

Claims

1. An antibody comprising at least one antigen-binding region capable of binding to 5T4 (Trophoblast glycoprotein), wherein the antibody is able to block binding to 5T4 of an antibody comprising a variable heavy chain (VH) region comprising the sequence set forth in SEQ ID NO: 5, and a variable light chain (VL) region comprising the sequence set forth in SEQ ID NO: 9 [059].
2. The antibody of claim 1, wherein said antibody blocks binding to 5T4 of an antibody selected from the group consisting of:
 - a) an antibody comprising a variable heavy chain (VH) region comprising the sequence set forth in SEQ ID NO: 40 and a variable light chain (VL) region comprising the sequence set forth in SEQ ID NO: 44 [207],
 - b) an antibody comprising a variable heavy chain (VH) region comprising the sequence set forth in SEQ ID NO: 47 and a variable light chain (VL) region comprising the sequence set forth in SEQ ID NO: 51 [226]; and
 - c) an antibody comprising a variable heavy chain (VH) region comprising the sequence set forth in SEQ ID NO: 5 and a variable light chain (VL) region comprising the sequence set forth in SEQ ID NO: 9 [059].
3. The antibody of claim 1 or 2, wherein said antibody blocks binding to 5T4 of an antibody selected from the group consisting of:
 - a) an antibody comprising a variable heavy chain (VH) region comprising the sequence set forth in SEQ ID NO: 40 and a variable light chain (VL) region comprising the sequence set forth in SEQ ID NO: 44 [207]; and
 - b) an antibody comprising a variable heavy chain (VH) region comprising the sequence set forth in SEQ ID NO: 47 and a variable light chain (VL) region comprising the sequence set forth in SEQ ID NO: 51 [226].
4. The antibody according to any one of the preceding claims, wherein 5T4 is human (*Homo sapiens*) 5T4, such the mature polypeptide sequence of SEQ ID NO: 1.
5. The antibody according to any one of claims 1 to 3, wherein 5T4 is cynomolgus monkey (*Macaca fascicularis*) 5T4, such as the mature polypeptide sequence of SEQ ID NO: 2.
6. The antibody according to any one of claims 1 to 3, wherein 5T4 is chicken (*Gallus gallus*) 5T4, such as the mature polypeptide sequence of SEQ ID NO: 3.

7. The antibody according to any one of the preceding claims, wherein 5T4 is human 5T4 such as the mature polypeptide of SEQ ID NO: 1 and cynomolgus monkey 5T4, such as the mature polypeptide of SEQ ID NO: 2.
8. The antibody according to any one of the preceding claims, wherein 5T4 is human 5T4, such as the mature polypeptide sequence of SEQ ID NO: 1, cynomolgus monkey 5T4, such as the mature polypeptide sequence of SEQ ID NO: 2 and chicken 5T4 such as the mature polypeptide sequence of SEQ ID NO: 3.
9. The antibody according to any one of the preceding claims, said antibody being able to bind human 5T4, cynomolgus monkey and/or chicken 5T4, with a binding affinity that corresponds to a K_D value $1E-7$ M or less, such as $5E-8$ M or less, $1E-8$ M or less, $5E-9$ M or less or such as $1E-9$ M or less such as with a binding affinity corresponding to a K_D value which is within the range of $1E-7$ to $5E-10$ M, such as within the range of $1E-7$ to $1E-9$ M, such as $5E-8$ to $5E-10$ M, $5E-8$ to $1E-9$ M, such as $1E-8$ to $5E-10$ M, $1E-8$ to $1E-9$ M or such as $1E-8$ to $5E-9$ M.
10. The antibody according to claim 9, wherein the binding affinity is determined by biolayer interferometry, optionally as set forth in Example 2 herein.
11. The antibody according to any one of claims 9 and 10, wherein the binding affinity is determined using a biolayer interferometry comprising the steps of:
 - I) Immobilizing the antibody at an amount of $1\text{ }\mu\text{g/mL}$ for 600 seconds on an anti-human IgG Fc Capture biosensor;
 - II) Determining association over a time period of 200 seconds and dissociation over a time period of 1000 seconds of 5T4ECDHis (mature protein of SEQ ID NO: 99) or cynomolgus monkey 5T4 (mature protein of SEQ ID NO: 2, or recombinant cynomolgus monkey 5T4 protein (Cusabio; cat. no. CSB-MP024093MOV), using 2-fold dilution series ranging from 100 nM to 1.56 nM.
 - III) Referencing the data to a buffer control (0 nM).
12. The antibody according to any one of claims 9 to 11, wherein the binding affinity is determined using an antibody as defined in any one of the preceding claims, which is a monospecific, bivalent antibody, such as an antibody which is a full length IgG1.
13. The antibody according to any one of the preceding claims, wherein said antibody recognizes an epitope or antibody binding region or binding site on 5T4, said antibody binding region, binding

site or epitope being recognized by any one of the antibodies selected from the group consisting of:

- a) an antibody comprising a VH region comprising the sequence set forth in SEQ ID NO: 5 and a VL region comprising the sequence set forth in SEQ ID NO: 9 [059],
 - 5 b) an antibody comprising a VH region comprising the sequence set forth in SEQ ID NO: 12 and a VL region comprising the sequence set forth in SEQ ID NO: 16 [076],
 - c) an antibody comprising a VH region comprising the sequence set forth in SEQ ID NO: 19 and a VL region comprising the sequence set forth in SEQ ID NO: 23 [085],
 - 10 d) an antibody comprising a VH region comprising the sequence set forth in SEQ ID NO: 26 and a VL region comprising the sequence set forth in SEQ ID NO: 30 [106],
 - e) an antibody comprising a VH region comprising the sequence set forth in SEQ ID NO: 33 and a VL region comprising the sequence set forth in SEQ ID NO: 37 [127],
 - f) an antibody comprising a VH region comprising the sequence set forth in SEQ ID NO: 40 and a VL region comprising the sequence set forth in SEQ ID NO: 44 [207]; and
 - 15 g) an antibody comprising a VH region comprising the sequence set forth in SEQ ID NO: 47 and a VL region comprising the sequence set forth in SEQ ID NO: 51 [226].
14. The antibody according to any one of the preceding claims, wherein said antibody binds to an antibody binding region, a binding site or an epitope on 5T4, which is not an antibody binding region or binding site or epitope bound by, or is different from an antibody binding region, a binding site or an epitope bound by an antibody selected from the group consisting of:
- 20 a) an antibody comprising a VH region comprising the sequence set forth in SEQ ID NO: 87 and a VL region comprising the sequence set forth in SEQ ID NO: 88 [H8],
 - b) an antibody comprising a VH region comprising the sequence set forth in SEQ ID NO: 83 and a VL region comprising the sequence set forth in SEQ ID NO: 84 [A1]; and
 - 25 c) An antibody comprising a VH region comprising the sequence set forth in SEQ ID NO: 85 and a VL region comprising the sequence set forth in SEQ ID NO: 86 [A3].
15. The antibody according to any one of the preceding claims, wherein the binding of said antibody to 5T4 is blocked by binding to 5T4 of an antibody comprising a variable heavy chain (VH) region comprising the sequence set forth in SEQ ID NO: 85 and a variable light chain (VL) region comprising the sequence set forth in SEQ ID NO: 86 [A3].
- 30 16. The antibody according to any one of the preceding claims, wherein said antibody shows displacement of an antibody bound to 5T4ECDHis (mature protein of SEQ ID NO: 99), said

antibody bound to 5T4 comprising a variable heavy chain (VH) region comprising the sequence set forth in SEQ ID NO: 85 and a variable light chain (VL) region comprising the sequence set forth in SEQ ID NO: 86 [A3].

17. The antibody according to claim 14 or 15, wherein cross-block, or the ability of an antibody as defined in any of the preceding claims to block binding of another antibody to 5T4 is determined by the fluorescence-activated cell sorting (FACS) assay, such as in an assay performed as described in Example 5.
18. The antibody according to any one of claims 14 to 16, wherein cross-block, or the ability of an antibody as defined in any of the preceding claims to block binding of another antibody to 5T4, is determined as the ability of an unconjugated antibody to block binding of a conjugated antibody, and is optionally determined in a procedure comprising the steps of:
- i) Providing a set of samples, each sample comprising a mixture of human ovary adenocarcinoma SK-OV-3 cells, an antibody which binds to 5T4 and is conjugated to fluorescein isothiocyanate (FITC) and an excess of unconjugated antibody targeting 5T4,
 - ii) Incubating the samples for 30 minutes at 4°C, and thereafter subjecting the samples to centrifugation,
 - iii) Removing the supernatant from each sample and resuspending the cells in buffer and determining mean fluorescence intensity (MFI) of the FITC using a flow cytometer; and
 - iv) Calculating the percentage of binding as following:
The difference in MFI between cells incubated with a mixture of FITC-conjugated antibodies and unconjugated antibodies and cells incubated without FITC-conjugated or unconjugated antibodies, multiplied by 100, and subsequently divided by the difference in MFI between cells incubated with a mixture of FITC-conjugated antibodies and IgG-b12 antibodies and cells incubated without FITC-conjugated or unconjugated antibodies.
19. The antibody according to any one of claims 14 to 17, wherein the ability of said antibody to block binding of another antibody to 5T4 or to displace another antibody bound to 5T4ECDHis (mature protein of SEQ ID NO: 99), is determined using biolayer interferometry, such as in an assay as described in Example 3.

20. The antibody according to any one of claims 14 to 18, wherein the ability of the antibody to block binding of another antibody to 5T4, or to displace another antibody bound to 5T4 is determined using biolayer interferometry in a procedure comprising the steps of:
- i) Immobilizing an antibody, according to any of the preceding claims, at an amount of 20 µg/mL in 10 mM sodium acetate buffer to an activated Amine-Reactive 2nd Generation biosensor,
 - ii) Quenching the biosensor with the immobilized antibody in ethanolamine pH 8.5,
 - iii) Immersing the biosensor with the immobilized antibody in a composition comprising 3.6 µg/mL (100 nM) of human 5T4ECDHis (mature protein of SEQ ID NO: 99) for a time period of 500 seconds, and then
 - iv) Immersing the biosensor with the immobilized antibody and 5T4ECDHis in a composition comprising 10 µg/mL of the other antibody targeting 5T4 and determining the association response over a time period of 500 seconds;
- wherein steps i)-iv) are performed at a temperature of 30°C and with shaking at 1000 rpm.
21. The antibody according to any one of the preceding claims, wherein said antibody binds to an epitope or antibody binding region on human 5T4 comprising the amino acid residues R73, Y92 and R94; the numbering of each amino acid residue referring to its position in SEQ ID NO: 1.
22. The antibody according to any one of the preceding claims, wherein said antibody binds to an epitope or antibody binding region on human 5T4 comprising the amino acid residues S69, R73, Y92 and R94; the numbering of each amino acid residue referring to its position in SEQ ID NO: 1.
23. The antibody according to any one of claims 1-21, wherein said antibody binds to an epitope or antibody binding region on human 5T4 comprising the amino acid residues R73, T74, Y92, R94 and N95; the numbering of each amino acid residue referring to its position in SEQ ID NO: 1.
24. The antibody according to any one of claims 21 to 23, wherein said amino acid residues are directly involved in the binding of the antibody.
25. The antibody according to any one of claims 21 to 24, wherein one or more of the following additional amino acid residues are involved binding of the antibody, such as indirectly involved in binding, e.g. by impacting protein folding and/or positioning of one or more amino acid residues directly involved in binding of the antibody: L89, F111, L117, F138, L144, D148, N152; the numbering of each amino acid residue referring to its position in SEQ ID NO: 1.

26. The antibody according to any one of the preceding claims, wherein said antibody binds to an epitope or antibody binding region on human 5T4 within which amino acid residues R73, Y92 and R94 are directly involved in binding the antibody, and wherein one or more of amino acid residues F111, F138, L144 and D148 are indirectly involved in said binding; the numbering of each amino acid residue referring to its position in SEQ ID NO: 1.
27. The antibody according to any one of claims 1 to 25, wherein said antibody binds to an epitope or antibody binding region on human 5T4 within which amino acid residues S69, R73, Y92 and R94 are directly involved in binding the antibody, and wherein one or more of amino acid residues F111, F138, and D148 are indirectly involved in said binding; the numbering of each amino acid residue referring to its position in SEQ ID NO: 1.
28. The antibody according to any one of claims 1 to 25, wherein said antibody binds to an epitope or antibody binding region on human 5T4 within which amino acid residues R73, T74, Y92, R94 and N95 are directly involved in binding the antibody, and wherein amino acid residue F138 is indirectly involved in said binding; the numbering of each amino acid residue referring to its position in SEQ ID NO: 1.
29. The antibody according to any one of claims 21 to 28, wherein the amino acid residues comprised by said epitope or antibody binding region and optionally the one or more additional amino acid residues are identified by alanine scanning of human 5T4 having the amino acid sequence set forth in SEQ ID NO: 1 or the mature polypeptide sequence of SEQ ID NO: 1.
30. The antibody according to claim 29, wherein the alanine scanning is performed as set forth or essentially as set forth in Example 16 herein.
31. The antibody according to claims 29 to 30, wherein the alanine scanning is performed by a procedure comprising the steps of:
- i) Expressing mutant human 5T4 polypeptides in which all amino acid residues in the extracellular domain of human 5T4 (corresponding to amino acid residues 32-355 of SEQ ID NO: 1), except cysteines and alanines, are individually substituted with alanine, and wild type 5T4 polypeptides (amino acid residues 32-355 of SEQ ID NO: 1) individually in human embryonic kidney cells, e.g. HEK 293 cells, such that for each mutant or wild type 5T4 a sample comprising 70-90.000 cells, such as 80.000 cells is provided,
 - ii) Incubating the cells in each sample with 20 µL of said antibody conjugated to fluorescein isothiocyanate (FITC)-conjugated antibody (3 µg/mL; in FACS buffer) for 40 minutes at

room temperature, and subsequently washing each sample twice in 150-180 μ L FACS buffer (phosphate-buffered saline + 0.1% [w/v] BSA + 0.02% [w/v] sodium azide) and resuspending the cells in each sample in 30 μ L FACS buffer,

- 5 iii) Determining, for each sample, the average amount of antibody bound per cell as the geometric mean of the fluorescence intensity (gMFI) for the viable, single cell population in said sample and normalizing the data for each test antibody against the binding intensity of a non-cross blocking 5T4-specific control antibody using the equation:

$$\text{Normalized } gMFI_{aa \text{ position}} = \text{Log}_{10} \left(\frac{gMFI_{Test \text{ Ab}}}{gMFI_{Control \text{ Ab}}} \right)$$

wherein 'aa position' refers to the position that was mutated into an alanine,

- 10 wherein the Z-score is calculated to express loss or gain of binding of the antibody, according to the calculation:

$$Z - \text{score}(\text{fold change}) = \frac{\text{Normalized } gMFI_{aa \text{ position}} - \mu}{\sigma}$$

wherein μ and σ are the mean and standard deviation, respectively, of the Normalized gMFI calculated from all mutants,

- 15 wherein data is excluded from the analysis if the gMFI of the control antibody for a particular 5T4 mutant is lower than the mean $gMFI_{Control \text{ Ab}} - 2.5 \times \text{SD}$ of the mean $gMFI_{Control \text{ Ab}}$ (from all mutants); and optionally

- 20 wherein data is excluded from the analysis if a residue binds with a Z-score just below -1.5 (e.g. between -1.5 and -1.8, such as between -1.5 and -1.7 or such as between -1.5 and -1.6) and that residue is predicted to be buried and spatially separated from the majority of residues, which are predicted to be surface-exposed and for which loss of binding or reduced binding is determined.

32. The antibody according to claim 31, wherein the non-cross blocking 5T4-specific control antibody in step iv) is a bispecific antibody comprising

- 25 - an antigen-binding region, which comprises a VH sequence as set forth in SEQ ID NO: 83 and a VL sequence as set forth in SEQ ID NO: 84 [A1]; and
- 25 - an antigen binding region, which comprises a VH sequence as set forth in SEQ ID NO: 97 and a VL sequence as set forth in SEQ ID NO: 98 [B12].

33. The antibody according to any one of claims 1 to 20, wherein said antibody binds to 5T4 such that there is loss of binding or binding is reduced if any one or more of the amino acid residues R73, Y92 and R94 is/are substituted with alanine; the numbering of each amino acid residue referring to its position in SEQ ID NO: 1.
- 5 34. The antibody according to any one of claims 1 to 20 and 33, wherein said antibody binds to 5T4 such that there is loss of binding or binding is reduced if any one or more of the amino acid residues S69, R73, Y92 and R94 is/are substituted with alanine; the numbering of each amino acid residue referring to its position in SEQ ID NO: 1.
- 10 35. The antibody according to any one of claims 1 to 20 and 33, wherein said antibody binds to 5T4 such that there is loss of binding or binding is reduced if any one or more of the amino acid residues R73, T74, Y92, R94 and N95 is/are substituted with alanine; the numbering of each amino acid residue referring to its position in SEQ ID NO: 1.
- 15 36. The antibody according to any one of claims 1 to 20 and 33 to 35, wherein said antibody binds to 5T4 such that there is loss of binding or binding is reduced if any one or more of the amino acid residues: L89, F111, L117, F138, L144, D148, N152 is/are substituted with alanine; the numbering of each amino acid residue referring to its position in SEQ ID NO: 1.
- 20 37. The antibody according to any one of claims 1 to 20 and 33 to 36, wherein said antibody binds to 5T4 such that there is loss of binding or binding is reduced if any one or more of the amino acid residues R73, Y92, R94, F111, F138, L144 and D148 is/are substituted with alanine; the numbering of each amino acid residue referring to its position in SEQ ID NO: 1.
38. The antibody according to any one of claims 1 to 20 and 33 to 36, wherein said antibody binds to 5T4 such that there is loss of binding or binding is reduced if any one or more of the amino acid residues S69, R73, Y92, R94, F111, F138, and D148 is/are substituted with alanine; the numbering of each amino acid residue referring to its position in SEQ ID NO: 1.
- 25 39. The antibody according to any one of claims 1 to 20 and 33 to 36, wherein said antibody binds to 5T4 such that there is loss of binding or binding is reduced if any one or more of the amino acid residues R73, T74, Y92, R94, N95 and F138 is/are substituted with alanine; the numbering of each amino acid residue referring to its position in SEQ ID NO: 1.
- 30 40. The antibody according to any one of claims 33 to 39, wherein the effect of alanine substitution is determined by alanine scanning of a polypeptide comprising amino acid residues 32-355 of SEQ ID NO: 1.

41. The antibody according to any one of claims 33 to 39, wherein the effect of alanine substitution is determined by a procedure as set forth or essentially as set forth in Example 16 herein.
42. The antibody according to any one of claims 33 to 39, wherein loss of binding is defined as a Z-score in binding being lower than 1.5; the Z-score optionally being calculated as set forth or essentially as set forth in Example 16 herein.
43. The antibody according to claim 42, wherein the effect of alanine substitution is determined by a procedure comprising the steps of:
- i) Expressing mutant human 5T4 polypeptides in which all amino acid residues in the extracellular domain of human 5T4 (corresponding to amino acid residues 32-355 of SEQ ID NO: 1), except cysteines and alanines, are individually substituted with alanine, and wild type 5T4 polypeptides individually in human embryonic kidney cells, e.g. HEK 293 cells, such that for each mutant or wild type 5T4 a sample comprising 70-90.000 cells, such as 80.000 cells is provided,
 - ii) Incubating the cells in each sample with 20 μ L of said antibody conjugated to fluorescein isothiocyanate (FITC)-conjugated antibody (3 μ g/mL; in FACS buffer) for 40 minutes at room temperature, and subsequently washing each sample twice in 150-180 μ L FACS buffer (phosphate-buffered saline + 0.1% [w/v] BSA + 0.02% [w/v] sodium azide) and resuspending the cells in each sample in 30 μ L FACS buffer,
 - iii) Determining, for each sample, the average amount of antibody bound per cell as the geometric mean of the fluorescence intensity (gMFI) for the viable, single cell population in said sample and normalizing the data for each test antibody against the binding intensity of a non-cross blocking 5T4-specific control antibody using the equation:

$$\text{Normalized } gMFI_{aa \text{ position}} = \text{Log}_{10} \left(\frac{gMFI_{Test Ab}}{gMFI_{Control Ab}} \right)$$

wherein 'aa position' refers to the position that was mutated into an alanine,

wherein the Z-score is calculated to express loss or gain of binding of the antibody, according to the calculation:

$$Z - \text{score}(\text{fold change}) = \frac{\text{Normalized } gMFI_{aa \text{ position}} - \mu}{\sigma}$$

wherein μ and σ are the mean and standard deviation, respectively, of the Normalized gMFI calculated from all mutants,

wherein data is excluded from the analysis if the gMFI of the control antibody for a particular 5T4 mutant is lower than the mean $\text{gMFI}_{\text{Control Ab}} - 2.5 \times \text{SD}$ of the mean $\text{gMFI}_{\text{Control Ab}}$ (from all mutants); and optionally

wherein data is excluded from the analysis if a residue binds with a Z-score just below -1.5 (e.g. between -1.5 and -1.8, such as between -1.5 and -1.7 or such as between -1.5 and -1.6) and that residue is predicted to be buried and spatially separated from the majority of residues, which are predicted to be surface-exposed and for which loss of binding or reduced binding is determined.

44. The antibody according to claim 43, wherein the non-cross blocking 5T4-specific control antibody in step iii) is a bispecific antibody comprising

- an antigen-binding region, which comprises a VH sequence as set forth in SEQ ID NO: 83 and a VL sequence as set forth in SEQ ID NO: 84 [A1]; and

- an antigen binding region, which comprising a VH sequence as set forth in SEQ ID NO: 97 and a VL sequence as set forth in SEQ ID NO: 98 [B12].

45. The antibody according to any of the preceding claims, wherein said antibody has reduced internalization capacity as shown by reduced cytotoxicity when conjugated to a cytotoxic moiety as compared to an antibody comprising a variable heavy chain (VH) region comprising the sequence set forth in SEQ ID NO: 87 and a variable light chain (VL) region comprising the sequence set forth in SEQ ID NO: 88 [H8].

46. The antibody according to claim 45, wherein cytotoxicity is determined using a procedure as set forth in Example 7, such as in a procedure comprising the steps of:

- i) Providing an monovalent antibody comprising a first Fab arm of an antibody as defined in any one of the preceding claims and a second Fab arm that is capable of binding to HIV viral protein gp120 (HIV-1 gp120) and is conjugated to Duostatin-3,
- ii) Contacting breast cancer cells MDA-MB-468 (ATCC clone HTB-132) or HCC1954 (ATCC clone CRL-1338) with said monovalent antibody for 5 days at 37°C; and
- iii) Determining the viability of the cells.

47. The antibody according to any one of the preceding claims, wherein said antigen-binding region capable of binding to 5T4 comprises a heavy chain variable region (VH) selected from the group consisting of:
- 5 a) a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 6, 7 and 8 [059],
 - b) a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 13, 14 and 15 [076],
 - c) a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 20, 21 and 22 [085],
 - 10 d) a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 27, 28 and 29 [106],
 - e) a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 34, 35 and 36 [127],
 - 15 f) a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 41, 42 and 43 [207],
 - g) a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 48, 49 and 50 [226], and
 - 20 h) a heavy chain variable region (VH) comprising CDR1, CDR2 and CDR3 sequences, said CDR1, CDR2 and CDR3 sequences comprising in total, at the most 1, 2, 3, 4, 5, 6, 7, 8, 9 or at the most 10 amino acid substitutions, when compared to the CDR1, CDR2 and CDR3 sequences defined in any one of a) to g).
48. The antibody according to any one of the preceding claims, wherein said antigen-binding region capable of binding to 5T4 comprises a heavy chain variable region (VH) selected from the group consisting of:
- 25 a) a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 6, 7 and 8 [059],
 - b) a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 41, 42 and 43 [207],
 - c) a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 48, 49 and 50 [226]; and
 - 30 d) a heavy chain variable region (VH) comprising CDR1, CDR2 and CDR3 sequences, said CDR1, CDR2 and CDR3 sequences comprising in total, at the most 1, 2, 3, 4, 5, 6, 7, 8, 9 or

at the most 10 amino acid substitutions, when compared to the CDR1, CDR2 and CDR3 sequences defined in any one of a) to c).

49. The antibody according to any one of the preceding claims, wherein said antigen-binding region capable of binding to 5T4 comprises a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 6, 7 and 8 [059].
50. The antibody according to any one of the preceding claims, wherein said antigen-binding region capable of binding to 5T4 comprises a heavy chain variable region (VH) selected from the group consisting of: a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 41, 42 and 43 [207].
51. The antibody according to any one of the preceding claims, wherein said antigen-binding region capable of binding to 5T4 comprises a heavy chain variable region (VH) selected from the group consisting of: a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 48, 49 and 50 [226].
52. The antibody according to any one of the preceding claims, wherein said antigen-binding region capable of binding to 5T4 comprises a heavy chain variable region (VH) and a light chain variable region (VL) selected from the group consisting of:
- a) a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 6, 7 and 8, respectively, and a light chain variable region (VL) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NO: 10, AAS and SEQ ID NO: 11, respectively [059],
 - b) a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 13, 14 and 15, respectively; and a light chain variable region (VL) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NO: 17, DAS and SEQ ID NO: 18, respectively [076],
 - c) a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 20, 21 and 22, respectively; and a light chain variable region (VL) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NO: 24, DAS and SEQ ID NO: 25, respectively [085],
 - d) a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 27, 28 and 29, respectively; and a light chain variable region (VL) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NO: 31, DVS and SEQ ID NO: 32, respectively [106],

- e) a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 34, 35 and 36, respectively; and a light chain variable region (VL) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NO: 38, DAS and SEQ ID NO: 39, respectively [127],
- 5 f) a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 41, 42 and 43, respectively, and a light chain variable region (VL) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NO: 45, DAS and SEQ ID NO: 46, respectively [207],
- 10 g) a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 48, 49 and 50, respectively, and a light chain variable region (VL) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NO: 52, DAS and SEQ ID NO: 53, respectively [226]; and
- 15 h) a heavy chain variable region (VH) and a light chain variable region (VL) region, each region comprising CDR1, CDR2 and CDR3 sequences, said CDR1, CDR2 and CDR3 sequences comprising in total, at the most 1, 2, 3, 4, 5, 6, 7, 8, 9 or at the most 10 amino acid substitutions, when compared to the CDR1, CDR2 and CDR3 sequences defined in any one of a) to g).
53. The antibody according to any one of the preceding claims, wherein the six complementarity-determining regions (CDRs) of the antigen binding region(s) capable of binding to 5T4 comprise,
- 20 in total, at the most 1, 2, 3, 4, 5, 6, 7, 8, 9 or at the most 10 amino acid substitutions, when compared to
- iv) the CDR sequences of SEQ ID NOs: 6, 7, 8, 10, AAS and SEQ ID NO: 11 [059],
- v) the CDR sequences of SEQ ID NOs.: 41, 42, 43, 45, DAS and SEQ ID NO: 46 [207]; or
- vi) the CDR sequences of SEQ ID NOs.: 48, 49, 50, 52, DAS and SEQ ID NO: 53 [226].
- 25 54. The antibody according to any one of claims 22 to 29, wherein 1, such as 2, 3, 4, 5, 6, 7, 8, 9 or 10 of the said amino acid substitutions is/are conservative amino acid substitution(s).
55. The antibody according to claim any one of the preceding claims, the antibody comprising one or two heavy chain variable regions in which the complementarity-determining region 3 (CDR3) comprises six consecutive amino acid residues of the sequence set forth in SEQ ID NO: 102 (YYGMDV) [059, 207, 226].
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56. The antibody according to claim 55, wherein the said six consecutive amino acid residues are the most C-terminal amino acid residues within the CDR3.
57. The antibody according to any one of the preceding claims, wherein said antigen-binding region capable of binding to 5T4 comprises one or two heavy chain variable region(s) (VH) comprising the CDR1 sequence of SEQ ID NO: 41 (GGSFSGYY), the CDR2 sequence of SEQ ID NO: 103 (IDHSX₁ST), and the CDR3 sequence of SEQ ID NO: 104 (AX₂WFGELX₃X₄YYYGMDV), and a light chain variable region (VL) comprising the CDR1 sequence of SEQ ID NO: 105 (QSVSSX₅), the CDR2 sequence DAS, and the CDR3 sequence of SEQ ID NO: 46 (QQRSNWPLT), and wherein X₁ is G or E, X₂ is A or G, X₃ is W or Y, X₄ is D or H and X₅ is Y or F [207, 226].
58. The antibody according to any one of the preceding claims, wherein said antigen-binding region capable of binding to 5T4 comprises a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 6, 7, and 8, respectively, and a light chain variable region (VL) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NO: 10, AAS and SEQ ID NO: 11, respectively [059].
59. The antibody according to any one of the preceding claims, wherein said antigen-binding region capable of binding to 5T4 comprises a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 41, 42 and 43, respectively, and a light chain variable region (VL) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NO: 45, DAS and SEQ ID NO: 46, respectively [207].
60. The antibody according to any one of the preceding claims, wherein said antigen-binding region capable of binding to 5T4 comprises a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 48, 49 and 50, respectively, and a light chain variable region (VL) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NO: 52, DAS and 53, respectively [226].
61. The antibody according to any one of the preceding claims, wherein said antigen-binding region capable of binding to 5T4 comprises a heavy chain variable region (VH) selected from the group consisting of:
- a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 5 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 5 [059],

- b) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 12 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 12 [076],
- 5 c) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 19 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 19 [085],
- d) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 26 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 26 [106],
- 10 e) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 33 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 33 [127],
- f) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 40 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 40 [207]; and
- 15 g) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 47 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 47 [226].
62. The antibody according to any one of the preceding claims, wherein said antigen-binding region
- 20 capable of binding to 5T4 comprises a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 5 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 5 [059].
63. The antibody according to any one of the preceding claims, wherein said antigen-binding region
- 25 capable of binding to 5T4 comprises a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 40 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 40 [207].
64. The antibody according to any one of the preceding claims, wherein said antigen-binding region
- 30 capable of binding to 5T4 comprises a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 47 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 47 [226].

65. The antibody according to any one of the preceding claims, wherein said antigen-binding region capable of binding to 5T4 comprises a heavy chain variable region (VH) and a light chain variable region (VL) selected from the group consisting of:
- 5 a) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 5 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 5, and a light chain variable region (VL) comprising the sequence of SEQ ID NO: 9 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 9 [059],
 - 10 b) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 12 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 12, and a light chain variable region (VL) comprising the sequence of SEQ ID NO: 16 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 16 [076],
 - 15 c) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 19 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 19, and a light chain variable region (VL) comprising the sequence of SEQ ID NO: 23 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 23 [085],
 - 20 d) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 26 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 26, and a light chain variable region (VL) comprising the sequence of SEQ ID NO: 30 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 30 [106],
 - 25 e) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 33 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 33, and a light chain variable region (VL) comprising the sequence of SEQ ID NO: 37 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 37 [127],
 - 30

- 5 f) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 40 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 40, and a light chain variable region (VL) comprising the sequence of SEQ ID NO: 44 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 44 [207],
- 10 g) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 47 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 47, and a light chain variable region (VL) comprising the sequence of SEQ ID NO: 51 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 51 [226].
66. The antibody according to any one of the preceding claims, wherein said antigen-binding region capable of binding to 5T4 comprises a heavy chain variable region (VH) and a light chain variable region (VL) selected from the group consisting of:
- 15 a) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 5, and a light chain variable region (VL) comprising the sequence of SEQ ID NO: 9 [059],
- b) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 12, and a light chain variable region (VL) comprising the sequence of SEQ ID NO: 16 [076],
- 20 c) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 19, and a light chain variable region (VL) comprising the sequence of SEQ ID NO: 23 [085],
- d) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 26, and a light chain variable region (VL) comprising the sequence of SEQ ID NO: 30 [106],
- 25 e) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 33, and a light chain variable region (VL) comprising the sequence of SEQ ID NO: 37 [127],
- f) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 40, and a light chain variable region (VL) comprising the sequence of SEQ ID NO: 44 [207]; and
- g) a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 47, and a light chain variable region (VL) comprising the sequence of SEQ ID NO: 51 [226].
- 30 67. The antibody according to any of the preceding claims, wherein the antibody is a full-length antibody, such as a full length IgG1 antibody.
68. The antibody according to any one of the preceding claims, which is a monovalent antibody.

69. The antibody according to any one of the preceding claims, which is a bivalent antibody.
70. The antibody according to any one of the preceding claims, which is a monospecific antibody.
71. The antibody according to any one of the preceding claims, which is a bispecific antibody.
72. The antibody according to any one of the preceding claims, comprising an antigen binding
5 region of an antibody that binds to CD3, such as human CD3 ϵ (epsilon), such as human CD3 ϵ
(epsilon) as specified in SEQ ID NO: 4.
73. The antibody according to claim 72, wherein the antigen-binding region that binds to CD3
comprises
10 a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ
ID NOs.: 54, 55 and 56, respectively; [wildtype anti-CD3 (SP34/humanized SP34,
WO2015001085 (Genmab)) – VH CDR sequences];
and, optionally
a light chain variable region (VL) comprising comprising the CDR1, CDR2, and CDR3
15 sequences of SEQ ID NO: 58, GTN and 59, respectively [wildtype anti-CD3, VL CDR
sequences].
74. The antibody according to claim 72 or 73, wherein the antigen binding region that binds to CD3
comprises
20 a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 57, or a
sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid
sequence identity to the sequence of SEQ ID NO: 57 [wildtype anti-CD3 – VH full length
sequence];
and, optionally
a light chain variable region (VL) comprising the sequence of SEQ ID NO: 60 or a sequence
25 having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity
to the sequence of SEQ ID NO: 60, [wild type anti-CD3 – VL full length sequence].
75. The antibody according to any one of claims 72 to 74, wherein said antibody has a lower human
CD3 ϵ binding affinity than an antibody having an antigen-binding region comprising a VH
sequence as set forth in SEQ ID NO: 57, and a VL sequence as set forth in SEQ ID NO: 60 [wild
30 type anti-CD3 (humanized SP34, WO2015001085 (Genmab)) VH and VL sequences], preferably
wherein said affinity is at least 5-fold lower, such as at least 10-fold lower, e.g. at least 20-fold

lower, at least 30 fold lower, at least 40 fold lower, at least 45 fold lower or such as at least 50-fold lower.

76. The antibody according to any one of claims 72 to 74, wherein said antigen binding region that binds to CD3 with an equilibrium dissociation constant K_D within the range of 200 – 1000 nM, such as within the range of 300 – 1000 nM, within the range of 400 – 1000 nM, within the range of 500 – 1000 nM, within the range of 300 – 900 nM within the range of 400 – 900 nM, within the range of 400 – 700 nM, within the range of 500 – 900 nM, within the range of 500 – 800 nM, within the range of 500 – 700 nM, within the range of 600 – 1000 nM, within the range of 600 – 900 nM, within the range of 600 – 800 nM, or such as within the range of 600 – 700 nM.
77. The antibody according to claim 72 or 75, wherein said antigen binding region that binds to CD3 with an equilibrium dissociation constant K_D within the range of 1 – 100 nM, such as within the range of 5 – 100 nM, within the range of 10 – 100 nM, within the range of 1 – 80 nM, within the range of 1 – 60 nM within the range of 1 – 40 nM, within the range of 1 – 20 nM, within the range of 5 – 80 nM, within the range of 5 – 60 nM, within the range of 5 – 40 nM, within the range of 5 – 20 nM, within the range of 10 – 80 nM, within the range of 10 – 60 nM, within the range of 10 – 40 nM, or such as within the range of 10 – 20 nM.
78. The antibody according to any one of claims 72 to 77, wherein
- the antigen binding region that binds to CD3 comprises a heavy chain variable (VH) region comprising a CDR1 sequence, a CDR2 sequence and a CDR3 sequence,
- the heavy chain variable (VH) region, when compared to a heavy chain variable (VH) region comprising the sequence set forth in SEQ ID NO: 57, has an amino acid substitution in one of the CDR sequences, the substitution being at a position selected from the group consisting of: T31, N57, H101, G105, S110 and Y114, the positions being numbered according to the sequence of SEQ ID NO: 57 [VH_huCD3-H1L1]; and
- the wild type light chain variable (VL) region comprises the CDR1, CDR2 and CDR3 sequences set forth in SEQ ID NO: 58, GTN and SEQ ID NO: 59, respectively.
79. The antibody according to claim 72, wherein the CDR1, CDR2 and CDR3 of the heavy chain variable (VH) region of the antigen binding region that binds to CD3 comprises, in total, at the most 1, 2, 3, 4 or 5 amino acid substitutions, when compared to the CDR1, CDR2 and CDR3 of the sequence set forth in SEQ ID NO: 57.

80. The antibody according to claim 72 or 73, wherein the amino acid sequences of the CDR1, CDR2 and CDR3 of the heavy chain variable (VH) region of the antigen binding region that binds to CD3 have at least 95% sequence identity, such as at least 96% sequence identity, at least 97% sequence identity, at least 98% sequence identity or at least 99% sequence identity to the amino acid sequences of the CDR1, CDR2 and CDR3 of the wild type heavy chain variable (VH) region, sequence identity being calculated based on an aligning an amino acid sequence consisting of the sequences of the CDR1, CDR2 and CDR3 of the heavy chain variable (VH) region of the antigen binding region that binds to CD with an amino acid sequence comprising the sequences of the CDR1, CDR2 and CDR3 of the wild type heavy chain variable (VH) region.
81. The antibody according to claims 72 to 74, wherein the antigen binding region that binds to CD3 comprises a mutation selected from the group consisting of: T31M, T31P, N57E, H101G, H101N, G105P, S110A, S110G, Y114M, Y114R, Y114V.
82. The antibody according to any one of the preceding claims, wherein when said antibody is a bispecific antibody which is devoid of, or has reduced Fc-mediated effector function ("inert" antibody), and comprises an antigen binding region of an antibody that binds to CD3, then the antibody :
- a) is capable of mediating concentration-dependent cytotoxicity of SK-OV-3 cells, when using purified PBMCs or T cells as effector cells e.g. when assayed as described in Example 14 herein,
 - b) is capable of mediating concentration-dependent cytotoxicity of MDA-MB-231 cells, when using purified T cells as effector cells e.g. when assayed as described in Example 13 herein,
 - c) is capable of activating T cells *in vitro* in the presence of MDA-MB-231 tumor cells; e.g. when assayed as described in Example 13 herein,
 - d) is capable of activating T-cells *in vitro* in the presence of BxPC-3, PANC-1, Ca Ski and/or SiHa tumor cells; e.g. when assayed as described in Example 17 herein,
 - e) is capable of inducing cytotoxicity of BxPC-3, PANC-1, Ca Ski and/or SiHa tumor cells when using purified T cells as effector cells e.g. when assayed as described in Example 17 herein; and/or
 - f) shows anti-tumor activity, such as delayed tumor outgrowth, in a humanized immune hematopoietic stem cell reconstitution mouse xenograft model, such as NOD.Cg-

Prkdc^{scid} Il2rg^{tm1Wjl}/SzJ inoculated with human MDA-MB-231 tumor cells; e.g. when determined as described in Example 15.

83. The antibody according to claim 82, wherein the ability of the antibody to mediate concentration-dependent cytotoxicity of SK-OV-3 cells is determined in an *in vitro* cytotoxicity assay comprising the steps of:
- i) isolating peripheral blood mononuclear cells (PBMCs) or T cells from healthy human donor buffy coats,
 - ii) providing
 - a first set of samples, wherein each sample comprises PBMCs and human ovary adenocarcinoma SK-OV-3 cells, and wherein the ratios PBMCs:SK-OV-3 cells in said samples are 1:2, 1:1, 2:1, 4:1, 8:1, and 12:1; and
 - a second set of samples, wherein each sample comprises T cells and human ovary adenocarcinoma SK-OV-3 cells and wherein the ratios of T cells:SK-OV-3 cells in said samples are 1:2, 1:1, 2:1, 4:1 and 8:1
 - iii) adding the antibody to each set of samples at concentrations ranging from 0.0128 ng/mL to 1000 ng/mL and incubating the samples for 72 hours at 37°C; and then
 - iv) assessing the viability of the SK-OV-3 cells using Resazurin (7-Hydroxy-3H-phenoxazin-3-one 10-oxide).
84. The antibody according to claim 82, wherein the ability to activate T cells *in vitro* in the presence of MDA-MB-231 tumor cells is determined in an assay comprising the steps of:
- i) Isolating T cells from healthy human donor buffy coats,
 - ii) Providing a set of samples, wherein each sample comprises T-cells and human breast adenocarcinoma MDA-MB-231 cells and wherein the ratio of T-cells: MDA-MB-231 cells in said samples is 8:1,
 - iii) adding the antibody to the set of samples at concentrations ranging from 0.0128 ng/mL to 1000 ng/mL and incubating the samples for 72 hours at 37°C,
 - iv) staining the T-cells with fluorescent-labeled antibodies against T-cell activation markers, such as CD69-APC, CD25-PE-Cy7 and CD279/PD1-BV604 antibodies, by incubation with said antibodies for 30 minutes at 4°C; and
 - v) analyzing the samples by flow cytometry.
85. The antibody according to claim 82, wherein activation of T cells *in vitro* in the presence of BxPC-3, PANC-1, Ca Ski and/or SiHa tumor cells is determined in an procedure comprising the steps of:

- i) Providing T cells isolated from healthy human donor buffy coats,
 - ii) Providing a set of samples, wherein each sample comprises said T cells and BxPC-3, PANC-1, Ca Ski or SiHa tumor cells and wherein the ratio of T cells: tumor cells in said samples is 4:1,
 - 5 iii) adding the antibody to the set of samples at concentrations ranging from 0.0128 ng/mL to 5000 ng/mL (such as 5-fold dilutions) and incubating the samples for 72 hours at 37°C,
 - iv) collecting from each sample 110 µL supernatant containing T cells and staining the T cells with fluorescent-labeled antibodies against T-cell markers, such as CD3-eFluor450, CD4-APC-eFluor780, DC8-AF700, and with antibodies against T-cell markers, such as 69-APC,
 - 10 CD25-PE-Cy7 and CD279/PD1-BV604 antibodies, by incubation with said antibodies for 30 minutes at 4°C; and
 - v) analyzing the samples by flow cytometry.
86. The antibody according to claim 82, wherein the ability to induce cytotoxicity of BxPC-3, PANC-1, Ca Ski and/or SiHa tumor cells is determined in a procedure comprising the steps of
- 15 i) Providing T cells isolated from healthy human donor buffy coats,
 - ii) Providing a set of test samples and control samples, wherein each sample comprises said T-cells and BxPC-3, PANC-1, Ca Ski or SiHa tumor cells which have been allowed to adhere to the bottom of a 96-well tissue culture plate and wherein the ratio of T-cells: tumor cells in said samples is 4:1,
 - 20 iii) adding the antibody to the set of test samples at concentrations ranging from 0.0128 ng/mL to 5000 ng/mL (such as 5-fold dilutions), while the control samples remain untreated or are incubated with 5 µM staurosporin, and incubating all samples for 72 hours at 37°C,
 - iv) Incubating the adherent cells in 10% (w/w) 7-hydroxy-3H-phenoxazin-3-one 10-oxide (Resazurin) in RPMI-1640 medium supplemented with 10% (w/w) donor bovine serum with iron and penicilin/streptomycin at 37°C for 4 hours,
 - 25 v) Measuring the absorbance of the cells; setting the absorbance of the cells incubated with staurosporin as 0% viability and the untreated cells as 100% viability and calculating the percentage viable cells as

$$x100 \% \text{ viable cells} = \left(\frac{[\text{absorbance sample} - \text{absorbance staurosporine treated cells}]}{[\text{absorbance untreated cells} - \text{absorbance staurosporine treated cells}]} \right)$$

87. The antibody according to any one of claims 72 and 78 to 84, wherein the antigen-binding region capable of binding to CD3 comprises:

- 5 a) a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NOs: 61, 55, and 56 [VH CDR1-T31P + Wild type VH CDRs 2,3], respectively, and a light chain variable region (VL) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NO: 58, the sequence GTN, and the sequence as set forth in SEQ ID NO: 59, respectively [Wild type VL CDRs 1,2,3], or
- 10 b) a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NOs: 63, 55, and 56 [VH CDR1-T31M + Wild type VH CDRs 2,3], respectively, and a light chain variable region (VL) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NO: 58, the sequence GTN, and the sequence as set forth in SEQ ID NO: 59, respectively [Wild type VL CDRs 1,2,3], respectively, or
- 15 c) a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NOs: 54, 65, and 56 [VH CDR-N57E + Wild type VH CDRs 1,3], respectively, and a light chain variable region (VL) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NO: 58, the sequence GTN, and the sequence as set forth in SEQ ID NO: 59, respectively [Wild type VL CDRs 1,2,3], respectively, or
- 20 d) a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NOs: 54, 55, and 67 [Wild type VH CDRs 1,2 + VH CDR3-H101G], respectively, and a light chain variable region (VL) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NO: 58, the sequence GTN, and the sequence as set forth in SEQ ID NO: 59, respectively [Wild type VL CDRs 1,2,3] ,
- 25 respectively.
- 30 e) a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NOs: 54, 55, and 69 [Wild type VH CDRs 1,2 + VH CDR3-H101N], respectively, and a light chain variable region (VL) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NO: 58, the sequence GTN, and the sequence as set forth in SEQ ID NO: 59, respectively [Wild type VL CDRs 1,2,3] , respectively;
- f) a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NOs: 54, 55, and 71 [Wild type VH CDRs 1,2 + VH CDR3-

- G105P], respectively, and a light chain variable region (VL) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NO: 58, the sequence GTN, and the sequence as set forth in SEQ ID NO: 59, respectively [Wild type VL CDRs 1,2,3] , respectively;
- 5 g) a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NOs: 54, 55, and 73 [Wild type VH CDRs 1,2 + VH CDR3-S110A], respectively, and a light chain variable region (VL) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NO: 58, the sequence GTN, and the sequence as set forth in SEQ ID NO: 59, respectively [Wild type VL CDRs 1,2,3],
- 10 respectively, or
- h) a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NOs: 54, 55, and 75 [Wild type VH CDRs 1,2 + VH CDR3-S110G], respectively, and a light chain variable region (VL) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NO: 58, the sequence GTN, and the
- 15 sequence as set forth in SEQ ID NO: 59, respectively [Wild type VL CDRs 1,2,3], respectively,
- i) a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NOs: 54, 55, and 77 [Wild type VH CDRs 1,2 + VH CDR3-Y114V], respectively, and a light chain variable region (VL) comprising CDR1, CDR2, and
- 20 CDR3 having the sequences as set forth in SEQ ID NO: 58, the sequence GTN, and the sequence as set forth in SEQ ID NO: 59, respectively [Wild type VL CDRs 1,2,3], respectively, or
- j) a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NOs: 54, 55, and 79 [Wild type VH CDRs 1,2 + VH CDR3-Y114M], respectively, and a light chain variable region (VL) comprising CDR1, CDR2, and
- 25 CDR3 having the sequences as set forth in SEQ ID NO: 58, the sequence GTN, and the sequence as set forth in SEQ ID NO: 59, respectively [Wild type VL CDRs 1,2,3], respectively, or
- k) a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 having the
- 30 sequences as set forth in SEQ ID NOs: 54, 55, and 81 [Wild type VH CDRs 1,2 + VH CDR3-Y114R], respectively, and a light chain variable region (VL) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NO: 58, the sequence GTN, and the

sequence as set forth in SEQ ID NO: 59, respectively [Wild type VL CDRs 1,2,3], respectively.

88. The antibody according to any one of claims 72 and 78 to 85, wherein the antigen-binding region capable of binding to CD3 comprises a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NOs: 54, 55, and 67 [Wild type VH CDRs 1,2 + VH CDR3-H101G], respectively, and a light chain variable region (VL) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NO: 58, the sequence GTN, and the sequence as set forth in SEQ ID NO: 59, respectively [Wild type VL CDRs 1,2,3], respectively.
89. The antibody according to any one of claims 72 and 78 to 85, wherein the antigen-binding region capable of binding to 5T4 comprises a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 6, 7 and 8, respectively, and a light chain variable region (VL) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NO: 10, AAS and SEQ ID NO: 11, respectively [059];
- and
- the antigen-binding region capable of binding to CD3 comprises a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NOs: 54, 55, and 67 [Wild type VH CDRs 1,2 + VH CDR3-H101G], respectively, and a light chain variable region (VL) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NO: 58, the sequence GTN, and the sequence as set forth in SEQ ID NO: 59, respectively [Wild type VL CDRs 1,2,3], respectively.
90. The antibody according to any one of claims 72 and 78 to 85, wherein the antigen-binding region capable of binding to 5T4 comprises a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 41, 42 and 43, respectively, and a light chain variable region (VL) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NO: 45, DAS and 46, respectively [207];
- and
- the antigen-binding region capable of binding to CD3 comprises a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NOs: 54, 55, and 67 [Wild type VH CDRs 1,2 + VH CDR3-H101G], respectively, and a light chain variable region (VL) comprising CDR1, CDR2, and CDR3 having the sequences as set

forth in SEQ ID NO: 58, the sequence GTN, and the sequence as set forth in SEQ ID NO: 59, respectively [Wild type VL CDRs 1,2,3] , respectively.

91. The antibody according to any one of claims 47 and 51 to 59, wherein

5 the antigen-binding region capable of binding to 5T4 comprises a heavy chain variable region (VH) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NOs.: 48, 49 and 50, respectively, and a light chain variable region (VL) comprising the CDR1, CDR2, and CDR3 sequences of SEQ ID NO: 52, DAS and 53, respectively [226];

and

10 the antigen-binding region capable of binding to CD3 comprises a heavy chain variable region (VH) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NOs: 54, 55, and 67 [Wild type VH CDRs 1,2 + VH CDR3-H101G], respectively, and a light chain variable region (VL) comprising CDR1, CDR2, and CDR3 having the sequences as set forth in SEQ ID NO: 58, the sequence GTN, and the sequence as set forth in SEQ ID NO: 59, respectively [Wild type VL CDRs 1,2,3], respectively.

15 92. The antibody according to any one of claims 72 and 78 to 91, wherein the antigen-binding region capable of binding to human CD3 comprises a VH sequence and a VL sequence selected from the group consisting of:

- a) a VH sequence as set forth in SEQ ID NO: 62 [VH T31P full length sequence] and a VL sequence as set forth in SEQ ID NO: 60 [Wild type full length sequence],
- 20 b) a VH sequence as set forth in SEQ ID NO: 64 [VH T31M full length sequence] and a VL sequence as set forth in SEQ ID NO: 60,
- c) a VH sequence as set forth in SEQ ID NO: 66 [VH N57E full length sequence] and a VL sequence as set forth in SEQ ID NO: 60,
- d) a VH sequence as set forth in SEQ ID NO: 68 [VH H101G full length sequence] and a VL sequence as set forth in SEQ ID NO: 60,
- 25 e) a VH sequence as set forth in SEQ ID NO: 70 [VH H101N full length sequence] and a VL sequence as set forth in SEQ ID NO: 60,
- f) a VH sequence as set forth in SEQ ID NO: 72 [VH G105P full length sequence] and a VL sequence as set forth in SEQ ID NO: 60,
- 30 g) a VH sequence as set forth in SEQ ID NO: 74 [VH S110A full length sequence] and a VL sequence as set forth in SEQ ID NO: 60,

- h) a VH sequence as set forth in SEQ ID NO: 76 [VH S110G full length sequence] and a VL sequence as set forth in SEQ ID NO: 60,
- i) a VH sequence as set forth in SEQ ID NO: 78 [VH Y114V full length sequence] and a VL sequence as set forth in SEQ ID NO: 60,
- 5 j) a VH sequence as set forth in SEQ ID NO: 80 [VH Y114M full length sequence] and a VL sequence as set forth in SEQ ID NO: 60; and
- k) a VH sequence as set forth in SEQ ID NO: 82 [VH Y114R full length sequence] and a VL sequence as set forth in SEQ ID NO: 60.
93. The antibody according to any one of claims 72 and 78 to 92, wherein the antigen-binding
10 region capable of binding to human CD3 comprises a VH sequence as set forth in SEQ ID NO: 68 [VH H101G full length sequence] and a VL sequence as set forth in SEQ ID NO: 60.
94. The antibody according to any one of claims 78 to 93, wherein
the antigen-binding region capable of binding to 5T4 comprises a heavy chain variable
region (VH) comprising the sequence of SEQ ID NO: 5 or a sequence having at least 90%, at
15 least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of
SEQ ID NO: 5 [059 - VH full length sequence];
and
the antigen-binding region capable of binding to human CD3 comprises a VH sequence as
set forth in SEQ ID NO: 68 [VH H101G full length sequence] and a VL sequence as set forth
20 in SEQ ID NO: 60.
95. The antibody according to any one of claims 72 and 78 to 93, wherein
the antigen-binding region capable of binding to 5T4 comprises a heavy chain variable
region (VH) comprising the sequence of SEQ ID NO: 40 or a sequence having at least 90%, at
least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of
25 SEQ ID NO: 40 [207 - VH full length sequence];
and
the antigen-binding region capable of binding to human CD3 comprises a VH sequence as
set forth in SEQ ID NO: 68 [VH H101G full length sequence] and a VL sequence as set forth
in SEQ ID NO: 60.
- 30 96. The antibody according to any one of claims 47 and 51 to 64, wherein
the antigen-binding region capable of binding to 5T4 comprises a heavy chain variable
region (VH) comprising the sequence of SEQ ID NO: 47 or a sequence having at least 90%, at

least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 47 [226 - VH full length sequence];

and

5 the antigen-binding region capable of binding to human CD3 comprises a VH sequence as set forth in SEQ ID NO: 68 [VH H101G full length sequence] and a VL sequence as set forth in SEQ ID NO: 60.

97. The antibody according to any of claims 72 and 78 to 94, wherein

10 the antigen-binding region capable of binding to 5T4 comprises a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 5 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 5, and a heavy chain light region (VL) comprising the sequence of SEQ ID NO: 9 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 9 [059];

and

15 the antigen-binding region capable of binding to human CD3 comprises a VH sequence as set forth in SEQ ID NO: 68 [VH H101G full length sequence] and a VL sequence as set forth in SEQ ID NO: 60.

98. The antibody according to any of claims 72, 78 to 93 and 95, wherein

20 the antigen-binding region capable of binding to 5T4 comprises a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 40 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 40, and a heavy chain light region (VL) comprising the sequence of SEQ ID NO: 44 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 44 [207 – VH + VL full length sequences];

25 and

the antigen-binding region capable of binding to human CD3 comprises a VH sequence as set forth in SEQ ID NO: 68 [VH H101G full length sequence] and a VL sequence as set forth in SEQ ID NO: 60.

99. The antibody according to any of claims 72, 78 to 93 and 96, wherein

30 the antigen-binding region capable of binding to 5T4 comprises a heavy chain variable region (VH) comprising the sequence of SEQ ID NO: 47 or a sequence having at least 90%, at

least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 47, and a heavy chain light region (VL) comprising the sequence of SEQ ID NO: 51 or a sequence having at least 90%, at least 95%, at least 97%, or at least 99% amino acid sequence identity to the sequence of SEQ ID NO: 51 [226 – VH + VL full length sequences];

5 and

the antigen-binding region capable of binding to human CD3 comprises a VH sequence as set forth in SEQ ID NO: 68 [VH H101G full length sequence] and a VL sequence as set forth in SEQ ID NO: 60.

100. The antibody according to any one of the preceding claims, wherein each antigen-binding region
10 comprises a heavy chain variable region (VH) and a light chain variable region (VL), and wherein said variable regions each comprise three CDR sequences, CDR1, CDR2 and CDR3, respectively, and four framework sequences, FR1, FR2, FR3 and FR4, respectively.

101. The antibody according to claim 100, wherein the antibody comprises two heavy chain constant regions (CH), and two light chain constant regions (CL).

15 102. The antibody according to claim 100 or 101, wherein said antibody comprises a first and a second heavy chain, each of said first and second heavy chain comprises at least a hinge region, a CH2 and CH3 region, wherein in said first heavy chain at least one of the amino acids in the positions corresponding to positions selected from the group consisting of T366, L368, K370, D399, F405, Y407 and K409 in a human IgG1 heavy chain has been substituted, and in said
20 second heavy chain at least one of the amino acids in the positions corresponding to a position selected from the group consisting of T366, L368, K370, D399, F405, Y407, and K409 in a human IgG1 heavy chain has been substituted, wherein said substitutions of said first and said second heavy chains are not in the same positions, and wherein the amino acid positions are numbered according to EU numbering.

25 103. The antibody according to any one of claims 100 to 102, wherein the amino acid in the position corresponding to K409 in a human IgG1 heavy chain is R in said first heavy chain, and the amino acid in the position corresponding to F405 in a human IgG1 heavy chain is L in said second heavy chain, or *vice versa*.

30 104. The antibody according to any one of the preceding claims, wherein the antibody comprises a first and a second heavy chain, and wherein in both the first and the second heavy chain, the

amino acid residues at the positions corresponding to positions L234 and L235 in a human IgG1 heavy chain according to EU numbering are F and E, respectively.

105. The antibody according to any one of the preceding claims, wherein antibody comprises a first and a second heavy chain, and wherein in both the first and the second heavy chain, the amino acid residue at the position corresponding to position D265 in a human IgG1 heavy chain according to EU numbering is A.
106. The antibody according to any one of the preceding claims, wherein
- a) the antigen-binding region(s) capable of binding to 5T4 is/are humanized, and/or
 - b) the antigen-binding region capable of binding to CD3, if present, is humanized.
107. The antibody according to any one of the preceding claims, wherein
- a) the antigen-binding region(s) capable of binding to 5T4 is/are human, and/or
 - b) the antigen-binding region capable of binding to CD3, if present, is human.
108. The antibody according to any one of the preceding claims, wherein
- a) the antigen-binding region(s) capable of binding to 5T4 is/are chimeric, and/or
 - b) the antigen-binding region capable of binding to CD3, if present, is chimeric.
109. The antibody according to any one of the preceding claims, wherein said antibody comprises a first and, optionally, a second heavy chain and wherein the first heavy chain, and the second heavy chain if present, is/are modified so that the antibody induces Fc-mediated effector function to a lesser extent relative to an identical non-modified antibody.
110. The antibody according to any one of the preceding claims, wherein said antibody comprises a kappa (κ) light chain.
111. The antibody according to any one of the preceding claims, wherein said antibody comprises a lambda (λ) light chain.
112. The antibody according to any of the preceding claims, wherein said antibody comprises a lambda (λ) light chain and a kappa (κ) light chain; e.g. an antibody with a heavy chain and a lambda light chain which comprise the binding region capable of binding to CD3, and a heavy chain and a kappa light chain which comprise the binding region capable of binding to 5T4.
113. An immunoconjugate or antibody-drug conjugate (ADC) comprising the antibody according to any one of the preceding claims, and a therapeutic moiety, such as a cytotoxic agent, a chemotherapeutic drug, a cytokine, an immunosuppressant, antibiotic, or a radioisotope.

114. A nucleic acid construct comprising

- a) a nucleic acid sequence encoding a heavy chain sequence of an antibody comprising an antigen-binding region capable of binding to 5T4 as defined in any one of claims 1-113, and/or
- 5 b) a nucleic acid sequence encoding a light chain sequence of an antibody comprising an antigen-binding region capable of binding to 5T4 as defined in any one of claims 72 to 113.

115. The nucleic acid construct according to claim 114, further comprising

- a) a nucleic acid sequence encoding a heavy chain sequence of an antibody comprising an antigen-binding region capable of binding to CD3 as defined in any one of claims 72 to 10 113; and/or
- b) a nucleic acid sequence encoding a light chain sequence of an antibody comprising an antigen-binding region capable of binding to CD3 as defined in any one of claims 72 to 113.

15 116. An expression vector comprising

- a) a nucleic acid sequence encoding a heavy chain sequence of an antibody comprising an antigen-binding region capable of binding to 5T4 as defined in any one of claims 1 to 112, and/or
- 20 b) a nucleic acid sequence encoding a light chain sequence of an antibody comprising an antigen-binding region capable of binding to 5T4 as defined in any one of claims 1 to 112.

117. An expression vector according to claim 116, further comprising

- a) a nucleic acid sequence encoding a heavy chain sequence of an antibody comprising an antigen-binding region capable of binding to CD3 as defined in any one of claims 72 to 25 112; and/or
- b) a nucleic acid sequence encoding a light chain sequence of an antibody comprising an antigen-binding region capable of binding to CD3 as defined in any one of claims 72 to 112.

118. A cell comprising a nucleic acid construct as defined in any one of claims 114 to 115, or an
30 expression vector as defined in claim 116 or 117, such as a cell that has been obtained by

transfecting a host cell with said nucleic acid construct or expression vector, such as a recombinant host cell.

119. The cell according to claim 118, wherein said host cell is of human origin, such as a human embryonic kidney (HEK) cell, such as a HEK/Expi cell, or is of rodent origin, such as a Chinese hamster ovary cell, such as a CHO/N50 cell.
120. A composition comprising an antibody as defined in any one of claims 1 to 112.
121. A pharmaceutical composition comprising an antibody as defined in any one of claims 1 to 112 and a pharmaceutically acceptable carrier.
122. The antibody as defined in any of claims 1 to 112 for use as a medicament.
123. The antibody as defined in any of claims 1 to 112 for use in the treatment of a disease.
124. The antibody for use according claim 122 or 123, wherein the disease is cancer.
125. The antibody for use according to claim 124, wherein the cancer is characterized by expression of 5T4 in at least some of the tumor cells.
126. The antibody for use according to any one of claims 122 to 125, wherein the cancer is selected from the group consisting of kidney/renal cancer, breast cancer, colorectal cancer, prostate cancer, ovarian cancer, bladder cancer, uterine/endometrial/ cervical cancer, lung cancer, gastro-intestinal cancer, stomach cancer, pancreatic cancer, thyroid cancer, head and neck cancer, lymphoma, acute myeloid leukemia.
127. A method of treating a disease, the method comprising administering an antibody as defined in any one of claims 1 to 112, the composition as defined in claim 120, or the pharmaceutical composition defined in claim 121, to a subject in need thereof.
128. The method according to claim 127, said method being for treatment of a cancer.
129. The method according to claim 128, wherein the cancer is selected from the group consisting of kidney/renal cancer, breast cancer, colorectal cancer, prostate cancer, ovarian cancer, bladder cancer, uterine/endometrial/cervical cancer, lung cancer, gastro-intestinal cancer, stomach cancer, pancreatic cancer, thyroid cancer, head and neck cancer, lymphoma, acute myeloid leukemia.
130. A method for producing an antibody as defined in any of claims 1 to 112, comprising the steps of

- a) culturing a host cell comprising an expression vector as defined in claim 114 or 117;
and
- b) and purifying said antibody from the culture medium.

131. A method for producing an antibody as defined in any one of claims 1 to 112, comprising the
5 steps of

- a) Providing an antibody capable of binding to 5T4 by culturing a host cell comprising an expression vector as defined in claim 116 or 117 under conditions allowing expression of the antibody capable of binding to 5T4, and purifying the antibody capable of binding to 5T4 from the culture medium;
- 10 b) Providing an antibody capable of binding to CD3 by culturing a host cell comprising an expression vector comprising
 - l) a nucleic acid sequence encoding a heavy chain sequence of an antibody comprising an antigen-binding region capable of binding to CD3 as defined in any one of claims 72 to 1123; and
 - 15 II) a nucleic acid sequence encoding a light chain sequence of an antibody comprising an antigen-binding region capable of binding to CD3 as defined in any one of claims 72 to 112;
 under conditions allowing expression of the antibody capable of binding to CD3, and purifying the antibody capable of binding to CD3 from the culture medium;
- 20 c) incubating said antibody capable of binding to 5T4 together with said antibody capable of binding to CD3 under reducing conditions sufficient to allow cysteines in the hinge region to undergo disulfide-bond isomerization, and
- d) obtaining said antibody.

132. A kit-of-parts, such as a kit for use as a companion diagnostic/for identifying within a population
25 of patients those patients which have a propensity to respond to treatment with an antibody as defined in any one of claims 1 to 112 or an immunoconjugate or antibody-drug conjugate (ADC) as defined in claim 113, or for predicting efficacy of said antibody or immunoconjugate or ADC when used in treatment of a patient, comprising an antibody as defined in any one of claims 1 to 112; and instructions for use of said kit.

30 133. An anti-idiotypic antibody, which binds to the antigen-binding region capable of binding to 5T4 as defined in any one of claims 1 to 112.