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(54) Title: THERAPEUTIC AGENTS

(57) Abstract: An immunoresponsive cell, such as a T-cell expressing (i)a second generation chimeric antigen receptor comprising: (a) a signalling region; (b) a co-stimulatory signalling region; (c) a transmembrane domain; and (d) a binding element that specifically interacts with a first epitope on a target antigen; and (ii)a chimeric costimulatory receptor comprising (e) a co-stimulatory signalling region which is different to that of (b); (f) a transmembrane domain; and (g) a binding element that specifically interacts with a second epitope on a target antigen. This arrangement is referred to as parallel chimeric activating receptors (pCAR). Cells of this type are useful in therapy, and kits and methods for using them as well as methods for preparing them are described and claimed.

The present invention relates to nucleic acids encoding novel chimeric antigen receptors (CARs), as well as to the CARs themselves, cells incorporating the nucleic acids and their use in therapy, in particular to methods in which they are used to facilitate a T-cell response to a selected target.

Background of the Invention

Reference to any prior art in the specification is not an acknowledgement or suggestion that this prior art forms part of the common general knowledge in any jurisdiction or that this prior art could reasonably be expected to be combined with any other piece of prior art by a skilled person in the art.

Chimeric antigen receptors (CARs), which may also be referred to as artificial T cell receptors, chimeric T cell receptors (TCR) or chimeric immunoreceptors are engineered receptors, are well known in the art. They are used primarily to transform immune effector cells, in particular T-cells, so as to provide those cells with a particular specificity. They are particularly under investigation in the field of cancer immunotherapy where they may be used in techniques such as adoptive cell transfer. In these therapies, T-cells are removed from a patient and modified so that they express receptors specific to the antigens found in a particular form of cancer. The T cells, which can then recognize and kill the cancer cells, are reintroduced into the patient.

First generation CARs provide a TCR-like signal, most commonly using CD3 zeta (z) and thereby elicit tumouricidal functions. However, the engagement of CD3z-chain fusion receptors may not suffice to elicit substantial IL-2 secretion and/ or proliferation in the absence of a concomitant co-stimulatory signal. In physiological T-cell responses, optimal lymphocyte activation requires the engagement of one or more co-stimulatory receptors (signal 2) such as CD28 or 4-1BB. Consequently, T cells have also been engineered so that they receive a co-stimulatory signal in a tumour antigen-dependent manner.

An important development in this regard has been the successful design of 'second generation CARs' that transduce a functional antigen-dependent co-stimulatory signal in human primary T

cells, permitting T-cell proliferation in addition to
tumouricidal activity. Second generation CARs most commonly
provide co-stimulation using modules derived from CD28 or 4-1BB.
The combined delivery of co-stimulation plus a CD3 zeta signal

5   renders second generation CARs clearly superior in terms of
function, when compared to their first generation counterparts
(CD3z signal alone). An example of a second generation CAR is
found in US Patent No 7,446,190.

10   More recently, so-called 'third generation CARs' have been
prepared. These combine multiple signalling domains, such as
CD28+4-1BB+CD3z or CD28+OX40+CD3z, to further augment potency.
In the 3rd generation CARs, the signalling domains are aligned
in series in the CAR endodomain and placed upstream of CD3z.

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In general however, the results achieved with these third
generation CARs have disappointingly represented only a marginal
improvement over 2nd generation configurations.

20   The use of cells transformed with multiple constructs has also
been suggested. For example, Kloss et al. Nature Biotechnology
2012, doi:10.1038/nbt.2459 describes the transduction of T-cells
with a CAR comprising a signal activation region (CD3 zeta
chain) that targets a first antigen and a chimeric co-

25   stimulatory receptor (CCR) comprising both CD28 and 4-1BB
costimulatory regions which targets a second antigen. The two
constructs bind to their respective antigens with different
binding affinities and this leads to a 'tumour sensing' effect
that may enhance the specificity of the therapy with a view to

30   reducing side effects.

It is desirable to develop systems whereby T-cells can be
maintained in a state that they can grow, produce cytokines and
deliver a kill signal through several repeated rounds of

35   stimulation by antigen-expressing tumour target cells. Provision
of sub-optimal co-stimulation causes T-cells to lose these
effector functions rapidly upon re-stimulation, entering a state

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known as "anergy". When CAR T-cells are sequentially re-
stimulated *in vitro*, they progressively lose effector properties
(eg IL-2 production, ability to proliferate) and differentiate
to become more effector-like - in other words, less likely to

5   manifest the effects of co-stimulation. This is undesirable for
a cancer immunotherapy since more differentiated cells tend to
have less longevity and reduced ability to undergo further
growth/ activation when they are stimulated repeatedly in the
tumour microenvironment.

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Summary of the Invention

The applicants have found that effective T-cell responses may be
generated using a combination of constructs in which multiple
co-stimulatory regions are arranged in distinct constructs.

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According to a first aspect of the present invention, there is
provided an immuno-responsive cell expressing
        (i)   a second generation chimeric antigen receptor
                comprising:

20   (a) a signalling region;
                (b) a co-stimulatory signalling region;
                (c) a transmembrane domain; and
                (d) a binding element that specifically interacts
                with a first epitope on a target antigen; and

25   (ii)   a chimeric costimulatory receptor comprising
                (e) a co-stimulatory signalling region which is
                different to that of (b);
                (f) a transmembrane domain; and
                (g) a binding element that specifically interacts

30   with a second epitope on a target antigen.

The applicants have found that the efficacy of this system is
good and in particular may be better than that achieved using
conventional third generation CARs having similar elements.

35   Constructs of the type of the invention may be called 'parallel
chimeric activating receptors' or 'pCAR'.

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In addition, the proliferation of the cells, their ability to maintain their cytotoxic potency and to release IL-2 is maintained over many repeated rounds of stimulation with antigen-expressing tumour cells.

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Without being bound by theory, the arrangement of the elements in the pCARs may be facilitating activity. For example, by definition, one of the co-stimulatory modules in a 3rd generation CAR must be placed away from its natural location close to the inner leaflet of the plasma membrane. This may cause it not to signal normally owing to impaired access to obligate membrane-associated partner molecules. Alternatively, close proximity of 2 co-stimulatory signalling modules in a 3rd generation CAR might lead to steric issues, preventing full engagement of one or more downstream signalling pathways. Both of these issues are avoided in the arrangement of the invention. Both the signalling moieties (b) and (e) may be fused directly to a transmembrane domain, ensuring that they are both adjacent to the plasma membrane within the cell. Furthermore, they may be spaced at distinct sites within the cell so that will not interact sterically with each other.

Suitable immuno-responsive cells for use in the first aspect of the invention include T-cells such as cytotoxic T-cells, helper T-cells or regulatory T-cells and Natural Killer (NK) cells. In particular, the immuno-responsive cell is a T-cell.

Suitable elements (a) above may include any suitable signalling region, including any region comprising an Immune-receptor-Tyrosine-based-Activation-Motif (ITAM), as reviewed for example by Love et al. Cold Spring Harbor Perspect. Biol 2010 2(6)1 a002485. In a particular embodiment, the signalling region comprises the intracellular domain of human CD3 [zeta] chain as described for example in US Patent No 7,446,190, or a variant thereof.

In particular, this comprises the domain, which spans amino acid residues 52-163 of the full-length human CD3 zeta chain. It has a number of polymorphic forms (e.g. Sequence ID: gb|AAF34793.1 and gb|AAA60394.1), which are shown respectively as SEQ ID NO 1 and 2:

RVKFSRSADAPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR   (SEQ ID NO 1)

RVKFSRSAEPPAYQQGQNQLYNELNLGRREEYDVLDKRRGRDPEMGGKPRRKNPQEGLYNELQK DKMAEAYSEIGMKGERRRGKGHDGLYQGLSTATKDTYDALHMQALPPR

                                                         (SEQ ID NO 2)

As used herein, the term 'variant' refers to a polypeptide sequence which is a naturally occurring polymorphic form of the basic sequence as well as synthetic variants, in which one or more amino acids within the chain are inserted, removed or replaced. However, the variant produces a biological effect which is similar to that of the basic sequence. For example, the variant mentioned above will act in a manner similar to that of the intracellular domain of human CD3 [zeta] chain. Amino acid substitutions may be regarded as "conservative" where an amino acid is replaced with a different amino acid in the same class with broadly similar properties. Non-conservative substitutions are where amino acids are replaced with amino acids of a different type or class.

Amino acid classes are defined as follows:

Class	Amino acid examples
Nonpolar:	A, V, L, I, P, M, F, W
Uncharged polar:	G, S, T, C, Y, N, Q
Acidic:	D, E
Basic:	K, R, H.

As is well known to those skilled in the art, altering the primary structure of a peptide by a conservative substitution

may not significantly alter the activity of that peptide because
the side-chain of the amino acid which is inserted into the
sequence may be able to form similar bonds and contacts as the
side chain of the amino acid which has been substituted out.

5 This is so even when the substitution is in a region which is
critical in determining the peptide's conformation.

Non-conservative substitutions may also be possible provided
that these do not interrupt the function of the polypeptide as

10 described above. Broadly speaking, fewer non-conservative
substitutions will be possible without altering the biological
activity of the polypeptides.

In general, variants will have amino acid sequences that will be

15 at least 70%, for instance at least 71%, 75%, 79%, 81%, 84%,
87%, 90%, 93%, 95%, 96% or 98% identical to the basic sequence,
for example SEQ ID NO 1 or SEQ ID NO 2.   Identity in this
context may be determined using the BLASTP computer program with
SEQ ID NO 2 or a fragment, in particular a fragment as described

20 below, as the base sequence. The BLAST software is publicly
available at http://blast.ncbi.nlm.nih.gov/Blast.cgi (accessible
on 12 March 2009).

The co-stimulatory signal sequence (b) is suitably located

25 between the transmembrane domain (c) and the signalling region
(a) and remote from the binding element (d).   Similarly the co-
stimulatory signal sequence (e) is suitably located adjacent the
transmembrane domain (f) and remote from the binding element
(g).

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Suitable co-stimulatory signalling regions for use as elements
(b) and (e) above are also well known in the art, and include
members of the B7/CD28 family such as B7-1, B7-2, B7-H1, B7-H2,

35 B7-H3, B7-H4, B7-H6, B7-H7, BTLA, CD28, CTLA-4, Gi24, ICOS, PD-
1, PD-L2 or PDCD6; or ILT/CD85 family proteins such as LILRA3,
LILRA4, LILRB1, LILRB2, LILRB3 or LILRB4; or tumour necrosis

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factor (TNF) superfamily members such as 4-1BB, BAFF, BAFF R,
CD27, CD30, CD40, DR3, GITR, HVEM, LIGHT, Lymphotoxin-alpha,
OX40, RELT, TACI, TL1A, TNF-alpha or TNF RII; or members of the
SLAM family such as 2B4, BLAME, CD2, CD2F-10, CD48, CD58, CD84,
CD229, CRACC, NTB-A or SLAM; or members of the TIM family such
as TIM-1, TIM-3 or TIM-4; or other co-stimulatory molecules such
as CD7, CD96, CD160, CD200, CD300a, CRTAM, DAP12, Dectin-1,
DPPIV, EphB6, Integrin alpha 4 beta 1, Integrin alpha 4 beta
7/LPAM-1, LAG-3 or TSLP R.

The selection of the co-stimulatory signalling regions may be
selected depending upon the particular use intended for the
transformed cells. In particular, the co-stimulatory signalling
regions selected for (b) and (e) above are those which may work
co-operatively or synergistically together. For example, the
co-stimulatory signalling regions for (b) and (e) may be
selected from CD28, CD27, ICOS, 4-1BB, OX40, CD30, GITR, HVEM,
DR3 or CD40.

In a particular embodiment, one of (b) or (e) is CD28 and the
other is 4-1BB or OX40.

In a particular embodiment, (b) is CD28.

In another particular embodiment (e) is 4-1BB or OX40 and in
particular, is 4-1BB. In another embodiment, (e) is CD27.

The transmembrane domains of (c) and (f) above may be the same
or different but in particular are different to ensure
separation of the constructs on the surface of the cell.
Selection of different transmembrane domains may also enhance
stability of the vector since inclusion of a direct repeat
nucleic acid sequence in the viral vector renders it prone to
rearrangement, with deletion of sequences between the direct
repeats. Where the transmembrane domains of (c) and (f) are
the same however, this risk can be reduced by modifying or

"wobbling" the codons selected to encode the same protein sequence.

Suitable transmembrane domains are known in the art and include for example, CD8α, CD28, CD4 or CD3z transmembrane domains.

Where the co-stimulatory signalling region comprises CD28 as described above, the CD28 transmembrane domain represents a suitable option. The full length CD28 protein is a 220 amino acid protein of SEQ ID NO 3

MLRLLLALNLFPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRASLHKGLDSAVE
VCVVYGNYSQQLQVYSKTGFNCDGKLGNESVTFYLQNLYVNQTDIYFCKIEVMYPPPYLDNEKS
NGTIIHVKGKHLCPSPLFPGPSKP**FWVLVVVGGVLACYSLLVTVAFIIFWV**RSKRSRLLHSDYM
NMTPRRPGPTRKHYQPYAPPRDFAAYRS   (SEQ ID NO 3)

where the transmembrane domain is shown in bold type.

In particular, one of the co-stimulatory signalling regions is based upon the hinge region and suitably also the transmembrane domain and endodomain of CD28. In particular, which comprises amino acids 114-220 of SEQ ID NO 3, shown below as SEQ ID NO 4.

IEVMYPPPYLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVAFIIF
WVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS   (SEQ ID NO 4)

In a particular embodiment, one of the co-stimulatory signalling regions (b) or (e) above is a modified form of SEQ ID NO 4 which includes a c-myc tag of SEQ ID No 5.

The c-myc tag is well known and is of SEQ ID NO 5

EQKLISEEDL (SEQ ID NO 5)

The c-myc tag may be added to the co-stimulatory signalling region (b) or (e) by insertion into the ectodomain or by

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replacement of a region in the ectodomain, which is therefore within the region of amino acids 1-152 of SEQ ID NO 3.

In a particularly preferred embodiment, the c-myc tag replaces MYPPPY motif in the CD28 sequence. This motif represents a potentially hazardous sequence. It is responsible for interactions between CD28 and its natural ligands, CD80 and CD86, so that it provides potential for off-target toxicity when CAR T-cells encounter a target cell that expresses either of these ligands. By replacement of this motif with a tag sequence as described above, the potential for unwanted side-effects is reduced.

Thus in a particular embodiment, the co-stimulatory signalling region (b) of the construct is of SEQ ID NO 6

IEVEQKLISEEDLLDNEKSNGTIIHVKGKHLCPSPLFPGPSKPFWVLVVVGGVLACYSLLVTVA
FIIFWVRSKRSRLLHSDYMNMTPRRPGPTRKHYQPYAPPRDFAAYRS   (SEQ ID NO 6)

Furthermore, the inclusion of a c-myc epitope means that detection of the CAR T-cells using a monoclonal antibody is facilitated. This is very useful since flow cytometric detection had proven unreliable when using some available antibodies.

In addition, the provision of a c-myc epitope tag could facilitate the antigen independent expansion of targeted CAR T-cells, for example by cross-linking of the CAR using the appropriate monoclonal antibody, either in solution or immobilised onto a solid phase (e.g. a bag).

Moreover, expression of the epitope for the anti-human c-myc antibody, 9e10, within the variable region of a TCR has previously been shown to be sufficient to enable antibody-mediated and complement mediated cytotoxicity both *in vitro* and *in vivo* (Kieback et al. (2008) Proc. Natl. Acad. Sci. USA, 105(2) 623-8). Thus, the provision of such epitope tags could

also be used as a "suicide system", whereby an antibody could be used to deplete CAR T-cells *in vivo,* in the event of toxicity.

The binding elements (d) and (g) will be different and will bind

5   the same, overlapping or different epitopes. In a particular embodiment the first and second epitopes are associated with the same receptor or antigen.   Thus the first and second epitopes as described above may, in some cases, be the same, or overlapping so that the binding elements (d) and (g) will

10   compete in their binding. Alternatively, the first and second epitopes may be different and associated with the same or different antigens depending upon the particular therapy being envisaged.   In one embodiment, the antigens are different but may be associated with the same disease such as the same

15   specific cancer.

As used herein, the term 'antigen' refers to any member of a specific binding pair that will bind to the binding elements. Thus the term includes receptors on target cells.

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Thus suitable binding elements (d) and (g) may be any element which provides the pCAR with the ability to recognize a target of interest. The target to which the pCARs of the invention are directed can be any target of clinical interest to which it

25   would be desirable to induce a T cell response. This would include markers associated with cancers of various types, including for example, one or more ErbB receptors or the $\alpha_v\beta_6$ integrin, markers associated with prostate cancer (for example using a binding element that binds to prostate-specific membrane

30   antigen (PSMA)), breast cancer (for example using a binding element that targets Her-2 (also known as ErbB2)) and neuroblastomas (for example using a binding element that targets GD2), melanomas, small cell or non-small cell lung carcinoma, sarcomas and brain tumours. In a particular embodiment the

35   target is one or more ErbB dimers as described above or the receptor for colony stimulating factor-1 (CSF-1R) or the $\alpha_v\beta_6$

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integrin, all of which have been implicated in several solid
tumours.

The binding elements used in the pCARs of the invention may
comprise antibodies that recognize a selected target. For
convenience, the antibody used as the binding element is
preferably a single chain antibody (scFv) or single domain
antibody, from a camelid, human or other species. Single chain
antibodies may be cloned from the V region genes of a hybridoma
specific for a desired target. The production of such hybridomas
has become routine, and the procedure will not be repeated here.
A technique which can be used for cloning the variable region
heavy chain (VH) and variable region light chain (VL) has been
described in Orlandi et al., Proc. Natl Acad. Sci. (USA) 86:
3833-3837 (1989). Briefly, mRNA is isolated from the hybridoma
cell line, and reverse transcribed into complementary DNA
(cDNA), for example using a reverse transcriptase polymerase
chain reaction (RT-PCR) kit. Sequence-specific primers
corresponding to the sequence of the VH and VL genes are used.
Sequence analysis of the cloned products and comparison to the
known sequence for the VH and VL genes can be used to show that
the cloned VH gene matched expectations. The VH and VL genes are
then attached together, for example using an oligonucleotide
encoding a (gly4-ser)3 linker.

Alternatively, a binding element of a pCAR may comprise ligands
such as the T1E peptide (binds ErbB homo- and heterodimers),
colony-stimulating factor-1 (CSF-1) or IL-34 (both bind to the
CSF-1 receptor). The T1E peptide is a chimeric fusion protein
composed of the entire mature human EGF protein, excluding the
five most N-terminal amino acids (amino acids 971-975 of pro-
epidermal growth factor precursor (NP_001954.2)), which have
been replaced by the seven most N-terminal amino acids of the
mature human TGF-α protein (amino acids 40-46 of pro-
transforming growth factor alpha isoform 1 (NP_003227.1)).

In another embodiment, a binding element of a pCAR comprises an $\alpha_v\beta_6$ integrin-specific binding agent. The integrin αvβ6 is now regarded as a target in cancer as it has been found to be strongly upregulated in many types of cancer. $\alpha_v\beta_6$ has been
5   identified as a receptor for foot-and-mouth disease virus (FMDV) *in vitro* by binding through an RGD motif in the viral capsid protein, VP1. As a result, as described for example in US Patent No. 8,383,593, a range of peptides derived from FMDV and in particular, peptides originating from the VP1 protein of FMDV
10 and comprising an RGD motif showed increased binding potency and binding specificity. In particular, these peptides comprise the sequence motif

RGDLX^{5}X^{6}L   (SEQ ID NO 7) or

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RGDLX^{5}X^{6}I (SEQ ID NO 8),

wherein LX^{5}X^{6}L or LX^{5}X^{6}I is contained within an alpha helical structure, wherein X^5 and X^6 are helix promoting residues,
20 which have a conformational preference greater than 1.0 for being found in the middle of an [alpha]-helix (from Creighton, 1993 and Pace C. N. and Scholtz J. M. (1998), Biophysical Journal, Vol. 75, pages 422-427). In particular such residues are independently selected from the group consisting of Glu,
25 Ala, Leu, Met, Gln, Lys, Arg, Val, Ile, Trp, Phe and Asp.

Specific examples of such sequences include SEQ ID Nos 9-11 or variants thereof:

30 YTASARGDLAHLTTTHARHL   (SEQ ID NO 9)
GFTTGRRGDLATIHGMNRPF   (SEQ ID NO 10)
or
NAVPNLRGDLQVLAQKVART   (SEQ ID NO 11)

35 These peptides may form a particular group of binding elements for the CARs of the present application.

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For selected malignancies such as Hodgkin's lymphoma and some
breast cancers, two natural ligands are CSF-1 and IL-34 and
these form particularly suitable binding elements for (d) and
(g). They do however bind with different affinities. The
affinity of binding can impact on the activity observed. It may
be beneficial in this case to ensure that the binding element
with the lower binding affinity is used as binding element (b)
and that with the higher binding affinity is used as binding
element (g). In particular, in an embodiment, the relative
affinity of the second generation CAR (i) for its cognate target is
lower than that of the partnering TNFR-based chimeric co-
stimulatory receptor (ii). This does not preclude the use of high
or low affinity targeting moieties in each position provided that
this relative affinity relationship is maintained. Thus in the
case of the present invention, in a particular embodiment,
binding element (b) is CSF-1 which has a relatively low binding
affinity, whilst binding element (g) comprises IL-34 which has a
higher binding affinity.

Suitably the binding element is associated with a leader
sequence which facilitates expression on the cell surface. Many
leader sequences are known in the art, and these include the
macrophage colony stimulating factor receptor (FMS) leader
sequence or CD124 leader sequence.

In a further embodiment, the cells expressing the pCAR are
engineered to co-express a chimeric cytokine receptor, in
particular the 4αβ chimeric cytokine receptor. In 4αβ, the
ectodomain of the IL-4 receptor-α chain is joined to the
transmembrane and endodomains of IL-2/15 receptor-β. This allows
the selective expansion and enrichment of the genetically
engineered T-cells *ex vivo* by the culture of these cells in a
suitable support medium, which, in the case of 4αβ, would
comprise IL-4 as the sole cytokine support. Similarly, the
system can be used with a chimeric cytokine receptor in which

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the ectodomain of the IL-4 receptor-α chain is joined to the
transmembrane and endodomains of another receptor that is
naturally bound by a cytokine that also binds to the common γ
chain.

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As discussed, these cells are useful in therapy to stimulate a
T-cell mediated immune response to a target cell population.
Thus a second aspect of the invention provides a method for
stimulating a T cell mediated immune response to a target cell
10   population in a patient in need thereof, said method comprising
administering to the patient a population of immuno-responsive
cells as described above, wherein the binding elements (d) and
(g) are specific for the target cell.

15   In a third aspect of the invention, there is provided a method
for preparing an immuno-responsive cell according to any one of
the preceding claims, said method comprising transducing a cell
with a first nucleic acid encoding a CAR of structure (i) as
defined above; and also a second nucleic acid encoding a CAR of
20   structure (ii) as defined above.

In particular, in this method, lymphocytes from a patient are
transduced with the nucleic acids encoding the CARs of (i) and
(ii).   In particular, T-cells are subjected to genetic
25   modification, for example by retroviral mediated transduction,
to introduce CAR coding nucleic acids into the host T-cell
genome, thereby permitting stable CAR expression.   They may
then be reintroduced into the patient, optionally after
expansion, to provide a beneficial therapeutic effect. Where the
30   cells such as the T-cells are engineered to co-express a
chimeric cytokine receptor such as 4αβ, the expansion step may
include an *ex vivo* culture step in a medium which comprises the
cytokine, such as a medium comprising IL-4 as the sole cytokine
support in the case of 4αβ. Alternatively, the chimeric cytokine
35   receptor may comprise the ectodomain of the IL-4 receptor-α
chain joined to the endodomain used by a common γ cytokine with

distinct properties, such as IL-7. In this setting, expansion of the cells in IL-4 may result in less cell differentiation, capitalizing on the natural ability of IL-7 to achieve this effect. In this way, selective expansion and enrichment of genetically engineered T-cells with the desired state of differentiation can be ensured.

In a fourth aspect of the invention, there is provided a combination of a first nucleic acid encoding a CAR of (i) above and a second nucleic acid encoding a CCR of (ii) above. As indicated previously, this combination is referred to as a pCAR. Suitable sequences for the nucleic acids will be apparent to a skilled person. The sequences may be optimized for use in the required immuno-responsive cell. However, in some cases, as discussed above, codons may be varied from the optimum or 'wobbled' in order to avoid repeat sequences. Particular examples of such nucleic acids will encode the preferred embodiments described above.

In order to achieve transduction, the nucleic acids of the fourth aspect of the invention are suitably introduced into a vector, such as a plasmid or a retroviral vector. Such vectors including plasmid vectors, or cell lines containing them form a further aspect of the invention.

The first and second nucleic acids or vectors containing them may be combined in a kit, which is supplied with a view to generating immuno-responsive cells of the first aspect of the invention in situ.

Parallel chimeric activating receptors (pCAR) encoded by the nucleic acids described above form a further aspect of the invention.

Detailed Description of the Invention
The invention will now be particularly described by way of example and with reference to the following Figures in which:

Figure 1 is a schematic diagram showing a panel of CARs and
pCARs (named C34B and 34CB) embodying the invention. All CARs
and pCARs were co-expressed in the SFG retroviral vector with
4αβ, a chimeric cytokine receptor in which the IL-4 receptor-α
ectodomain has been fused to the transmembrane and endodomain of
IL-2 receptor-β. Use of 4αβ allows selective enrichment and
expansion of gene-modified T-cells by culture in IL-4, since it
recruits the gamma c (γc) chain.

Figure 2 shows the results of an experiment using CARs shown in
Figure 1. T-cells (1 x 10⁶ cells) expressing these CARs and pCARs
(or untransduced (UT) as control) were co-cultivated *in vitro*
for 24 hours with T47D tumour cells that express (T47D-FMS) or
lack (T47D) the cognate target antigen (Colony-stimulating
factor-1 receptor (CSF-1R), encoded by *c-fms*). Residual viable
tumour cells were then quantified by MTT assay.

Figure 3 shows a representative experiment in which T-cells that
express CARs and pCARs of Figure 1 (or untrans(duced) T-cells as
control) were subjected to successive rounds of Ag stimulation
in the absence of exogenous cytokine. Stimulation was provided
by weekly culture on T47D FMS monolayers and T-cell numbers were
enumerated at the indicated intervals.

Figure 4 shows pooled data from 7 similar replicate experiments
to that shown in Figure 3, indicating the fold expansion of CAR
T-cells that occurred in the week after each cycle of
stimulation.

Figure 5 shows illustrative cytotoxicity assays performed at the
time of stimulation cycles 2, 6, 9 and 12 in the experiment
shown in Figure 3. This follows from the testing of T-cells for
their ability to to kill T47D FMS and unmodified T47D monolayers
(MTT assay), twenty four hours after the time of each re-
stimulation cycle.

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Figure 6 shows the results of testing of supernatant, removed from cultures one day after each cycle of stimulation, for IL-2 and IFN-γ content by ELISA.

Figure 7 demonstrates the establishment of an *in vivo* xenograft model of CSF-1R-expressing anaplastic large cell lymphoma, which allowed subsequent testing of anti-tumour activity of CAR and pCAR-engineered T-cells. The model was established using K299 cells, engineered to express firefly luciferase (luc) and red fluorescent protein (RFP). Figure 7A shows tumour formation following the intravenous injection of the indicated doses of K299 luc cells, quantified by bioluminescence imaging (BLI). Representative BLI images are shown in Figure 7B in mice that received 2 million tumour cells. Expression of RFP+ tumour cells (Figure 7C) in the indicated tissues are shown, demonstrating that tumours only formed in lymph nodes in this model. Expression of the CSF-1R on five representative lymph node tumours is shown in Figure 7D.

Figure 8 shows the results of therapeutic studies in which K299 luc cells were injected intravenously in SCID Beige mice (n=9 per group, divided over 2 separate experiments). After 5 days, mice were treated with CAR T-cells. Pooled bioluminescence emission from tumours is shown in Figure 8A. Bioluminescence emission from individual mice is shown in Figure 8B and survival of mice shown in Figure 8C.

Figure 9 shows the weights of animals used in the therapeutic study over time.

Figures 10-13 show the results of analysis of the expression of 'exhaustion markers' from dual CAR (C34B) expressing T-cells of the invention where Figure 10 shows the results for PD1 analysis, Figure 11 shows the results for TIM3 analysis, Figure

12 shows the results of LAG3 analysis and Figure 13 shows the results for 2B4 analysis.

Figure 14 is a schematic diagram of a panel of CARs and constructs targeted to the integrin αvβ6 which have been prepared including a pCAR (named SFG TIE-41BB/A20-28z) embodying the invention. A20-28z is a second generation CAR that is targeted using the A20 peptide derived from foot and mouth disease virus. A20 binds with high affinity to αvβ6 and with 85-1000 fold lower affinity to other RGD-binding integrins. C20-28z is a matched control in which key elements of A20 have been mutated to abrogate integrin binding activity. All CARs have been co-expressed with 4αβ, as described in Figure 1.

Figure 15 is a series of histograms obtained by flow cytometry illustrating integrin expression in A375 puro and Panc1 cells. Cells were stained with anti-β6 (Biogen Idec) followed by secondary anti-mouse PE, anti-αvβ3 or anti-αvβ5 (both APC conjugated, Bio-Techne). Gates were set based on secondary antibody alone or isotype controls.

Figure 16 is a series of graphs illustrating the cytotoxicity of CARs including the pCARs of the invention targeted to αvβ6. T-cells expressing the indicated CARs and pCARs were co-cultivated with αvβ6-negative (Panc1 and A375 puro) or αvβ6-positive (Bxpc3 and A375 puro β6) tumour cells. Data show the mean ±_SEM of 2-7 independent experiments, each performed in triplicate. *$p<0.05$; **$p<0.01$; ***$p<0.001$.

Figure 17 is a series of graphs showing production of IFN-γ by CARs including pCARs of the invention, targeted to αvβ6. T-cells expressing the indicated CARs and pCARs were co-cultivated with αvβ6-negative (Panc1 and A375 puro) or αvβ6-positive (Bxpc3 and A375 puro β6) tumour cells. Data show the mean ±_SEM of 5-6 independent experiments, each performed in duplicate. *$p<0.05$; **$p<0.01$; ***$p<0.001$; ns - not significant.

Figure 18 shows the results of re-stimulation experiments using the CAR and pCAR-engineered T-cells described above and indicating the ability of A20-28z/T1E-41BB pCAR T-cells to

5   undergo repeated antigen stimulation, accompanied by expansion of T-cells and destruction of target cells that do (Bxpc3) or do not (Panc1) express the αvβ6 integrin.

Figure 19 shows the results of re-stimulation experiments using

10   pCAR-engineered T-cells in which A20-28z was co-expressed with T1E-41BB, T1E-CD27 or T1E-CD40, allowing the comparative evaluation of co-stimulation by additional members of the TNF receptor family. Control T-cells were non-transduced (NT) while CARs contained truncated (tr) endodomains. T-cells were re-

15   stimulated on target cells that do (Bxpc3) or do not (Panc1) express the αvβ6 integrin, making comparison with unstimulated T-cells. In the case of Bxpc3 cells, superior expansion (Figure 19A) accompanied by sustained cytotoxic activity (Figure 19B) was observed with A20-28z/T1E-CD27 T-cells. By contrast, with

20   Panc1 cells, superior expansion (Figure 19A) accompanied by sustained cytotoxic activity (Figure 19B) was observed with A20-28z/T1E-CD27 T-cells. These data demonstrate that additional members of the TNF receptor family can also deliver co-stimulation using the pCAR format.

25

Example 1
A panel of CARs targeted against the CSF-1 receptor (encoded by c-FMS), which is over-expressed in Hodgkin's lymphoma,

30   anaplastic large cell lymphoma and some solid tumours such as triple negative breast cancer were prepared and are illustrated schematically in Figure 1. The panel of CARs included both second and third generation CARs with either of the two natural ligands, CSF-1 or IL-34, as the targeting moieties. Although

35   both CSF-1 and IL-34 bind to CSF-1 receptor, IL-34 binds with much higher affinity (34-fold higher than CSF-1).

The constructs SFG C28ζ and SFG CTr were cloned in the SFG retroviral vector as NcoI/XhoI fragments, ensuring that their start codons are at the site of the naturally occurring NcoI site, previously occupied by the deleted *env* gene. Gene expression is achieved from the Moloney murine leukaemia virus (MoMLV) long terminal repeat (LTR), which has promoter activity and virus packaging of the RNA is ensured by the MoMLV ψ packaging signal, which is flanked by splice donor and acceptor sites.

All other constructs were designed and cloned using the Polymerase Incomplete Primer Extension (PIPE) cloning method. PIPE cloning method is a PCR-based alternative to conventional restriction enzyme- and ligation-dependent cloning methods. It eliminates the need to incorporate restriction sites, which could encode additional unwanted residues into expressed proteins. The PIPE method relies on the inefficiency of the amplification process in the final cycles of a PCR reaction, possibly due to the decreasing availability of dNTPs, which results in the generation of partially single-stranded (PIPE) PCR products with overhanging 5'ends. A set of vector-specific primers was used for PCR vector linearization and another set of primers with 5'-vector-end overlapping sequences then used for insert amplification, generating incomplete extension products by PIPE. In a following step, the PIPE products were mixed and the single-stranded overlapping sequences annealed and assembled as a complete SFG CAR construct. Successful cloning was confirmed by diagnostic restriction digestion. DNA sequencing was performed on all constructs to confirm that the predicted coding sequence was present, without any PCR-induced mutations (Source Bioscience, UK).

The panel included two "dual targeted" Chimeric Activating Receptors (pCARS) in which CSF-1 or IL-34 are coupled to 28z and 4-1BB, or vice versa. The dual targeted pCAR combinations were then stoichiometrically co-expressed in the same T-cell population using a *Thosea Asigna* (T)2A-containing retroviral

vector. One of these CARs was designated 'C34B' (CSF1-28z plus IL34-41BB) and the other was named '34CB' (IL34-28z plus CSF1-41BB).

In these dual targeted CAR T-cells, both co-stimulatory motifs (CD28/ 4-1BB) are placed in their natural location, close to the membrane, physically separated from each other and co-expressed in the same T-cell.

All CARs were co-expressed with an IL-4 responsive 4αβ receptor using an additional T2A element in the vector. This enables enrichment/ expansion of T-cells using IL-4, making it easier to compare the function of these diverse cell populations after selection.

The main focus of the experiments was to test the behaviour of the T-cells on repeated re-stimulation with tumour target cells that either express or lack the FMS/ CSF-1 receptor target. In each cycle, 1 million of the indicated IL-4 expanded CAR T-cells were suspended in RPMI + human AB serum and cultured with a confluent monolayer (24 well dish) of the antigen-expressing target (T47D FMS) or antigen null target (T47D).

Thereafter, if the CAR T-cells had persisted and destroyed the monolayer, 1 million T-cells were removed and re-stimulated in an identical manner each week. Total cell number was extrapolated at each time-point depending on the expansion of T-cells that occurred in each weekly cycle.

Throughout all of these experiments, T-cells were cultured in the absence of any exogenous cytokine such as IL-2 or IL-4 – so they had to make their own cytokines in order to persist and expand. Cytokine (IFN-γ and IL-2) production was measured by ELISA in supernatants harvested from T-cell/ tumour cell co-cultures, providing a second marker of effective co-stimulation.

It was found (Figure 2) that on their first exposure to a tumour monolayer that expresses target (FMS encoded CSF-1 receptor), all CARs that are predicted to kill do so (pooled data from 12 expts). The controls are UT (untransduced), P4 (targets an irrelevant antigen, PSMA) and CT4 in which the endodomain is truncated. As expected, none of the CAR T-cells kill tumour cells that lack CSF-1 receptor (T47D).

A representative re-stimulation experiment is shown in Figure 3. Pooled re-stimulation data from 7 experiments is shown in Figure 4. In this case, proliferation on the first cycle was similar for most of the constructs, although the IL-34 targeted second and third generation constructs were poorer. This may be because the affinity of the IL-34 targeting moiety is too high.

In the later cycles however, the C34B dual pCAR combination (a CSF-1 targeted 28z second generation CAR co-expressed with an IL-34 targeted 4-1BB co-stimulatory motif) consistently emerged as clearly superior.

In the experiment shown in Figure 3, supernatant was collected 24 hours after the time of each re-stimulation cycle and was analysed for cytokine content (IFN-γ and IL-2) by ELISA. The percentage of residual tumour cell viability was measured by MTT assay (representative examples shown in Figure 5). The cytokine production results are shown in Figure 6. It was found that only the C34B CAR T-cells retained the ability to make IL-2 throughout each cycle of stimulation. This was lost by all of the other CAR combinations after the first cycle. Sustained retention of the ability to make IL-2 through recursive re-stimulation is not usually seen with CAR T-cells and this suggests that this delivery of dual co-stimulation is fundamentally altering the differentiation of these cells *in vitro*, delaying the onset of anergy.

Number of viable T-cells post monolayer destruction on consecutive cycles of Ag-stimulation was also monitored and the results are shown in Figure 5. After the second cycle of re-stimulation, all CARs except C34B begin to lose the ability to achieve CSF-1R-dependent tumour cell killing. By contrast, T-cells that express C34B retain antigen-dependent potency in this cytotoxic assay for up to 13 iterative cycles of re-stimulation, but never elicit cytotoxicity against unmodified T47D cells.

Also, so-called "exhaustion markers" on these T-cells (PD1, TIM3, 2B4 and LAG3) were also measured by flow cytometry. The results are shown in Figures 10-13. As expected, the percentage of T cells that expressed various exhaustion markers progressively increased on the re-stimulated T-cells, but this did not retard the proliferation, tumour cell destruction or cytokine release by the C34B cells, upon antigen stimulation. This suggests that the superior function of C34B is not the result of delayed upregulation of exhaustion markers.

In summary, the pCAR approach of the invention seems to maintain the cells in a state whereby they retain responsiveness to antigen through more cycles of re-stimulation. There are indications that it may retard differentiation beyond controlled memory state and it appears to delay the onset of anergy while retaining the ability of the cells to make IL-2 upon activation.

Example 2
Analysis of effects *in vivo*
A panel of CARs used in Example 1 above were tested for anti-tumour activity using a highly aggressive *in vivo* xenograft model in which the CSF-1 receptor target is expressed at low levels and in which disease is disseminated throughout lymph nodes (Figure 7). Tumour cells were tagged with firefly luciferase, allowing the non-invasive monitoring of disease burden.

SCID/Beige mice were randomised into 6 groups (9 animals per group combined over two independent experiments) and were inoculated intravenously (IV) with 2x10⁶ K299 tumour cells, re-suspended in 200µL PBS. On day 5, the groups were treated with
5   one of the therapeutic regimens indicated below:

• C4B group: 20x10⁶ C4B T-cells IV

• C34B group: 20x10⁶ C34B T-cells IV

• 43428Bz: 20x10⁶ 43428Bz T-cells IV

• 34CB group: 20x10⁶ 34CB T-cells IV

10   • UT (Untransduced) group: 20x10⁶ untransduced T-cells IV

• NT (Non-treated) group: 200µL PBS IV

Tumour growth was monitored using bioluminescence imaging (BLI) at appropriate time-points for the duration of the study.

15

The results are shown in Figure 8. Again, the best performing system was that of the pCAR, C34B, indicated by lower average BLI emission (Figure 8A-B), delayed tumour progression or tumour regression, leading to prolonged survival of mice (Figure 8C).

20

Animals were weighed throughout the experiment and no significant toxicity was noted (Figure 9).

Example 3
25   Selection of targeting moieties to engineer pCARs that elicit T-cell activation in an αvβ6-dependent manner.

A panel of CARs that target αvβ6 integrin alone or together with the extended ErbB family were prepared and are shown schematically in Figure 14. The binding element used in this
30   case was A20 peptide (SEQ ID NO 11) derived from the GH-loop of the capsid protein VP1 from Foot and Mouth Disease Virus (serotype 01 BFS)(US8,927,501). This was placed downstream of a CD124 signal peptide and fused to CD28 and CD3ζ endodomains to form A20-28ζ, a 2nd generation CAR. A control (C20-28ζ) was
35   prepared comprising a similar construct but with a scrambled targeting peptide (named C20) in which the key RGDL motif was

replaced with AAAA. A second control comprised A20 fused to a CD28 truncated endodomain (A20-Tr).

To create the pCAR of the invention (named TIE-41BB/A20-28z), A20-28z was co-expressed with a chimeric co-stimulatory receptor comprising a pan-ErbB targeted peptide (T1E) fused to a CD8α transmembrane and a 41BB endodomain.

Where indicated, CARs were co-expressed with the 4αβ chimeric cytokine receptor to allow for IL-4-mediated enrichment in vitro. Equimolar co-expression of the IL-4-responsive 4αβ chimeric cytokine receptor, in which the IL-4 receptor α ectodomain is fused to the transmembrane and endodomain of the shared IL-2/15 receptor β, was achieved using a Thosea Asigna (T)2A ribosomal skip peptide. These chimeric molecules were expressed in human T-cells by retroviral gene transfer.

The integrin expression pattern of cancer cell lines A375 was assessed using flow cytometry (Figure 15), and these were separated into αvβ6-negative (Panc1 and A375 puro) or αvβ6-positive (Bxpc3 and A375 puro β6) tumour cells. These cells were co-cultured with CAR T-cells at an effector:target ratio of 1:1 for either 24, 28 or 72 hours, after which time, cytotoxicity was assessed by MTT assay and expressed relative to untreated tumour cells. The results are shown in Figure 16.

These data show that A20-28z CAR T-cells kill all target cells that express αvβ6 integrin (Bxpc3 and A375 β6 puro), but spare targets that lack this integrin (Panc1 and A375 puro). Secondly, the control CARs C20-28z and A20-Tr are inactive in these assays. Thirdly, T-cells that express the T1E-41BB/ A20-28z pCAR cause efficient killing of target cells that express αvβ6 integrin (Bxpc3 and A375 β6 puro). All of these results are as expected. Notably however, T-cells that express the T1E-41BB/ A20-28z pCAR also cause the killing of target cells that lack αvβ6 (Panc1 and A375 puro). This indicates that, within a pCAR configuration, the ability of the A20 peptide to bind non-αvβ6

integrins with low affinity is sufficient to trigger the activation of these engineered T-cells.

Production of IFN-γ by the pCAR and control engineered T-cells was then assessed. Tumour cells that lacked αvβ6 (Panc1 and A375 puro) or expressed αvβ6 (Bxpc3 and A375 puro β6) were co-cultured with genetically engineered T-cells at an effector:target ratio of 1:1 and supernatant was collected after 24, 48 or 72 hours. Levels of IFN-γ were quantified by ELISA (eBioscience). The results are shown in Figure 17. As expected, the controls did not generate significant quantities of IFN-γ while A20-28z CAR T-cells released IFN-γ when cultured with αvβ6-positive (Bxpc3 and A375 puro β6) tumour cells. Notably, T-cells that express the pCAR of the invention, TIE-41BB/A20z, produce more IFN-γ than A20-28z T-cells when cultured with αvβ6-positive (Bxpc3) tumour cells. In addition, TIE-41BB/A20z+ T-cells produced IFN-γ when cultured with αvβ6-negative (Panc1 and A375 puro) tumour cells. Once again, this demonstrates that, within a pCAR configuration, low affinity binding of the A20 peptide to non-αvβ6 integrins is sufficient to trigger the activation of these engineered T-cells.

Next, the CAR T-cell populations were re-stimulated bi-weekly in the absence of IL-2 support on Panc1 (αvβ6 negative) or Bxpc3 tumour cells (αvβ6 positive). Tumour cells were co-cultured with CAR T-cells derived from a patient with pancreatic ductal adenocarcinoma (PDAC) at an effector:target ratio of 1:1 (Figure 18). T-cells were initially added at 2×10^5 cells/well and were counted 72hrs after co-culture to assess expansion (top panels). Cytotoxicity was assessed at 72hrs post-addition of T-cells by MTT assay (bottom panels). If there were a sufficient number of T-cells (2×10^5), T-cells were re-stimulated on a fresh tumour monolayer and the process repeated a further 72hrs later.

Results are shown in Figure 18. These illustrate that A20-28z/T1E-41BB+ T-cells undergo a number of rounds of expansion

accompanied by IL-2 release (data not shown) and destruction of αvβ6+ Bxpc3 cells. Once again, they also underwent a number of rounds of expansion accompanied by IL-2 release and destruction of Panc1 tumour cells.

Overall, the results clearly showed that the pCAR comprising A20-28z/T1E-41BB exhibits enhanced *in vitro* functionality compared to a 2nd generation CAR targeted against αvβ6. Furthermore, the A20-28z/T1E-41BB+ T-cells also undergo activation by Panc1 or A375 puro cells, which express minimal to undetectable levels of this integrin. Taken with the findings obtained using the C34B pCAR (examples 1 and 2), this indicates that the pCAR configuration allows T-cell activation to occur upon serial re-stimulation when a high affinity binding interaction occurs with the 41BB CCR while a lower affinity interaction occurs with the 28z 2nd generation CAR.

Example 4
Use of an alternative TNF receptor family member, CD27 to engineer a functional pCAR.
Using the A20-28z/T1E-41BB pCAR as starting material, additional pCARs were engineered in which the 41BB module was replaced by alternative members of the TNF receptor family, namely CD27 or CD40. Control pCARs were engineered in which endodomains were truncated (tr). Target cells that express (Bxpc3) or lack (Panc1) αvβ6 were plated at a density of 5×10^4 cells per well of a 24 well plate. After 24 hours, 5×10^4 pCAR T-cells were added to target cells or empty wells ("unstimulated"), without exogenous cytokine support. After a further 72 hours, T-cells were harvested from the wells and were counted (Figure 19A). An MTT assay was performed to determine the percentage viability of the residual target cells, making comparison with control target cells that had been plated without addition of T-cells (Figure 19B). If T-cells proliferated after each cycle of stimulation, they were re-stimulated on fresh target cells, exactly as described above. Proliferation of pCAR T-cells (Figure 19A) and MTT assay (Figure 19B) were performed after 72 hours as before.

Iterative re-stimulation of pCAR T-cells and assessment of target cell killing was continued in this manner until T-cells no longer proliferated over the course of each 72 hour cycle.

5   These data once again confirm the superior functionality of the A20-28z/T1E-41BB pCAR when T-cells are stimulated on Panc1 target cells, indicated by sustained T-cell proliferation and tumour cell killing. This provides further confirmation that low affinity binding of the A20 peptide to non-αvβ6 integrins is

10   sufficient to trigger the activation of these engineered T-cells. Notably however, the A20-28z/T1E-CD27 pCAR achieved the greatest level of proliferation (Figure 19A) and sustained tumour cell killing (Figure 19B) when re-stimulated on αvβ6-expressing Bxpc3 cells. By contrast, CD40-based pCARs exhibited

15   modest function in these assays. Together, these data demonstrate that a number of TNF receptor family members can be employed to engineer pCARs that demonstrate superior functionality, exemplified by CD27 or 41BB.

20

CLAIMS

1.   An immuno-responsive T-cell or Natural Killer (NK)-cell construct expressing

(i)   a second generation chimeric antigen receptor (CAR) comprising:

(a) a signalling region;

(b) a co-stimulatory signalling region;

(c) a transmembrane domain; and

(d) a binding element that specifically interacts with a first epitope on a target antigen; and

(ii)   a chimeric costimulatory receptor (CCR) comprising

(e) a co-stimulatory signalling region which is different to that of (b);

(f) a transmembrane domain; and

(g) a binding element that specifically interacts with a second epitope on a target antigen.

2.   An immuno-responsive cell according to claim 1 which is a T-cell.

3.   An immuno-responsive cell according to claim 1 or claim 2 wherein the co-stimulatory signalling regions for (b) and (e) are selected from CD28, CD27, ICOS, 4-1BB, OX40, CD30, GITR, HVEM, DR3 or CD40.

4.   An immuno-responsive cell according to claim 3, wherein one of (b) or (e) is CD28 and the other is 4-1BB or OX40.

5.   An immuno-responsive cell according to claim 3, wherein (b) is CD28 and (e) is 4-1BB or CD27.

6.   An immuno-responsive cell according to any one of the preceding claims, wherein the transmembrane domains of (c) and (f) are selected from CD8α and CD28 transmembrane domains.

7.   An immuno-responsive cell according to any one of the preceding claims, wherein the first and second epitopes are associated with the same receptor or antigen.

8.   An immuno-responsive cell according to any one of the preceding claims which co-expresses a chimeric cytokine receptor.

9.   An immuno-responsive cell according to claim 8, wherein the chimeric cytokine receptor is $4\alpha\beta$.

10.   An immuno-responsive cell according to any one of the preceding claims, wherein at least one of binding element (d) or binding element (g) is a ligand for an ErbB dimer, a receptor for colony stimulating factor-1 (CSF-1R) or an $\alpha_v\beta_6$ integrin-specific binding agent.

11.   An immuno-responsive cell according to any one of the preceding claims, wherein binding element (d) comprises CSF-1 and binding element (g) comprises IL-34; or wherein binding element (d) is an $\alpha_v\beta_6$ integrin-specific binding agent which is a peptide comprising the sequence motif
    RGDLX^{5}X^{6}L (SEQ ID NO 7) or
    RGDLX^{5}X^{6}I (SEQ ID NO 8),
wherein LX^{5}X^{6}L or LX^{5}X^{6}I is contained within an alpha helical structure, wherein X^5 and X^6 are helix promoting residues; and binding element (g) is a TIE peptide.

12.   An immuno-responsive cell according to any one of the preceding claims, wherein binding affinity of binding element (d) is lower than that of binding element (g).

13.   A method for preparing an immuno-responsive cell according to any one of the preceding claims, said method comprising transducing a cell with a first nucleic acid encoding a CAR of structure (i) as defined in claim 1; and also a second nucleic acid encoding a CCR of structure (ii) as defined in claim 1.

14.   A method according to claim 13, wherein the immuno-responsive cell comprises a chimeric cytokine receptor, and wherein an expansion step is carried out in the presence of said cytokine.

15.   A combination of a first nucleic acid encoding a CAR of (i) as defined in claim 1 and a second nucleic acid encoding a CCR of (ii) as defined in claim 1.

16.   A vector or combination of vectors comprising a combination according to claim 15.

17.   A kit comprising a combination according to claim 15 or claim 16.

18.   A method of stimulating a T-cell mediated immune response to a target cell population in a patient in need thereof, said method comprising administering to the patient an immuno-responsive cell according to any one of claims 1 to 12, a combination of the first and second nucleic acid according to claim 15, or a vector or combination of vectors according to claim 16, wherein the binding elements (d) and (g) are specific for the target cell, thereby stimulating a T-cell mediated immune response to a target cell population in the patient in need thereof.

19.   Use of an immuno-responsive cell according to any one of claims 1 to 12, a combination of the first and second nucleic acid according to claim 15, or a vector or combination of vectors according to claim 16 in the preparation of a medicament for stimulating a T-cell mediated immune response to a target cell population, wherein the binding elements (d) and (g) are specific for the target cell.

20.   A method of treating cancer in a patient in need thereof, said method comprising administering to the patient an immuno-responsive cell according to any one of claims 1 to 12, a combination of the first and second nucleic acid according to claim 15, or a vector or combination of vectors according to claim 16, to stimulate a T-cell

mediated immune response to a target cancer cell population in the patient, thereby treating cancer in the patient in need thereof.

21. Use of an immuno-responsive cell according to any one of claims 1 to 12, a combination of the first and second nucleic acid according to claim 15, or a vector or combination of vectors according to claim 16 in the preparation of a medicament for the treatment of cancer in a patient in need thereof, wherein the medicament stimulates a T-cell mediated immune response to a target cancer cell population in the patient.
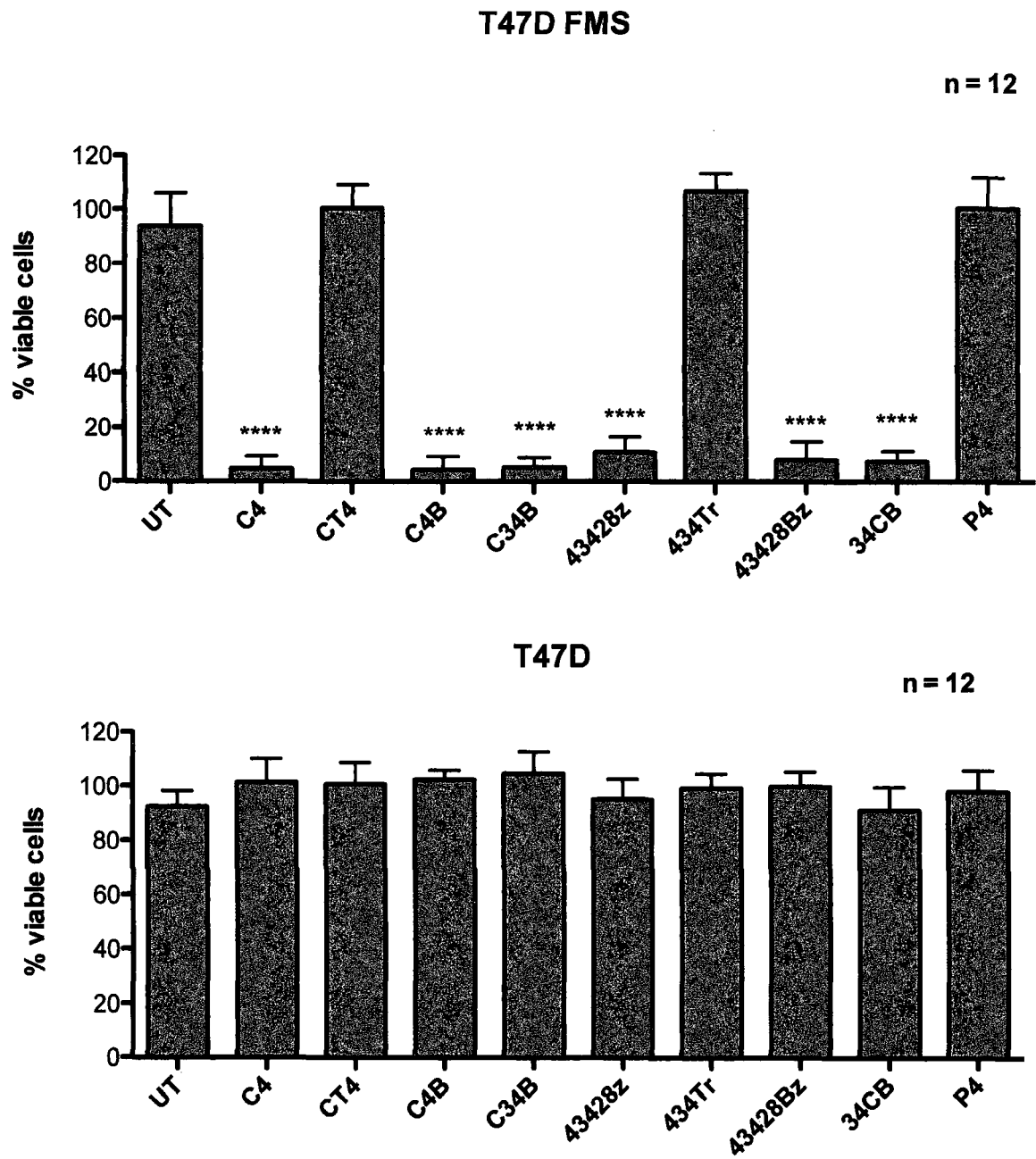
22. The method of claim 20 or the use of claim 21, wherein the cancer is selected from the group consisting of prostate cancer, breast cancer, neuroblastoma, melanoma, small cell or non-small cell lung carcinoma, sarcoma and brain tumours.

23. A method of providing a therapy to a patient in need thereof, said method comprising administering to the patient an immuno-responsive cell according to any one of claims 1 to 12, a combination of the first and second nucleic acid according to claim 15, or a vector or combination of vectors according to claim 16, to stimulate a T-cell mediated immune response to a target cell population in the patient, thereby providing a therapy to the patient in need thereof.

24. Use of an immuno-responsive cell according to any one of claims 1 to 12, a combination of the first and second nucleic acid according to claim 15, or a vector or combination of vectors according to claim 16 in the preparation of a medicament for providing a therapy to a patient in need thereof, wherein the medicament stimulates a T-cell mediated immune response to a target cell population in the patient.
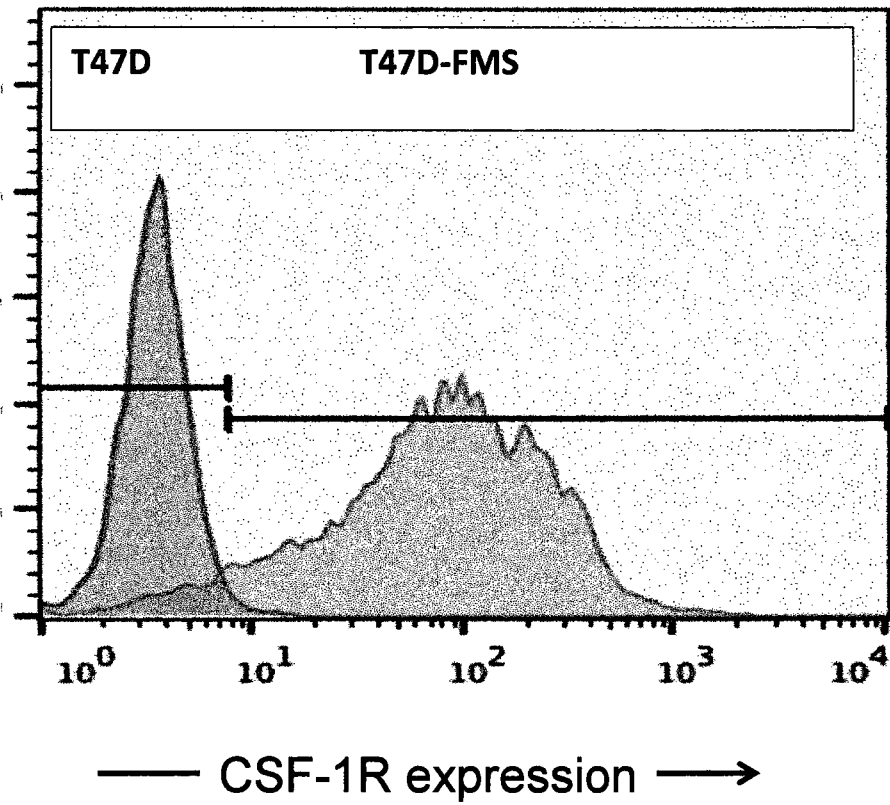
Figure 1

SFG C34B

SFG 34CB

Figure 2

— CSF-1R expression →

Figure 3

Figure 4

Figure 5

Interferon-γ

Interleukin-2

Cycle of re-stimulation

C34B   34CB
C4   43428z
C4B   43428Bz
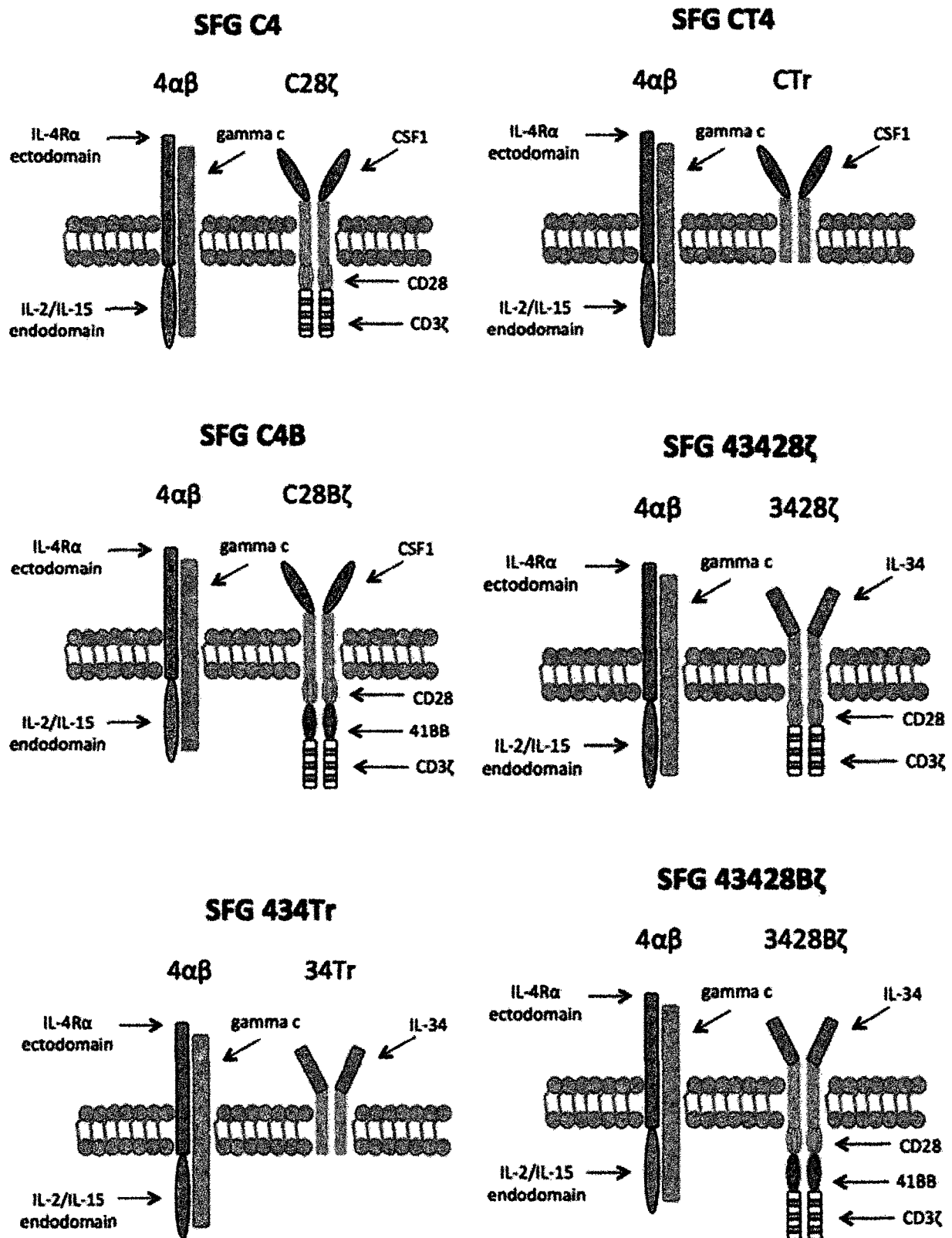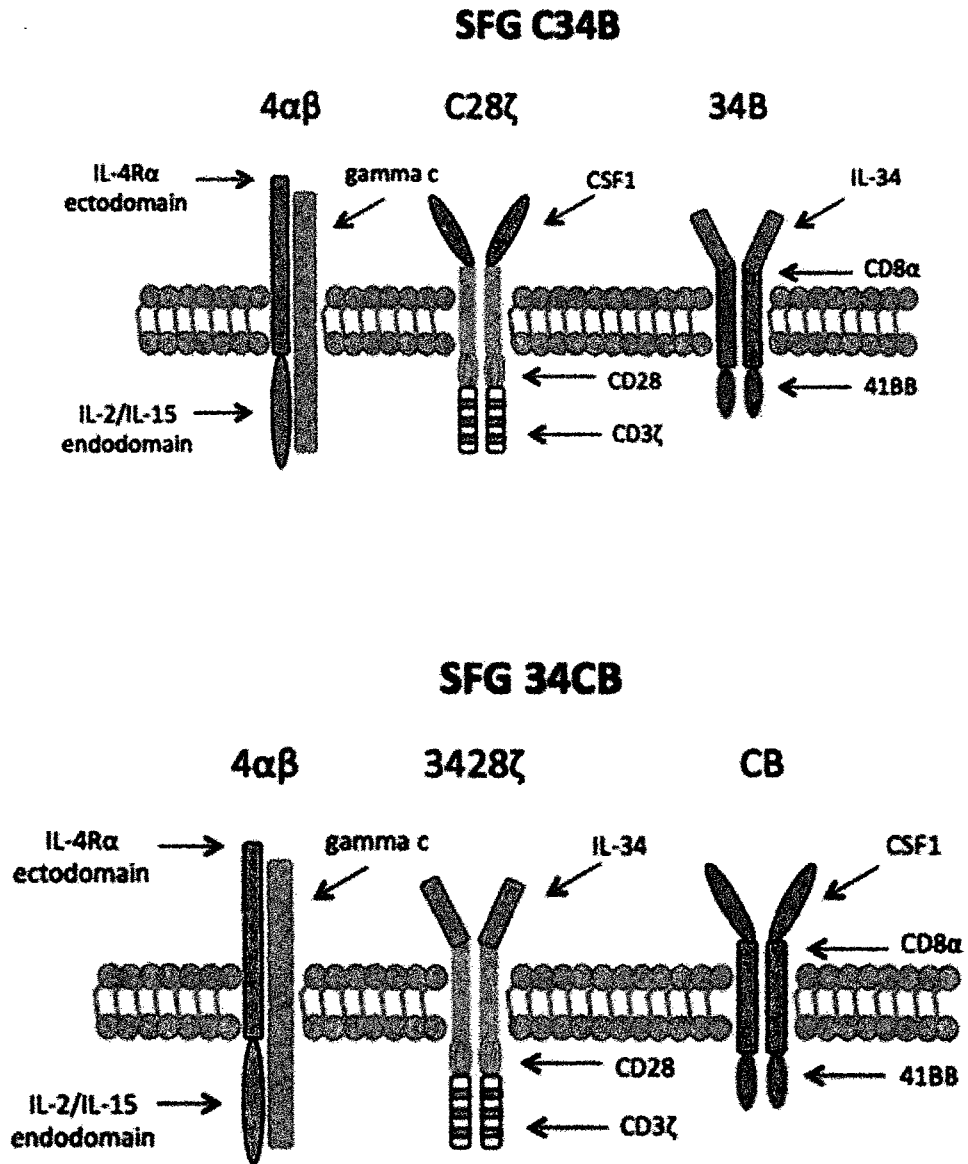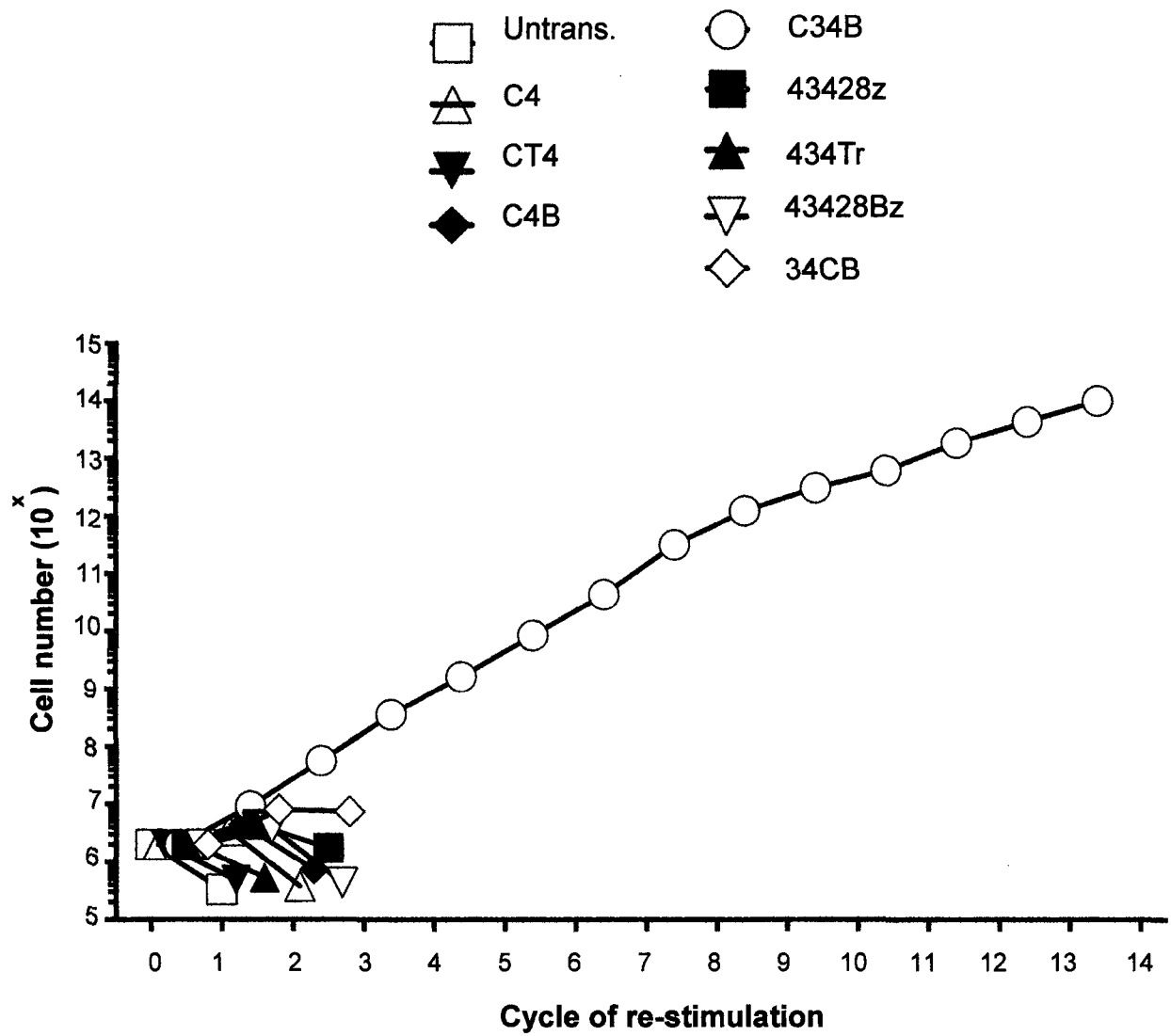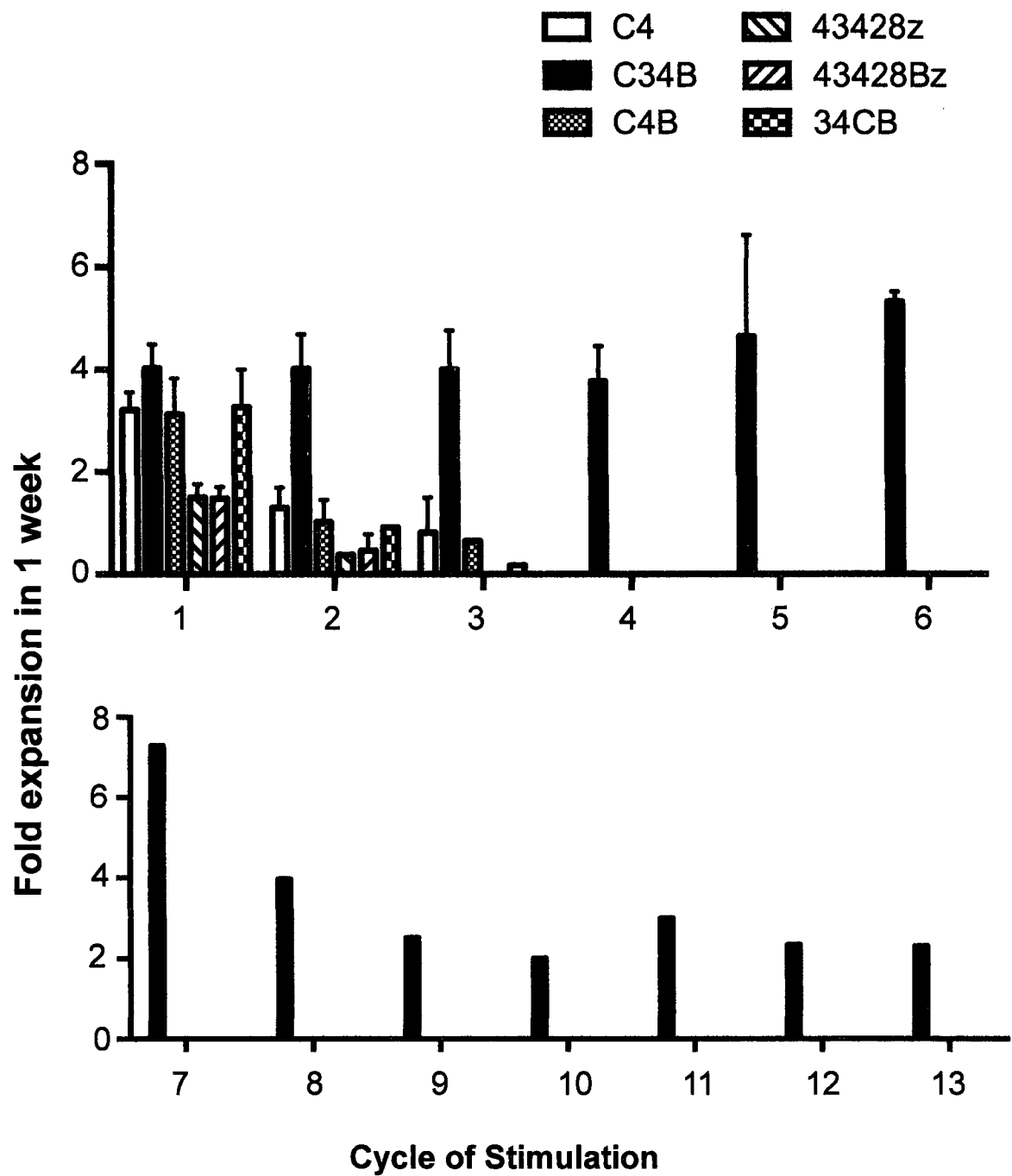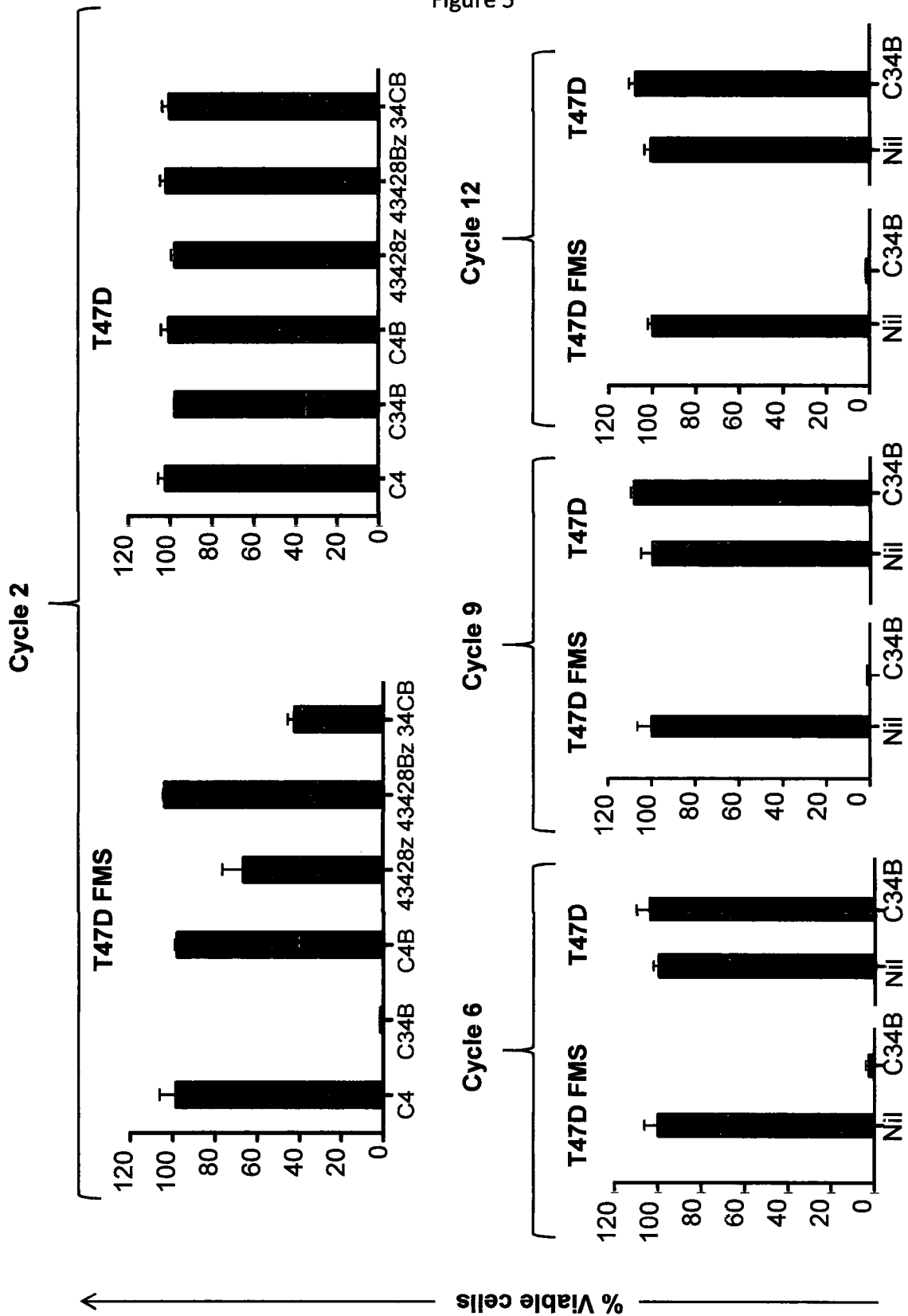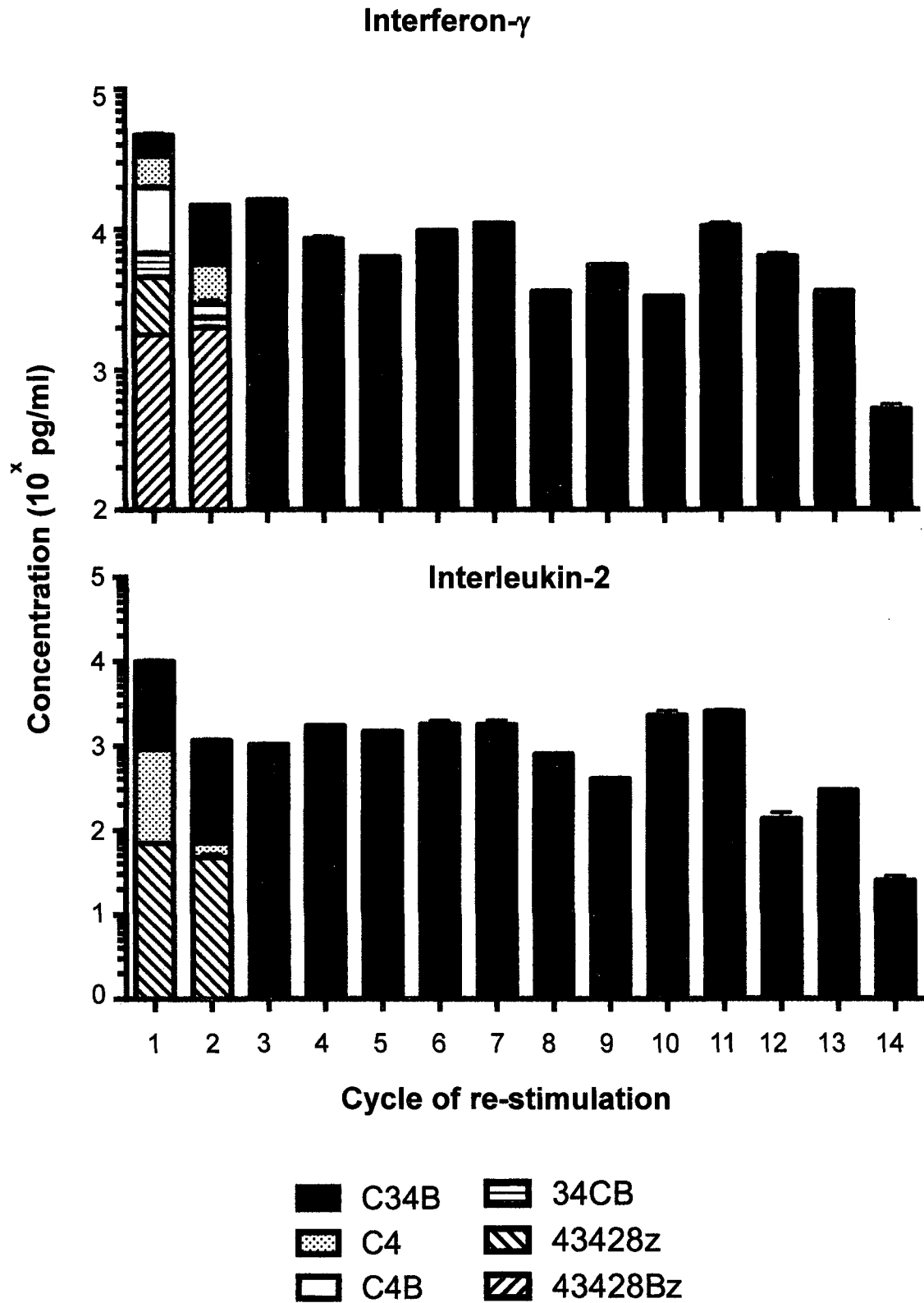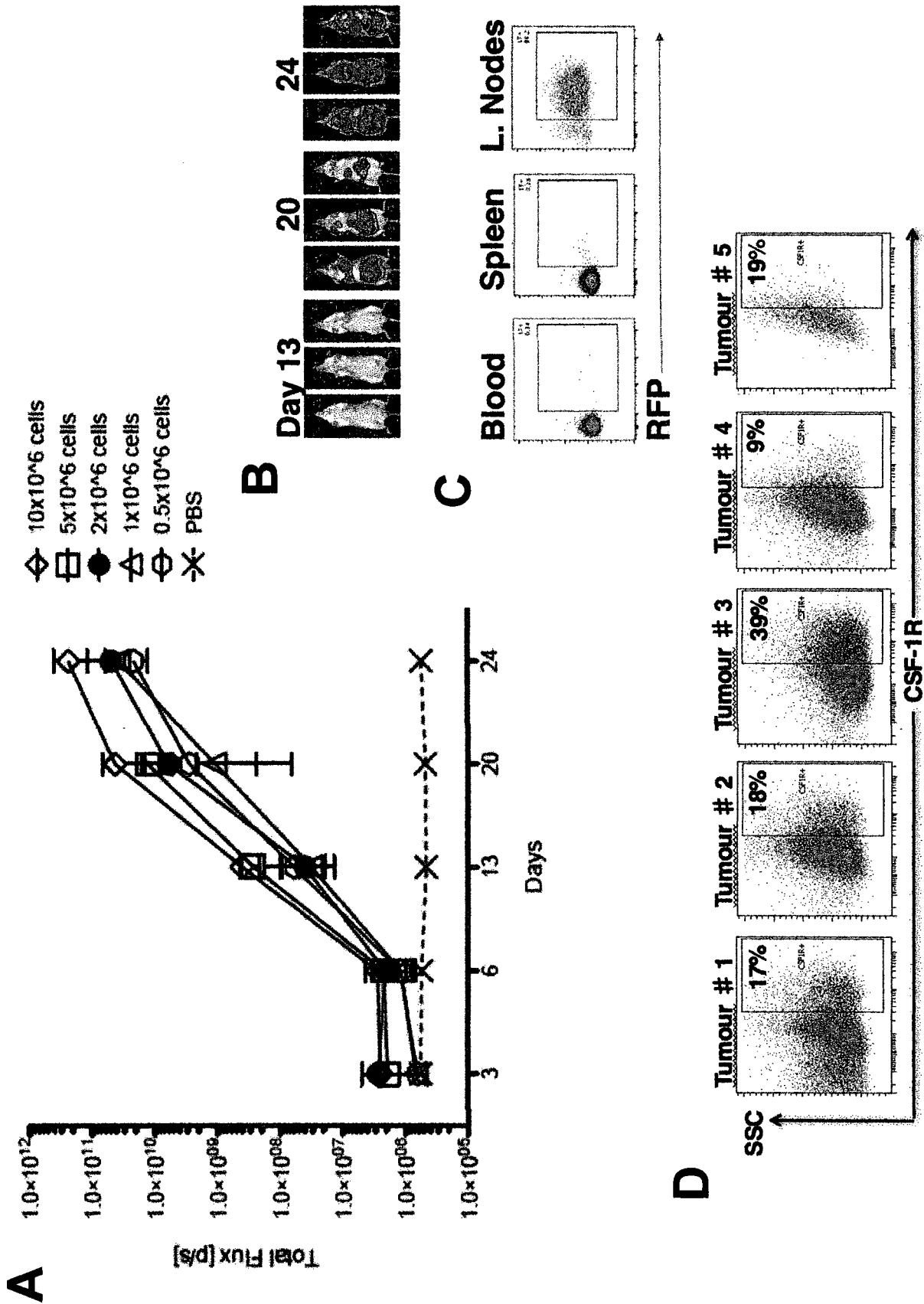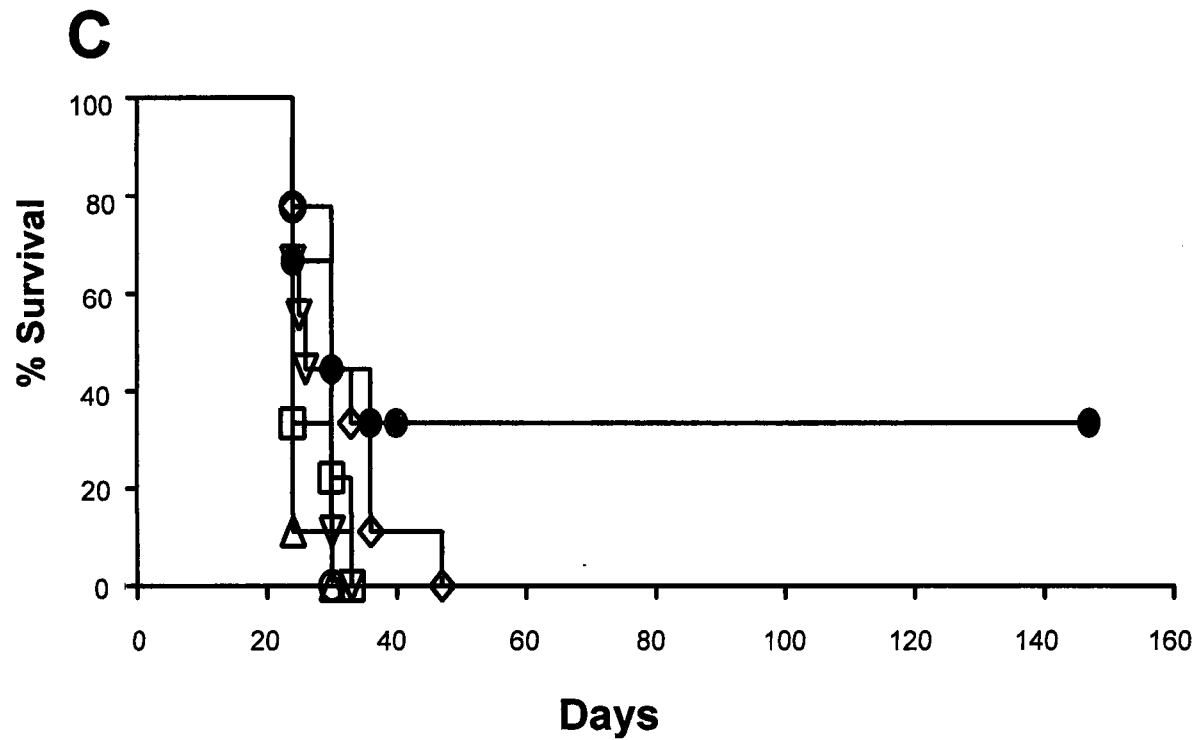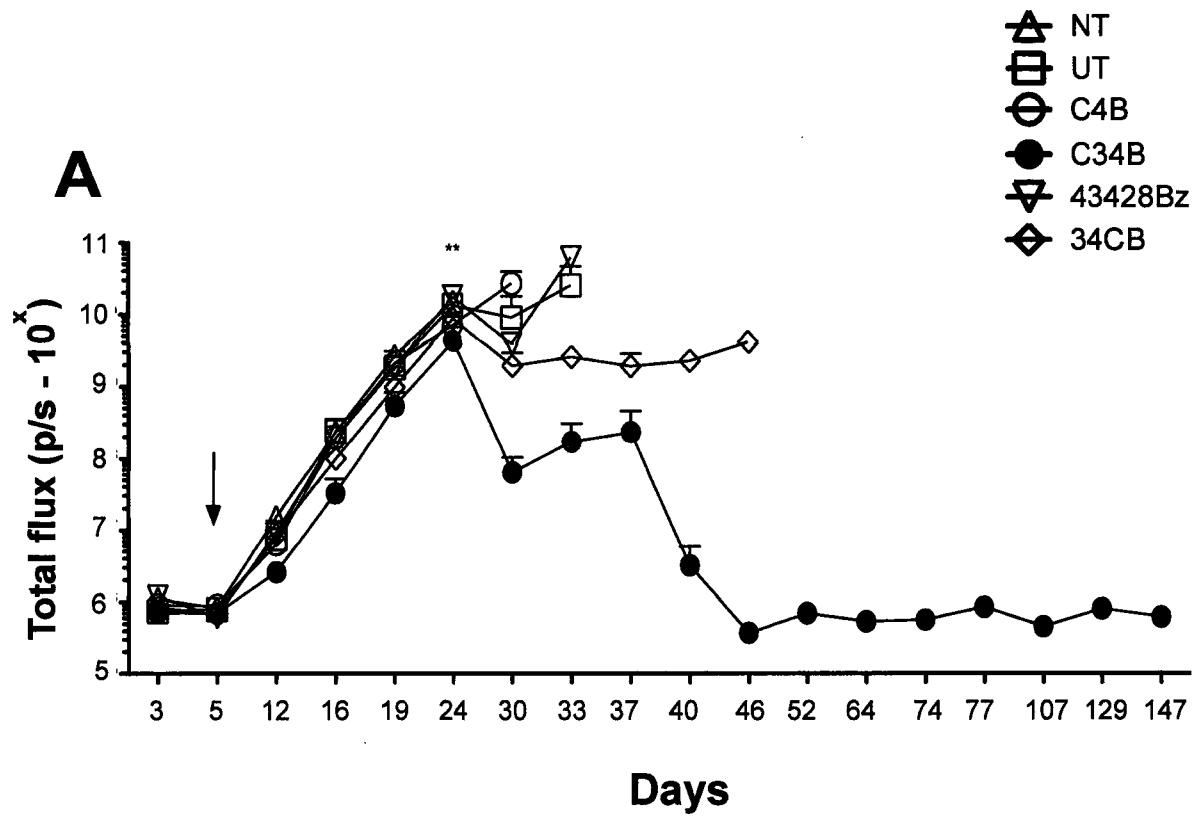
Figure 8

Figure 8 continued
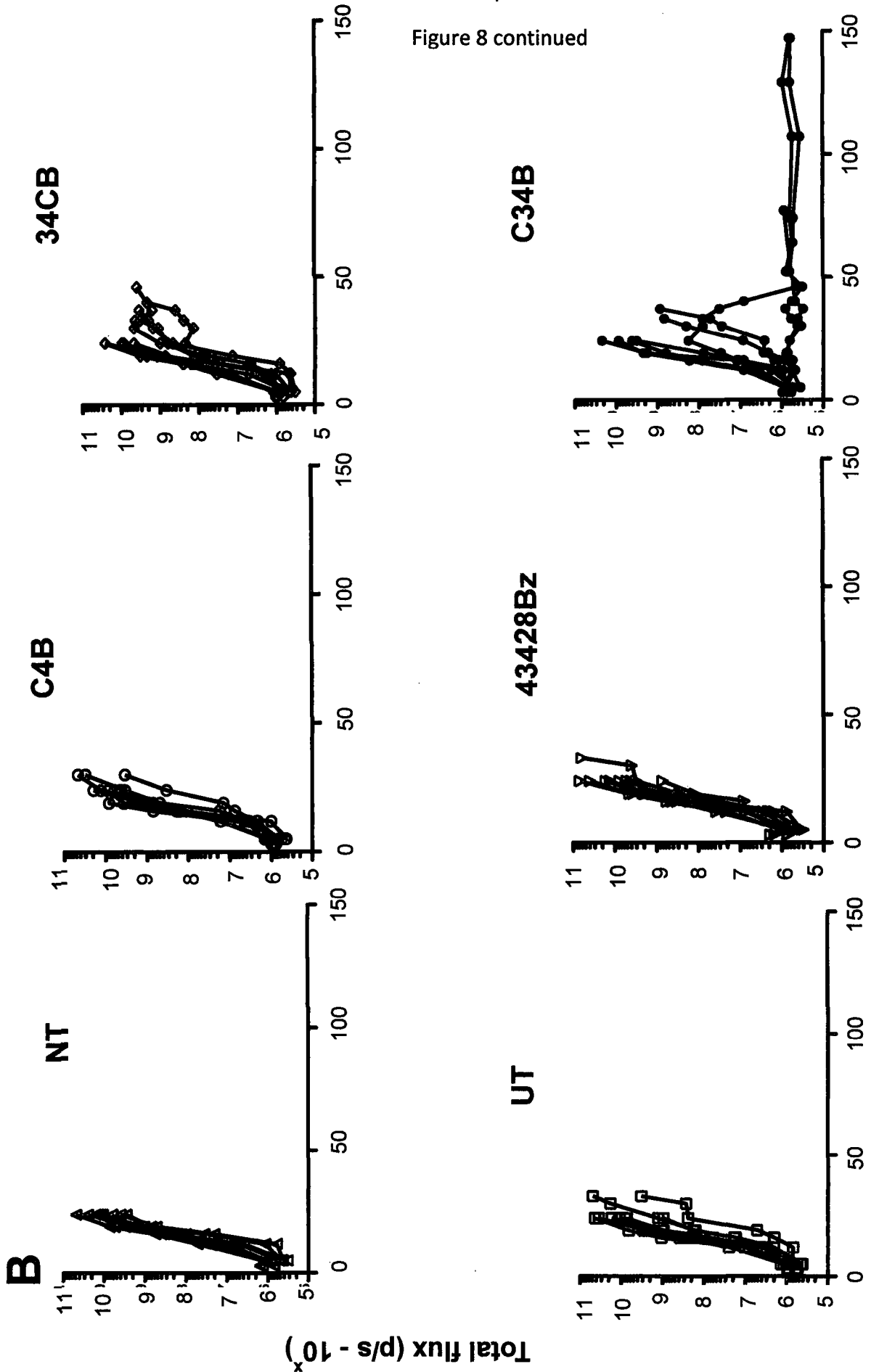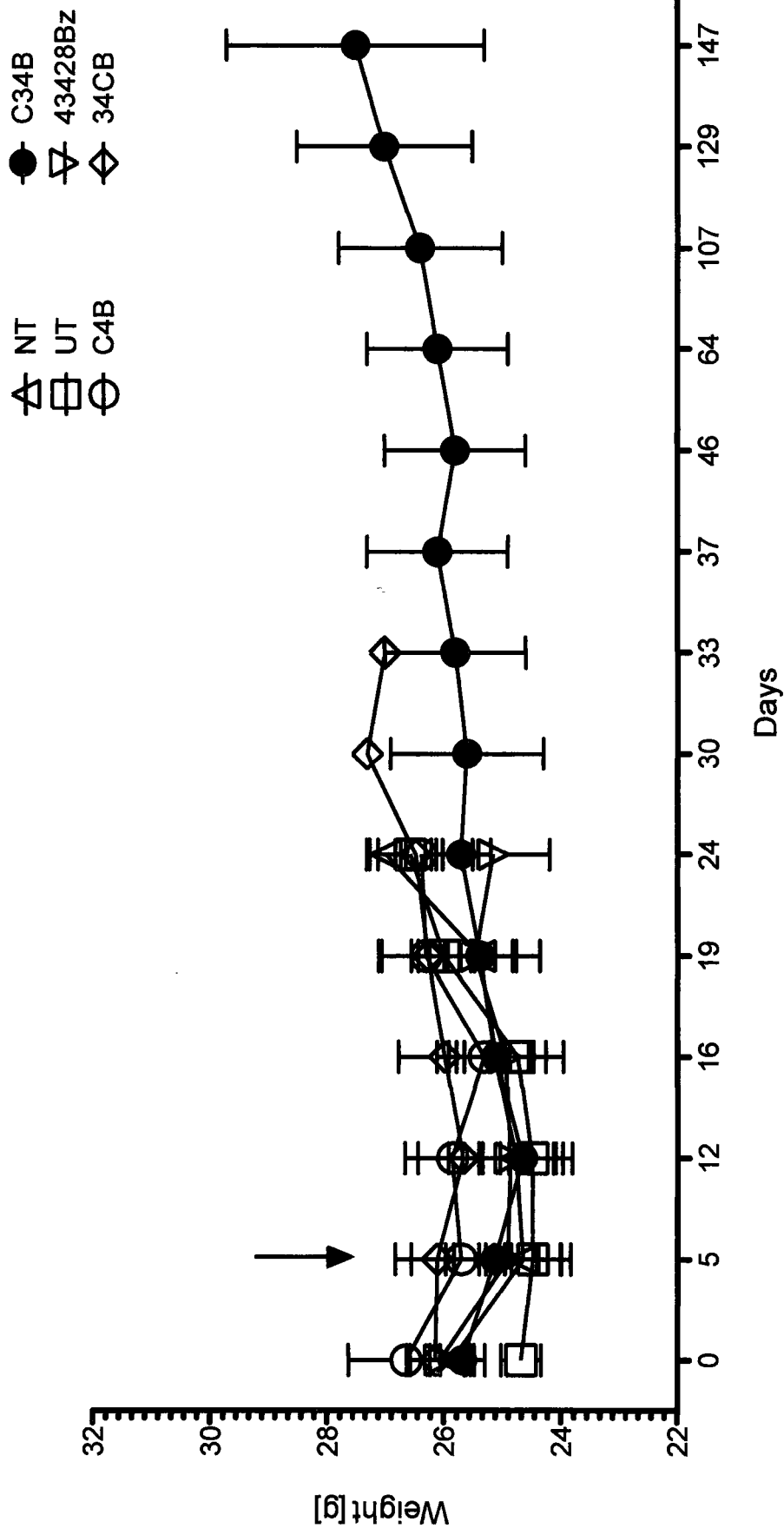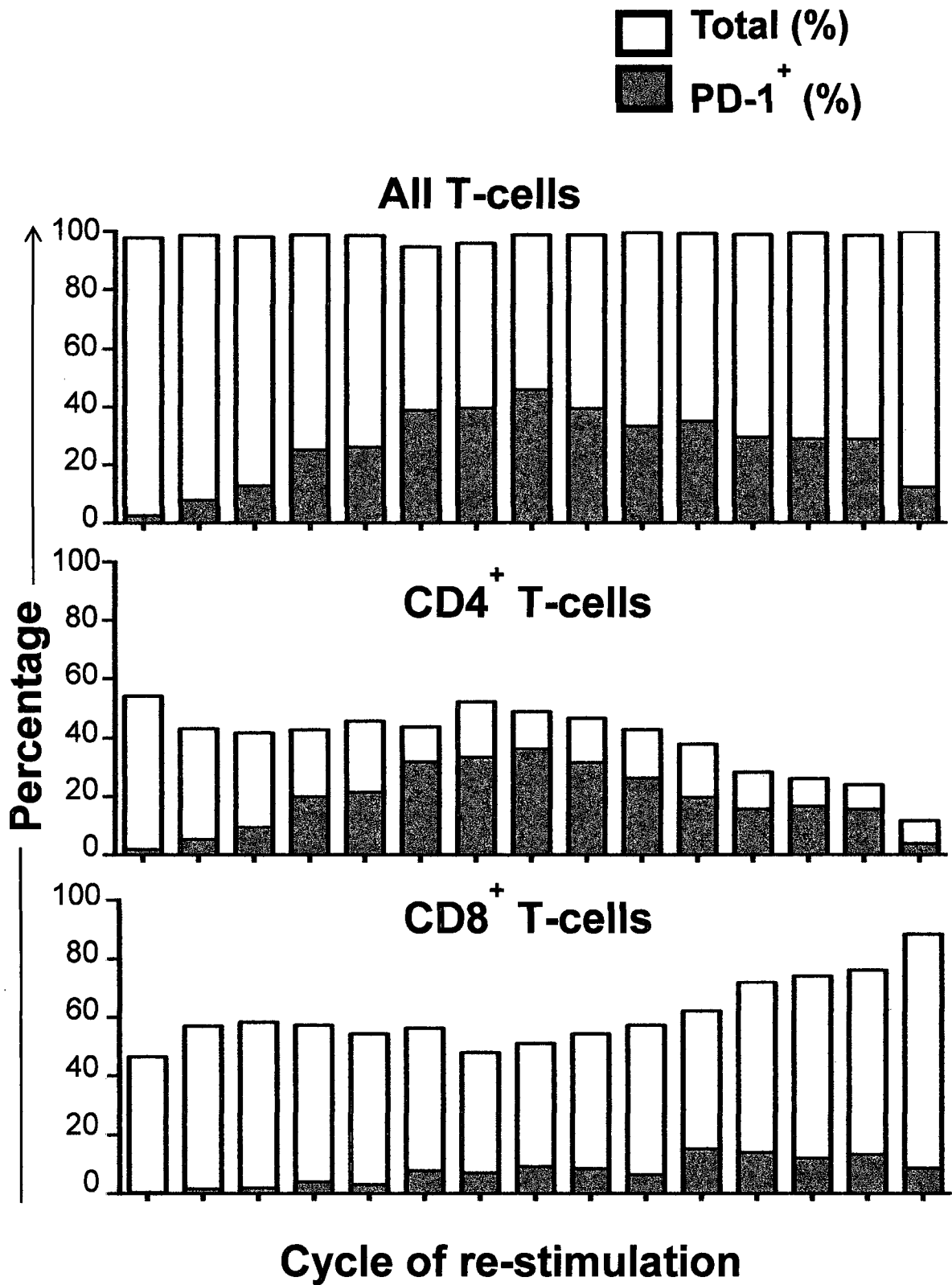
Figure 9

Figure 10

Figure 11

All T-cells

CD4$^+$ T-cells

CD8$^+$ T-cells

Cycle of re-stimulation
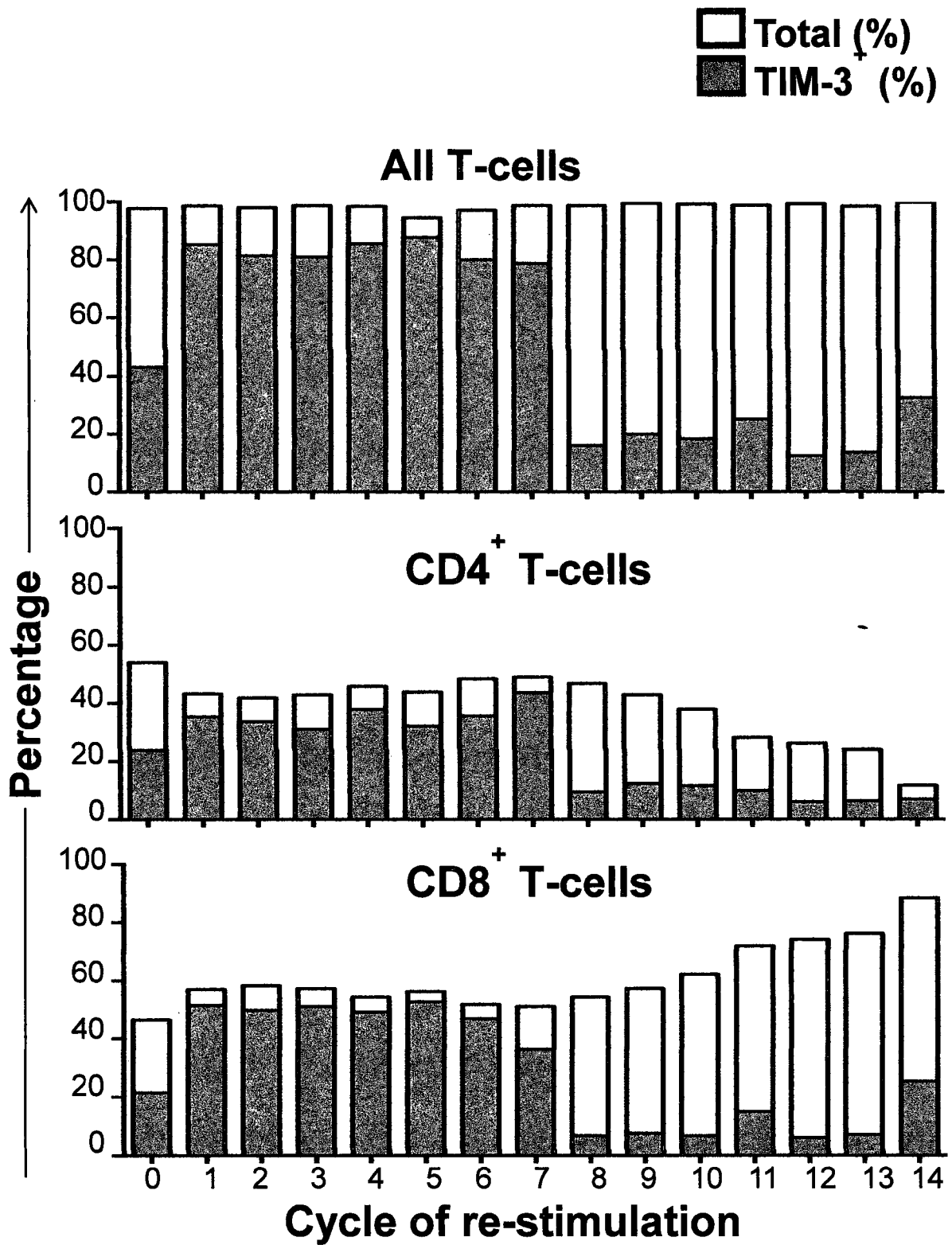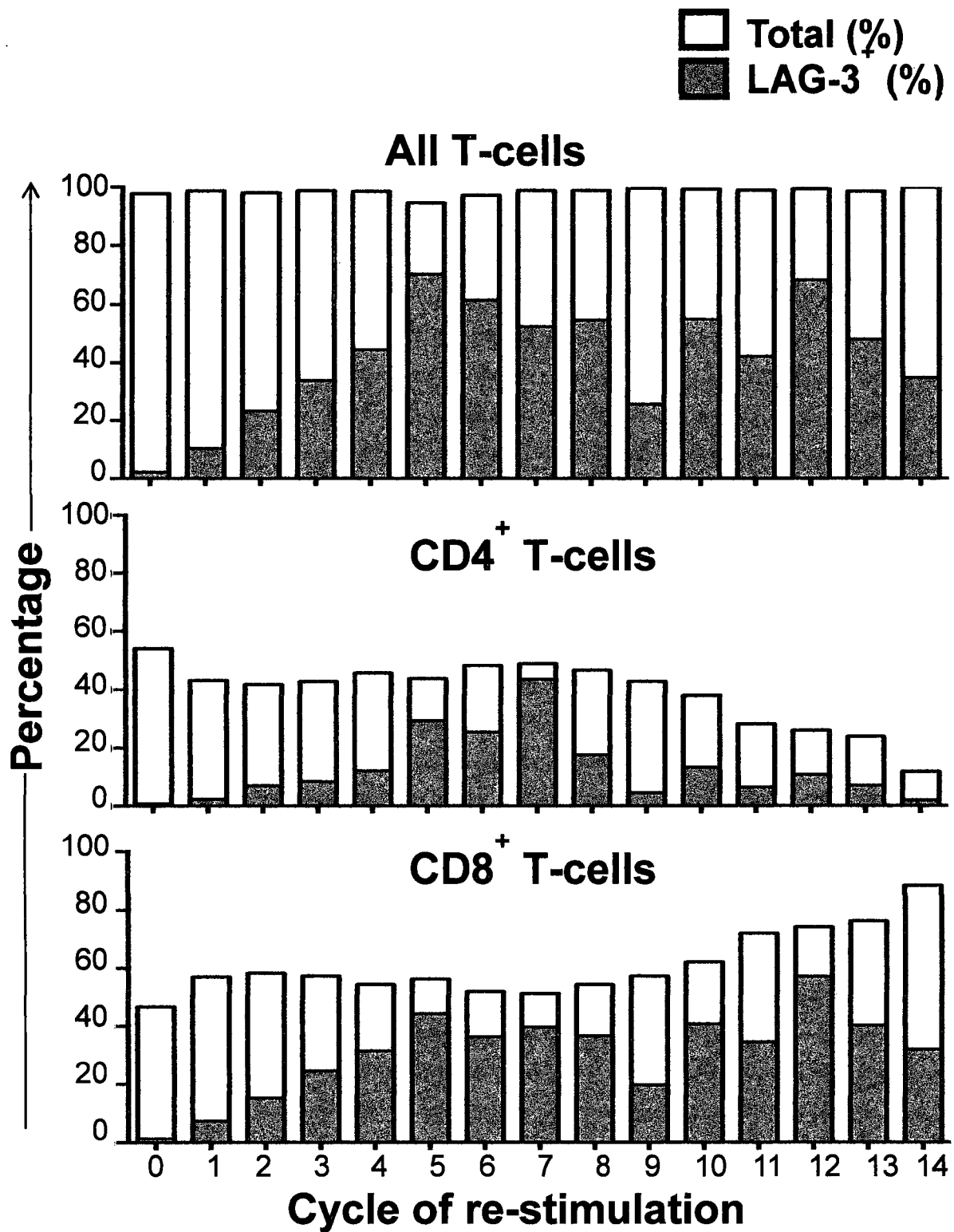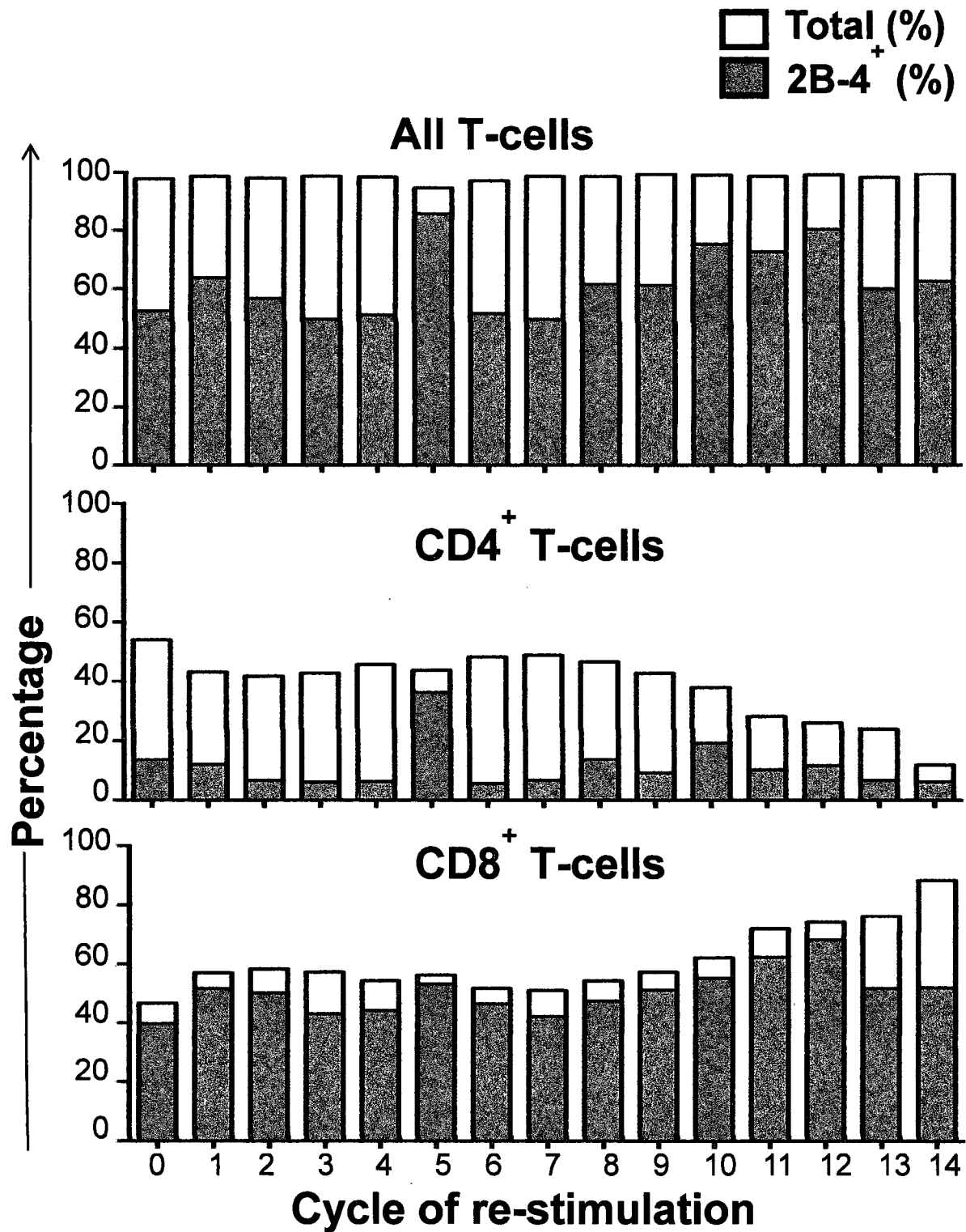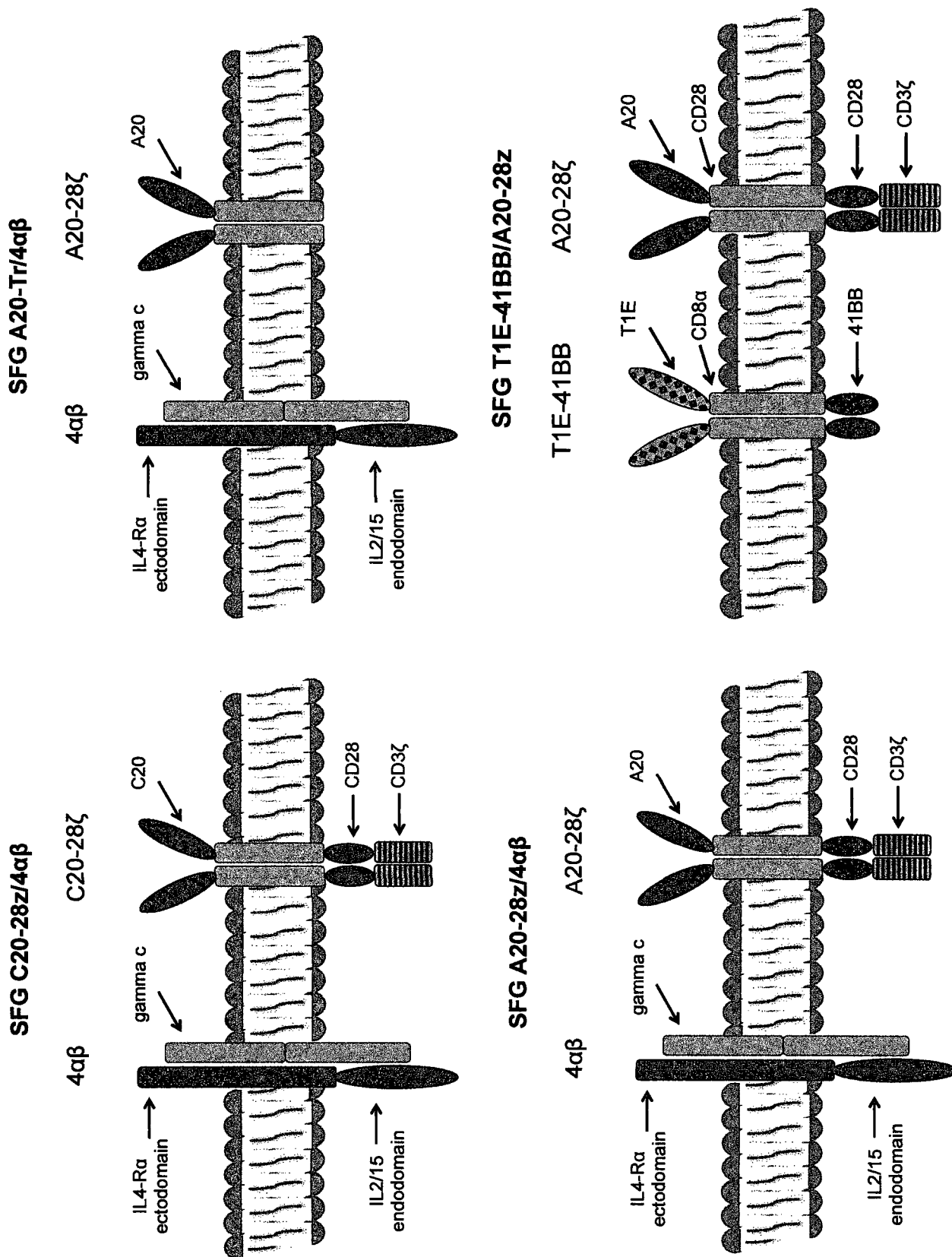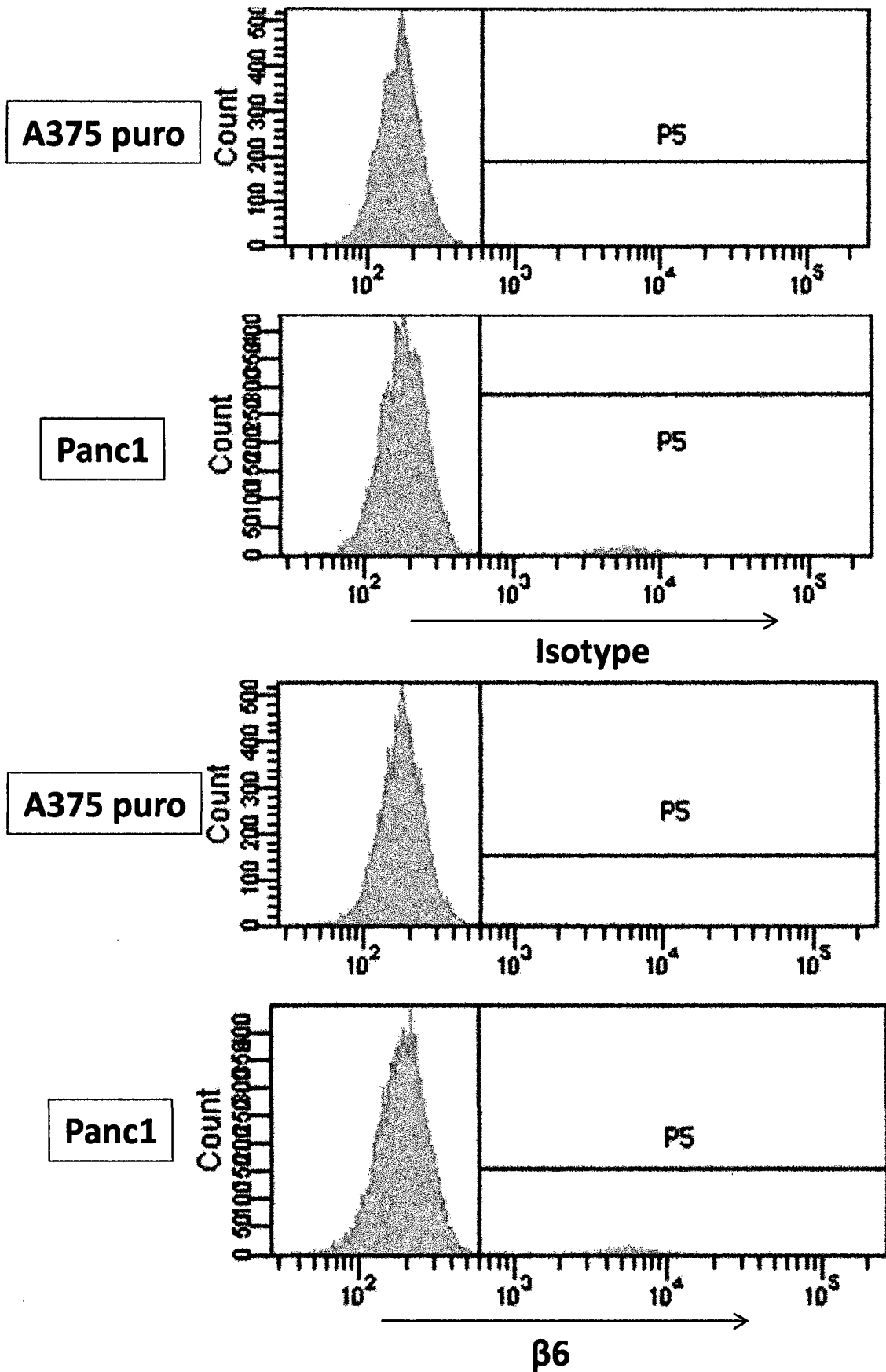
Figure 15

Figure 15 continued
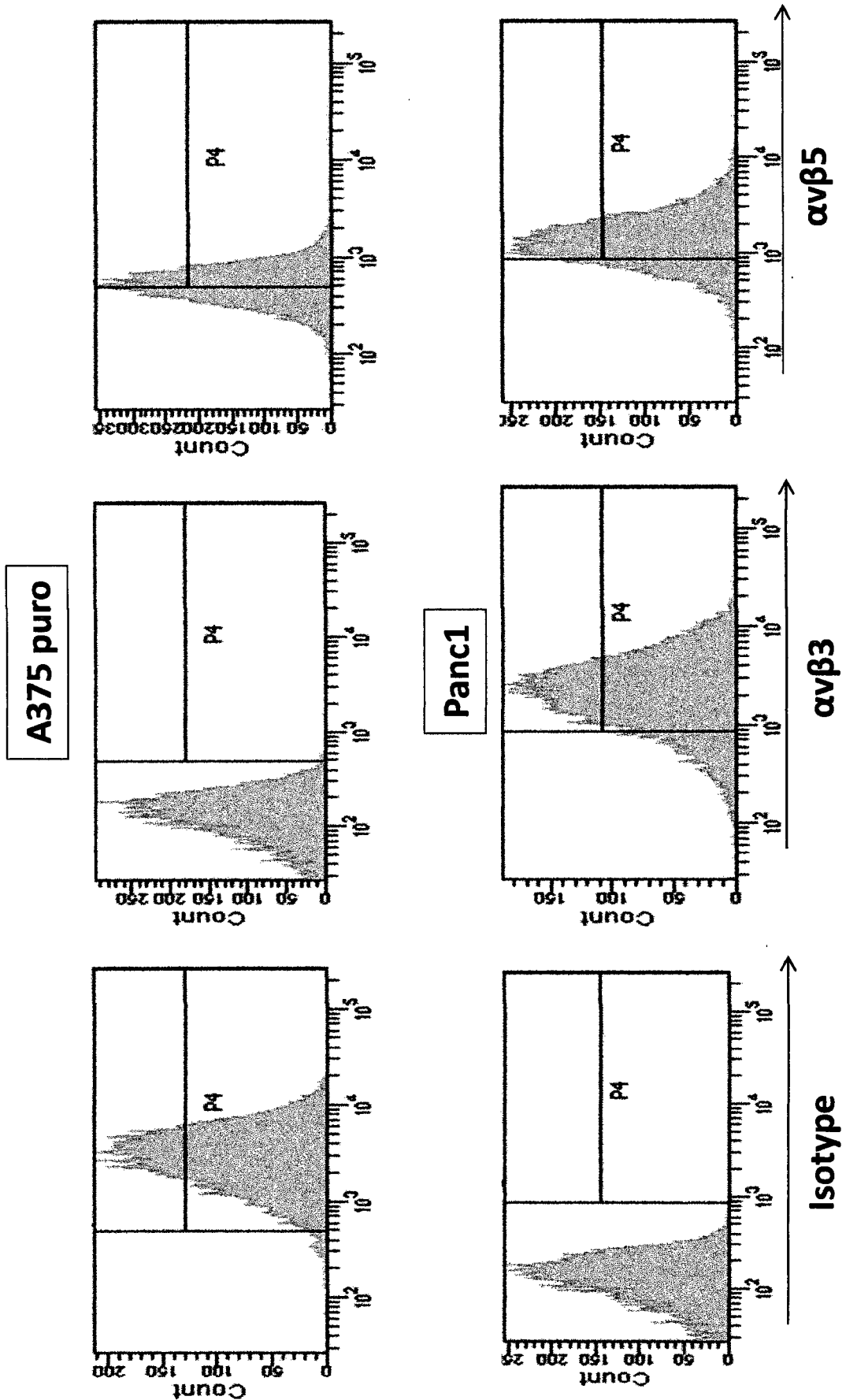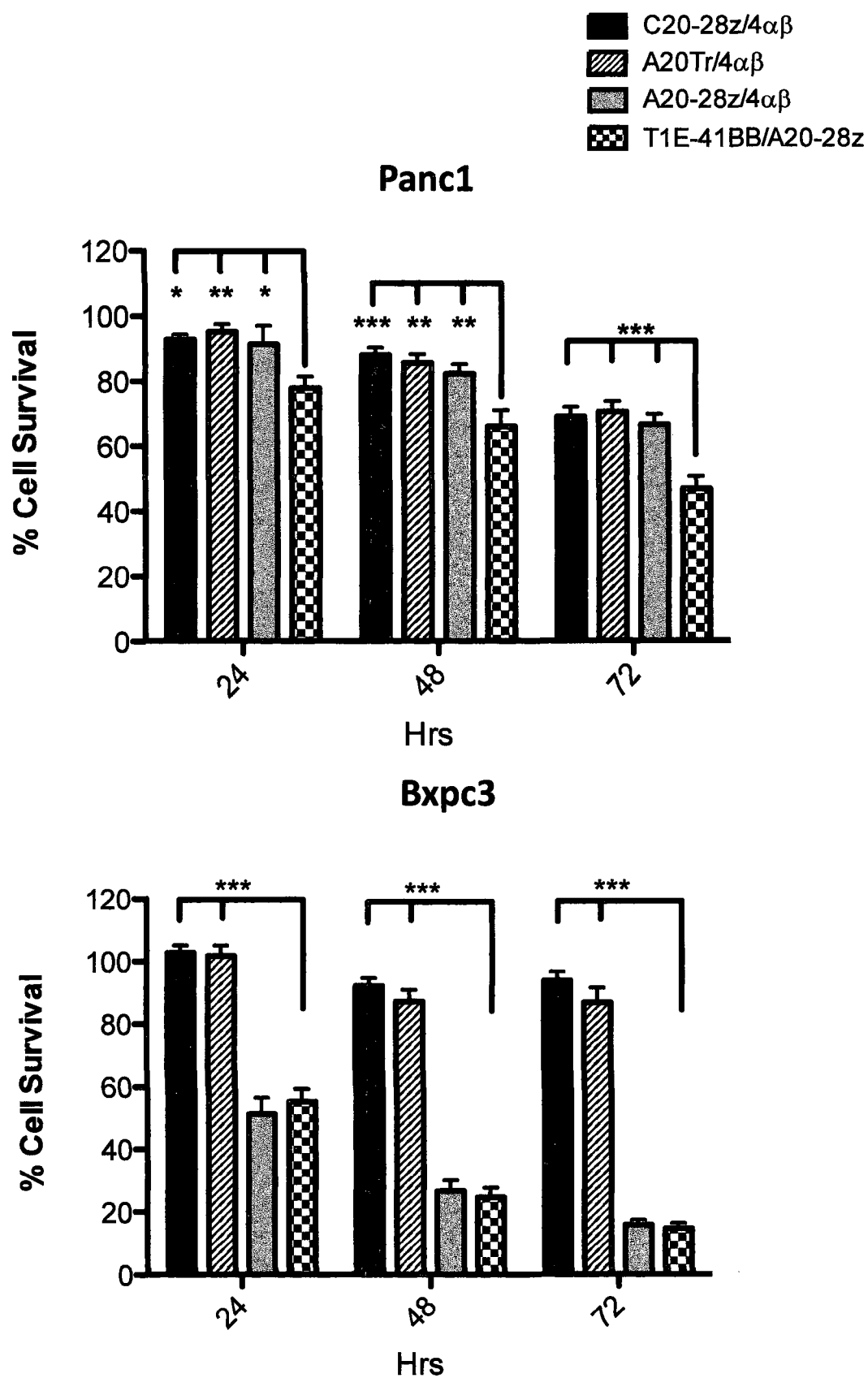
Figure 16

Panc1

Bxpc3

Hrs

Figure 16 continued
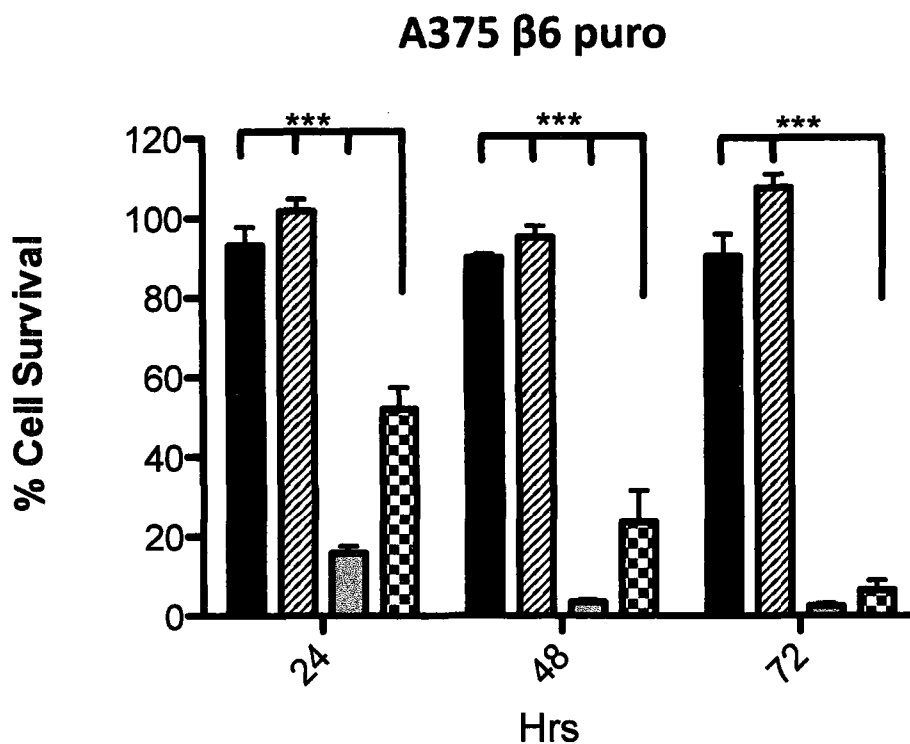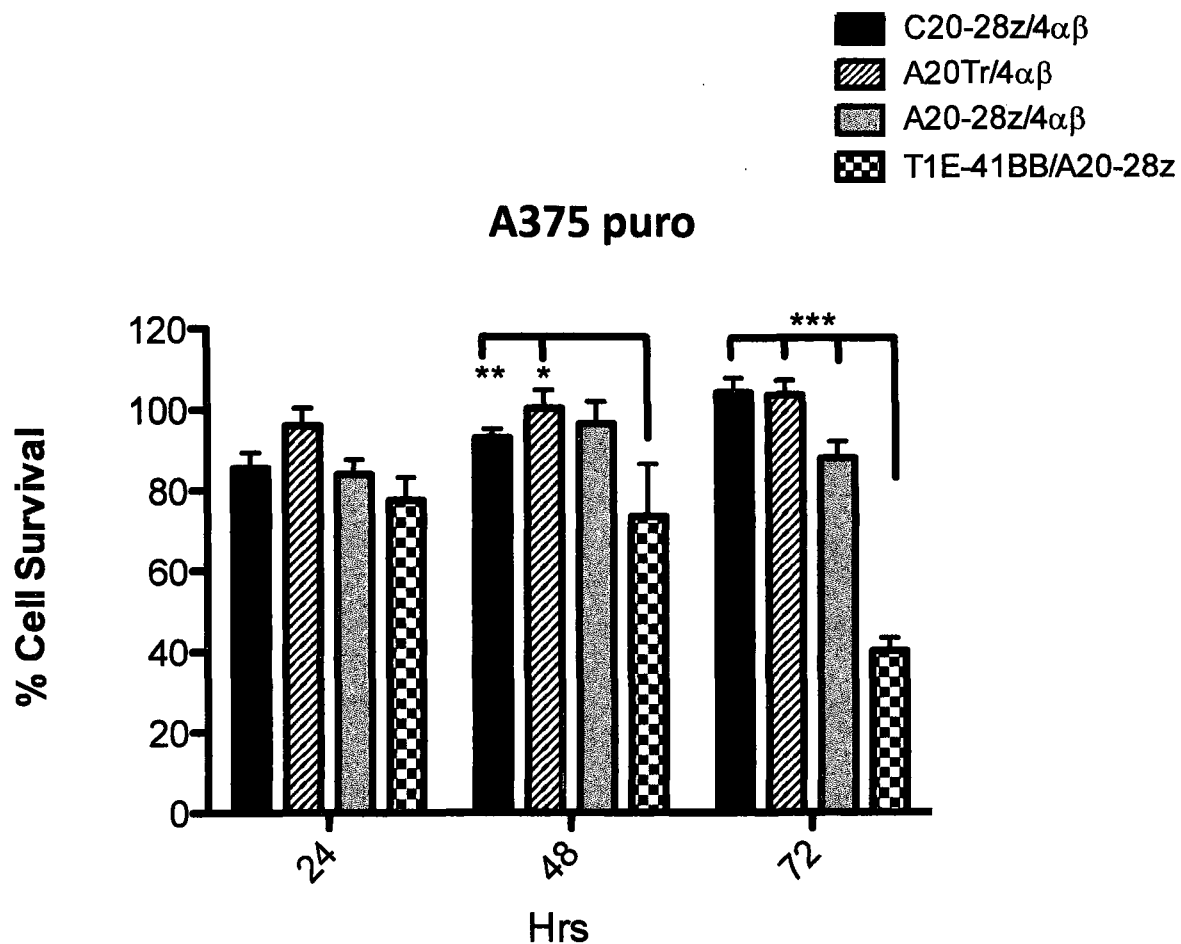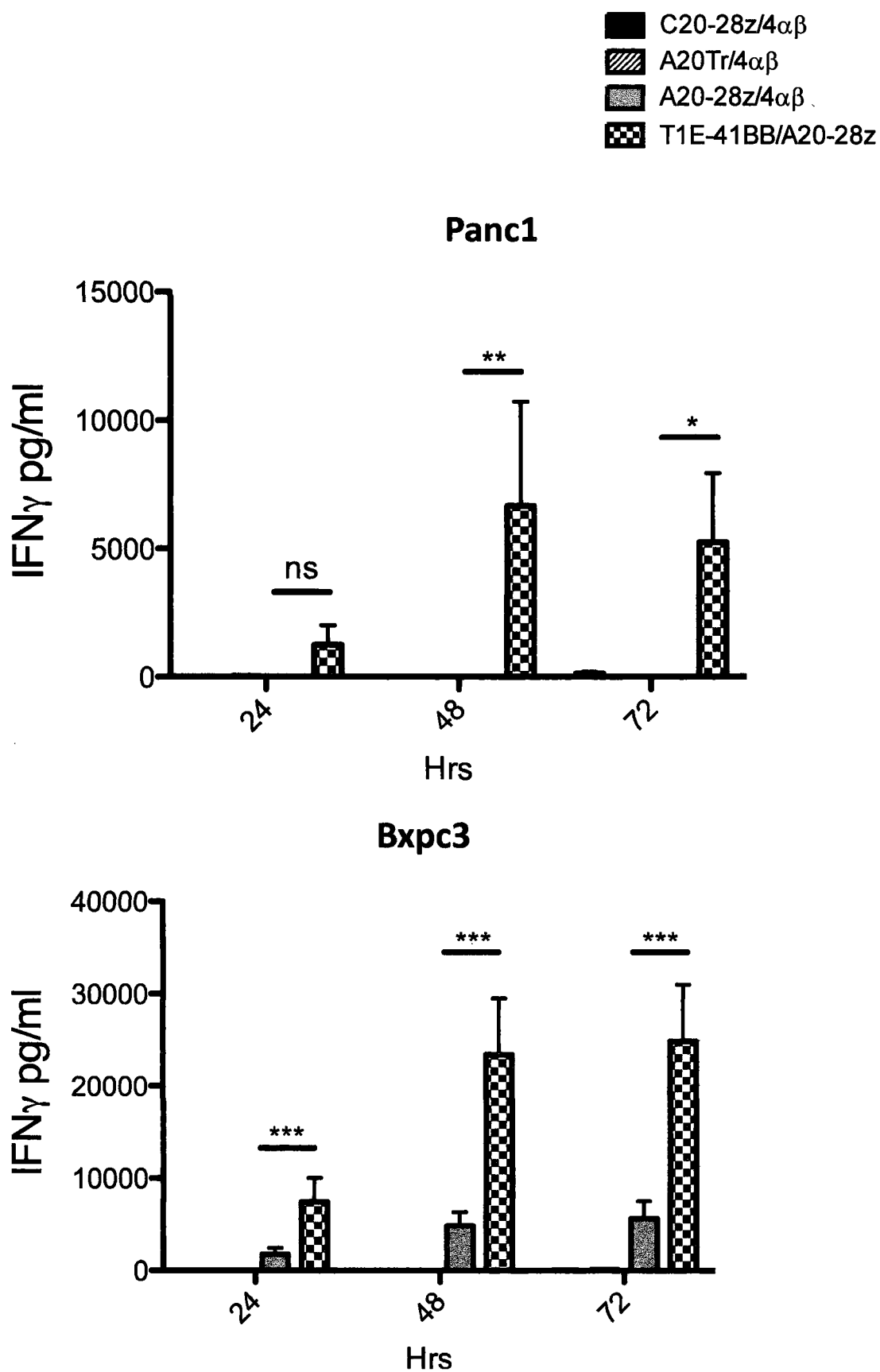
Figure 17

Panc1

Bxpc3

Figure 17 continued

■ C20-28z/4αβ
▨ A20Tr/4αβ
▨ A20-28z/4αβ
▨ T1E-41BB/A20-28z

A375 puro

A375 β6 puro

Figure 18

Panc1

Bxpc3

■	C20-28z/4αβ
▨	A20Tr/4αβ
▨	A20-28z/4αβ
▨	A20-28z/T1E-41BB

A

Legend:
- ● NT
- ○ T1E-tr/A20-tr
- ■ T1E-tr/A20-28z
- ⊟ T1E-41BB/A20-28z
- ▲ T1E-CD27/A20-28z
- △ T1E-CD40/A20-28z

BxPC-3

Panc1

Unstimulated
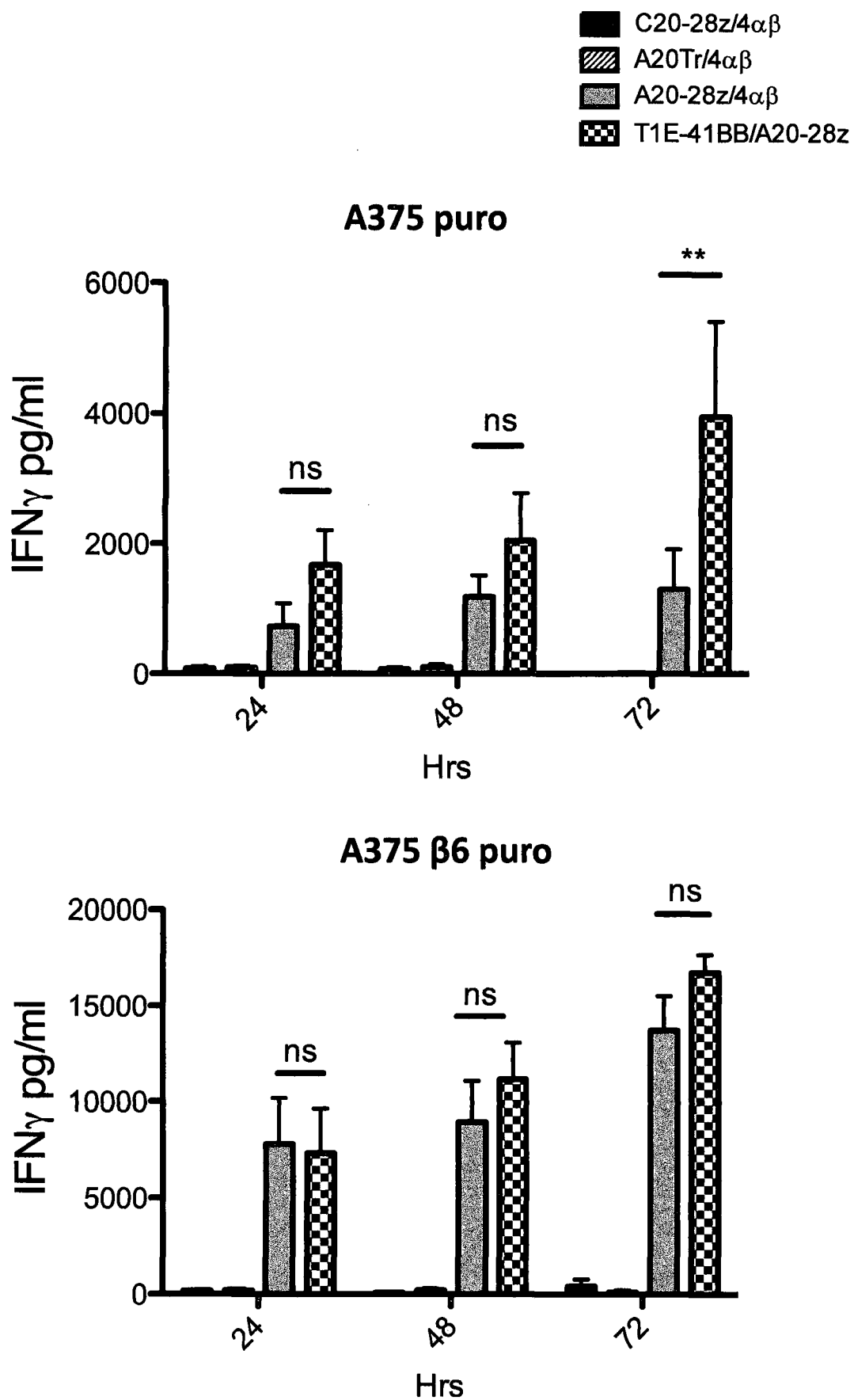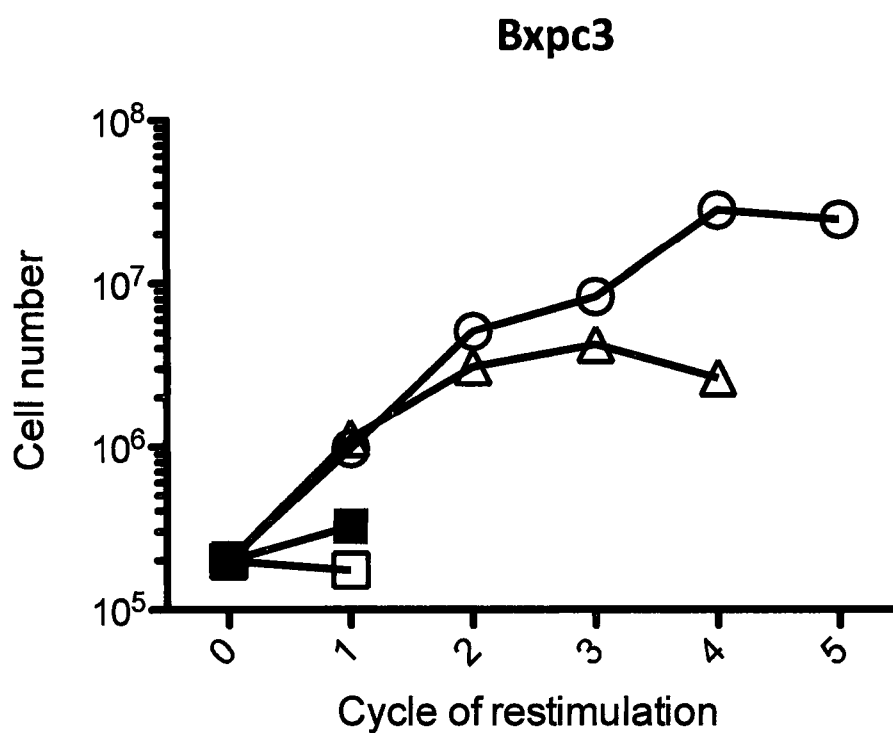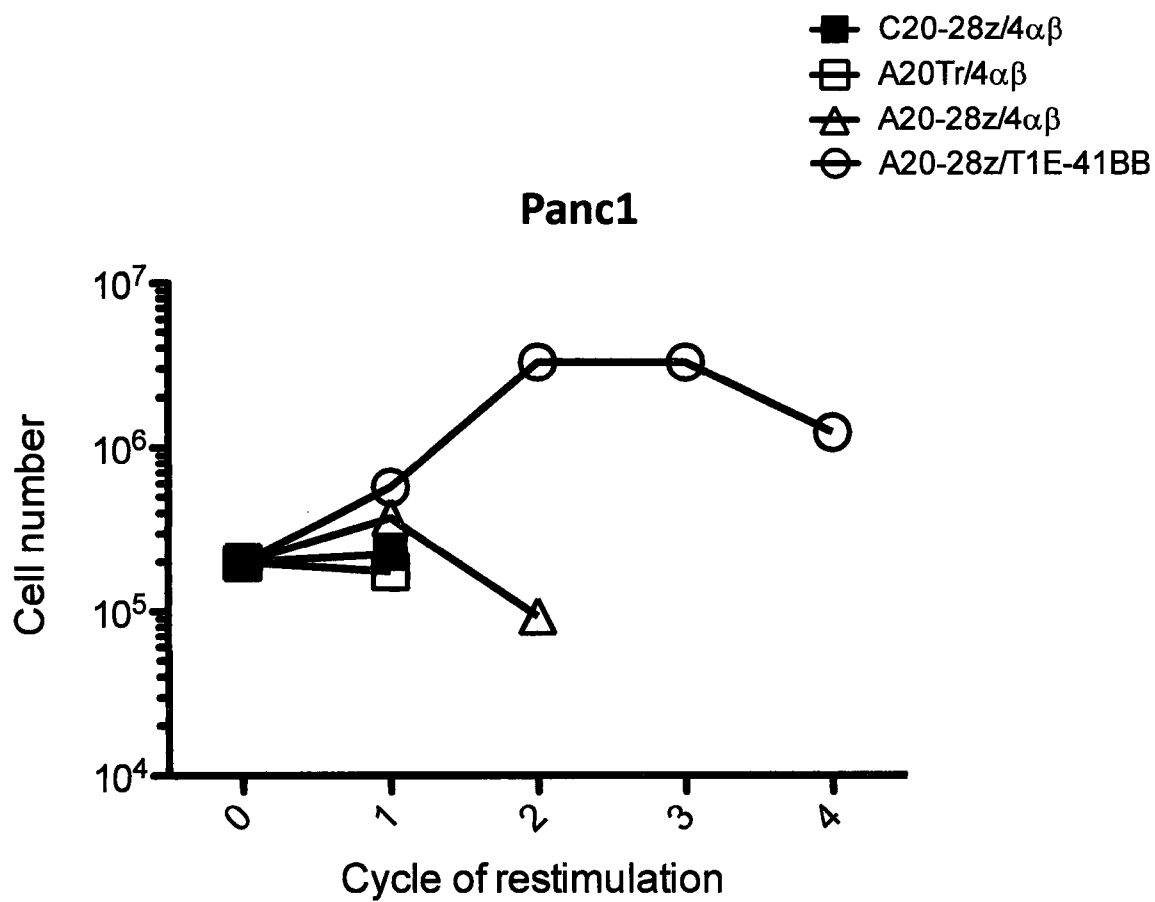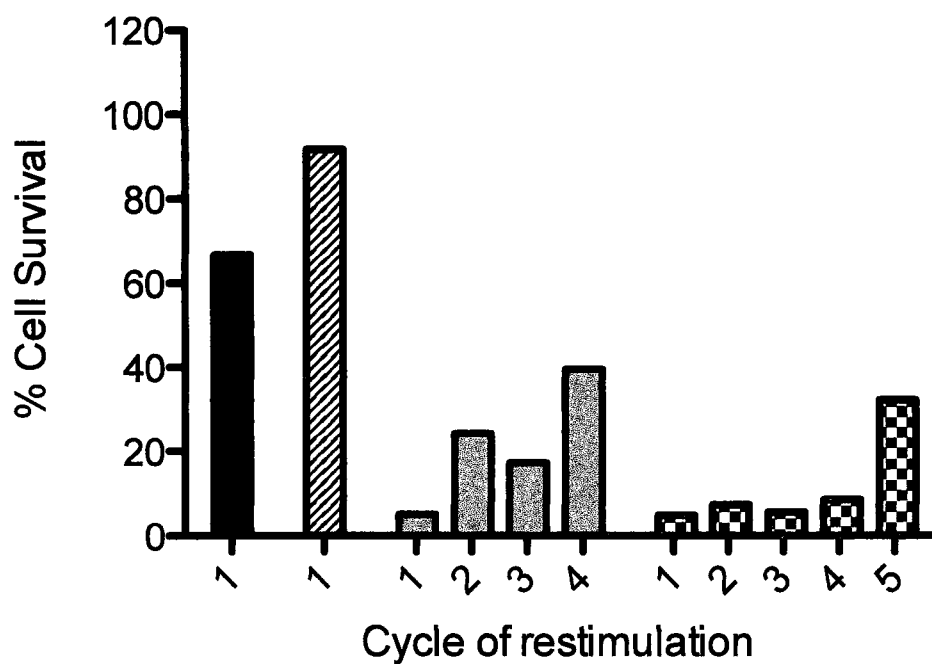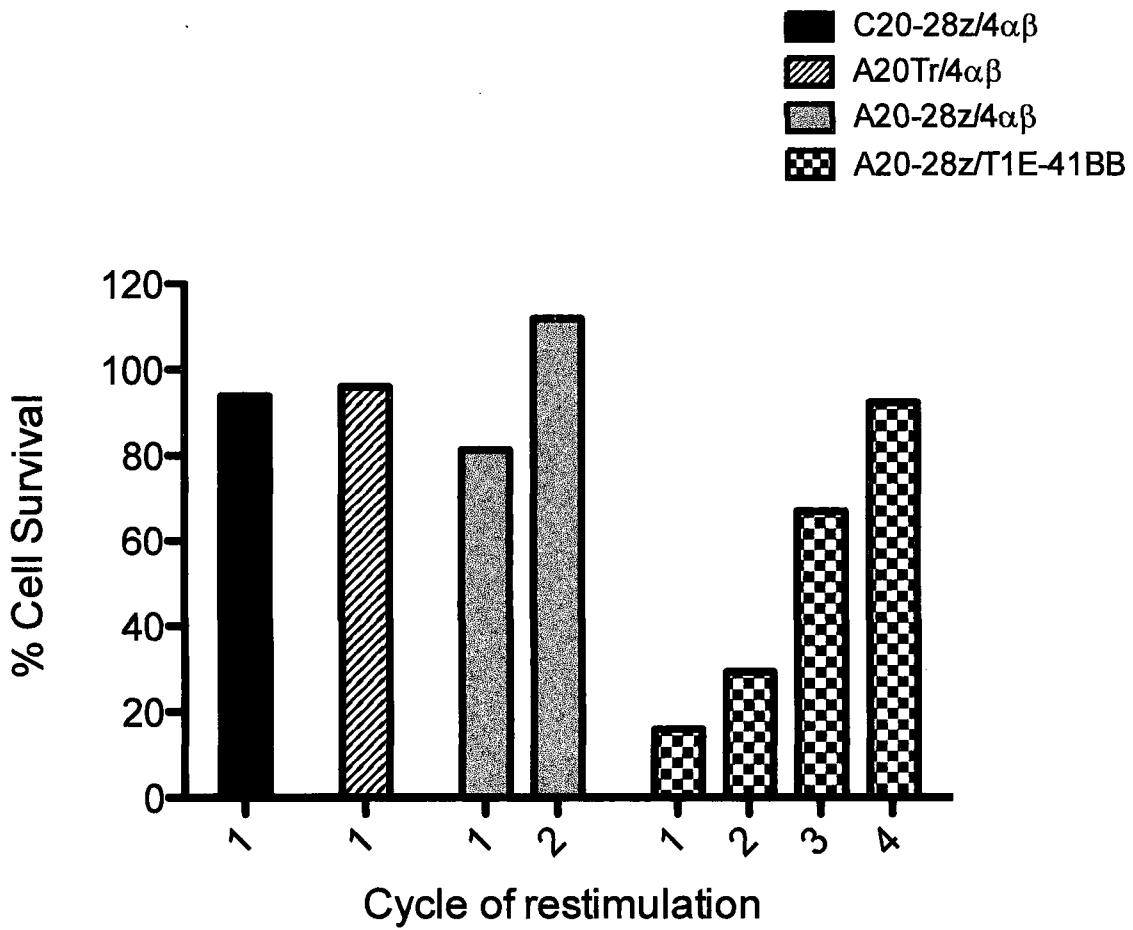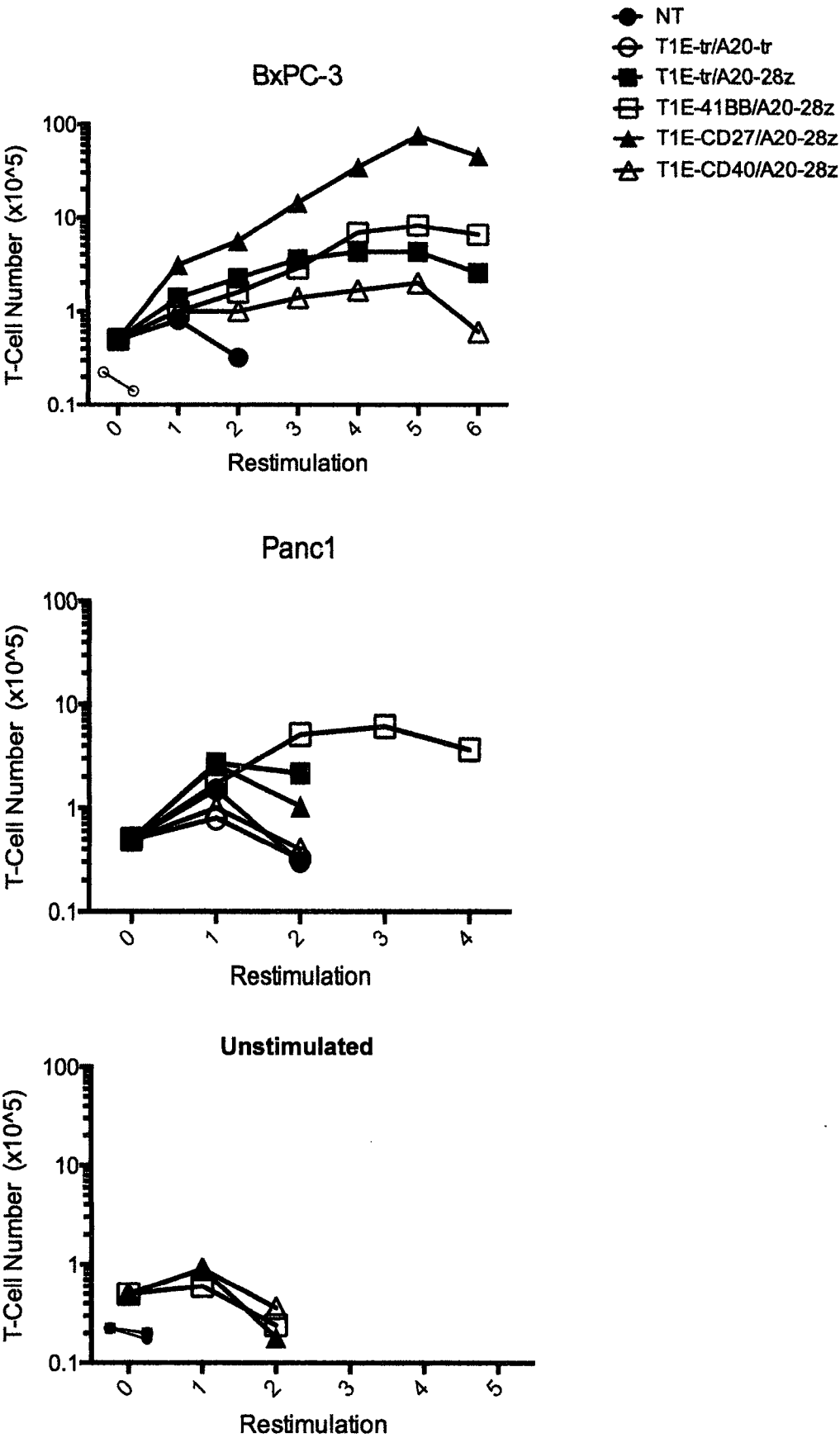
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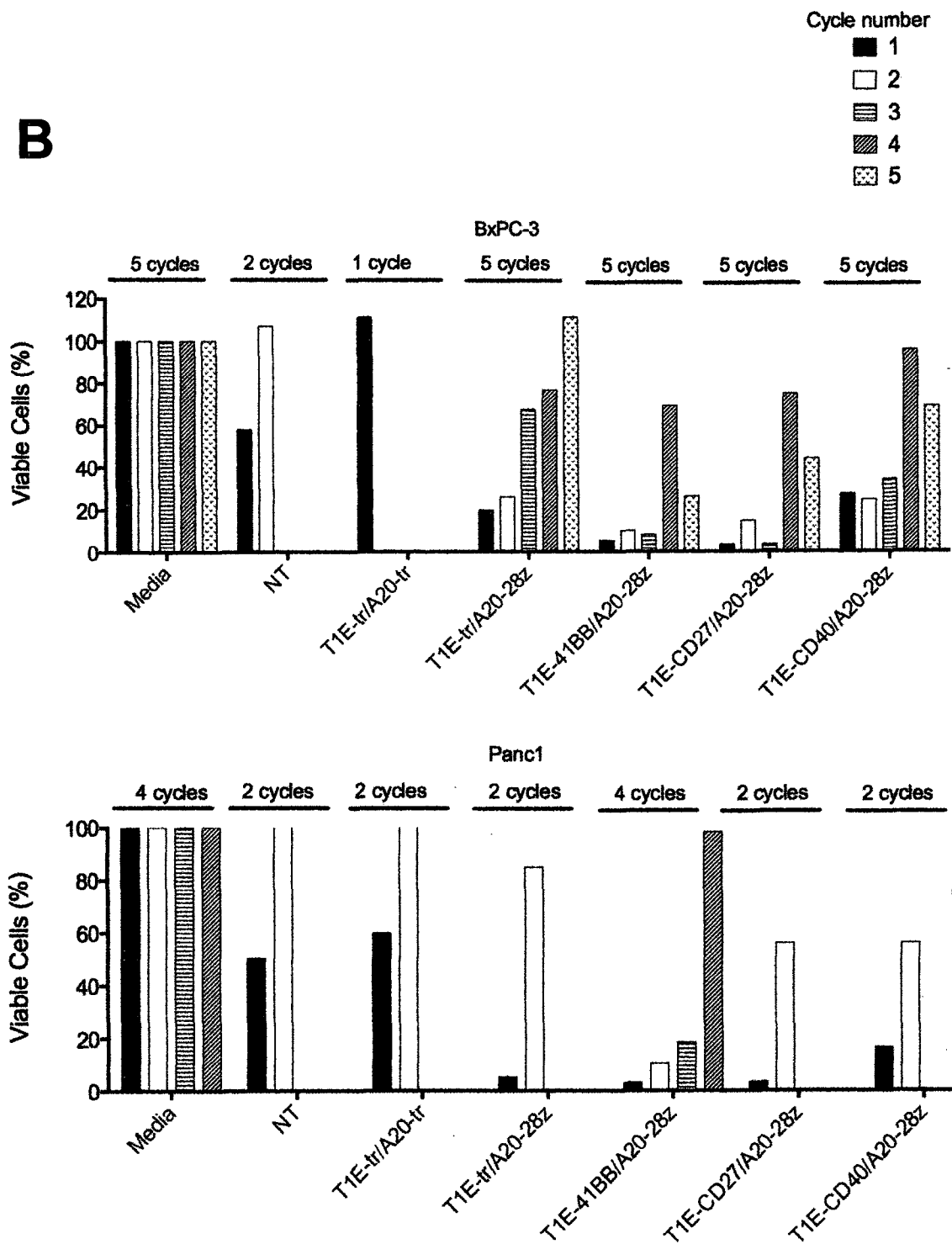
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Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
            35   40   45
Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
        50   55   60
Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65   70   75   80
Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
                85   90   95
Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                100   105   110

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Asp Val Leu Asp Lys Arg Arg Gly Arg Asp Pro Glu Met Gly Gly Lys
            35   40   45
Pro Arg Arg Lys Asn Pro Gln Glu Gly Leu Tyr Asn Glu Leu Gln Lys
        50   55   60
Asp Lys Met Ala Glu Ala Tyr Ser Glu Ile Gly Met Lys Gly Glu Arg
65   70   75   80
Arg Arg Gly Lys Gly His Asp Gly Leu Tyr Gln Gly Leu Ser Thr Ala
                85   90   95
Thr Lys Asp Thr Tyr Asp Ala Leu His Met Gln Ala Leu Pro Pro Arg
                100   105   110

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<213> Homo sapiens

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            20   25   30
Asp Asn Ala Val Asn Leu Ser Cys Lys Tyr Ser Tyr Asn Leu Phe Ser
        35   40   45
Arg Glu Phe Arg Ala Ser Leu His Lys Gly Leu Asp Ser Ala Val Glu
    50   55   60
Val Cys Val Val Tyr Gly Asn Tyr Ser Gln Gln Leu Gln Val Tyr Ser
65   70   75   80
Lys Thr Gly Phe Asn Cys Asp Gly Lys Leu Gly Asn Glu Ser Val Thr
                85   90   95
Phe Tyr Leu Gln Asn Leu Tyr Val Asn Gln Thr Asp Ile Tyr Phe Cys
            100   105   110
Lys Ile Glu Val Met Tyr Pro Pro Pro Tyr Leu Asp Asn Glu Lys Ser
            115   120   125
Asn Gly Thr Ile Ile His Val Lys Gly Lys His Leu Cys Pro Ser Pro
        130   135   140
Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly
145   150   155   160
Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile
                165   170   175
Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met
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Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val Val Val Gly Gly
            35   40   45
Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala Phe Ile Ile Phe
    50   55   60
Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser Asp Tyr Met Asn
65   70   75   80
Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His Tyr Gln Pro Tyr
                85   90   95
Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
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            20   25   30
Pro Ser Pro Leu Phe Pro Gly Pro Ser Lys Pro Phe Trp Val Leu Val
            35   40   45
Val Val Gly Gly Val Leu Ala Cys Tyr Ser Leu Leu Val Thr Val Ala
        50   55   60
Phe Ile Ile Phe Trp Val Arg Ser Lys Arg Ser Arg Leu Leu His Ser
65   70   75   80
Asp Tyr Met Asn Met Thr Pro Arg Arg Pro Gly Pro Thr Arg Lys His
                85   90   95
Tyr Gln Pro Tyr Ala Pro Pro Arg Asp Phe Ala Ala Tyr Arg Ser
                100   105   110

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Val Ala Arg Thr
            20