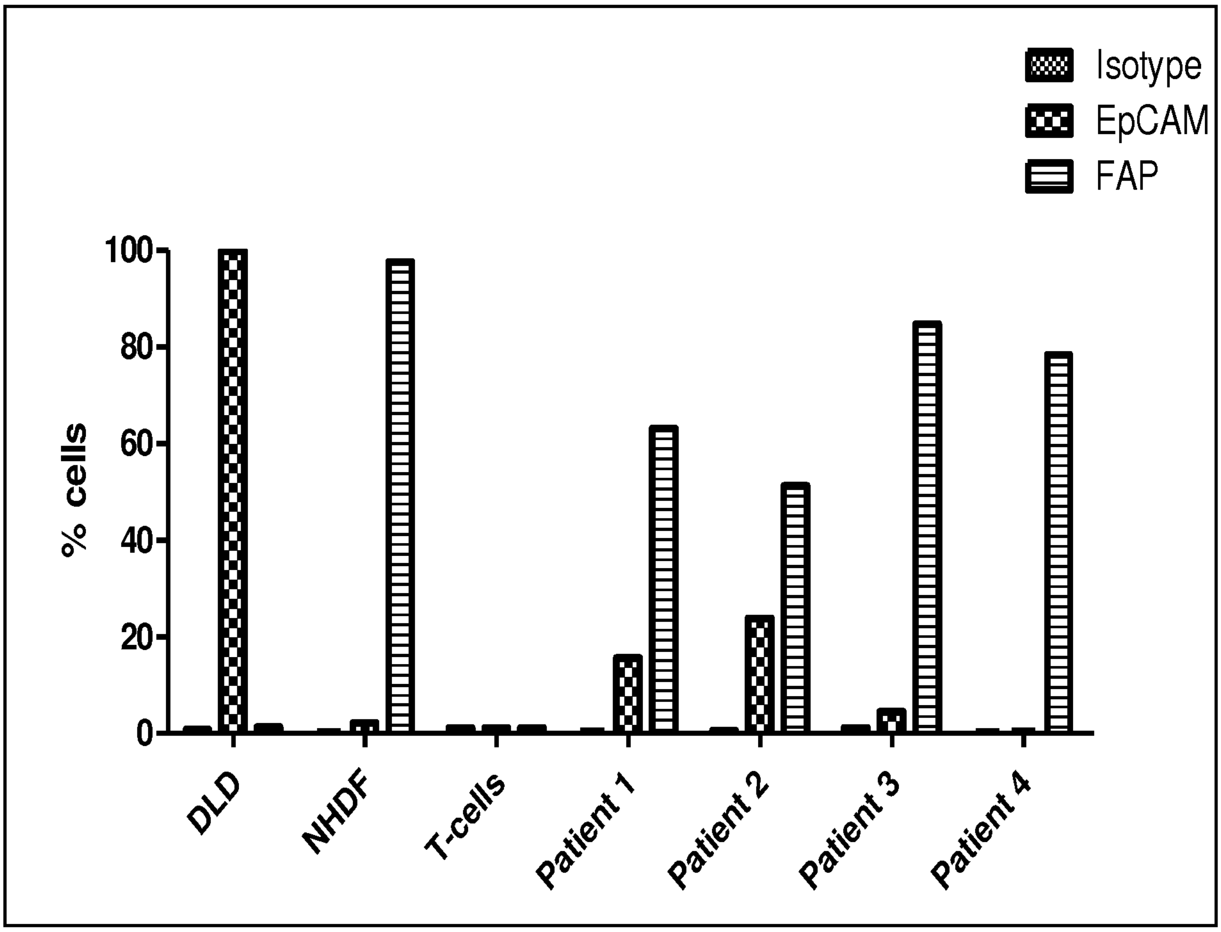


Figure 17A

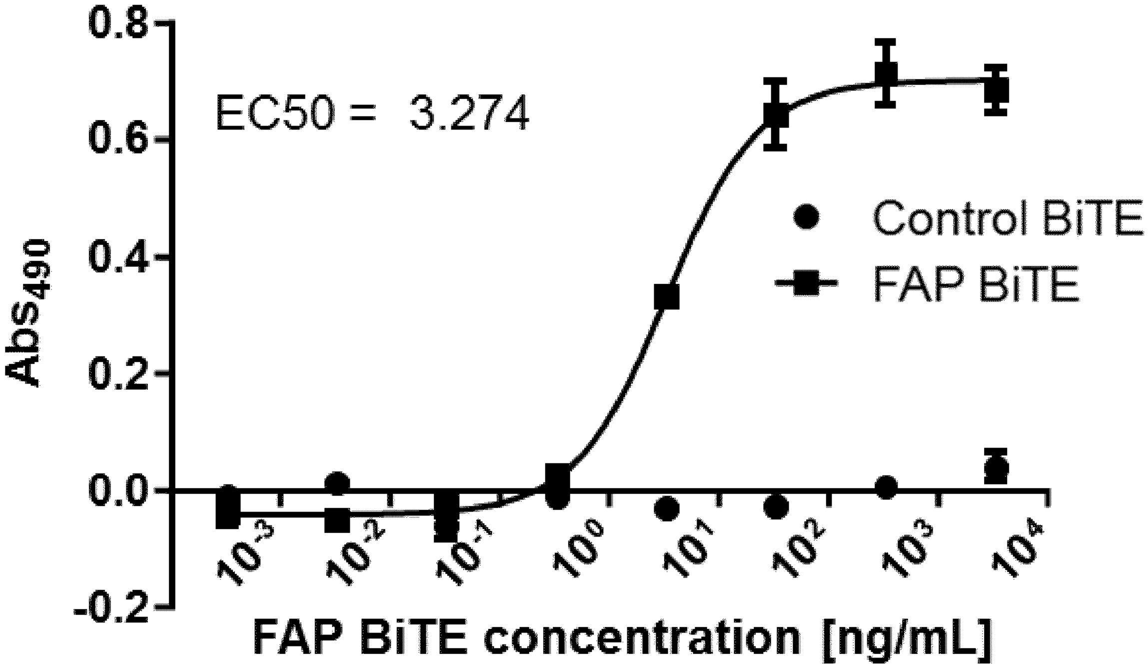


Figure 17B

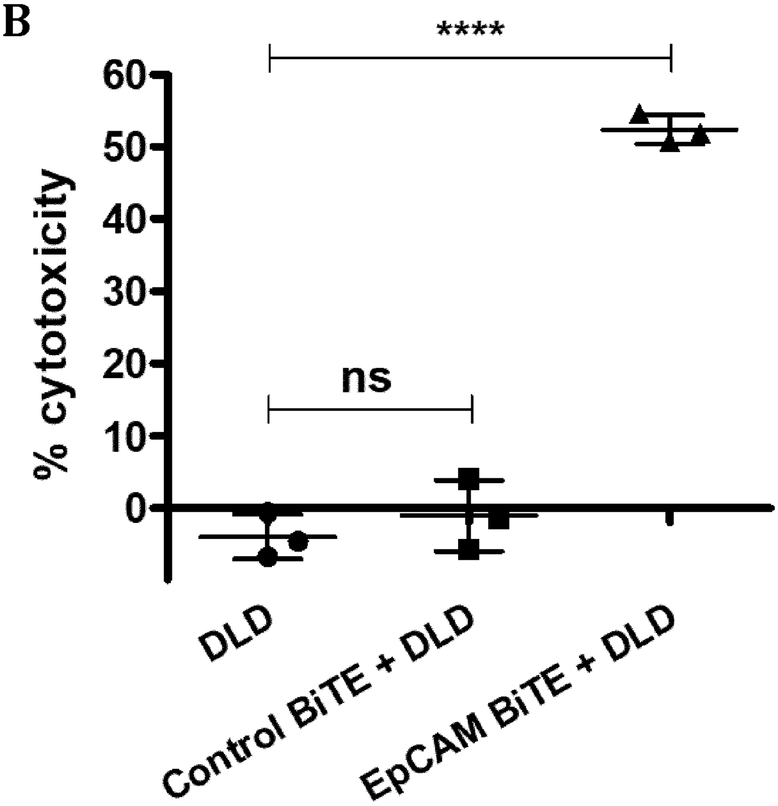
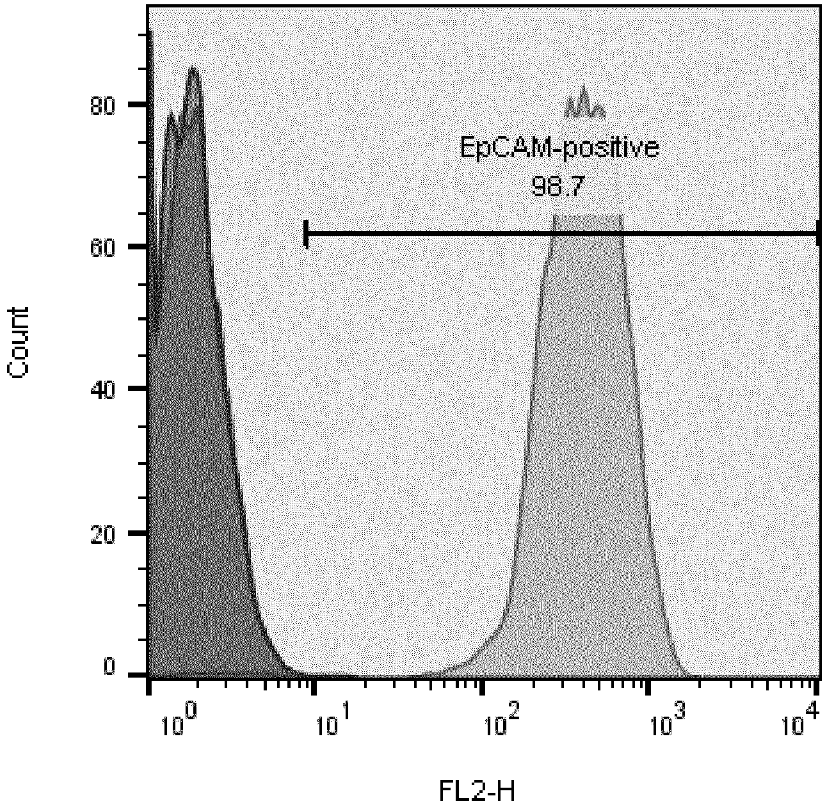


Figure 17C



	Sample Name	EpCAM-positive :: Freq. of Parent	Geometric Mean : FL2-H
■	[DLD unstained.021]	0.40	1.77
▨	[DLD iso.022]	0.36	1.81
□	[DLD ep.023]	98.7	361

Figure 18A

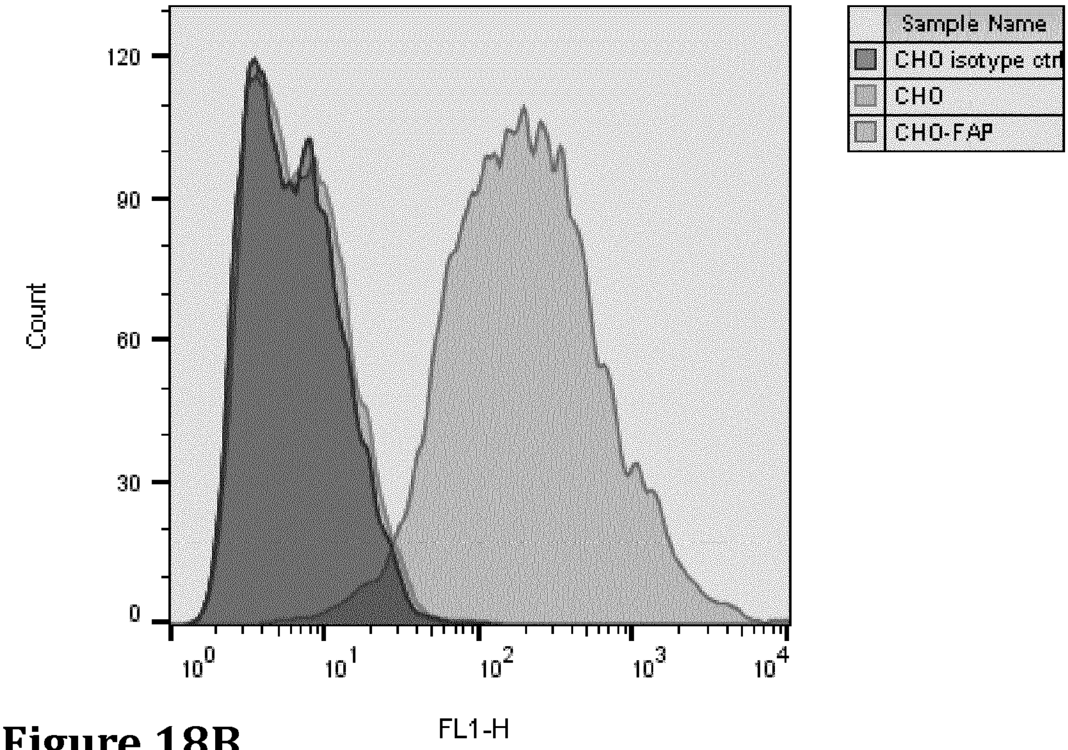


Figure 18B

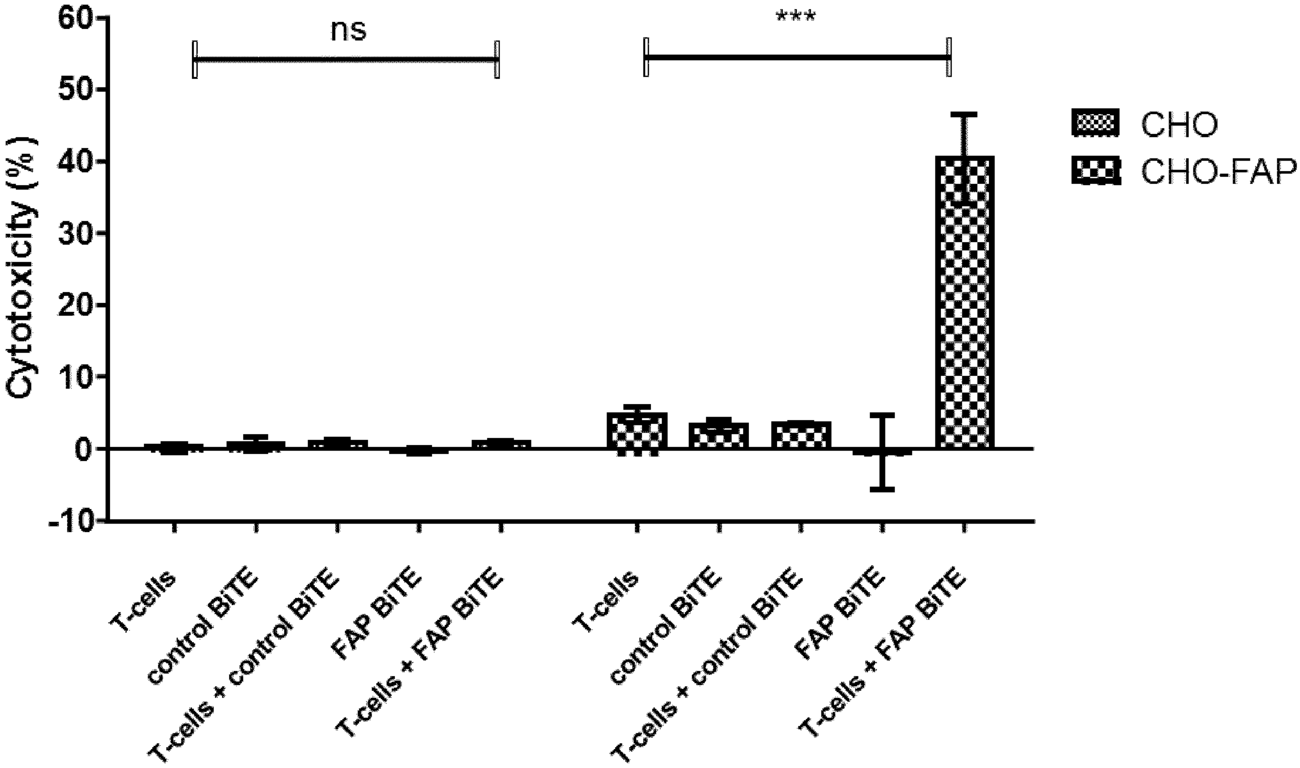


Figure 19

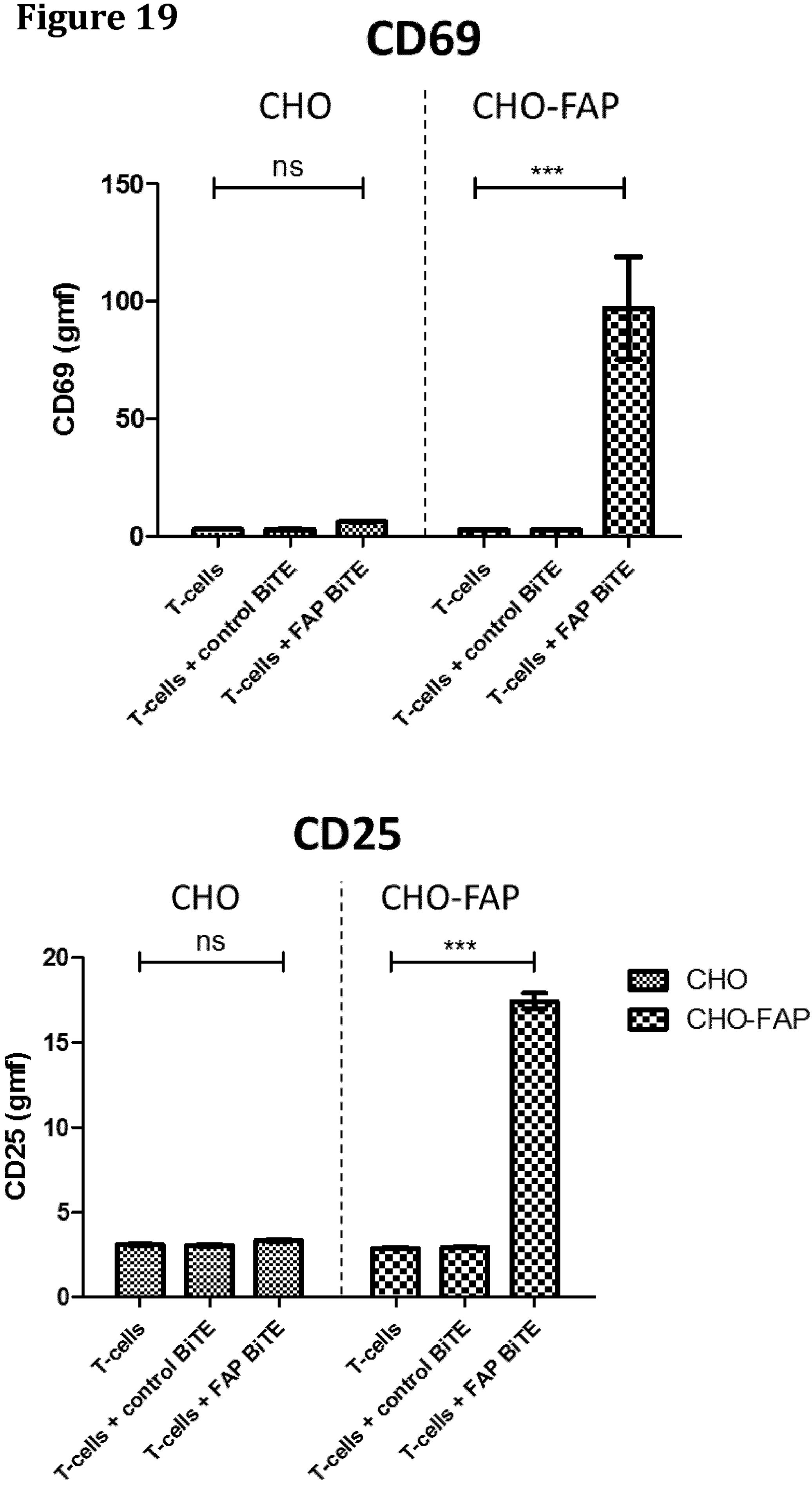

CD69
CHO
CHO-FAP
ns
***
150
100
50
0
CD69 (gmf)
T-cells
T-cells + control BiTE
T-cells + FAP BiTE
T-cells
T-cells + control BiTE
T-cells + FAP BiTE
CD25
CHO
CHO-FAP
ns
***
20
15
10
5
0
CD25 (gmf)
CHO
CHO-FAP
T-cells
T-cells + control BiTE
T-cells + FAP BiTE
T-cells
T-cells + control BiTE
T-cells + FAP BiTE

Figure 20

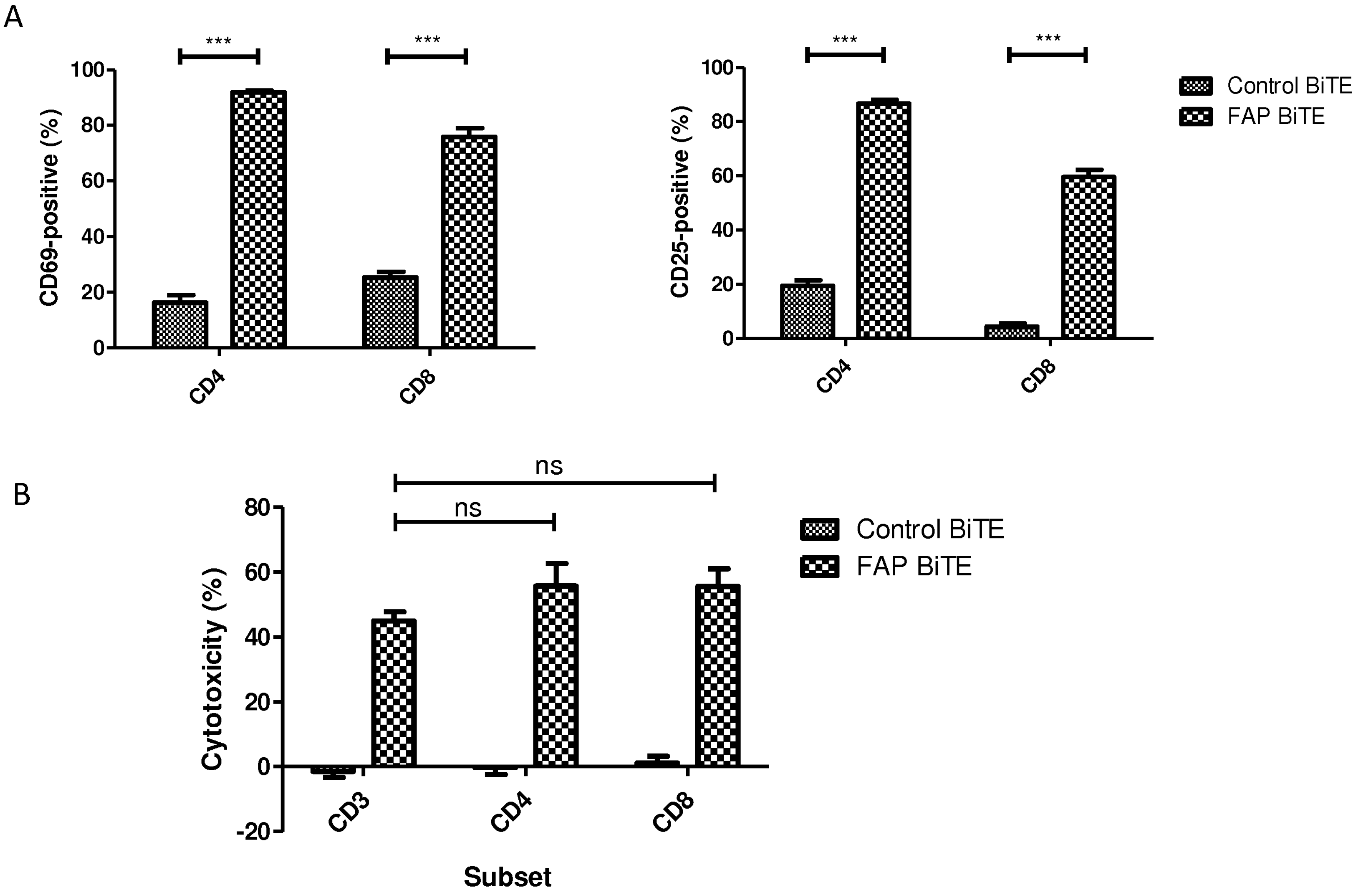

A
***
***
CD69-positive (%)
100
80
60
40
20
0
CD4
CD8
***
***
CD25-positive (%)
100
80
60
40
20
0
CD4
CD8
Control BiTE
FAP BiTE
B
ns
ns
Cytotoxicity (%)
80
60
40
20
0
-20
CD3
CD4
CD8
Subset
Control BiTE
FAP BiTE

Figure 21

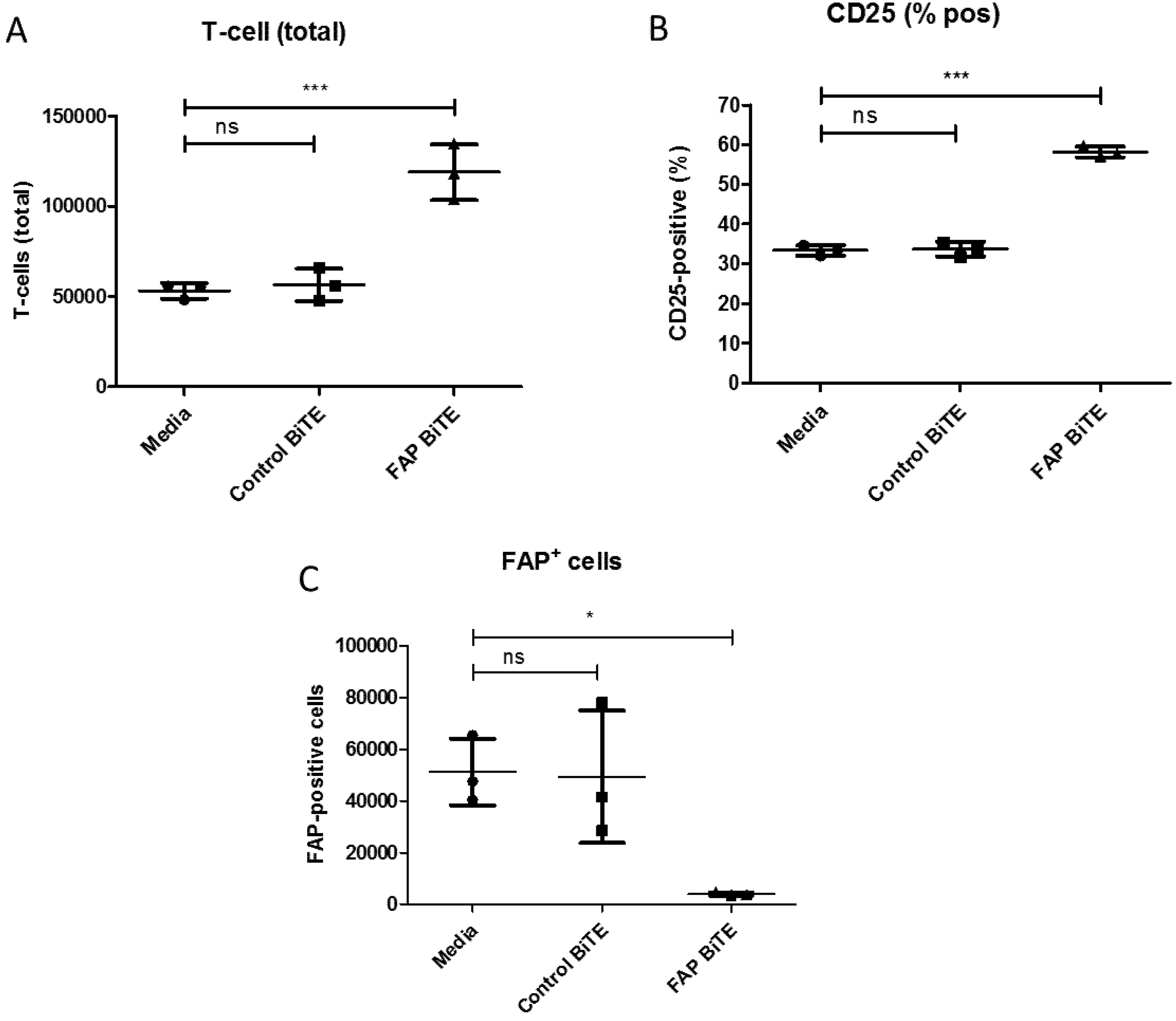

A
T-cell (total)
T-cells (total)
150000
100000
50000
0
ns
***
Media
Control BiTE
FAP BiTE
B
CD25 (% pos)
CD25-positive (%)
70
60
50
40
30
20
10
0
ns
***
Media
Control BiTE
FAP BiTE
C
FAP$^+$ cells
FAP-positive cells
100000
80000
60000
40000
20000
0
ns
*
Media
Control BiTE
FAP BiTE

Figure 22

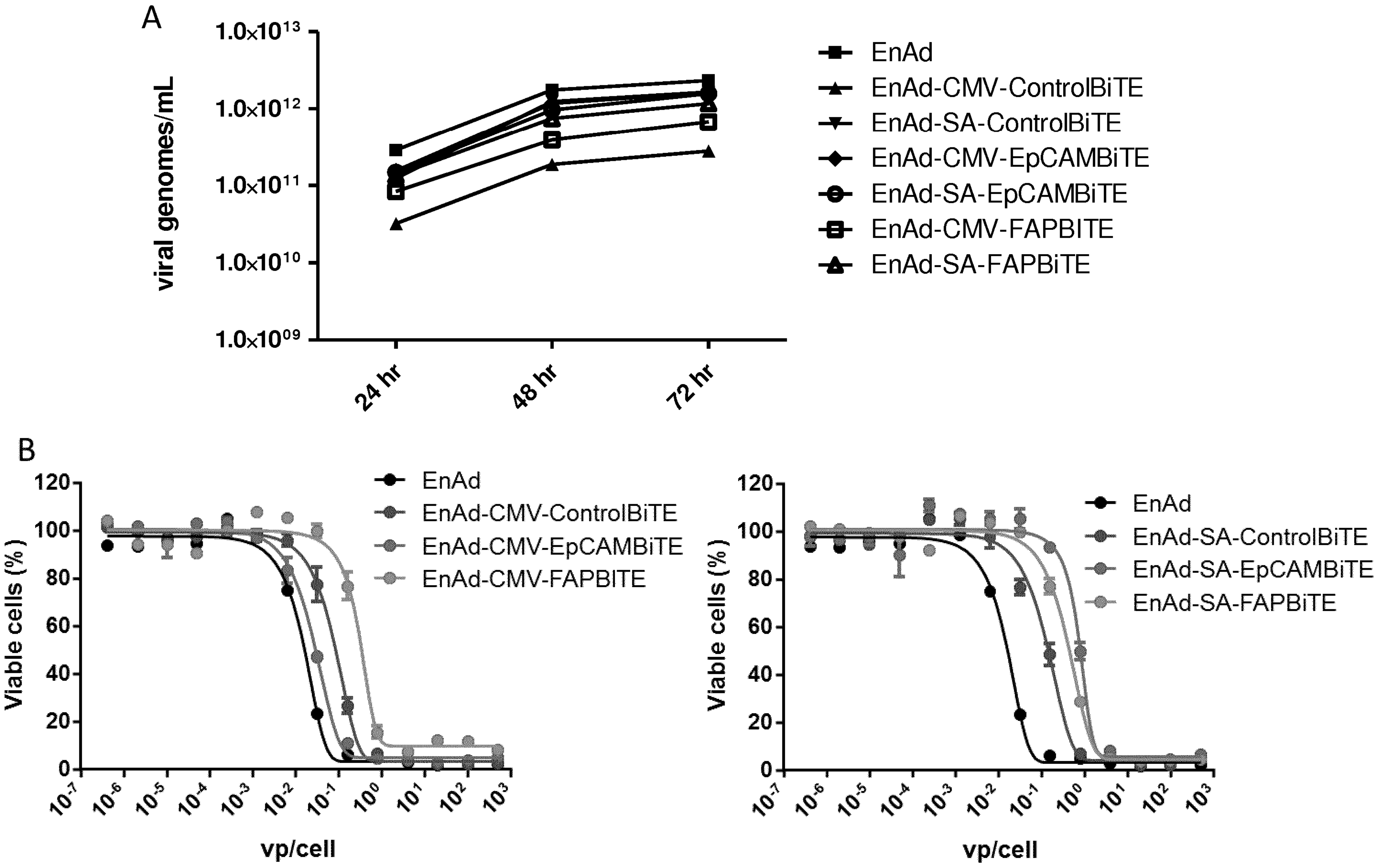
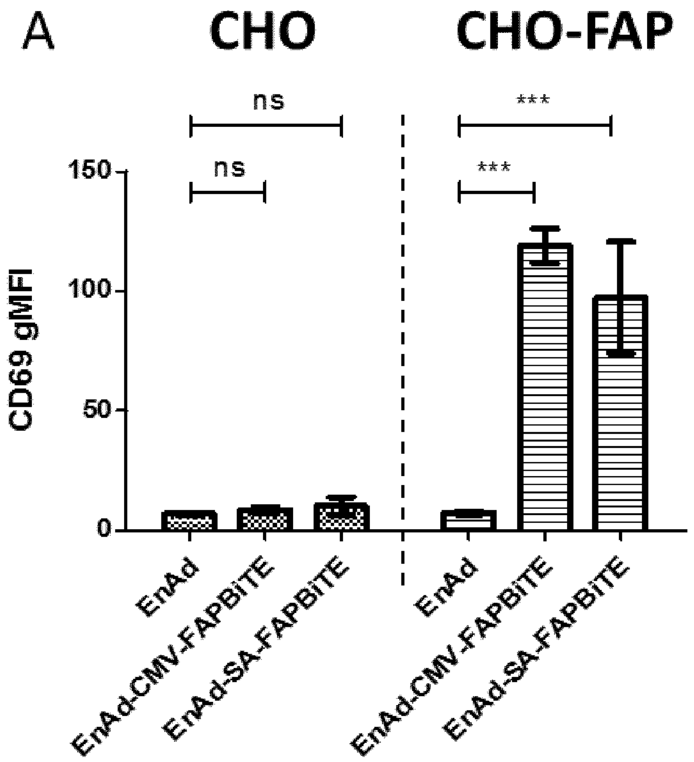

A
1.0×10¹³
1.0×10¹²
1.0×10¹¹
1.0×10¹⁰
1.0×10⁰⁹
viral genomes/mL
24 hr
48 hr
72 hr
EnAd
EnAd-CMV-ControlBiTE
EnAd-SA-ControlBiTE
EnAd-CMV-EpCAMBiTE
EnAd-SA-EpCAMBiTE
EnAd-CMV-FAPBITE
EnAd-SA-FAPBiTE
B
Viable cells (%)
120
100
80
60
40
20
0
10⁻⁷
10⁻⁶
10⁻⁵
10⁻⁴
10⁻³
10⁻²
10⁻¹
10⁰
10¹
10²
10³
vp/cell
EnAd
EnAd-CMV-ControlBiTE
EnAd-CMV-EpCAMBiTE
EnAd-CMV-FAPBITE
Viable cells (%)
vp/cell
EnAd
EnAd-SA-ControlBiTE
EnAd-SA-EpCAMBiTE
EnAd-SA-FAPBiTE

Figure 23A


A
CHO
CHO-FAP
ns
ns
***
***
CD69 gMFI
150
100
50
0
EnAd
EnAd-CMV-FAPBiTE
EnAd-SA-FAPBiTE
EnAd
EnAd-CMV-FAPBiTE
EnAd-SA-FAPBiTE

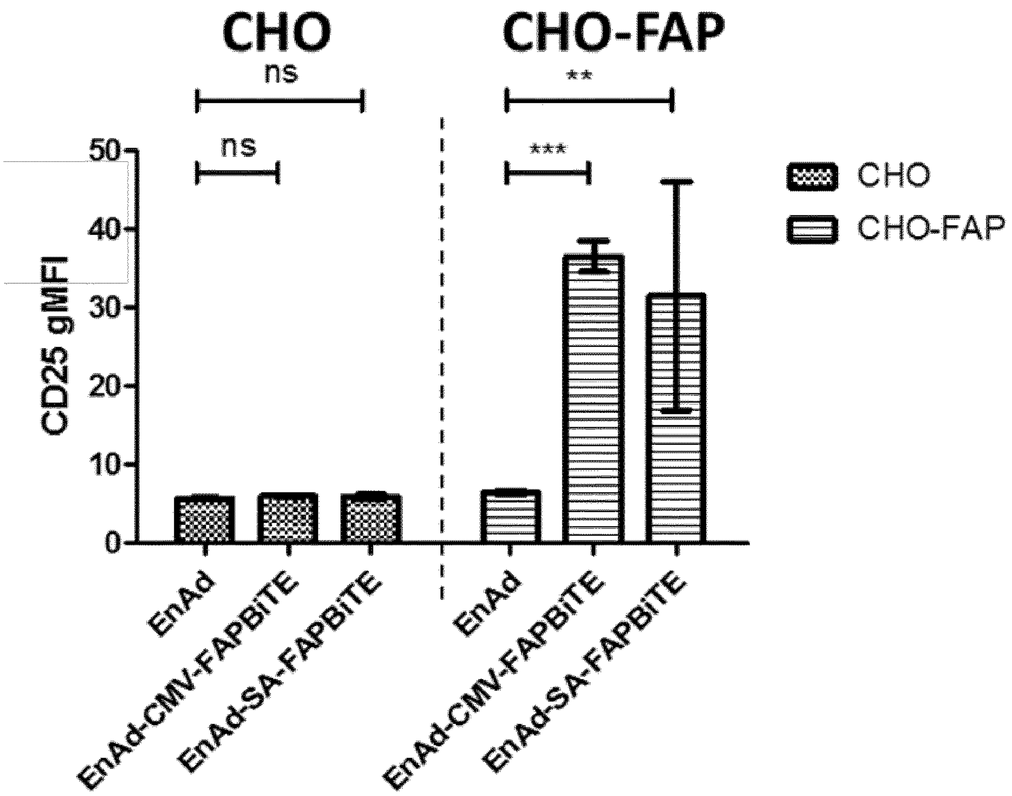

CHO
CHO-FAP
ns
ns
**
***
CD25 gMFI
50
40
30
20
10
0
EnAd
EnAd-CMV-FAPBiTE
EnAd-SA-FAPBiTE
EnAd
EnAd-CMV-FAPBiTE
EnAd-SA-FAPBiTE
CHO
CHO-FAP

Figure 23B

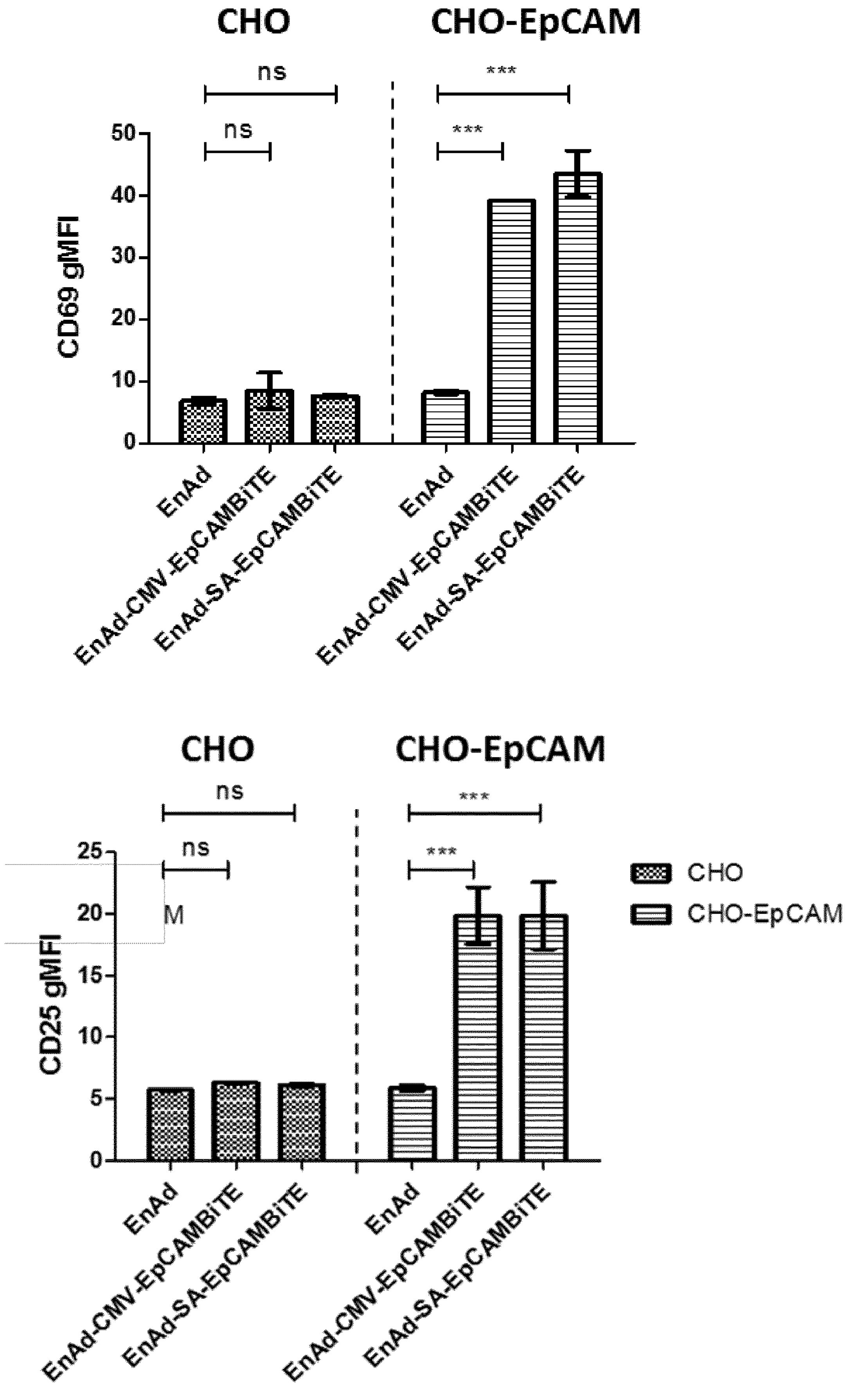
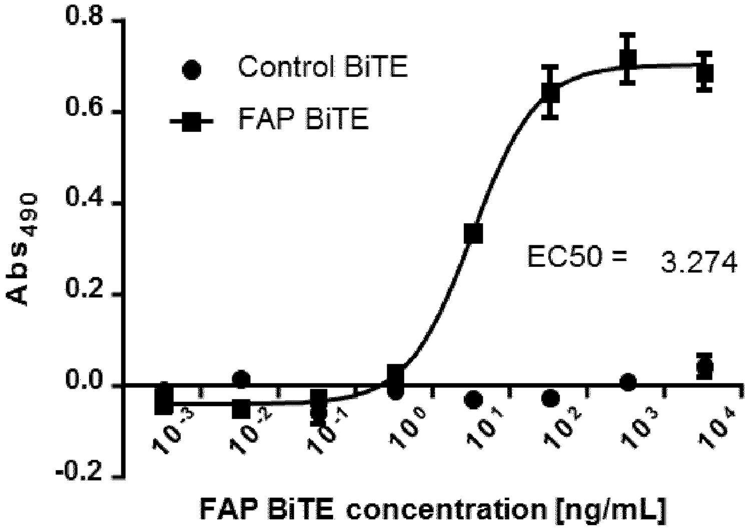
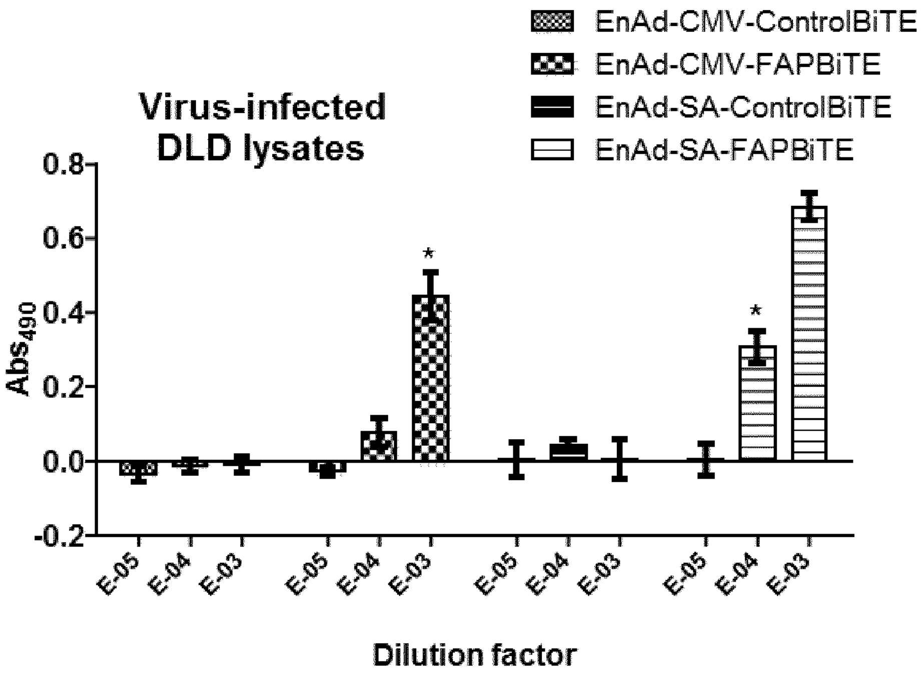

CHO
CHO-EpCAM
ns
ns
***
***
50
40
30
20
10
0
CD69 gMFI
EnAd
EnAd-CMV-EpCAMBiTE
EnAd-SA-EpCAMBiTE
EnAd
EnAd-CMV-EpCAMBiTE
EnAd-SA-EpCAMBiTE
CHO
CHO-EpCAM
ns
ns
***
***
25
20
15
10
5
0
M
CD25 gMFI
▩ CHO
▤ CHO-EpCAM
EnAd
EnAd-CMV-EpCAMBiTE
EnAd-SA-EpCAMBiTE
EnAd
EnAd-CMV-EpCAMBiTE
EnAd-SA-EpCAMBiTE

Figure 24


0.8
0.6
0.4
0.2
0.0
-0.2
Abs490
Control BiTE
FAP BiTE
EC50 = 3.274
10-3
10-2
10-1
100
101
102
103
104
FAP BiTE concentration [ng/mL]


EnAd-CMV-ControlBiTE
EnAd-CMV-FAPBiTE
EnAd-SA-ControlBiTE
EnAd-SA-FAPBiTE
Virus-infected DLD lysates
0.8
0.6
0.4
0.2
0.0
-0.2
Abs490
*
*
E-05
E-04
E-03
E-05
E-04
E-03
E-05
E-04
E-03
E-05
E-04
E-03
Dilution factor

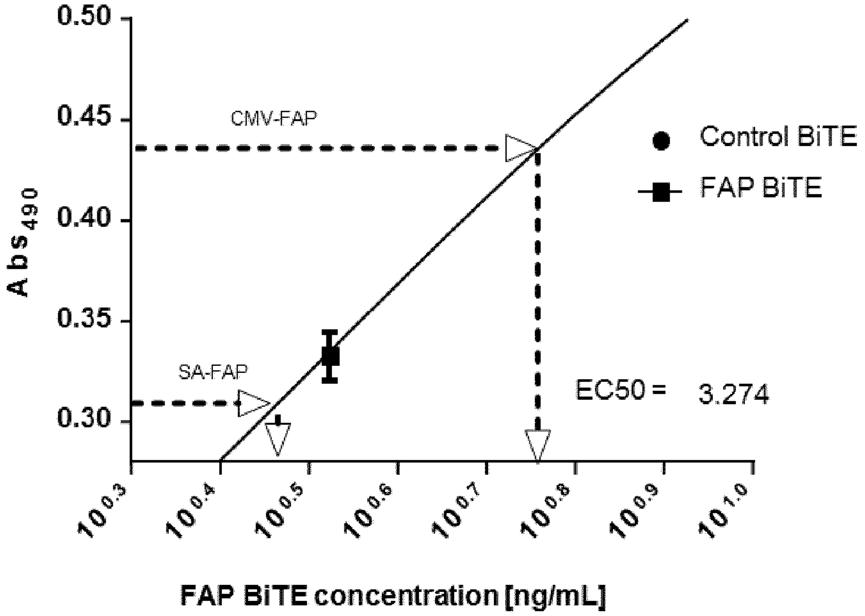

0.50
0.45
0.40
0.35
0.30
Abs490
CMV-FAP
SA-FAP
Control BiTE
FAP BiTE
EC50 = 3.274
100.3
100.4
100.5
100.6
100.7
100.8
100.9
101.0
FAP BiTE concentration [ng/mL]

Figure 25

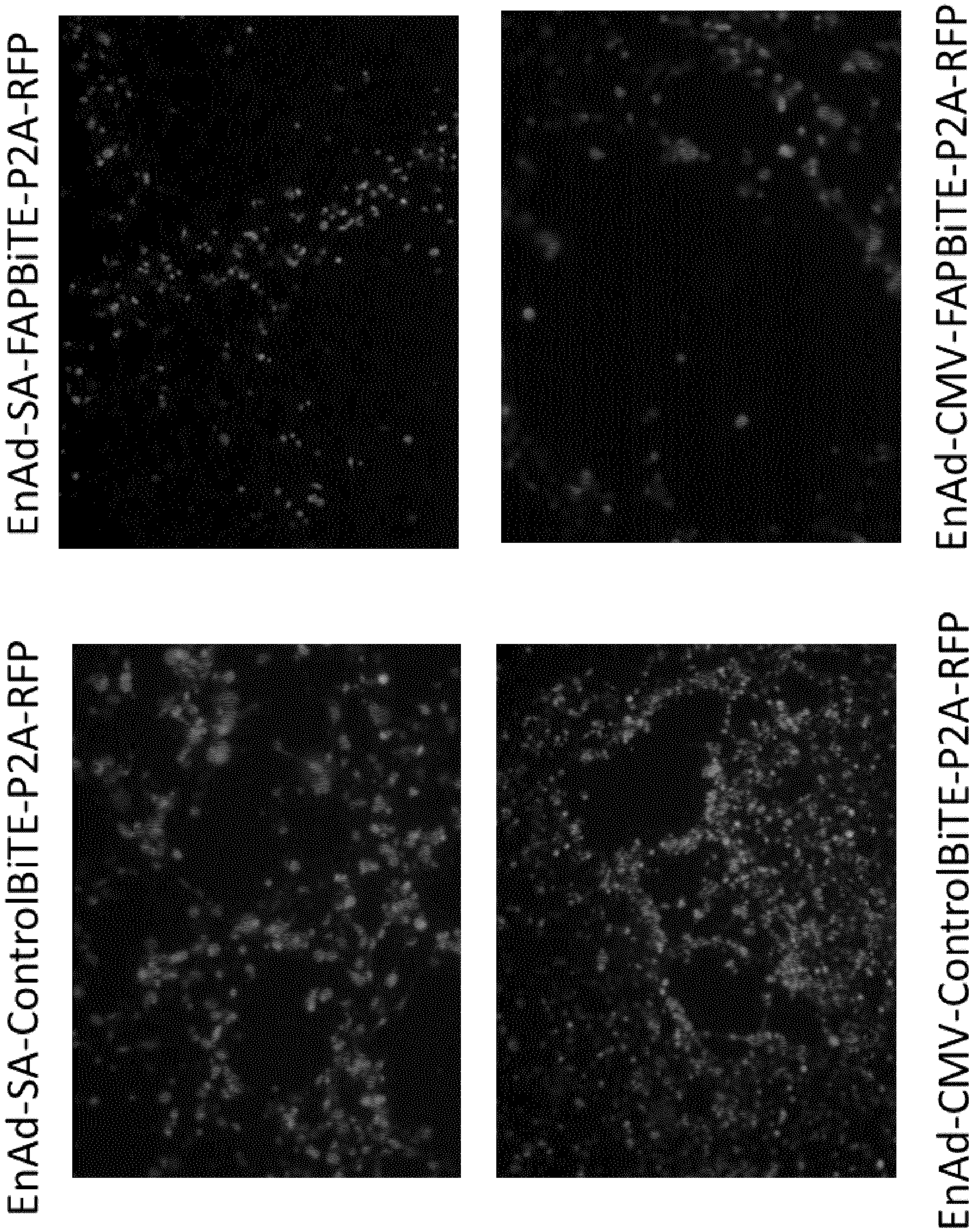

EnAd-SA-FAPBiTE-P2A-RFP
EnAd-CMV-FAPBiTE-P2A-RFP
EnAd-SA-ControlBiTE-P2A-RFP
EnAd-CMV-ControlBiTE-P2A-RFP

Figure 26A

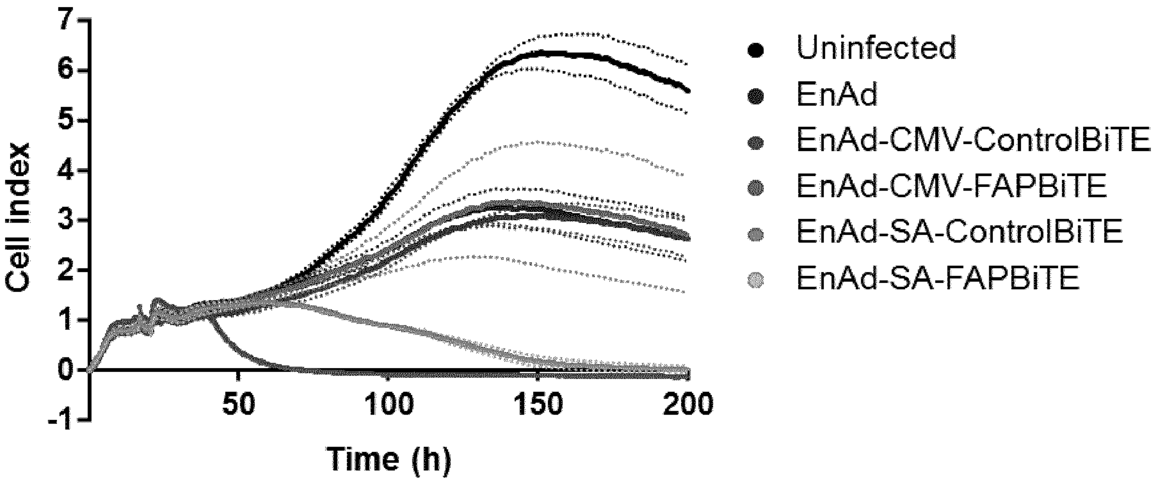


Figure 26B

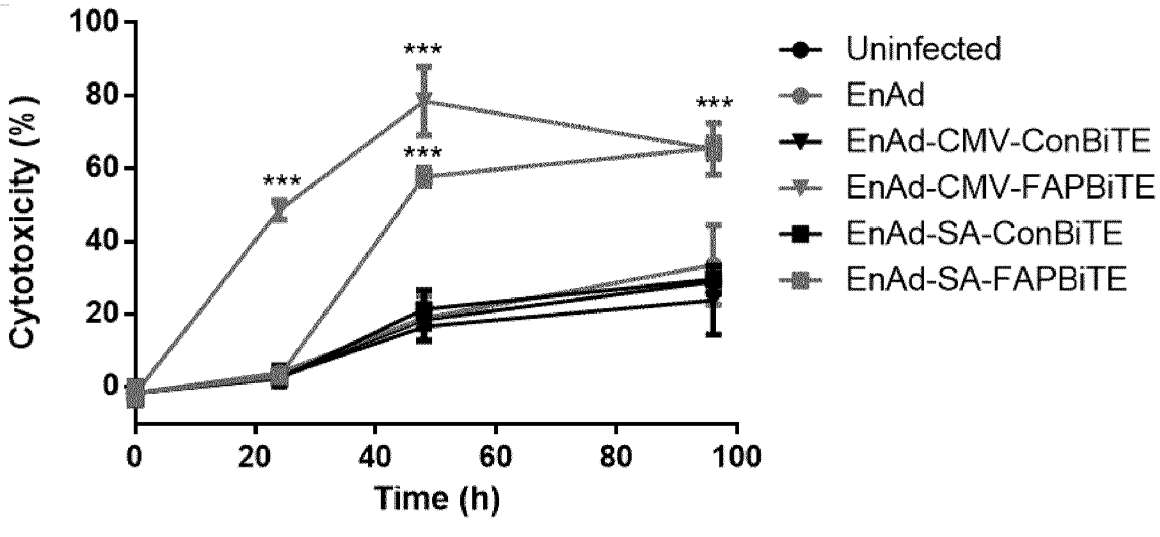


Figure 27

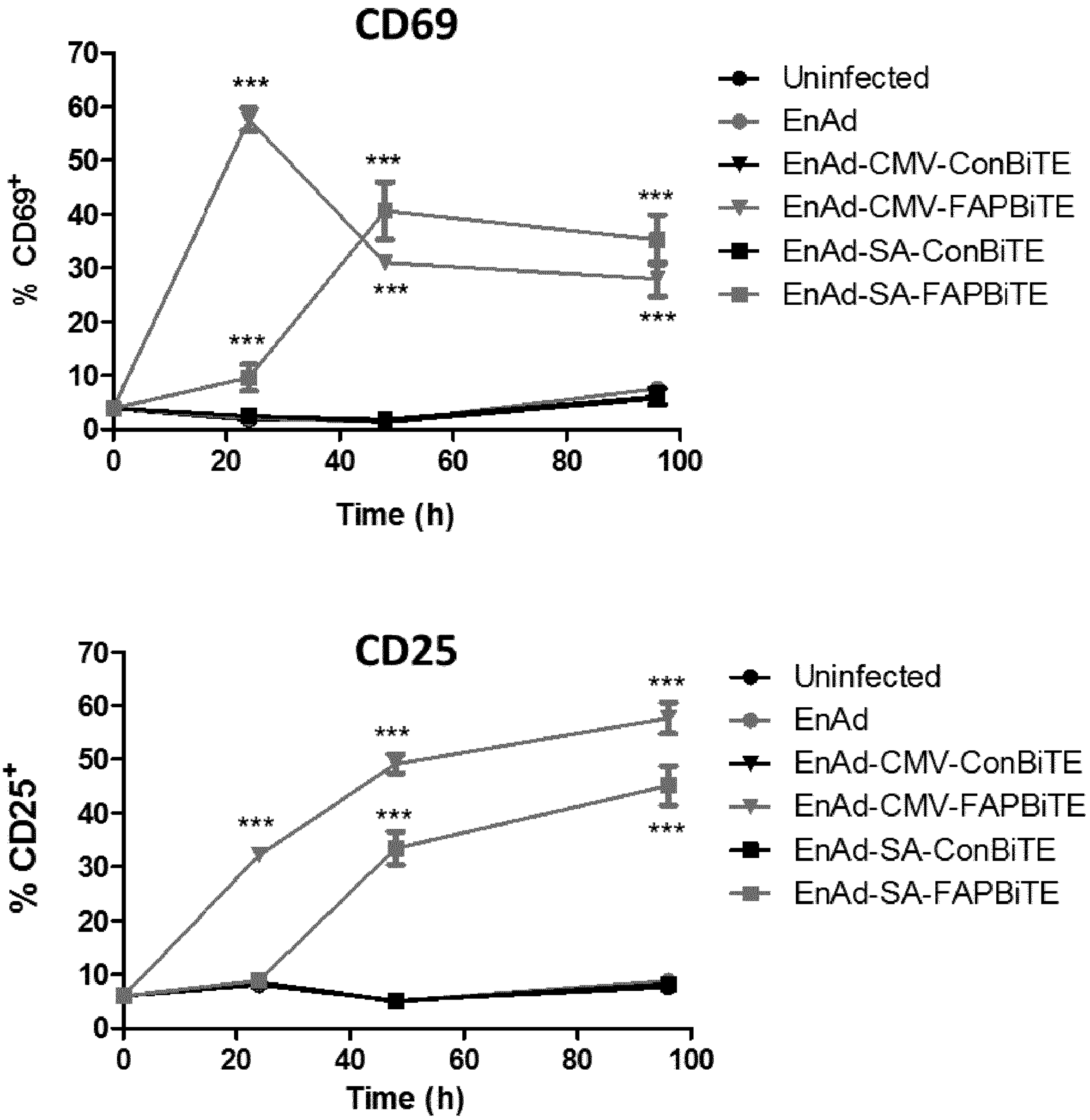

CD69
% CD69+
Time (h)
0
10
20
30
40
50
60
70
0
20
40
60
80
100
***
Uninfected
EnAd
EnAd-CMV-ConBiTE
EnAd-CMV-FAPBiTE
EnAd-SA-ConBiTE
EnAd-SA-FAPBiTE
CD25
% CD25+
Time (h)

Figure 28

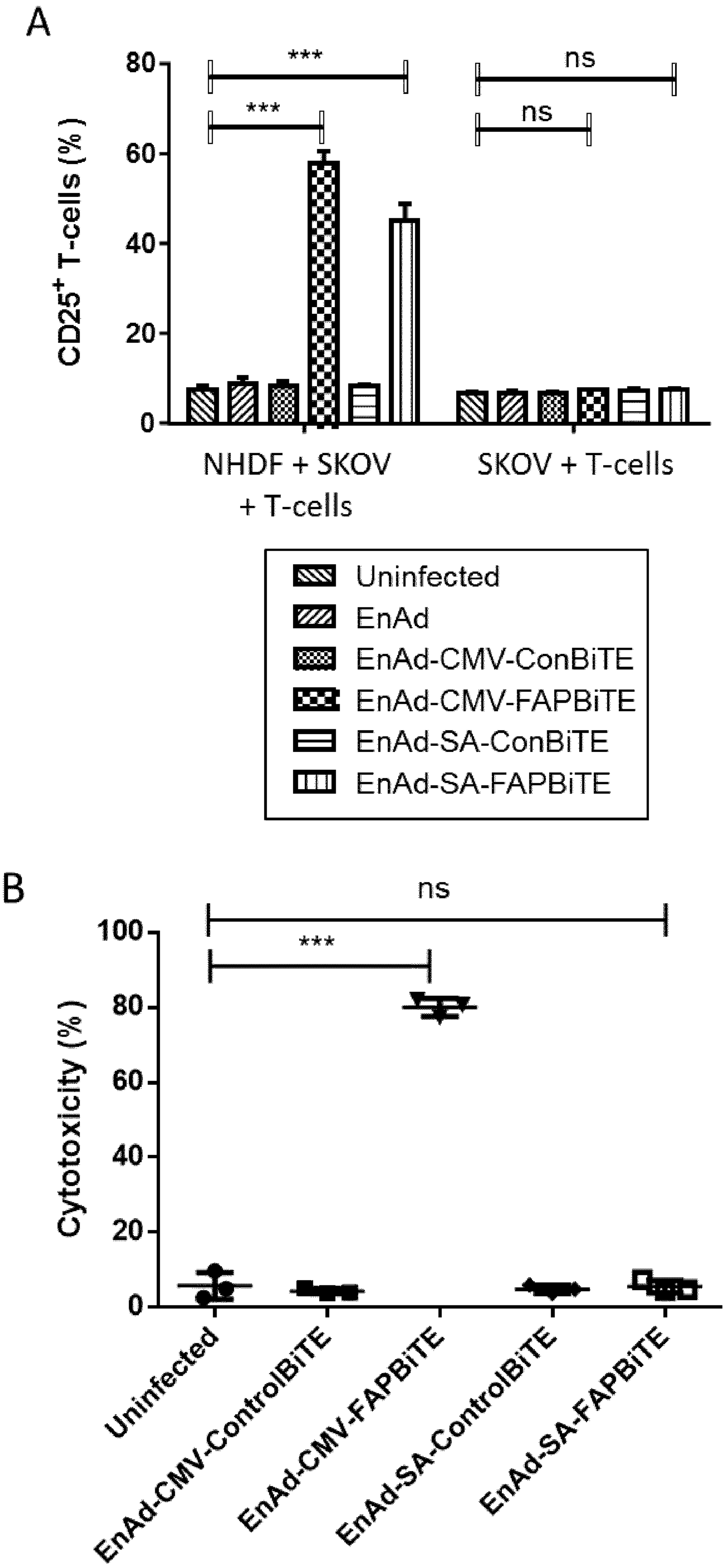
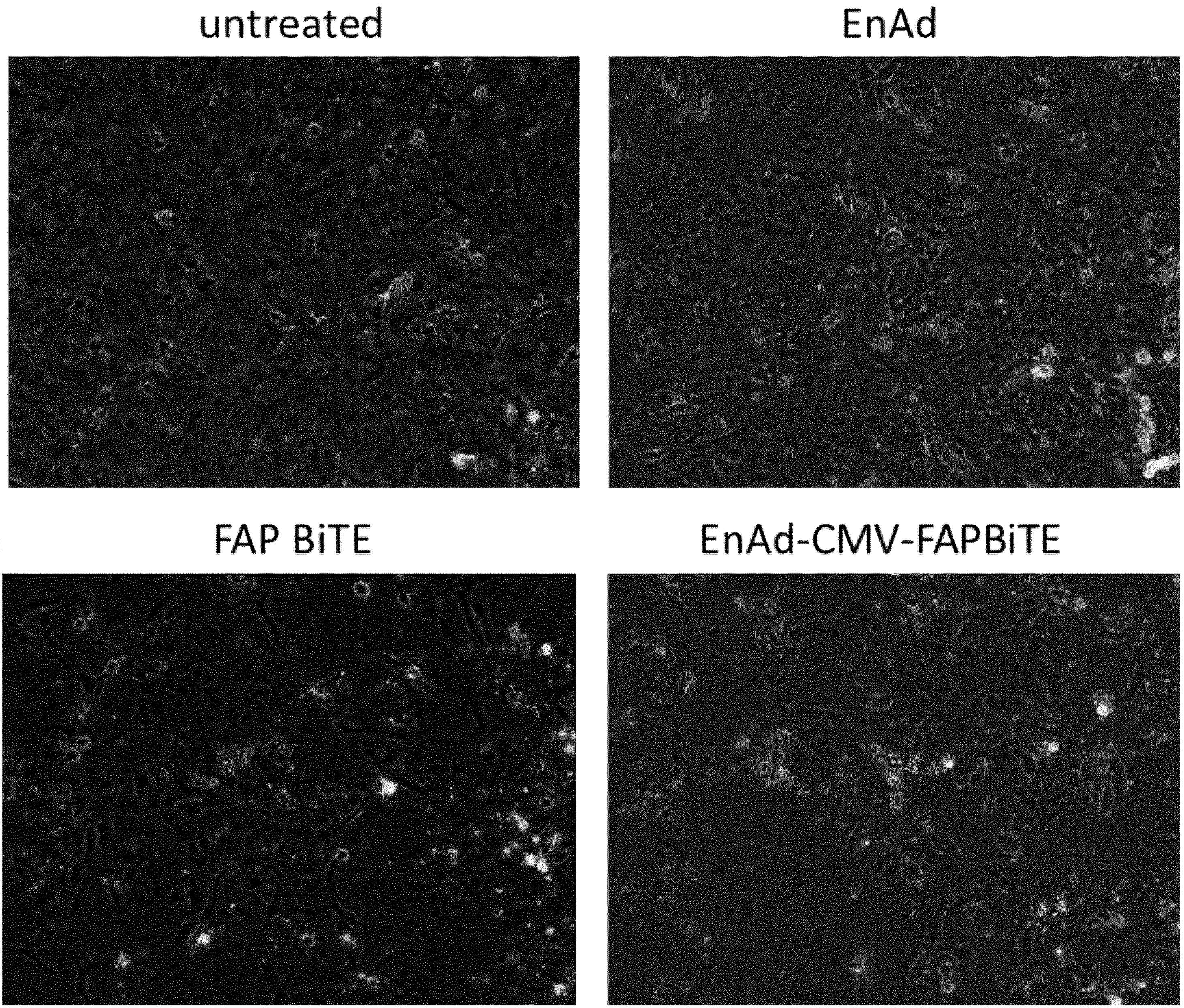
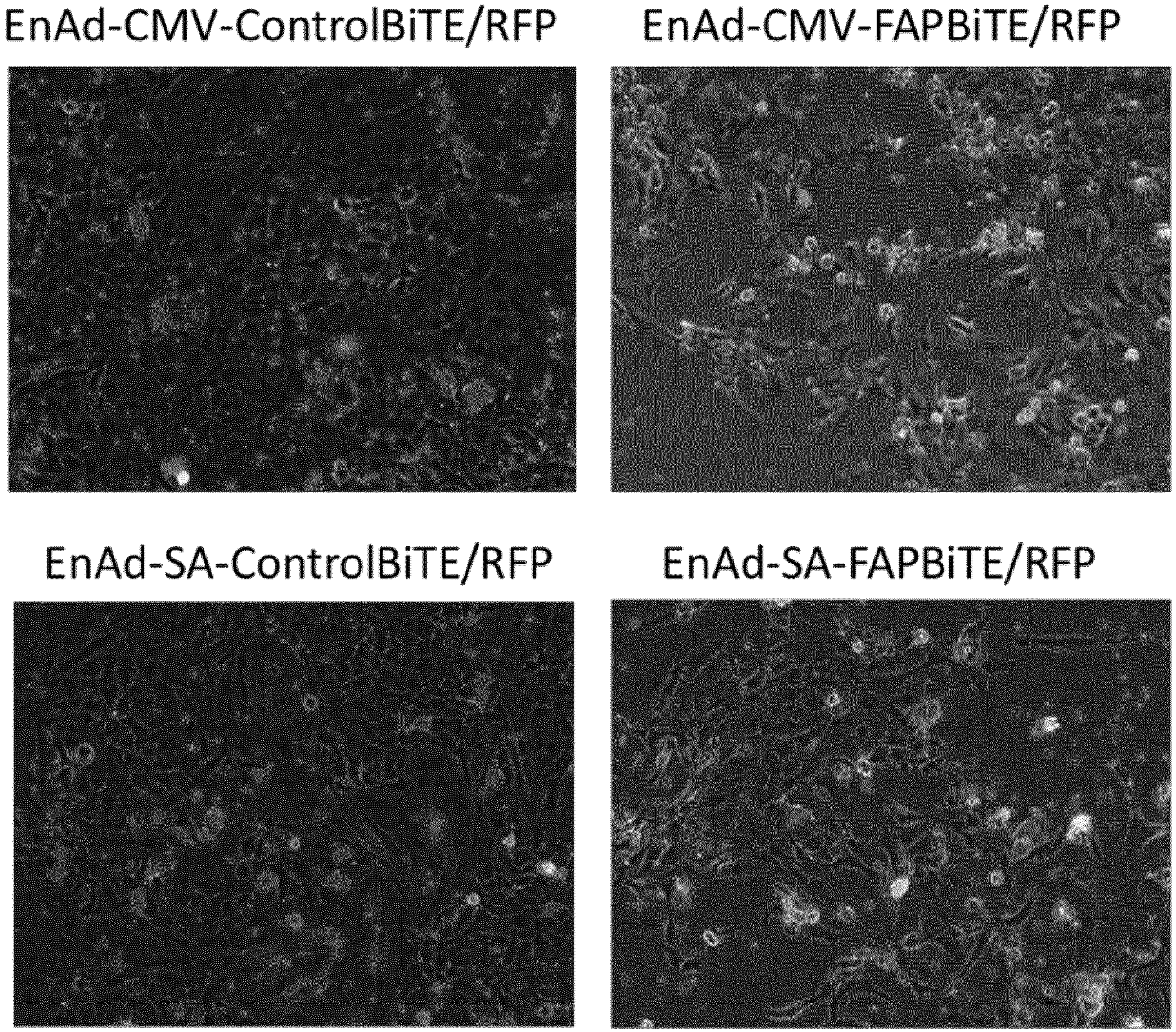

A
CD25⁺ T-cells (%)
80
60
40
20
0
***
***
ns
ns
NHDF + SKOV + T-cells
SKOV + T-cells
Uninfected
EnAd
EnAd-CMV-ConBiTE
EnAd-CMV-FAPBiTE
EnAd-SA-ConBiTE
EnAd-SA-FAPBiTE
B
Cytotoxicity (%)
100
80
60
40
20
0
ns
***
Uninfected
EnAd-CMV-ControlBiTE
EnAd-CMV-FAPBiTE
EnAd-SA-ControlBiTE
EnAd-SA-FAPBiTE

Figure 29



- SKOV (unstained)
- NHDF (red)
- caspase stain (green)
- Virus – 100 vp/cell

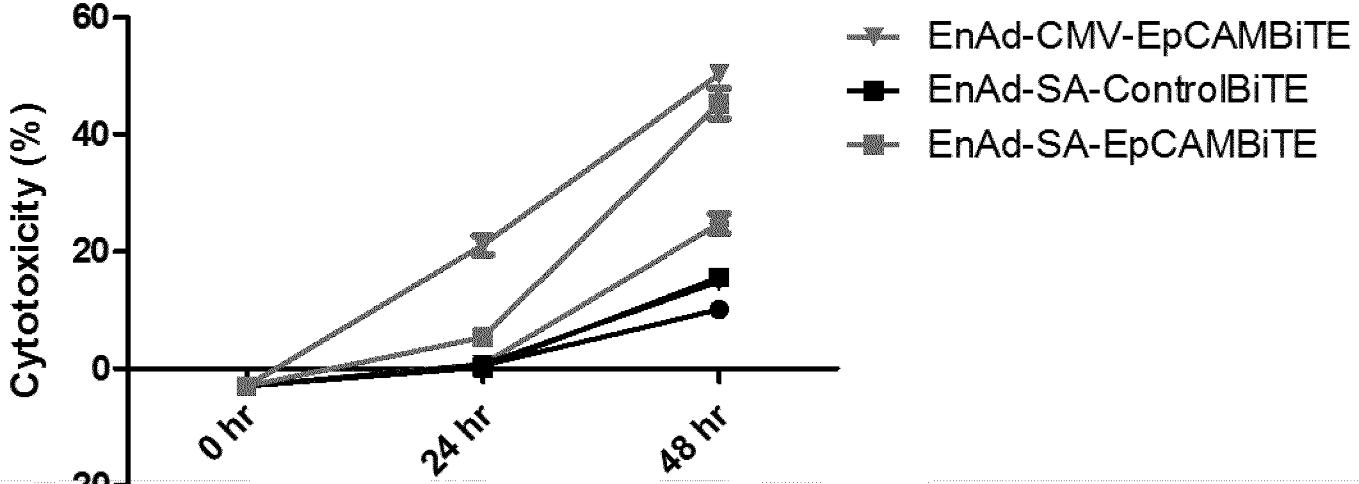
Figure 30



- SKOV (unstained)
- NHDF (green)
- RFP virus (red) – MOI of 1 for CMV, 10 for SA

Figure 31

With T-cells added



No T-cells added

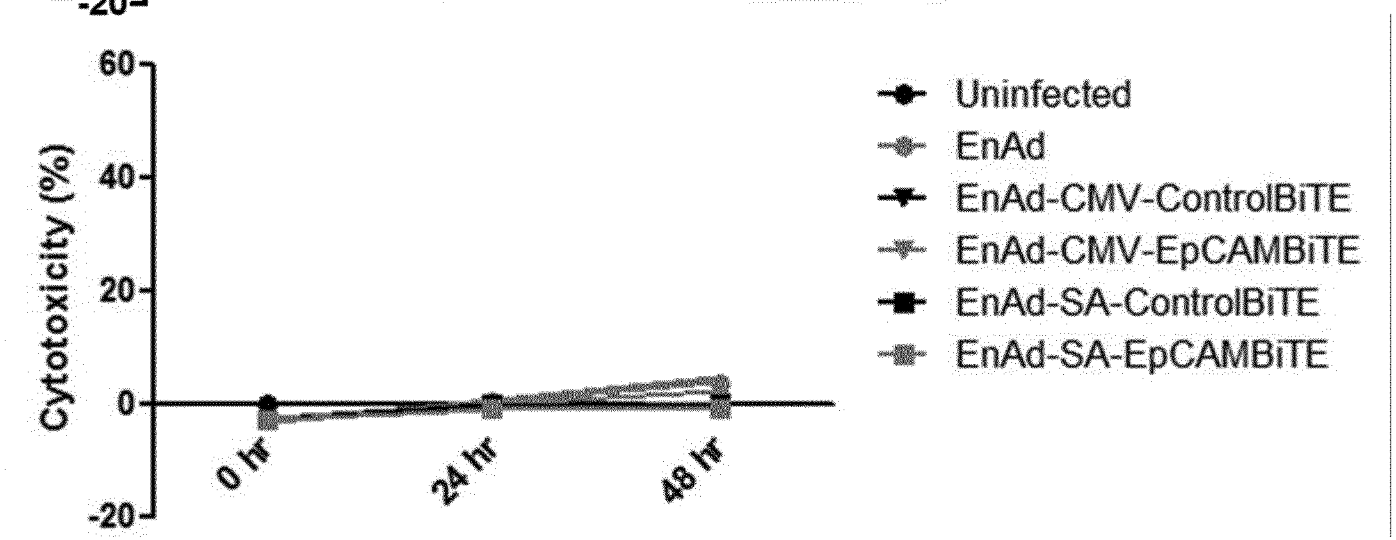
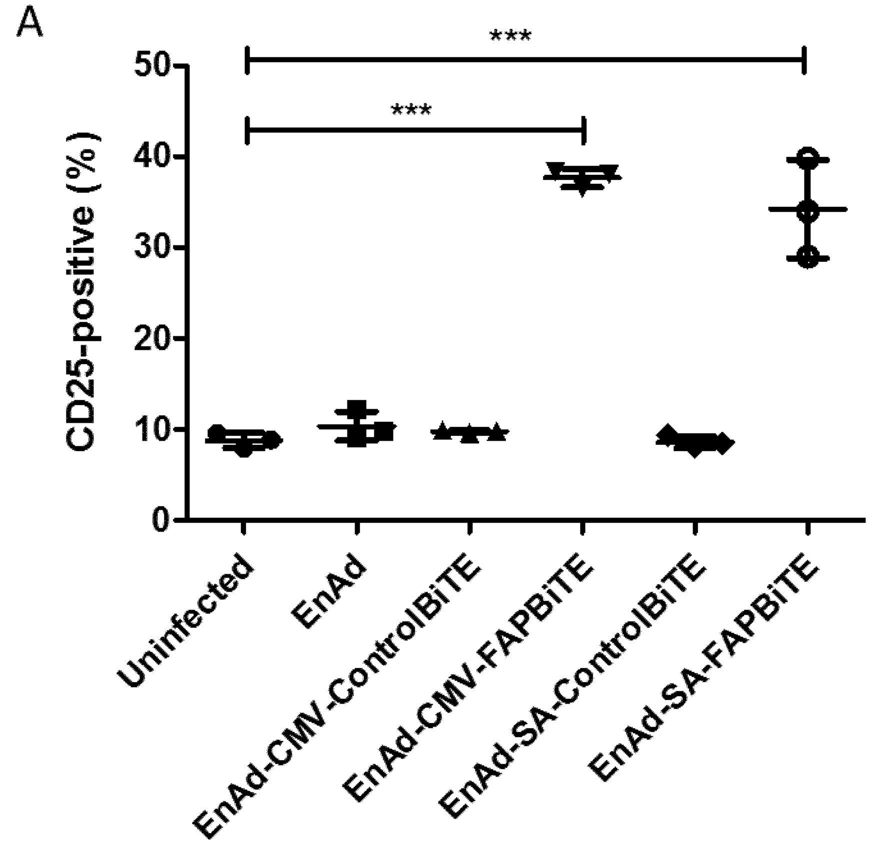


Figure 32


A
***
***
CD25-positive (%)
50
40
30
20
10
0
Uninfected
EnAd
EnAd-CMV-ControlBiTE
EnAd-CMV-FAPBiTE
EnAd-SA-ControlBiTE
EnAd-SA-FAPBiTE

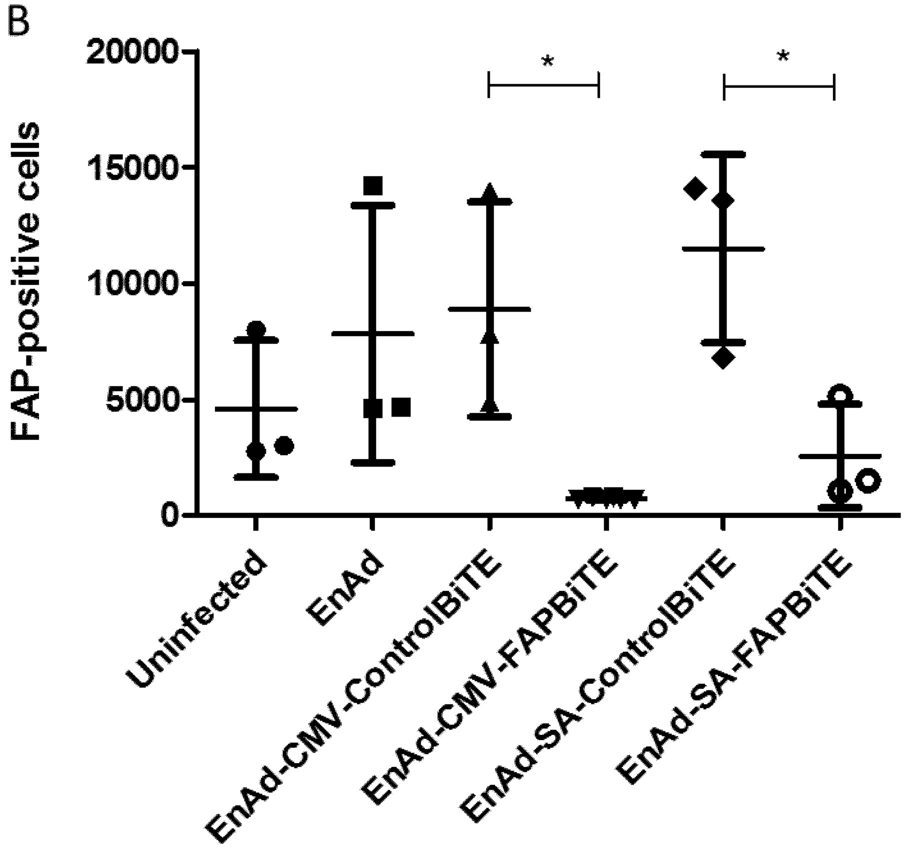
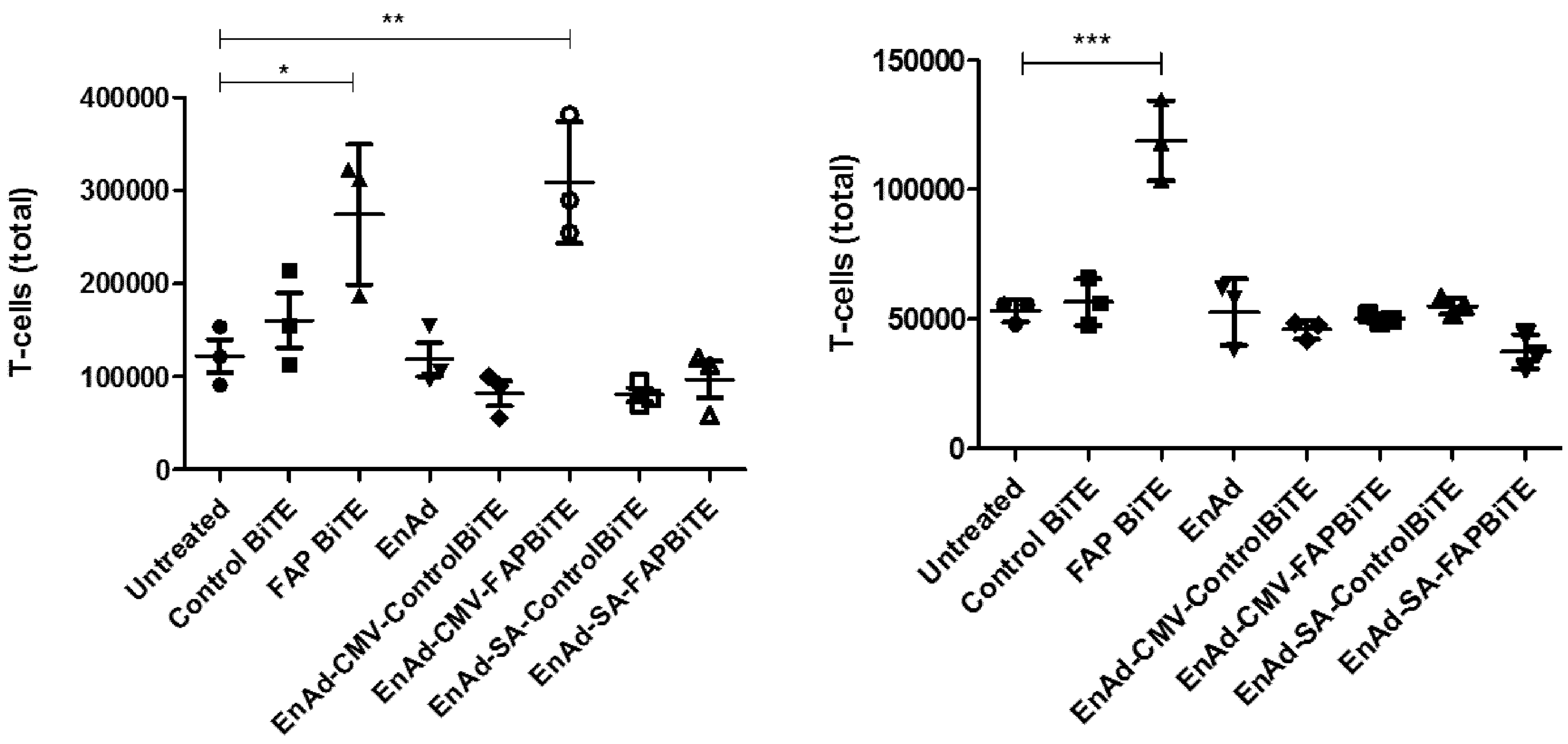

B
*
*
FAP-positive cells
20000
15000
10000
5000
0
Uninfected
EnAd
EnAd-CMV-ControlBiTE
EnAd-CMV-FAPBiTE
EnAd-SA-ControlBiTE
EnAd-SA-FAPBiTE

Figure 33



Media

Ascites fluid

Figure 34

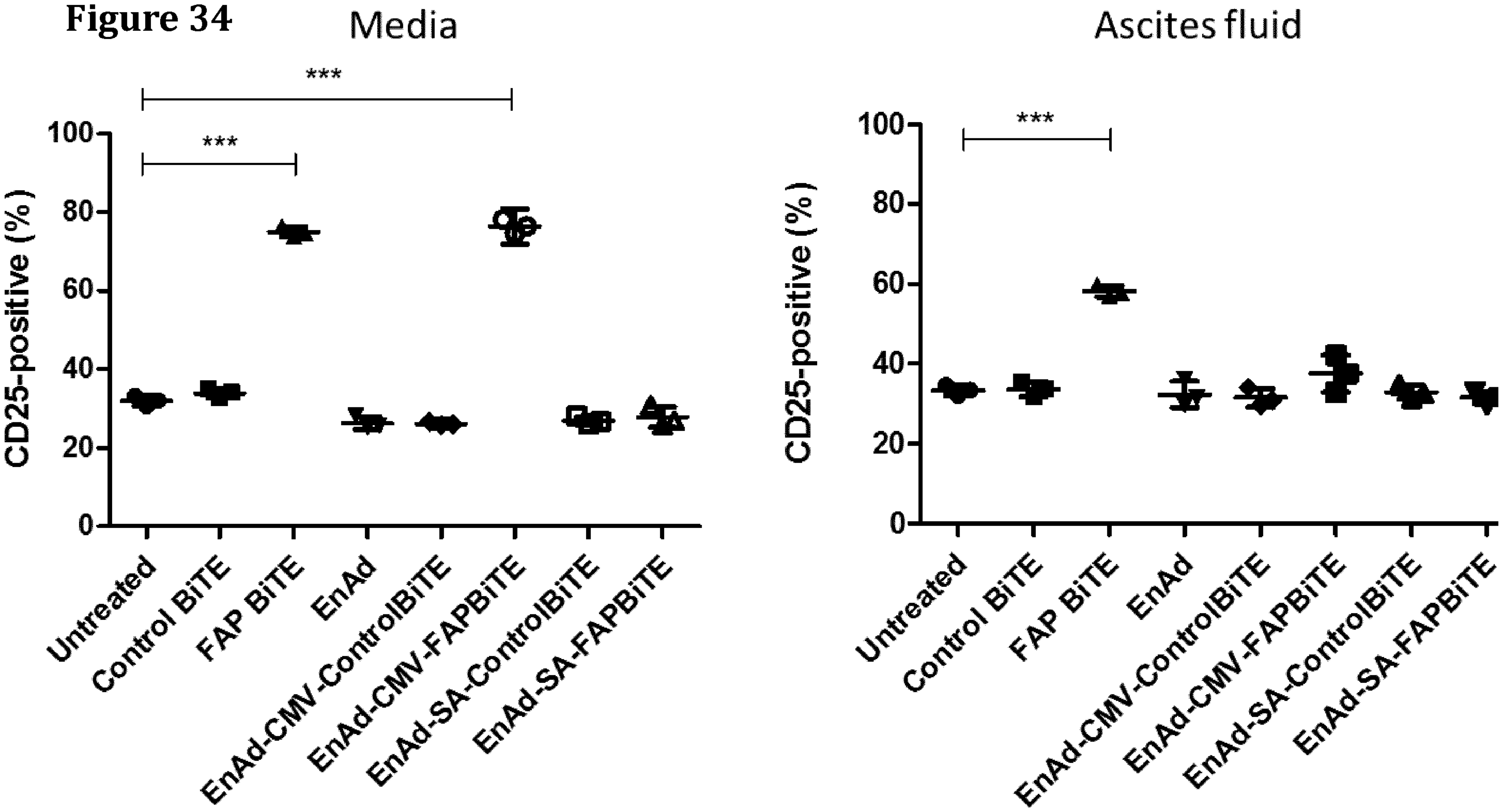

Media
***
***
CD25-positive (%)
100
80
60
40
20
0
Untreated
Control BiTE
FAP BiTE
EnAd
EnAd-CMV-ControlBiTE
EnAd-CMV-FAPBiTE
EnAd-SA-ControlBiTE
EnAd-SA-FAPBiTE
Ascites fluid
***
CD25-positive (%)
100
80
60
40
20
0
Untreated
Control BiTE
FAP BiTE
EnAd
EnAd-CMV-ControlBiTE
EnAd-CMV-FAPBiTE
EnAd-SA-ControlBiTE
EnAd-SA-FAPBiTE

Figure 35

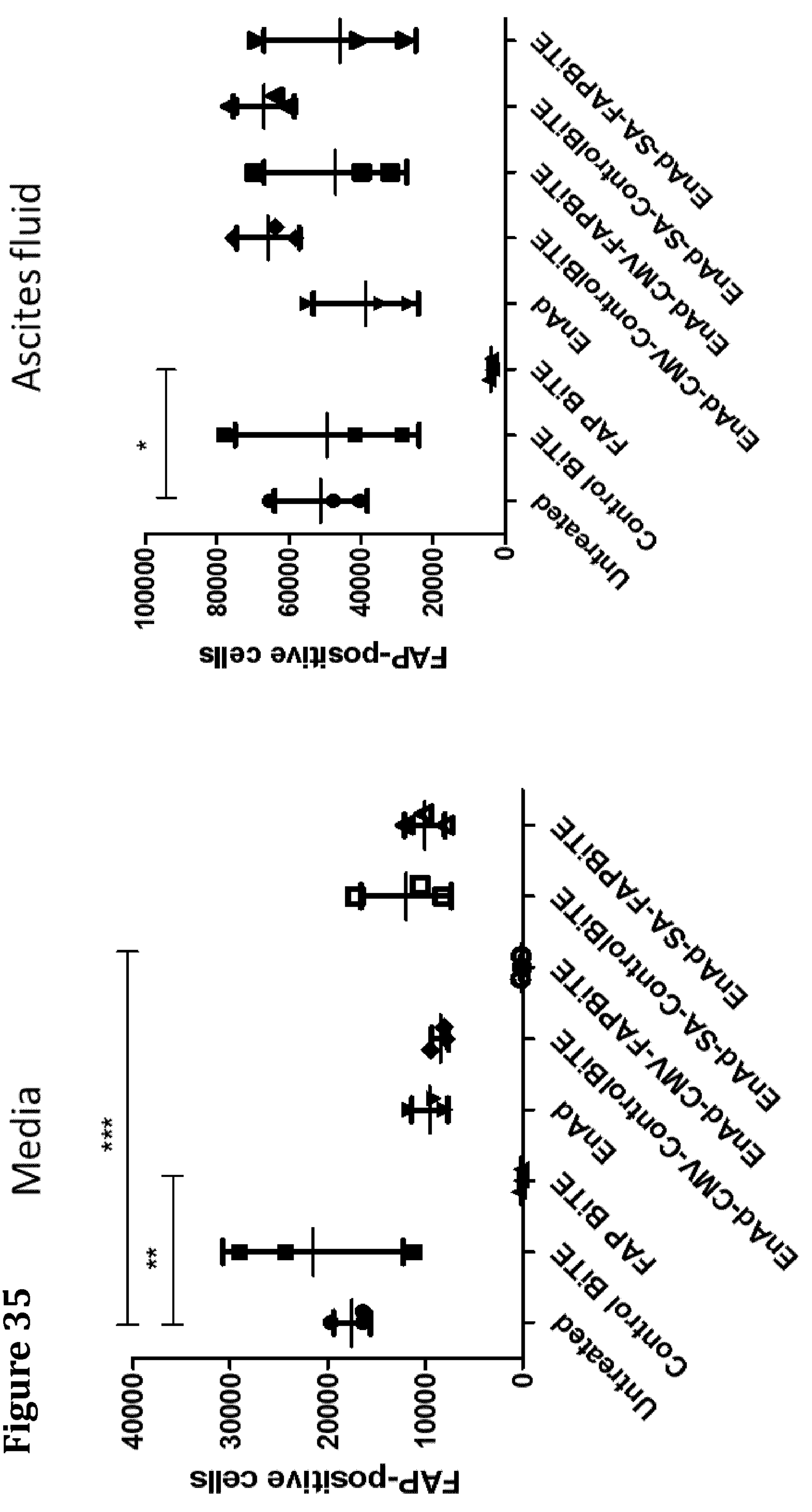

Media
FAP-positive cells
40000
30000
20000
10000
0
**
***
Untreated
Control BiTE
FAP BiTE
EnAd
EnAd-CMV-ControlBiTE
EnAd-CMV-FAPBiTE
EnAd-SA-ControlBiTE
EnAd-SA-FAPBiTE
Ascites fluid
FAP-positive cells
100000
80000
60000
40000
20000
0
*
Untreated
Control BiTE
FAP BiTE
EnAd
EnAd-CMV-ControlBiTE
EnAd-CMV-FAPBiTE
EnAd-SA-ControlBiTE
EnAd-SA-FAPBiTE

Figure 36

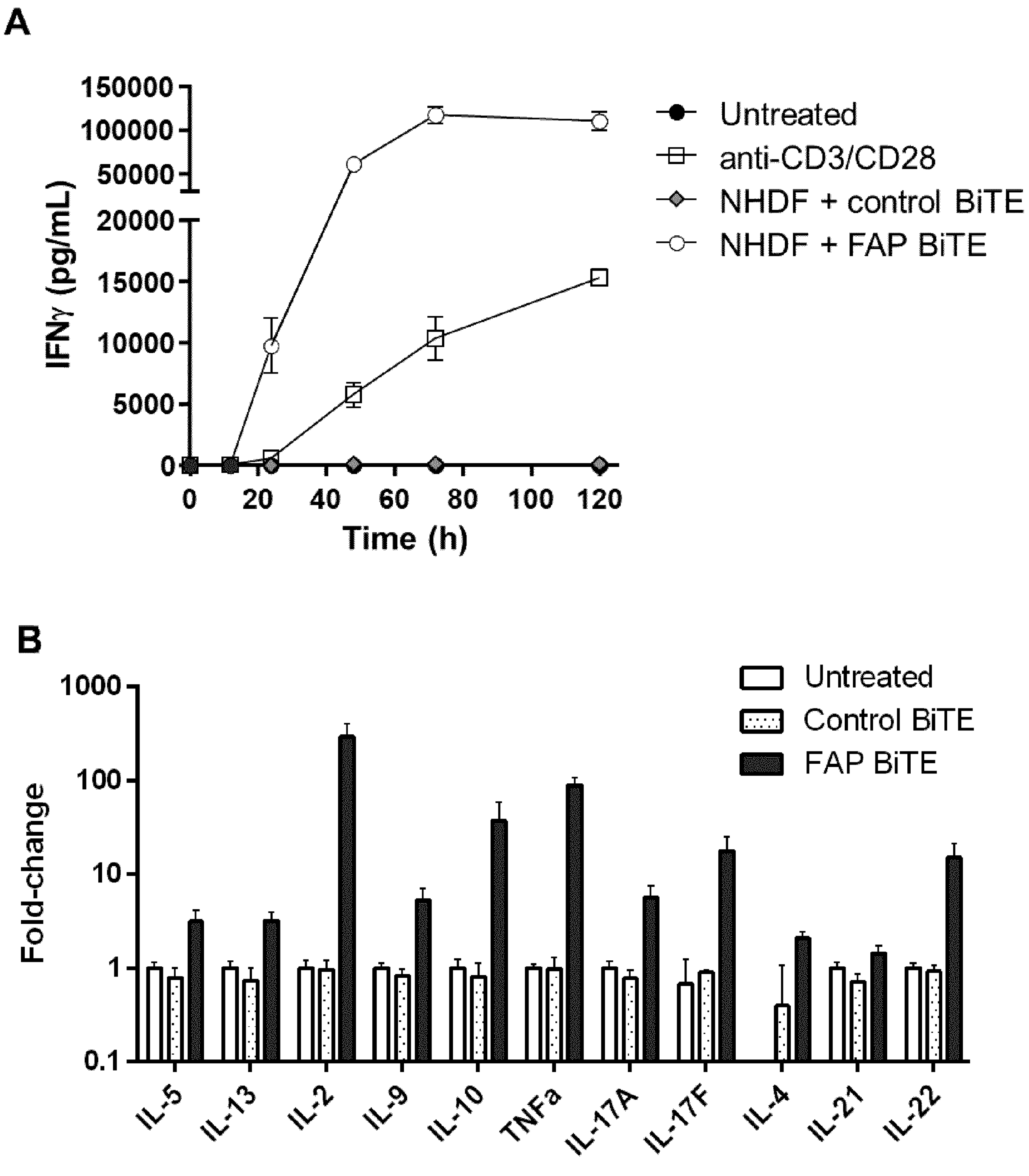

A
IFNγ (pg/mL)
150000
100000
50000
20000
15000
10000
5000
0
0
20
40
60
80
100
120
Time (h)
Untreated
anti-CD3/CD28
NHDF + control BiTE
NHDF + FAP BiTE
B
Fold-change
1000
100
10
1
0.1
IL-5
IL-13
IL-2
IL-9
IL-10
TNFa
IL-17A
IL-17F
IL-4
IL-21
IL-22
Untreated
Control BiTE
FAP BiTE

Figure 37

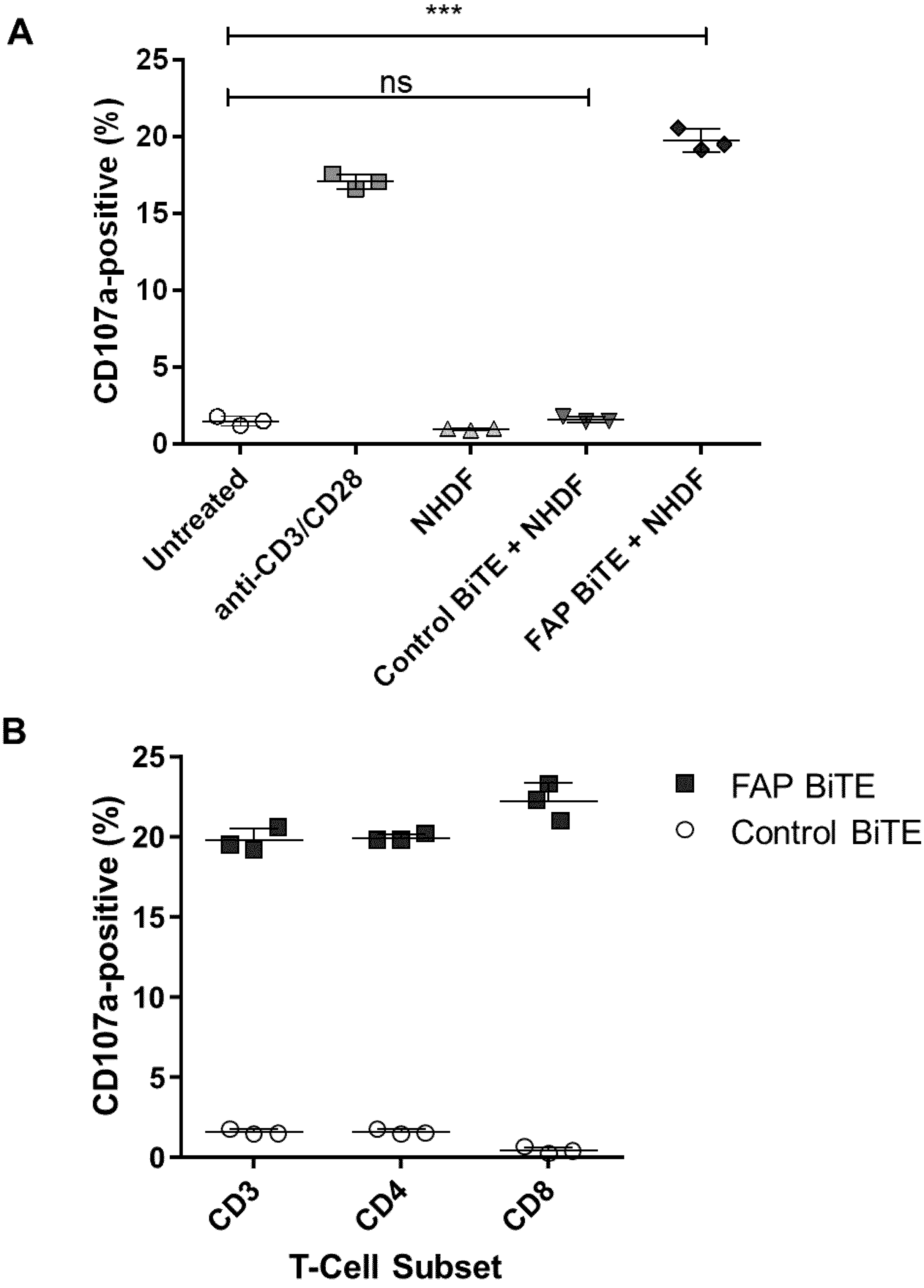

A
***
ns
CD107a-positive (%)
25
20
15
10
5
0
Untreated
anti-CD3/CD28
NHDF
Control BiTE + NHDF
FAP BiTE + NHDF
B
CD107a-positive (%)
25
20
15
10
5
0
CD3
CD4
CD8
T-Cell Subset
FAP BiTE
Control BiTE

Figure 37 cont.

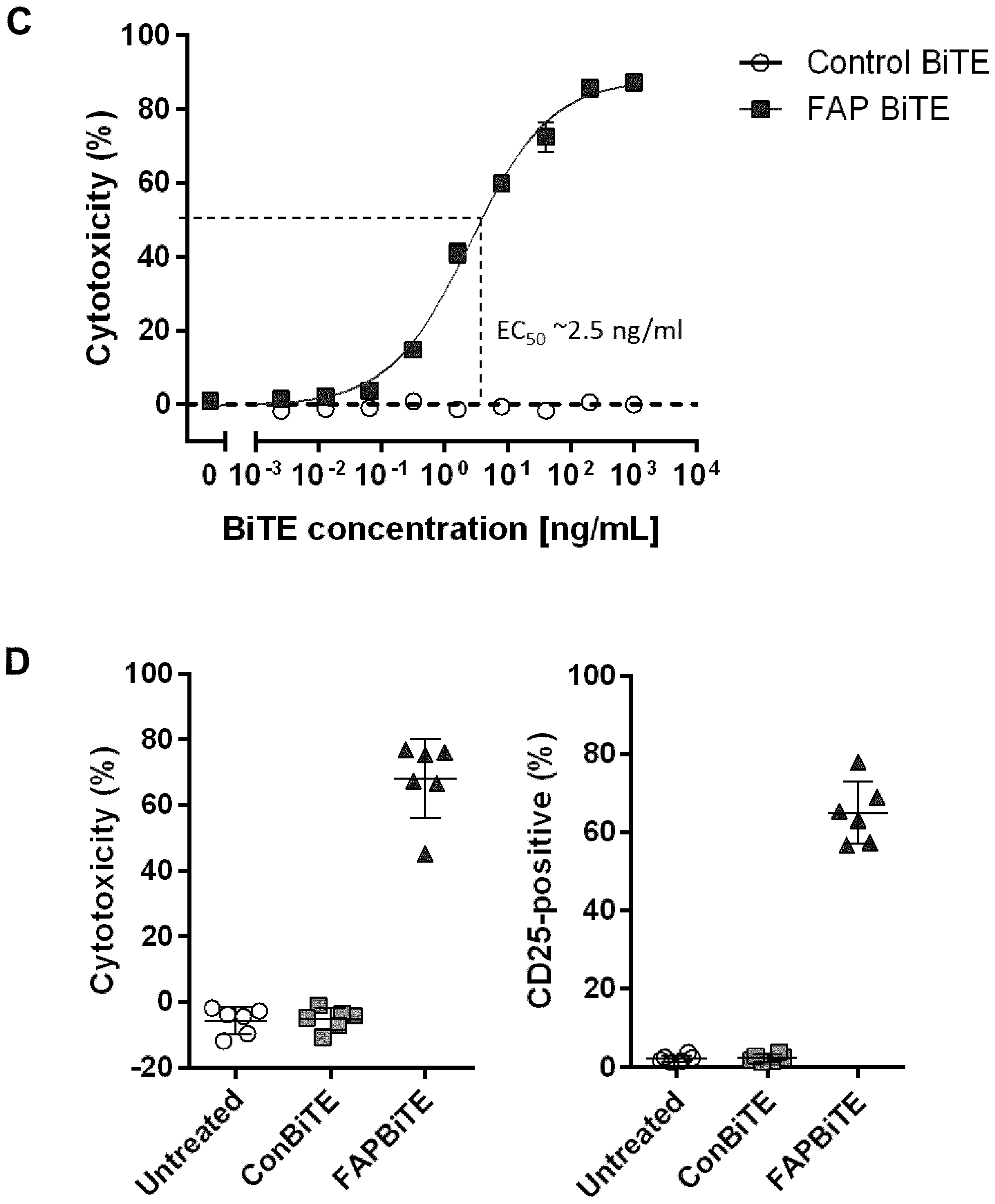
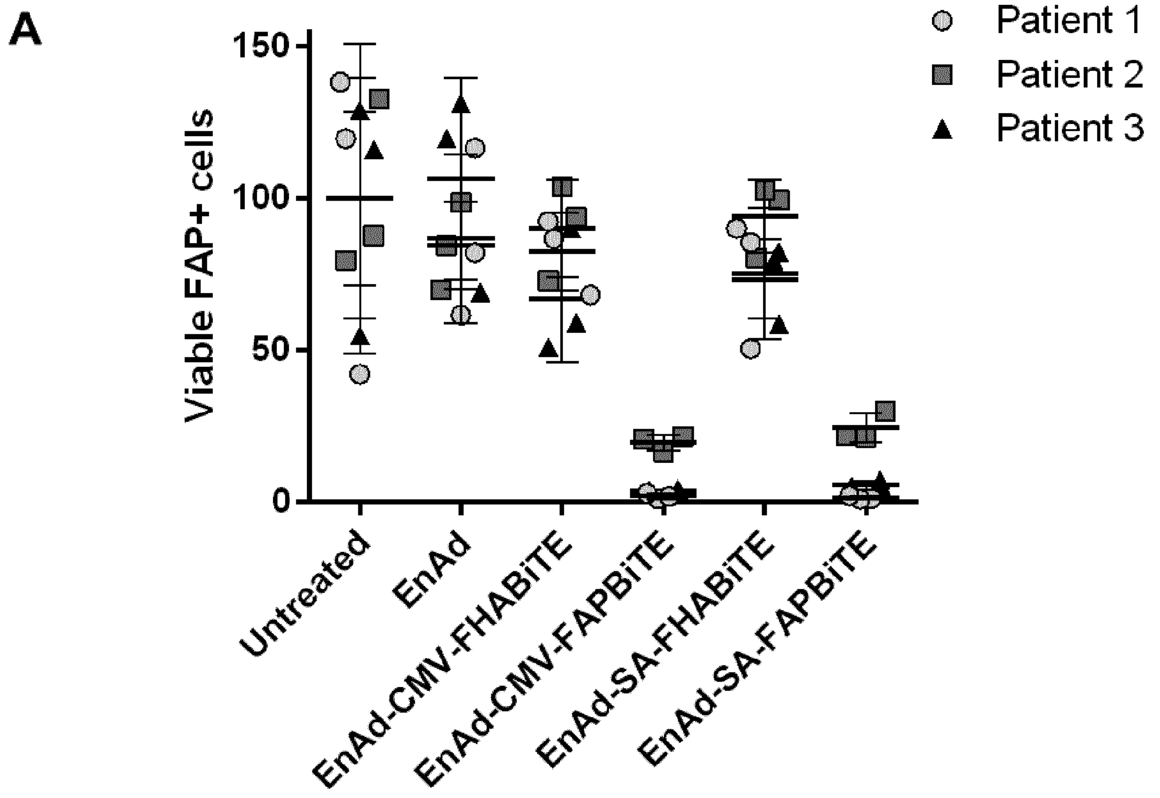


Figure 38


A
Viable FAP+ cells
150
100
50
0
Untreated
EnAd
EnAd-CMV-FHABiTE
EnAd-CMV-FAPBiTE
EnAd-SA-FHABiTE
EnAd-SA-FAPBiTE
Patient 1
Patient 2
Patient 3

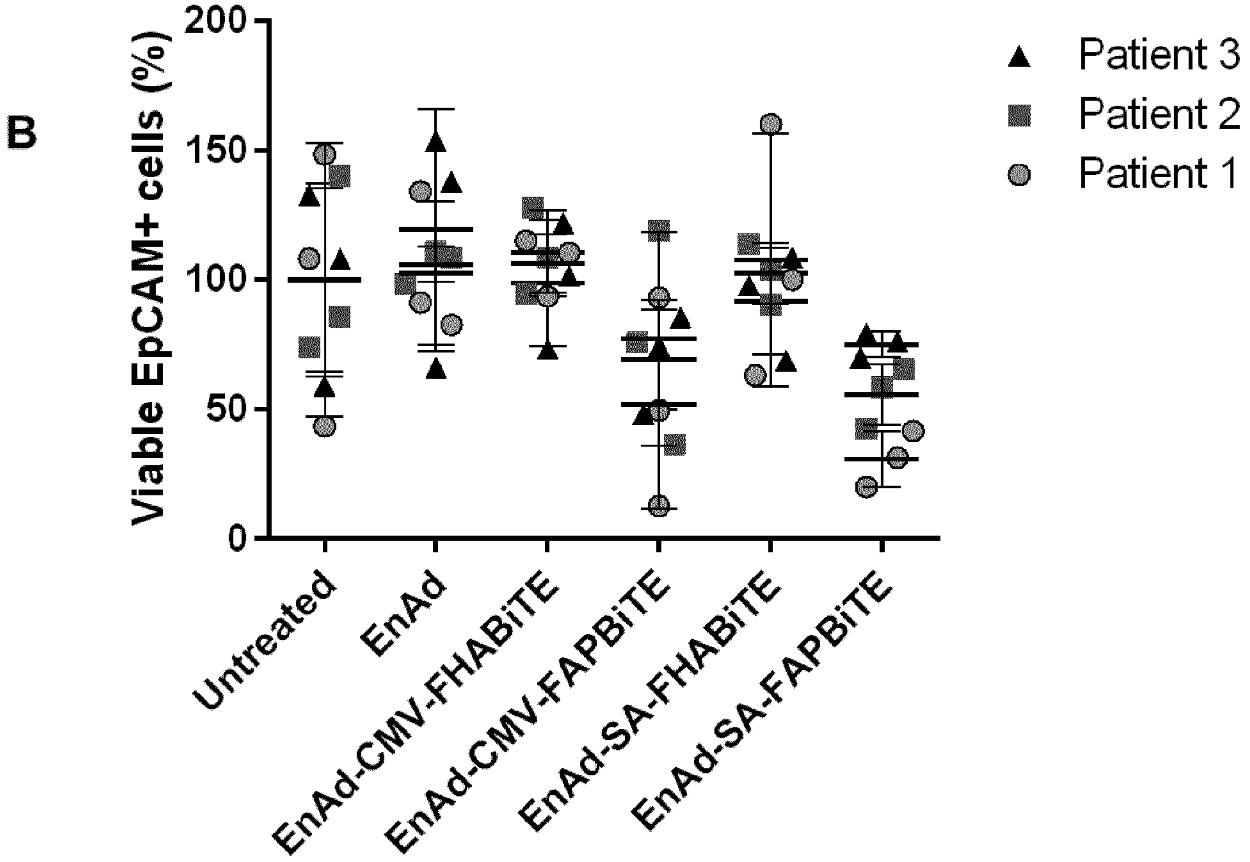

B
Viable EpCAM+ cells (%)
200
150
100
50
0
Untreated
EnAd
EnAd-CMV-FHABiTE
EnAd-CMV-FAPBiTE
EnAd-SA-FHABiTE
EnAd-SA-FAPBiTE
Patient 3
Patient 2
Patient 1

Figure 38 Cont.

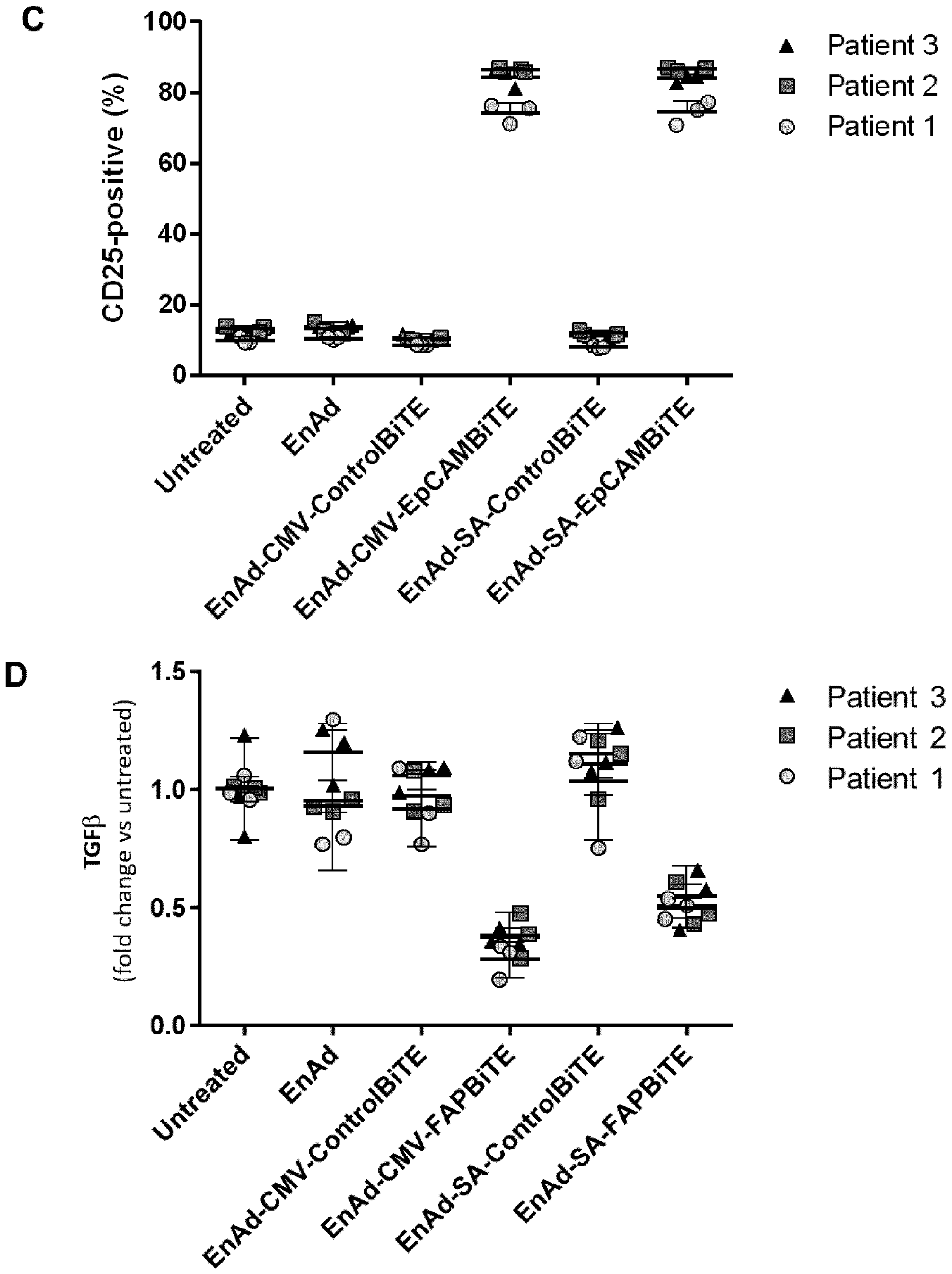


Figure 39

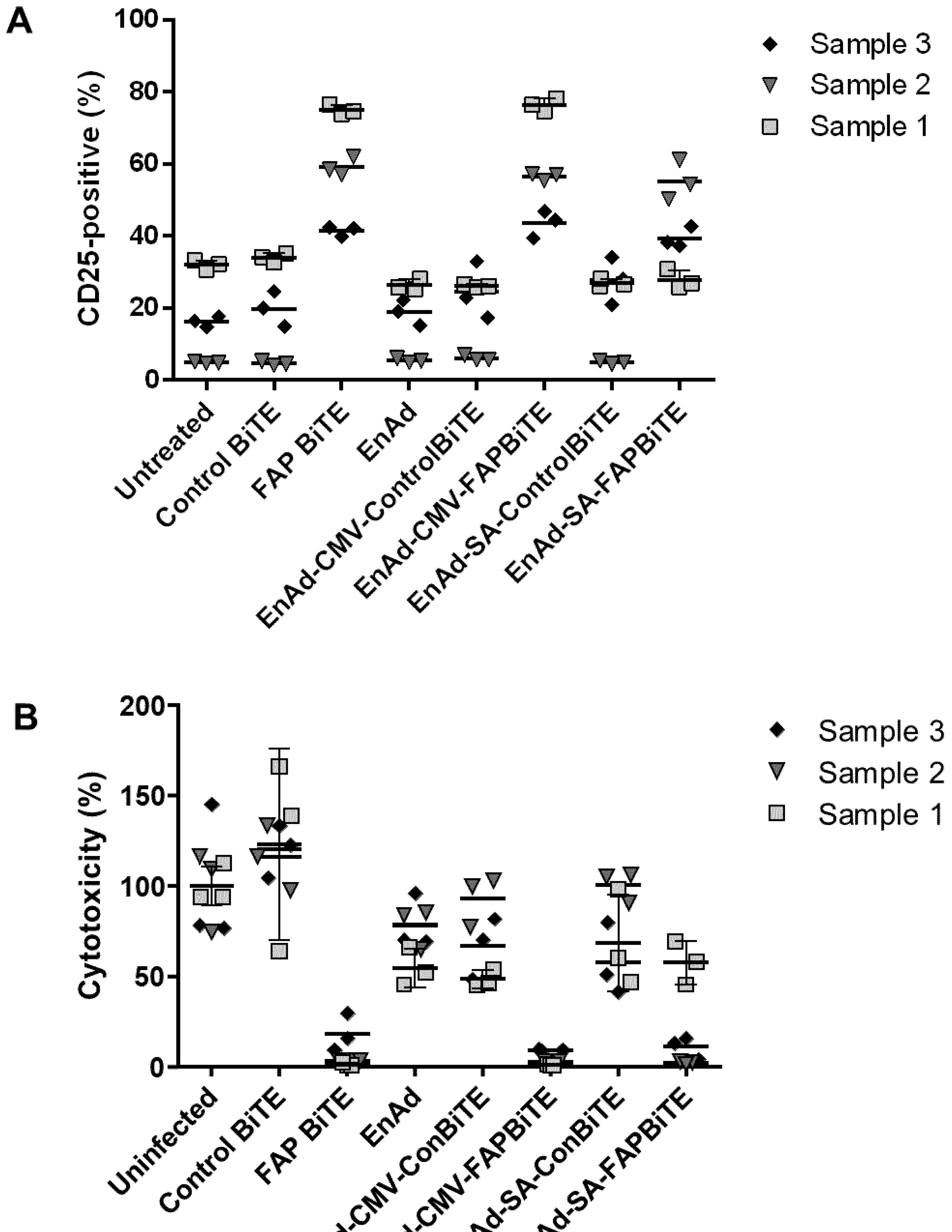

A
100
80
60
40
20
0
CD25-positive (%)
Untreated
Control BiTE
FAP BiTE
EnAd
EnAd-CMV-ControlBiTE
EnAd-CMV-FAPBiTE
EnAd-SA-ControlBiTE
EnAd-SA-FAPBiTE
Sample 3
Sample 2
Sample 1
B
200
150
100
50
0
Cytotoxicity (%)
Uninfected
Control BiTE
FAP BiTE
EnAd
EnAd-CMV-ConBiTE
EnAd-CMV-FAPBiTE
EnAd-SA-ConBiTE
EnAd-SA-FAPBiTE
Sample 3
Sample 2
Sample 1

Figure 40

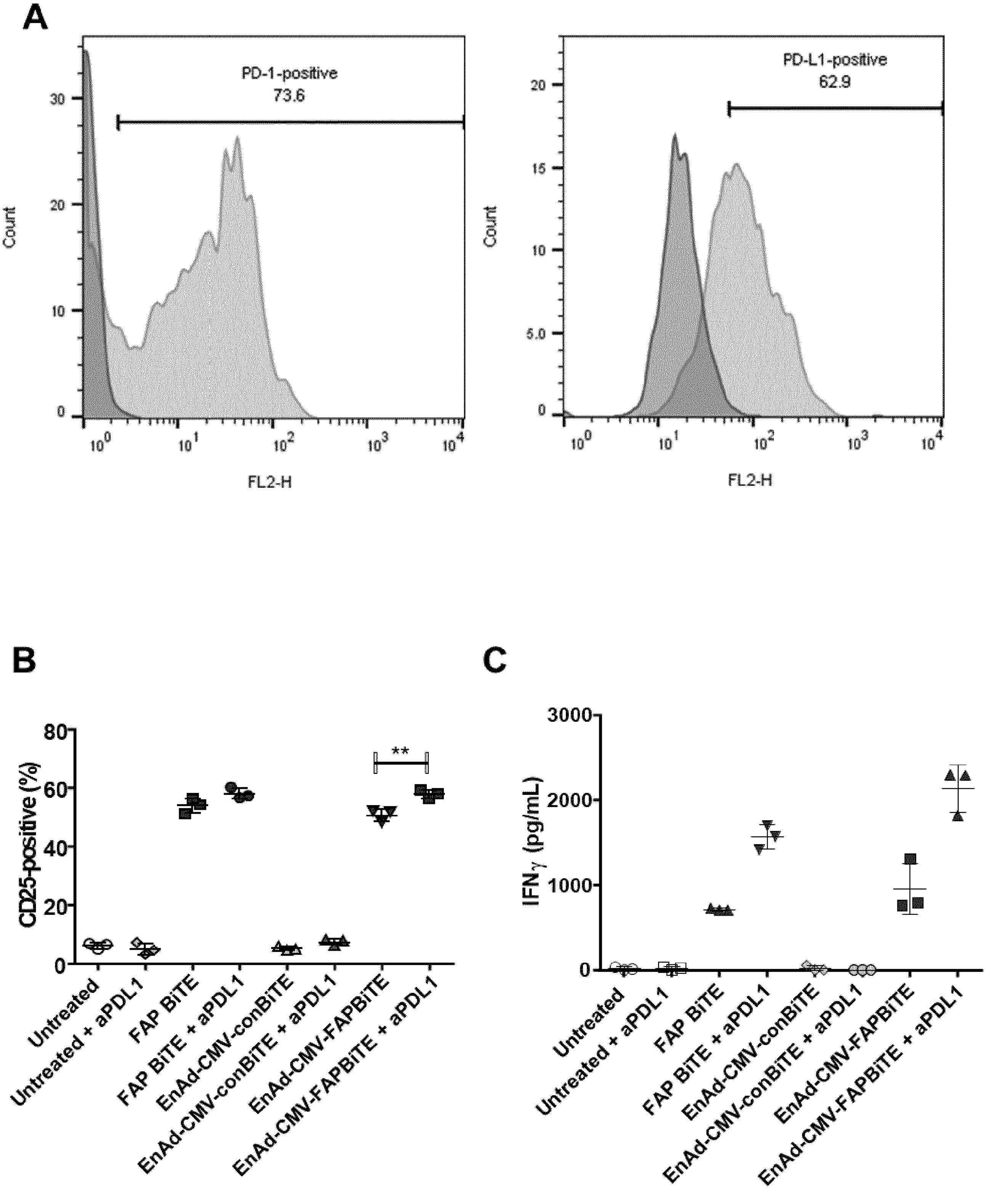

A
PD-1-positive
73.6
Count
30
20
10
0
10^0
10^1
10^2
10^3
10^4
FL2-H
PD-L1-positive
62.9
Count
20
15
10
5.0
0
10^0
10^1
10^2
10^3
10^4
FL2-H
B
CD25-positive (%)
80
60
40
20
0
**
Untreated
Untreated + aPDL1
FAP BiTE
FAP BiTE + aPDL1
EnAd-CMV-conBiTE
EnAd-CMV-conBiTE + aPDL1
EnAd-CMV-FAPBiTE
EnAd-CMV-FAPBiTE + aPDL1
C
IFNγ (pg/mL)
3000
2000
1000
0
Untreated
Untreated + aPDL1
FAP BiTE
FAP BiTE + aPDL1
EnAd-CMV-conBiTE
EnAd-CMV-conBiTE + aPDL1
EnAd-CMV-FAPBiTE
EnAd-CMV-FAPBiTE + aPDL1

Figure 40 cont.

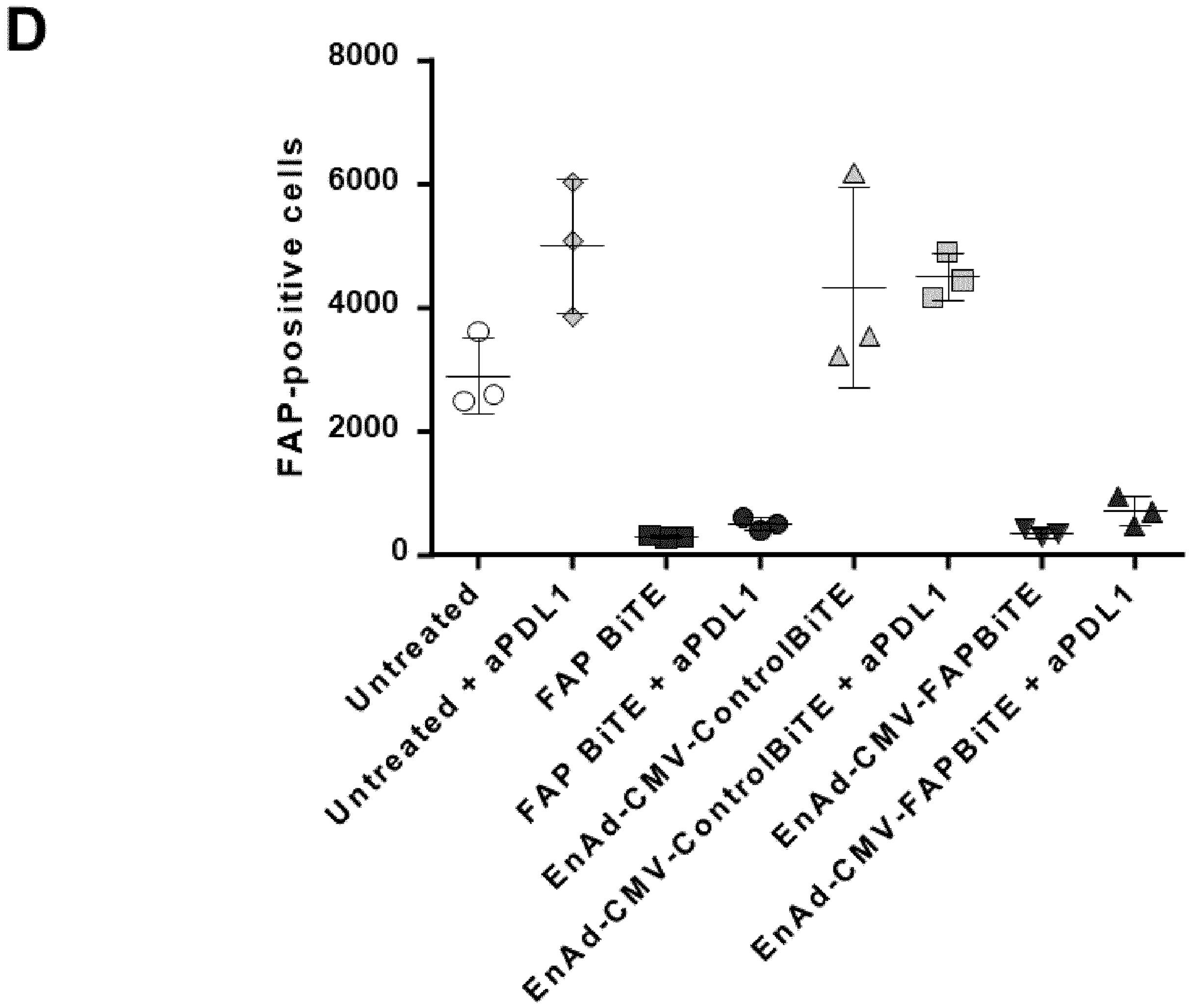


Figure 41

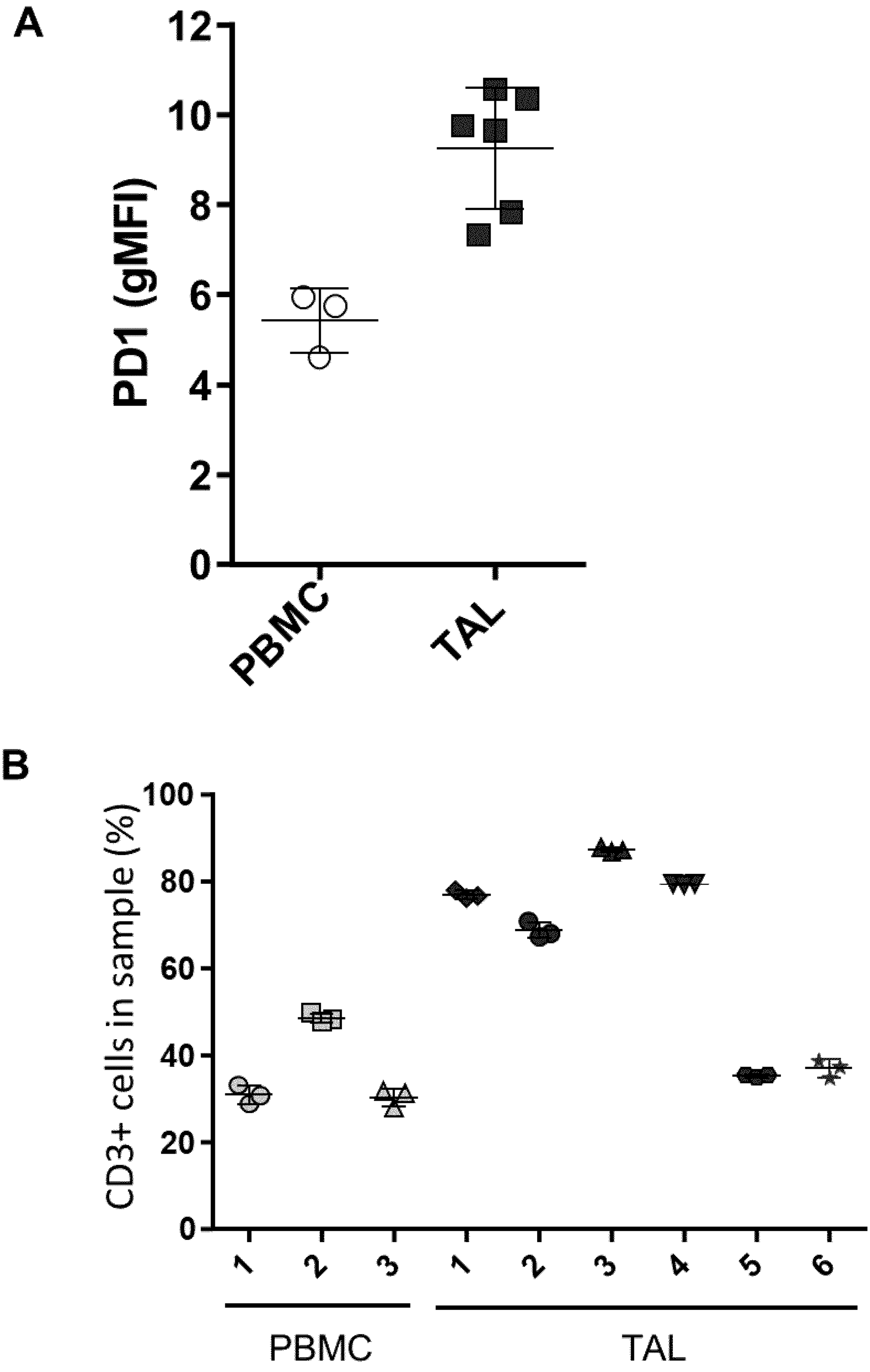
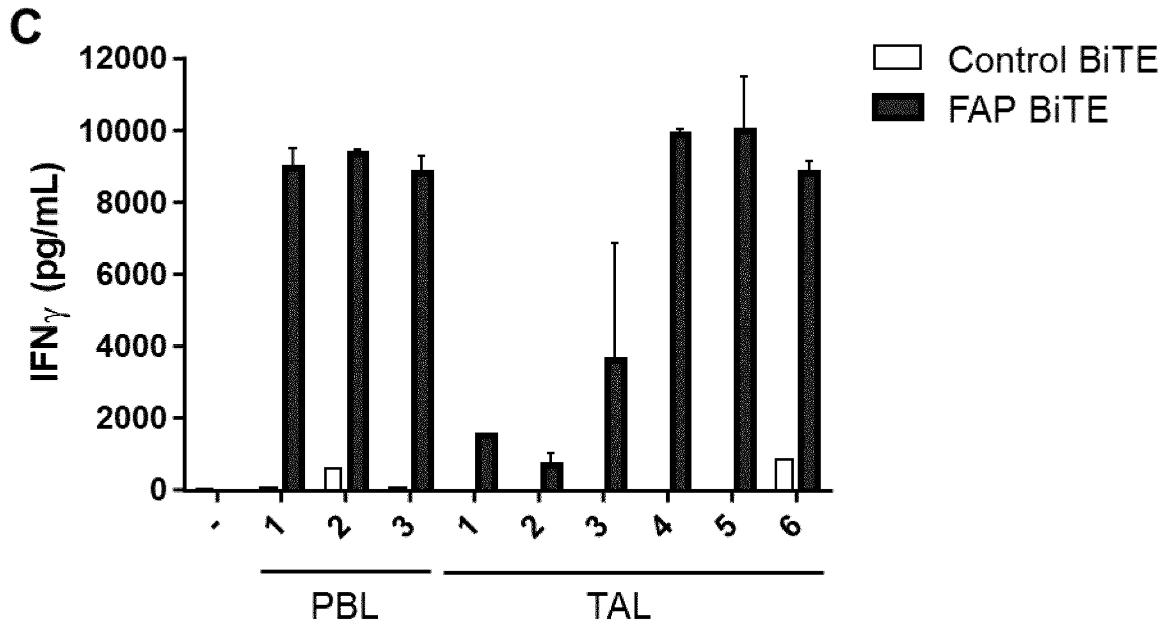

A
PD1 (gMFI)
12
10
8
6
4
2
0
PBMC
TAL
B
CD3+ cells in sample (%)
100
80
60
40
20
0
1
2
3
1
2
3
4
5
6
PBMC
TAL

Figure 41 cont.



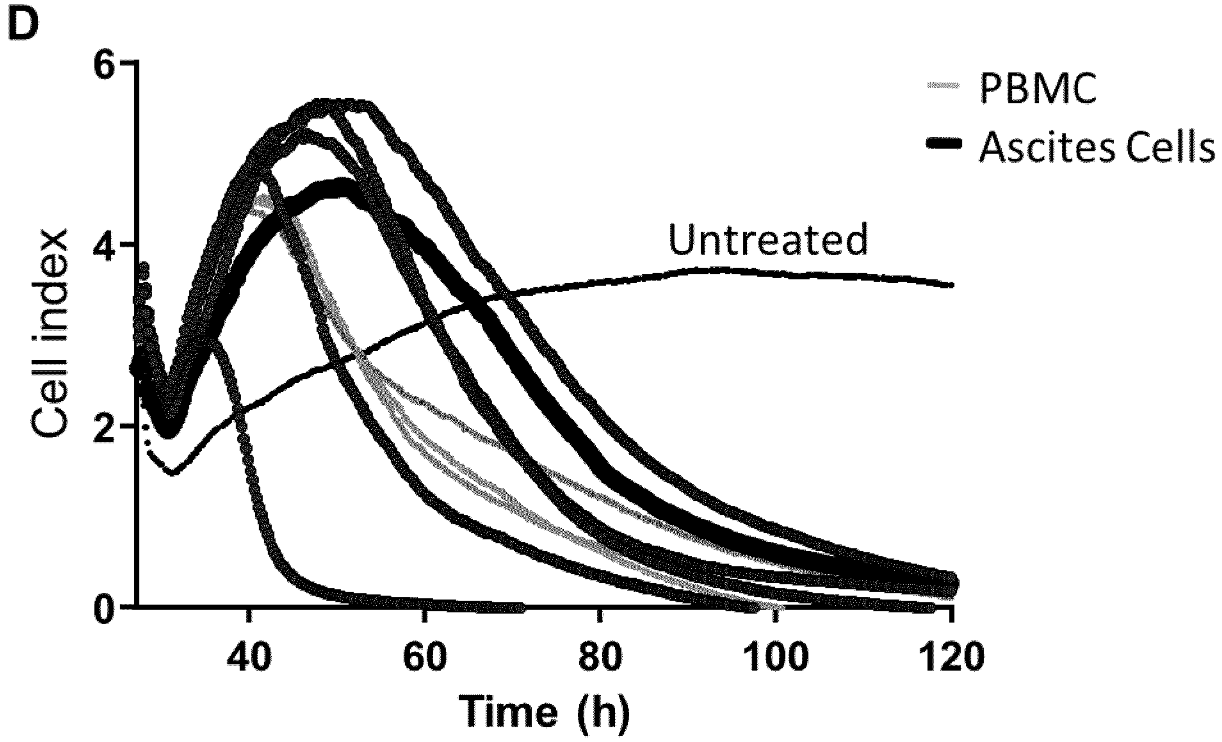


Figure 42

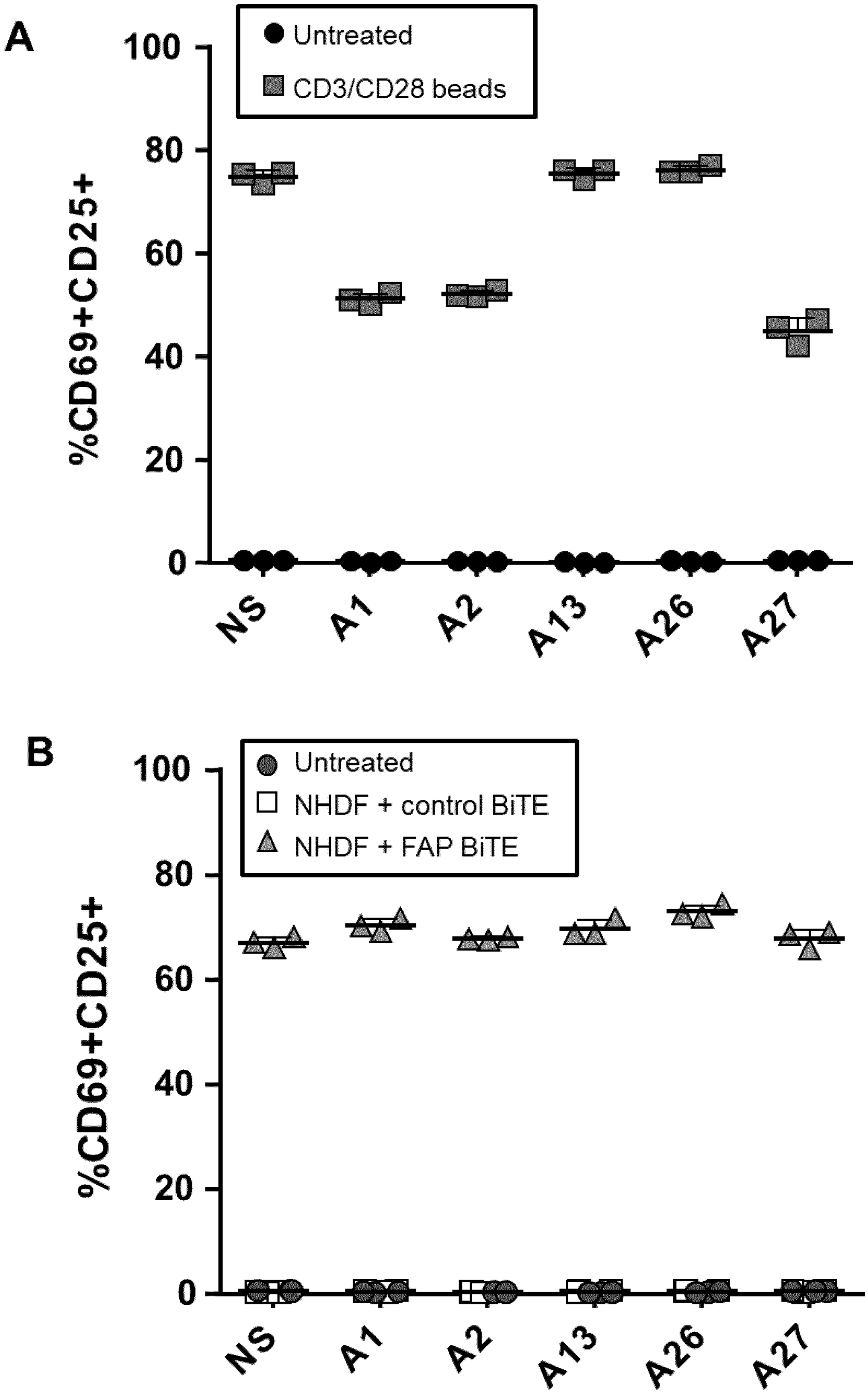

A
Untreated
CD3/CD28 beads
%CD69+CD25+
100
80
60
40
20
0
NS
A1
A2
A13
A26
A27
B
Untreated
NHDF + control BiTE
NHDF + FAP BiTE
%CD69+CD25+
100
80
60
40
20
0
NS
A1
A2
A13
A26
A27

Figure 43

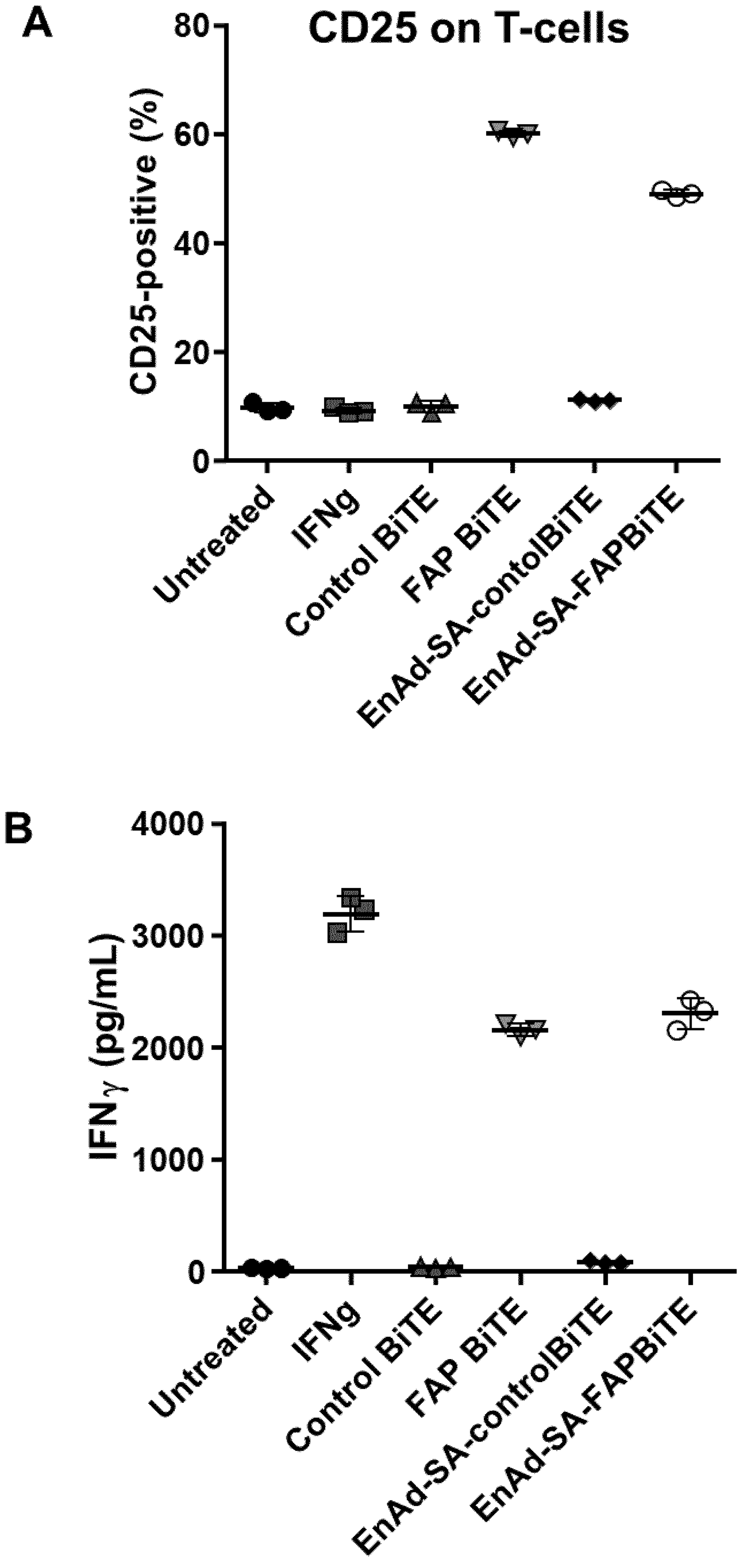

A
CD25 on T-cells
CD25-positive (%)
0
20
40
60
80
Untreated
IFNg
Control BiTE
FAP BiTE
EnAd-SA-contolBiTE
EnAd-SA-FAPBiTE
B
IFNγ (pg/mL)
0
1000
2000
3000
4000
Untreated
IFNg
Control BiTE
FAP BiTE
EnAd-SA-controlBiTE
EnAd-SA-FAPBiTE

Figure 43 cont.

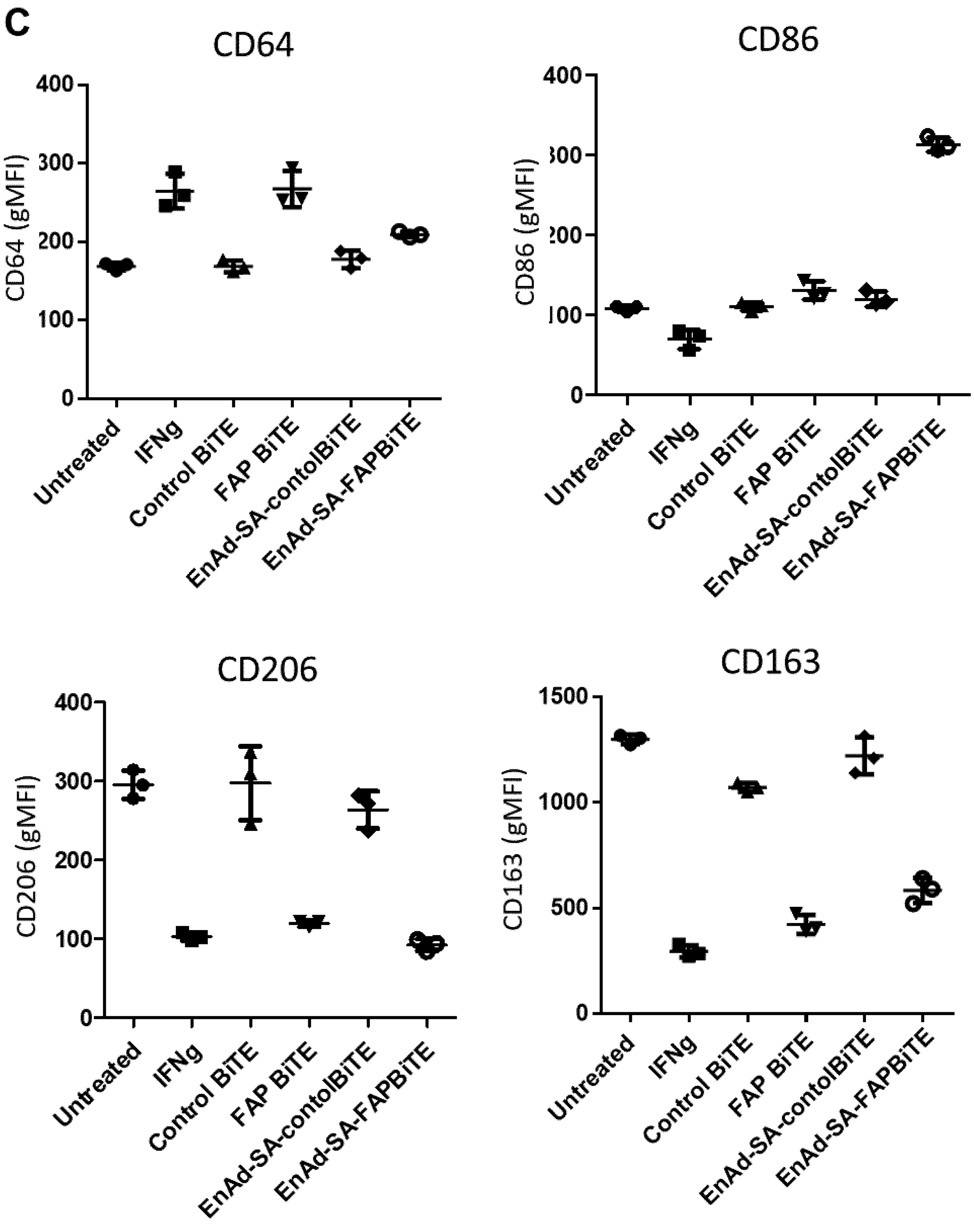
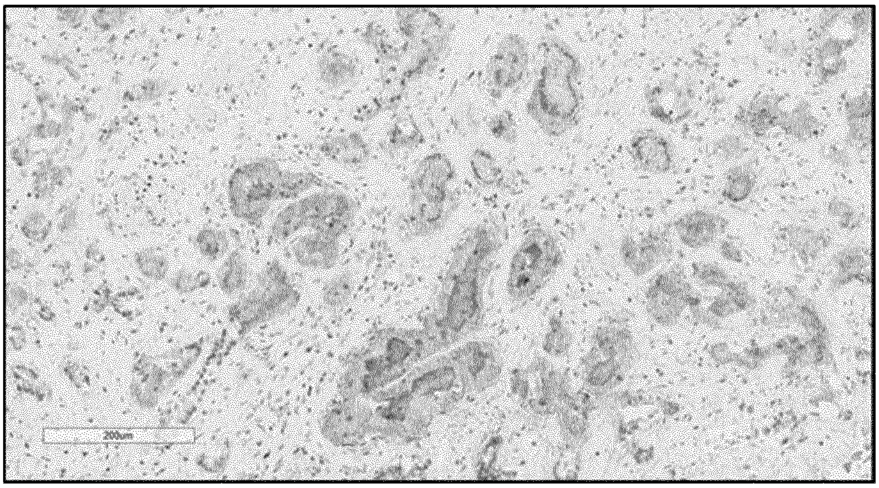
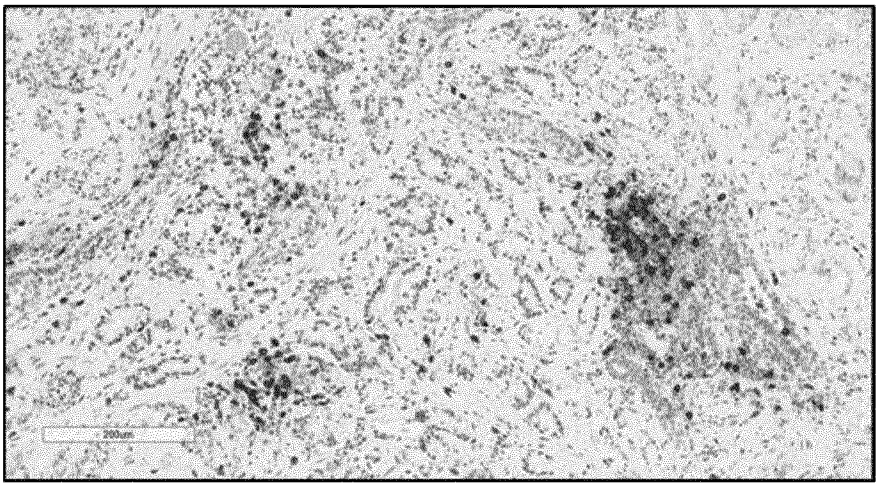


Figure 44

A EpCAM Staining



B CD8 Staining



C FAP Staining

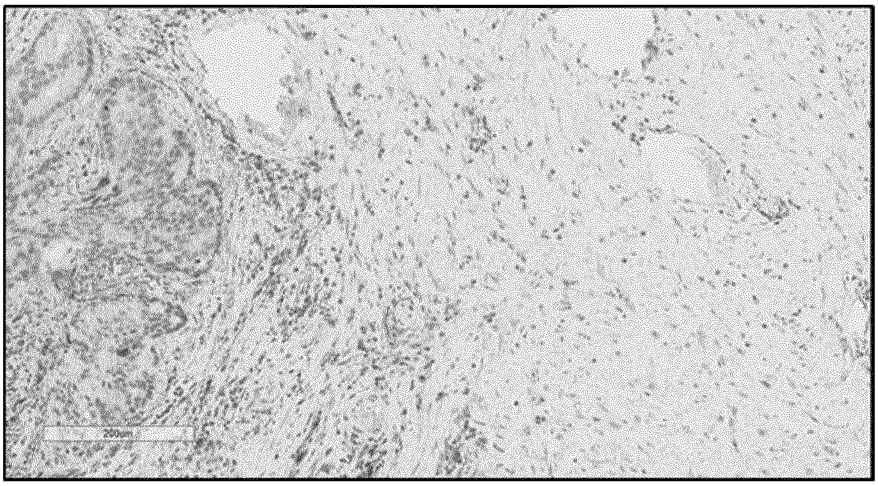
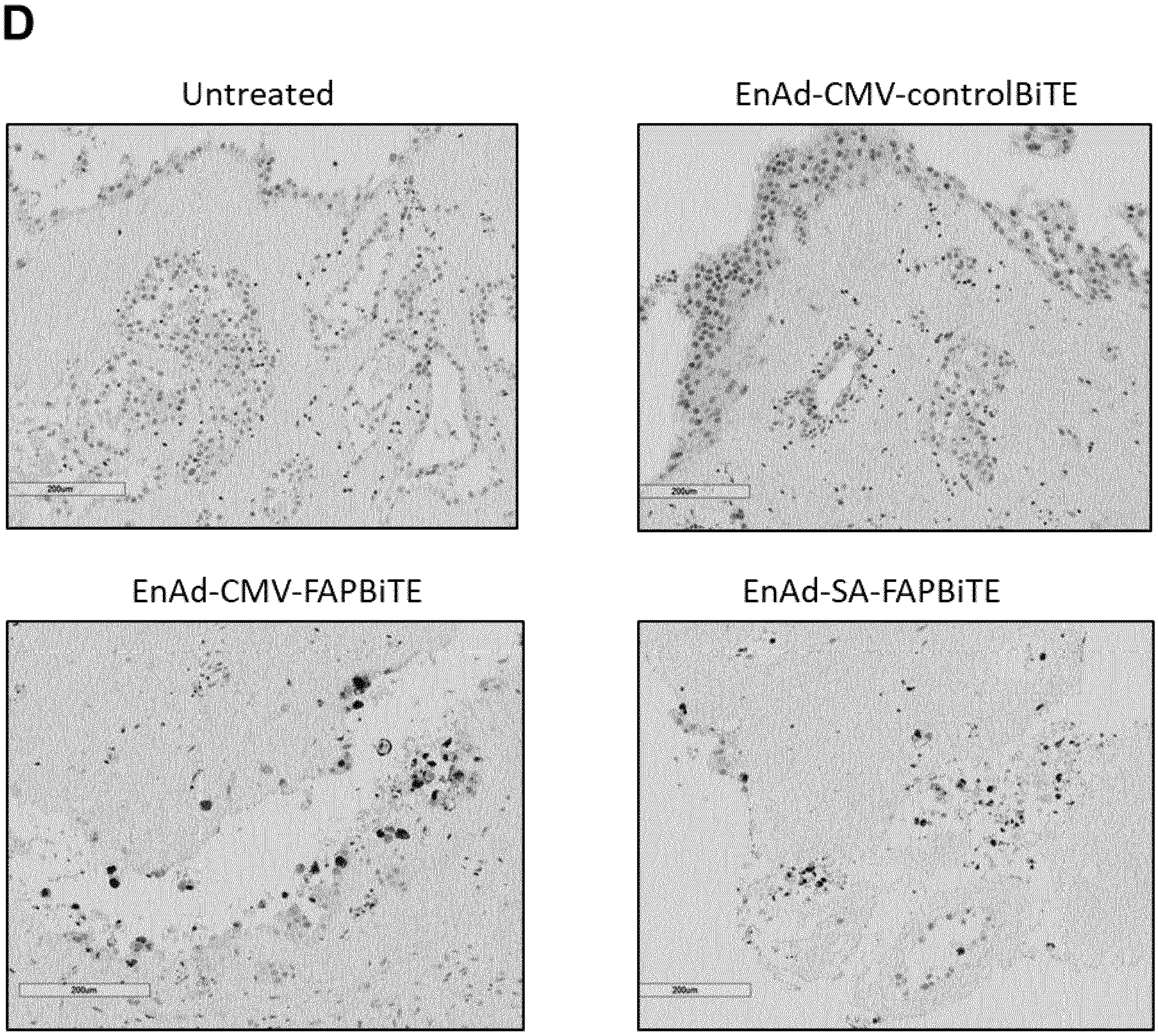


Figure 44 Cont.



D

Untreated

EnAd-CMV-controlBiTE

EnAd-CMV-FAPBiTE

EnAd-SA-FAPBiTE

Figure 44 Cont.

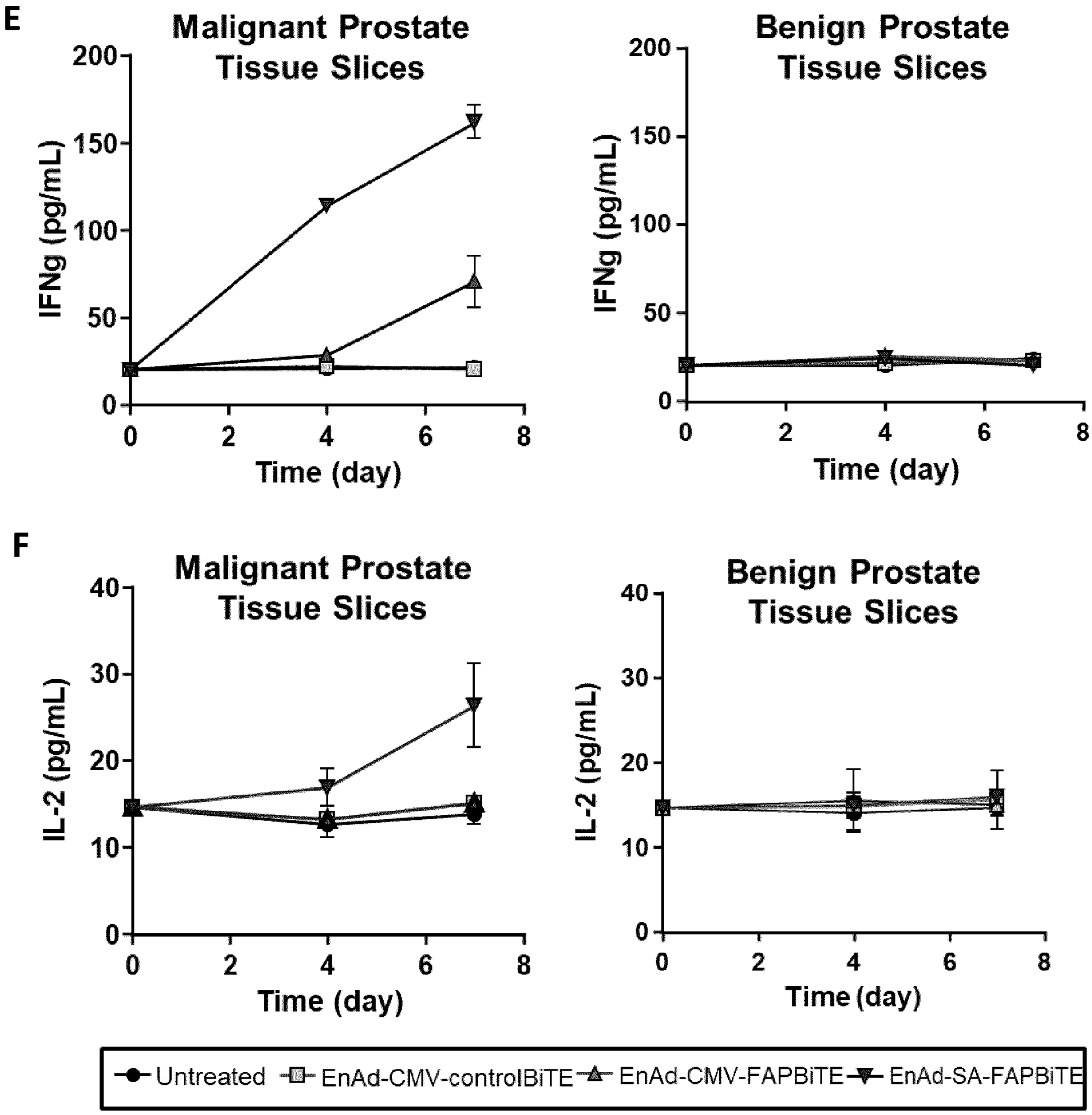


Figure 45

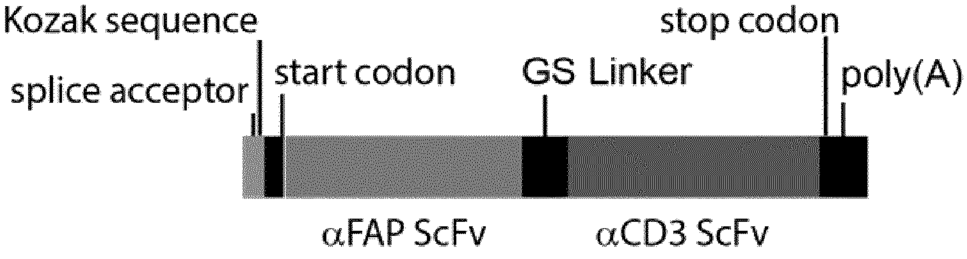


Figure 46

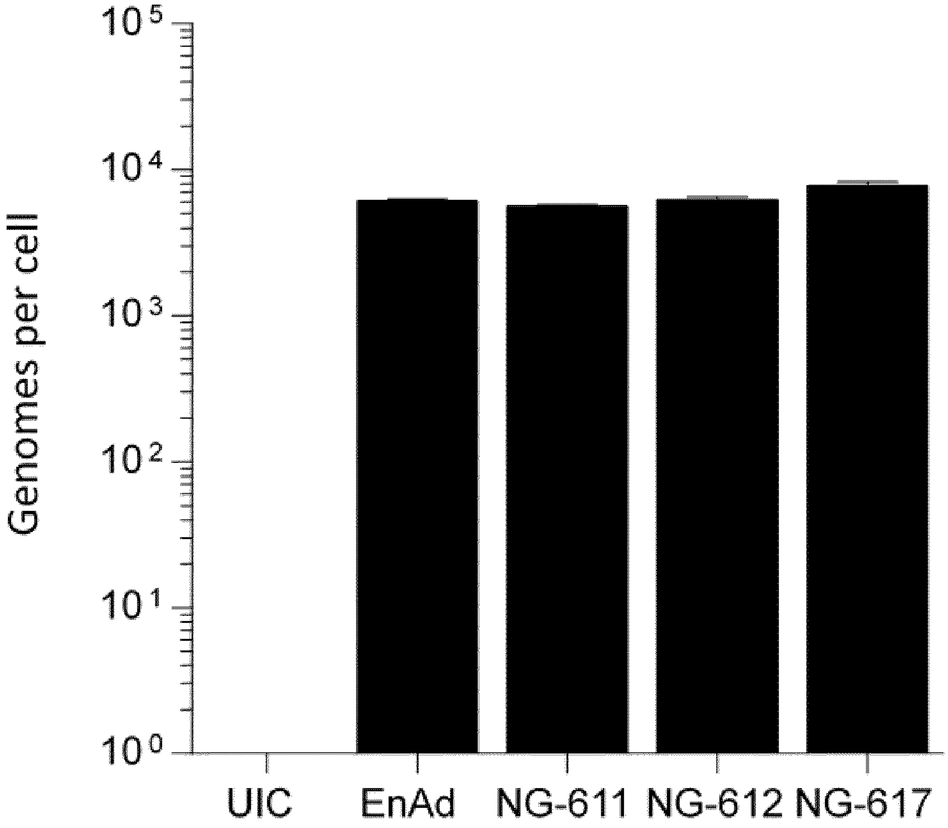

Genomes per cell
10^5
10^4
10^3
10^2
10^1
10^0
UIC
EnAd
NG-611
NG-612
NG-617

Figure 47

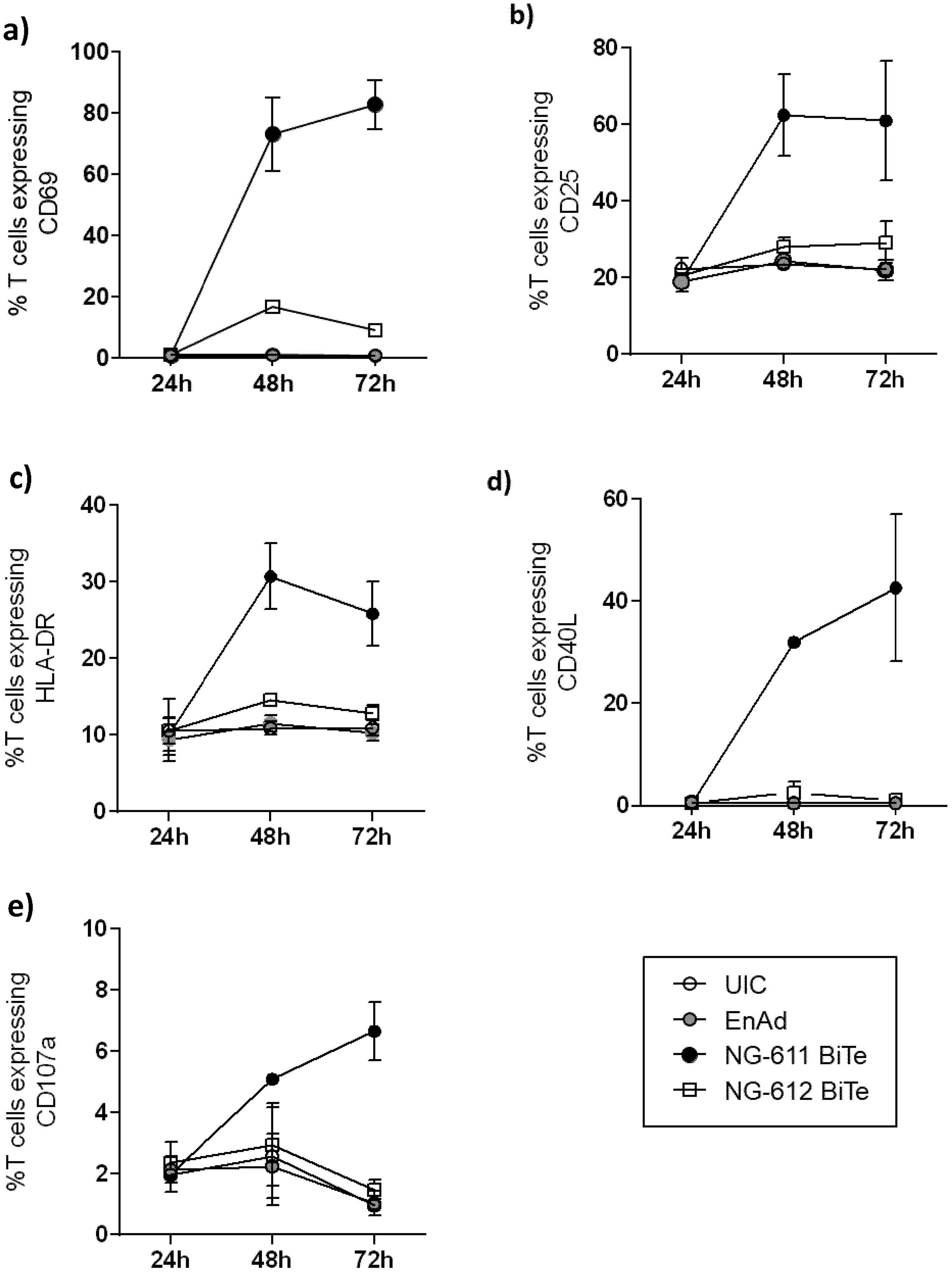

a)
% T cells expressing CD69
0
20
40
60
80
100
24h
48h
72h
b)
% T cells expressing CD25
0
20
40
60
80
24h
48h
72h
c)
% T cells expressing HLA-DR
0
10
20
30
40
24h
48h
72h
d)
% T cells expressing CD40L
0
20
40
60
24h
48h
72h
e)
% T cells expressing CD107a
0
2
4
6
8
10
24h
48h
72h
UIC
EnAd
NG-611 BiTe
NG-612 BiTe

Figure 48

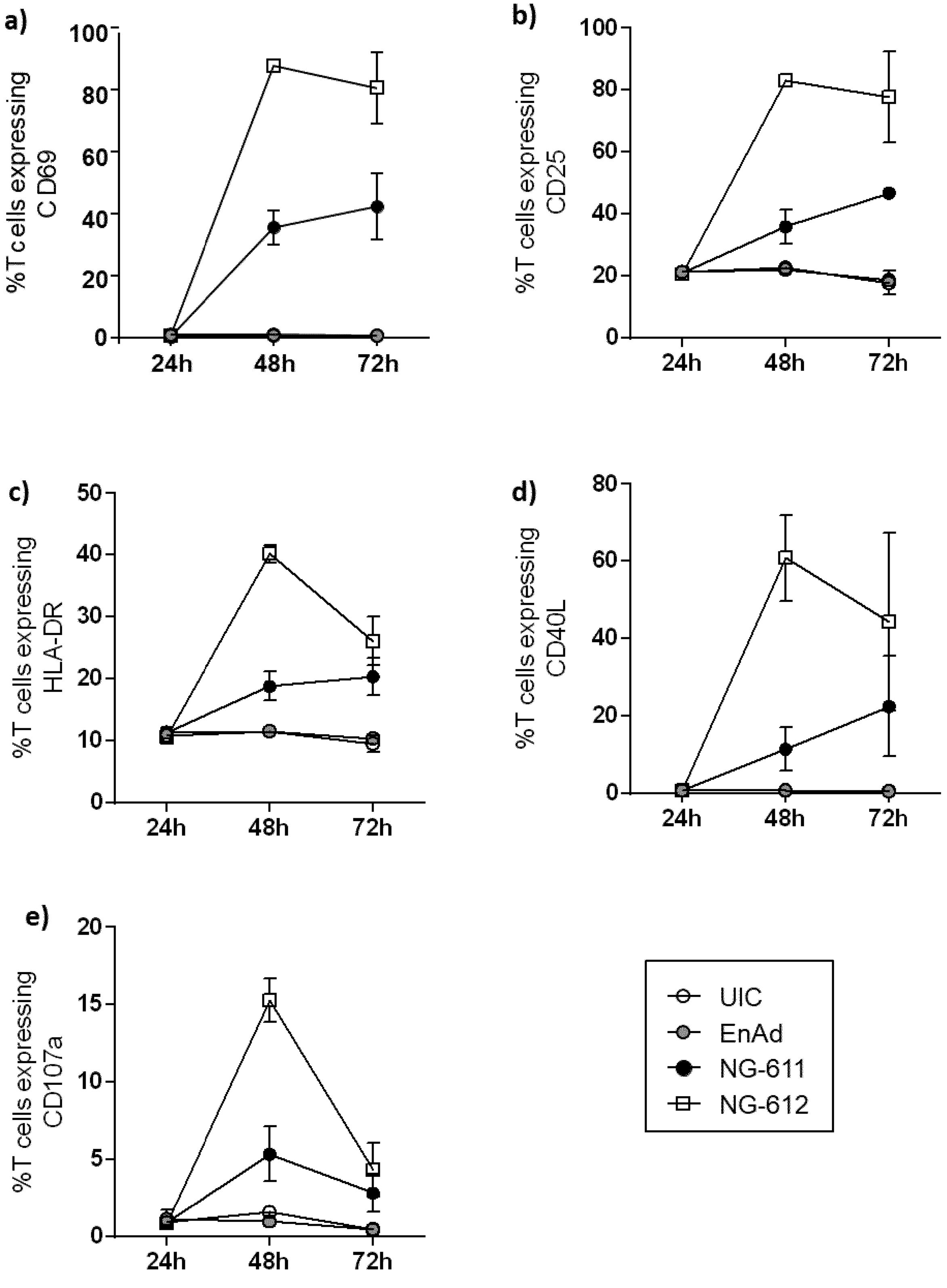

a)
%T cells expressing C D69
0
20
40
60
80
100
24h
48h
72h
b)
%T cells expressing CD25
0
20
40
60
80
100
24h
48h
72h
c)
%T cells expressing HLA-DR
0
10
20
30
40
50
24h
48h
72h
d)
%T cells expressing CD40L
0
20
40
60
80
24h
48h
72h
e)
%T cells expressing CD107a
0
5
10
15
20
24h
48h
72h
UIC
EnAd
NG-611
NG-612

Figure 49

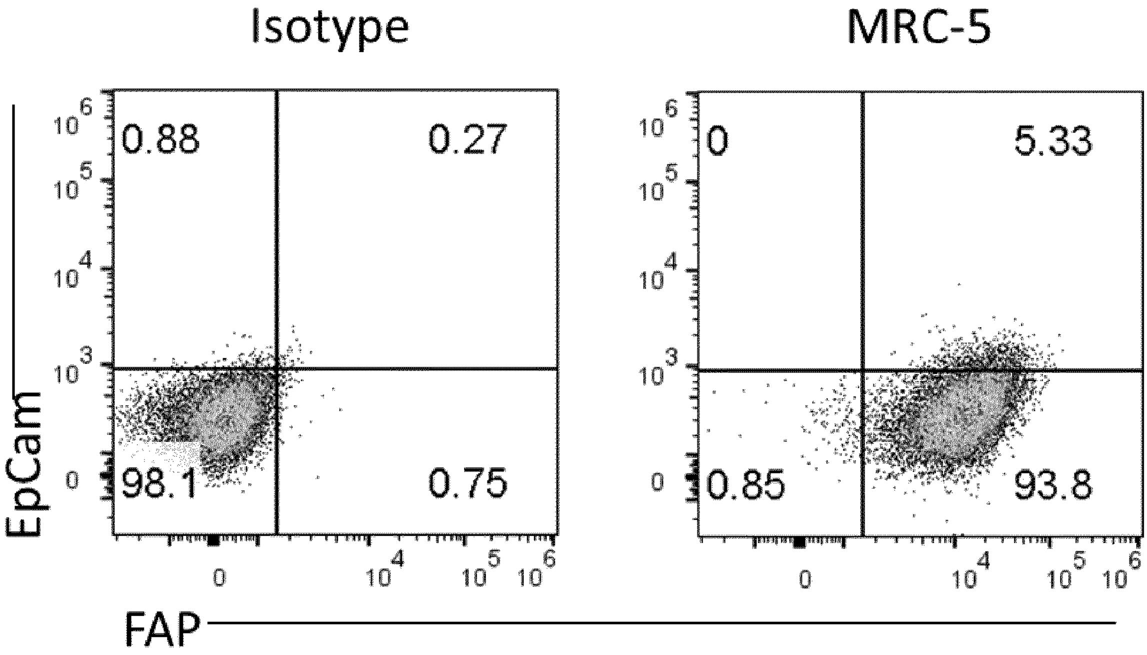

Isotype
MRC-5
EpCam
FAP
0.88
0.27
98.1
0.75
0
5.33
0.85
93.8
10^6
10^5
10^4
10^3
0

Figure 50A

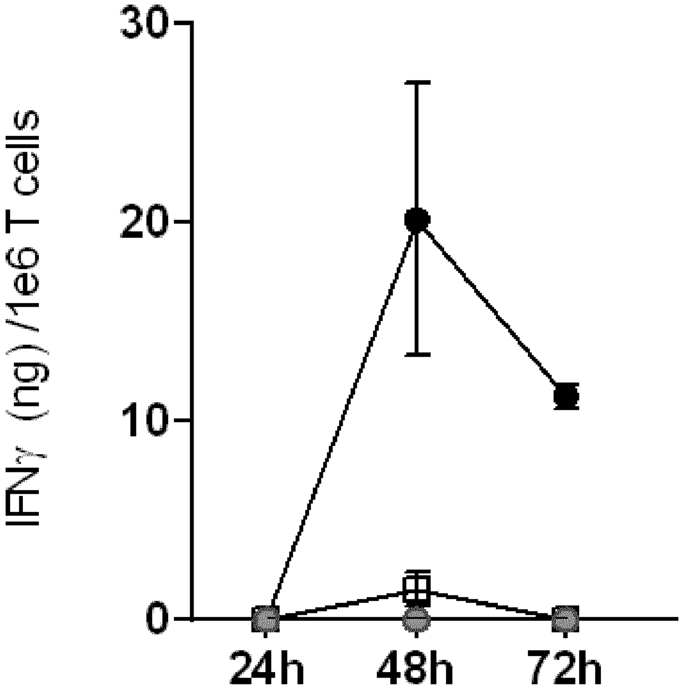


Figure 50B

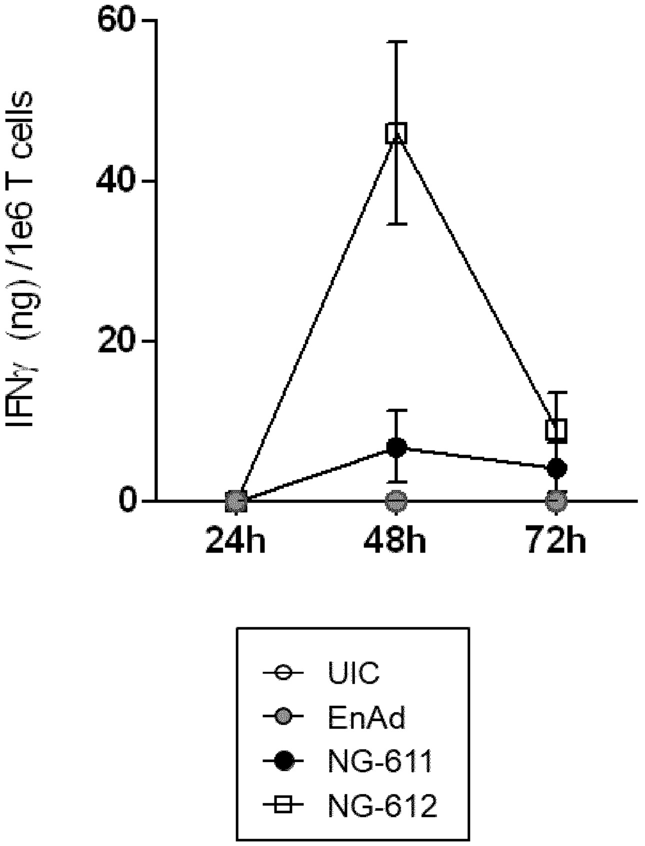
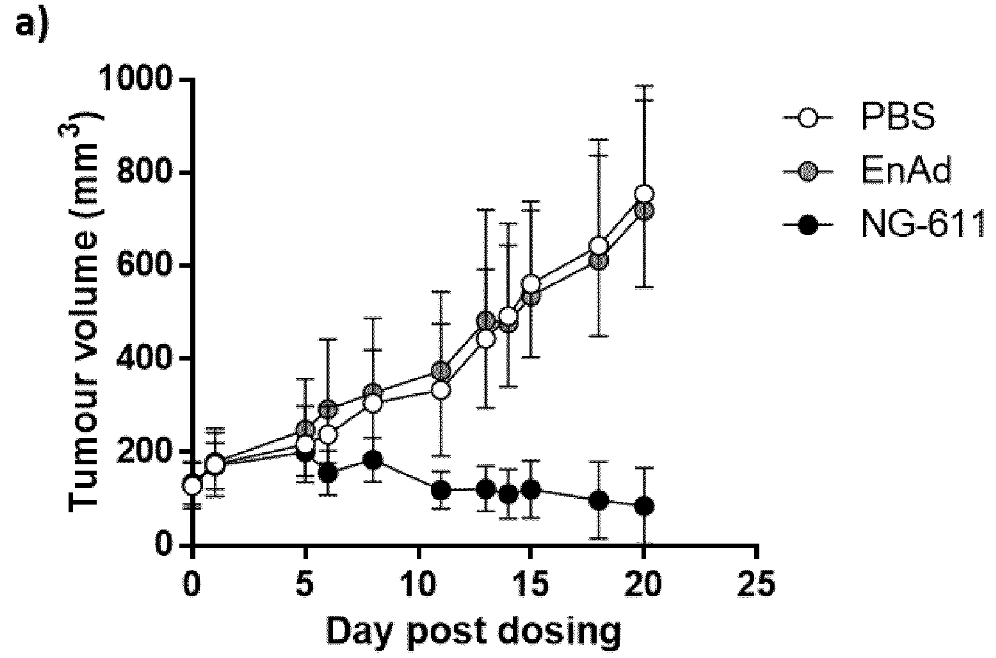


Figure 51


a)
Tumour volume (mm³)
1000
800
600
400
200
0
0
5
10
15
20
25
Day post dosing
PBS
EnAd
NG-611

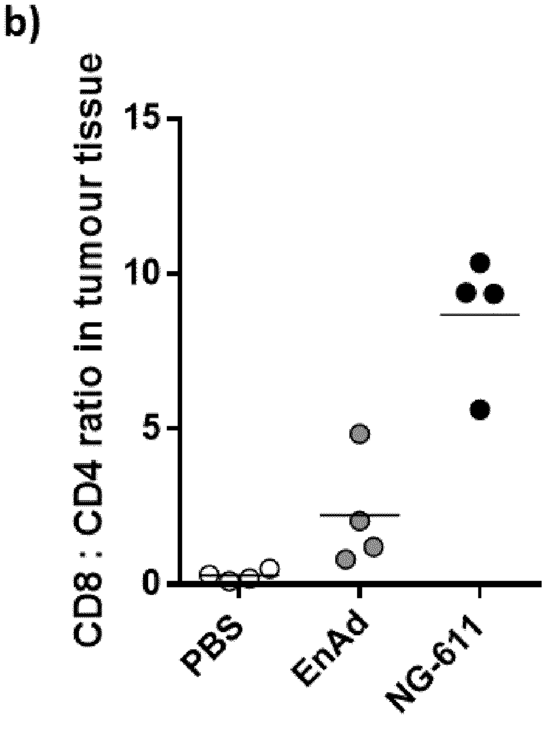

b)
CD8 : CD4 ratio in tumour tissue
15
10
5
0
PBS
EnAd
NG-611

Figure 52

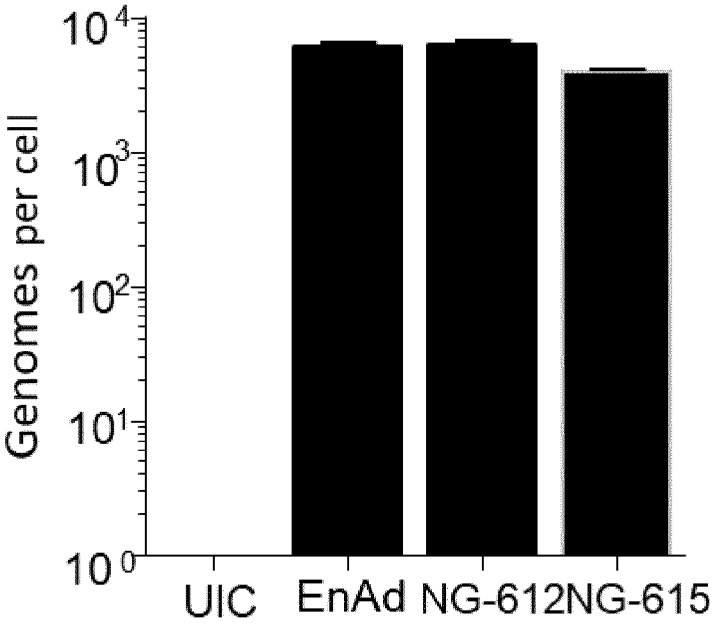


Figure 53

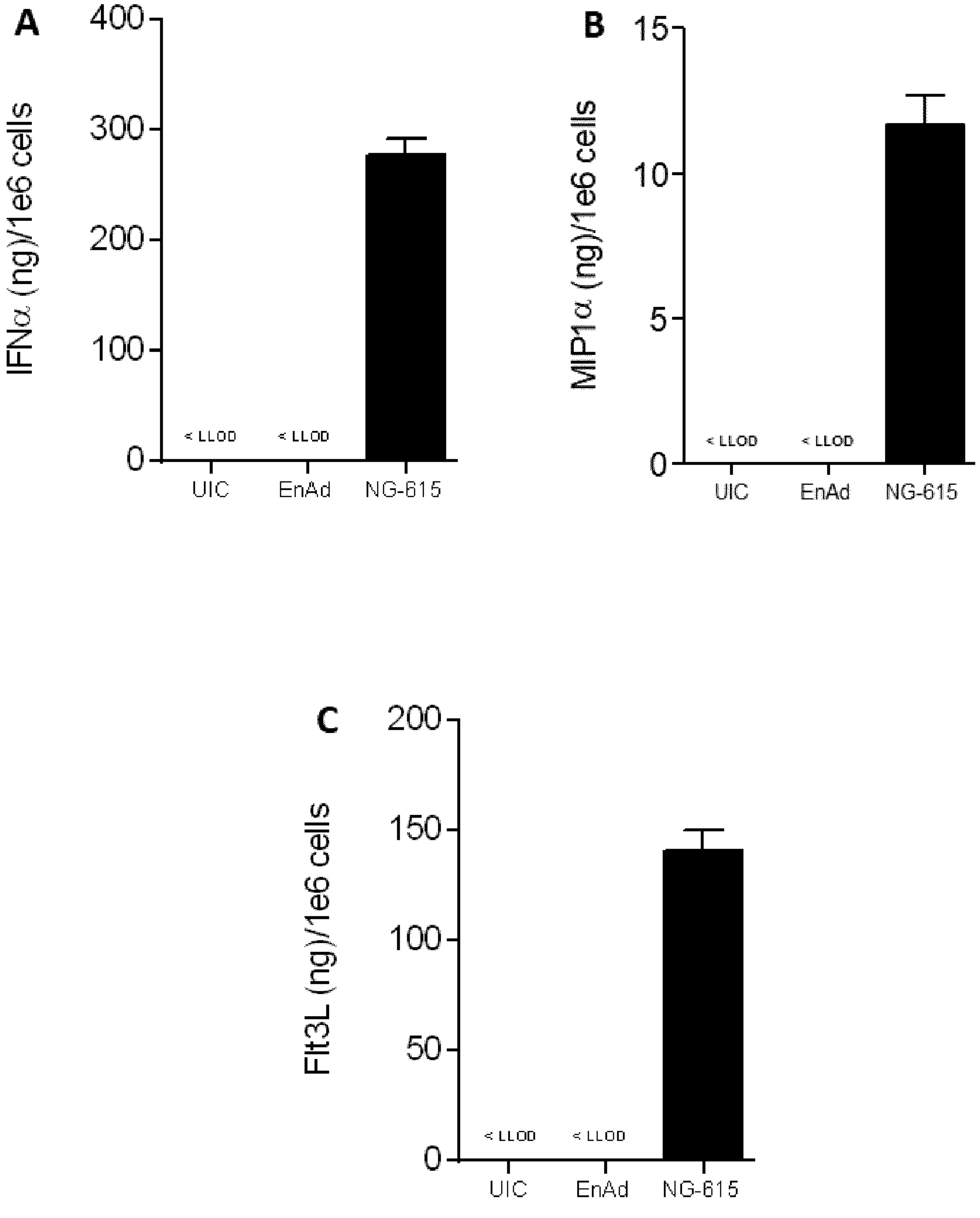

A
IFNα (ng)/1e6 cells
400
300
200
100
0
< LLOD
< LLOD
UIC
EnAd
NG-615
B
MIP1α (ng)/1e6 cells
15
10
5
0
< LLOD
< LLOD
UIC
EnAd
NG-615
C
Flt3L (ng)/1e6 cells
200
150
100
50
0
< LLOD
< LLOD
UIC
EnAd
NG-615

Figure 54

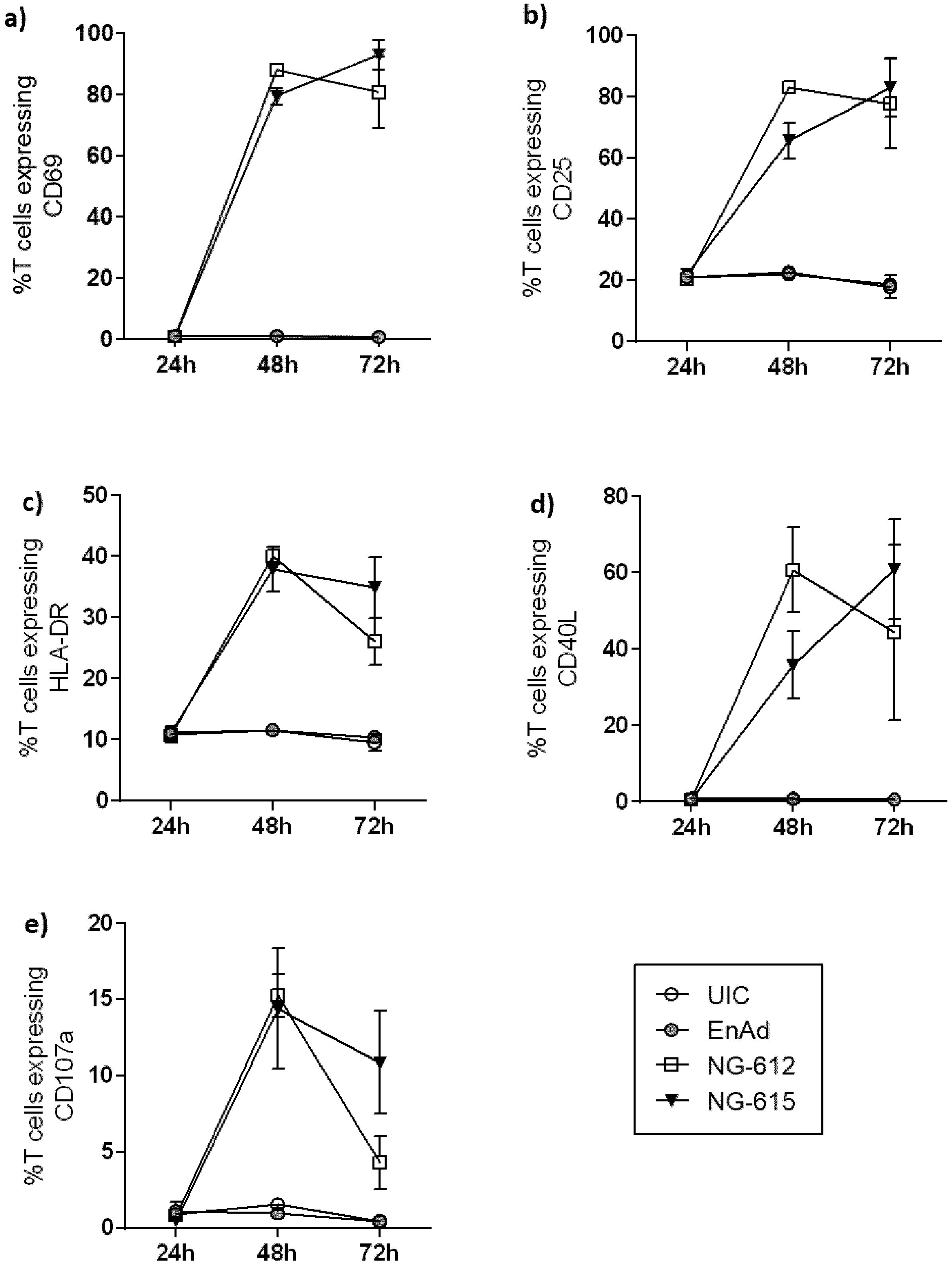
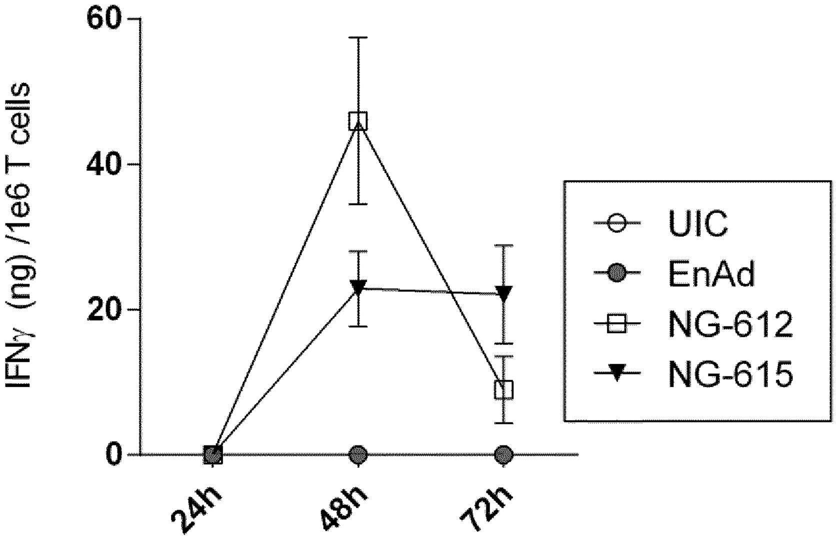

a)
%T cells expressing CD69
100
80
60
40
20
0
24h
48h
72h
b)
%T cells expressing CD25
100
80
60
40
20
0
24h
48h
72h
c)
%T cells expressing HLA-DR
50
40
30
20
10
0
24h
48h
72h
d)
%T cells expressing CD40L
80
60
40
20
0
24h
48h
72h
e)
%T cells expressing CD107a
20
15
10
5
0
24h
48h
72h
UIC
EnAd
NG-612
NG-615

Figure 55



INTERNATIONAL SEARCH REPORT

International application No
PCT/EP2018/073160

A. CLASSIFICATION OF SUBJECT MATTER
INV. A61K39/39 A61K39/395 A61K35/761 C07K14/52 C07K14/715
C07K16/28 C07K16/40 C12N15/861 A61P35/00
ADD.

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
A61K C07K C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

EPO-Internal, BIOSIS, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	YU FENG ET AL: "Cancer Associated Fibroblasts-Targeted Oncolytic Virus Results in Enhanced Antitumor Activity in Mouse Model", MOLECULAR THERAPY, vol. 23, no. Suppl. 1, May 2015 (2015-05), page S246, XP002786686, 18TH ANNUAL MEETING OF THE AMERICAN-SOCIETY-OF-GENE-AND-CELL-THERAPY (ASGCT); NEW ORLEANS, LA, USA; MAY 13 -16, 2015 the whole document ----- -/--	1-20

☒ Further documents are listed in the continuation of Box C.

☒ See patent family annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier application or patent but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search 21 November 2018	Date of mailing of the international search report 04/12/2018
Name and mailing address of the ISA/ European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Fax: (+31-70) 340-3016	Authorized officer Lonnoy, Olivier

1

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP2018/073160

Box No. I **Nucleotide and/or amino acid sequence(s) (Continuation of item 1.c of the first sheet)**

1. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of a sequence listing:

   a. ☒ forming part of the international application as filed:

      ☒ in the form of an Annex C/ST.25 text file.

      ☐ on paper or in the form of an image file.

   b. ☐ furnished together with the international application under PCT Rule 13*ter*.1(a) for the purposes of international search only in the form of an Annex C/ST.25 text file.

   c. ☐ furnished subsequent to the international filing date for the purposes of international search only:

      ☐ in the form of an Annex C/ST.25 text file (Rule 13*ter*.1(a)).

      ☐ on paper or in the form of an image file (Rule 13*ter*.1(b) and Administrative Instructions, Section 713).

2. ☐ In addition, in the case that more than one version or copy of a sequence listing has been filed or furnished, the required statements that the information in the subsequent or additional copies is identical to that forming part of the application as filed or does not go beyond the application as filed, as appropriate, were furnished.

3. Additional comments:

C(Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	CARLOS ALBERTO FAJARDO ET AL: "Oncolytic Adenoviral Delivery of an EGFR-Targeting T-cell Engager Improves Antitumor Efficacy", CANCER RESEARCH, vol. 77, no. 8, 15 April 2017 (2017-04-15), pages 2052-2063, XP055388559, & 102ND ANNUAL MEETING OF THE AMERICAN-ASSOCIATION-FOR-CANCER-RESEARCH (AACR); ORLANDO, FL, USA; APRIL 02 -06, 2011 ISSN: 0008-5472, DOI: 10.1158/0008-5472.CAN-16-1708 page 2060, column 1, line 11 - column 2, line 2 -----	1-20
A	WO 2015/155370 A1 (PSIOXUS THERAPEUTICS LTD [GB]) 15 October 2015 (2015-10-15) claim 1 -----	1-20

1

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No
PCT/EP2018/073160

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 2015155370 A1	15-10-2015	EP 3131563 A1	22-02-2017
		US 2017035818 A1	09-02-2017
		WO 2015155370 A1	15-10-2015