

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 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/or chicken 5T4 such as the mature polypeptide sequence of SEQ ID NO: 3.

5. ~~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.~~
6. ~~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.~~
7. ~~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.~~
8. ~~The antibody according to any one of claims 1-6, 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.~~
9. ~~The antibody according to any one of claims 6 to 8, wherein said amino acid residues are directly involved in the binding of the antibody.~~
10. ~~The antibody according to any one of claims 6 to 9, 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.~~
11. ~~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.~~
12. ~~The antibody according to any one of claims 1 to 10, 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.
- 5 ~~13. The antibody according to any one of claims 1 to 10, 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.~~
- 10 ~~14. The antibody according to any one of claims 1 to 5, 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.~~
- 15 ~~15. The antibody according to any one of claims 1 to 5 and 14, 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.~~
- 20 ~~16. The antibody according to any one of claims 1 to 5 and 14, 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.~~
- 25 ~~17. The antibody according to any one of claims 1 to 5 and 14 to 16, 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.~~
- 30 ~~18. The antibody according to any one of claims 1 to 5 and 14 to 17, 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.~~
- 30 ~~19. The antibody according to any one of claims 1 to 5 and 14 to 17, 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.~~

	20.	The antibody according to any one of claims 1 to 5 and 14 to 17, 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.
5	21.	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: <ul style="list-style-type: none"> 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],
10		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],
15		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],
20		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],
25		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],
30		f)b) 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], and g)c) 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
- 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).
22. ~~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].~~
- 23.2. ~~_____~~ The antibody according to ~~any one of the preceding claims~~ claim 1, 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].
- 24.3. ~~_____~~ The antibody according to ~~any one of the preceding claims~~ claim 1, 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].
- 25.4. ~~_____~~ The antibody according to ~~any one of the preceding claims~~ claim 1, 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].

~~26-5.~~_____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 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],
- 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 [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 [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 [106],~~
- ~~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)b) 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~~
- ~~g)c) 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].~~

25 ~~27-6.~~_____The antibody according to any one of the preceding claims 1, 2 and 5, wherein said 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 [059].

30 ~~28-7.~~_____The antibody according to any one of the preceding claims 1, 3 and 5, wherein said 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 [207].

~~29-8.~~_____The antibody according to any one of the preceding claims 1, 4 and 5, wherein said 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].

5 ~~30-9.~~_____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:

- 10** 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],
- 15** 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],
- 20** 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],
- 25** 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],
- 30** 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],

- 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].

~~31-10.~~ 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],~~
- ~~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],~~
- 20 ~~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],~~
- ~~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],~~
- 25 ~~f) b) 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) c) 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].~~

~~32-11.~~ The antibody according to any of the preceding claims, wherein the antibody is a full-length antibody, such as a full length IgG1 antibody.

- 30 ~~33-12.~~ The antibody according to any one of the preceding claims, which is a monospecific antibody.

- 34-13.** The antibody according to any one of the preceding claims 1 to 11, which is a bispecific antibody.
- 35-14.** The antibody according to ~~any one of the preceding claim 13s~~, comprising an antigen binding region of an antibody ~~that capable of~~ bindings to CD3, such as human CD3ε (epsilon), such as human CD3ε (epsilon) as specified in SEQ ID NO: 4.
- 36-15.** The antibody according to claim ~~14~~35, wherein the antigen-binding region ~~that capable of bindings~~ to CD3 comprises
- 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 sequences of SEQ ID NO: 58, GTN and 59, respectively [wildtype anti-CD3, VL CDR sequences].
- 37-16.** The antibody according to claim 14 or 15~~35 or 36~~, wherein the antigen binding region ~~that capable of bindings~~ to CD3 comprises
- 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 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].
- 38-17.** The antibody according to any one of claims 14 to 16~~35 to 37~~, wherein said antigen binding region ~~that capable of bindings~~ 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.

39-18. The antibody according to any one of claims 14 or 1635 or 37, wherein said antigen binding region ~~that capable of bindings~~ 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.

40-19. The antibody according to any one of claims 14 to 1835 to 39, wherein the antigen binding region ~~that capable of bindings~~ 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: T31M, T31P, N57E, H101G, H101N, G105P, S110A, S110G, Y114M, Y114R, Y114V ~~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.

~~41. The antibody according to claims 35 to 37, 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.~~

42-20. The antibody according to any one of claims 14 and 1935 and 40 to 41, wherein the antigen-binding region capable of binding to CD3 comprises:

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

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
- 5 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
- 10 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] , respectively.
- 15 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] ,
- 20 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
- 25 sequence as set forth in SEQ ID NO: 59, respectively [Wild type VL CDRs 1,2,3] , respectively;
- 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
- 30 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

- 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 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 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 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 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.
- 25 ~~43-21.~~_____The antibody according to any one of claims 14 and 1935 and ~~40 to 41~~, 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.
- 30 ~~44-22.~~_____The antibody according to any one of claims 14 and 1935 and ~~40 to 41~~, 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];

5 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.

10

~~45-23.~~ The antibody according to any one of claims 14 and 19 ~~14 and 19 to 35 and 40 to 41~~, 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];

15

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.

20

~~46-24.~~ The antibody according to any one of claims 14 and 19 to 21 ~~14 and 19 to 21 to 24~~, 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.: 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];

25

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

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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** ~~47-25.~~ The antibody according to any one of claims 14 and 19 to 24~~35 and 40 to 46~~, 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],
 - 10** 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,
 - 15** 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,
 - 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,
 - 20** 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,
 - 25** 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.

- 30** ~~48-26.~~ The antibody according to any one of claims 14 and 19 to 25~~35 and 40 to 47~~, wherein 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.

- 5** ~~49-27.~~ 27. The antibody according to any one of claims 19 to 26~~40 to 48~~, 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 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 in SEQ ID NO: 60.
- 10** ~~50-28.~~ 28. The antibody according to any one of claims 14 and 19 to 26~~35 and 40 to 48~~, 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 SEQ ID NO: 40 [207 - VH full length sequence];
- 15** 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.
- 20** ~~51-29.~~ 29. The antibody according to any one of claims 14, 19 to 21, and 24 to 26~~21 to 29~~, 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
- 25** 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** ~~52-30.~~ 30. The antibody according to any of claims 14 and 19 to 27~~35 and 40 to 49~~, 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 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

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.

~~53-31.~~ The antibody according to any of claims 14, 19 to 26 and 28~~35, 40 to 48 and 50~~, 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 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];

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.

~~54-32.~~ The antibody according to any of claims 14, 19 to 25 and 29~~35, 40 to 47 and 51~~, 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, 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];

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.

~~55-33.~~ The antibody according to any one of the preceding claims, wherein each antigen-binding region 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.

~~56-34.~~ The antibody according to claim ~~33~~⁵⁵, wherein the antibody comprises two heavy chain constant regions (CH), and two light chain constant regions (CL).

5 ~~57-35.~~ The antibody according to claim ~~33 or 34~~^{55 or 56}, 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 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.~~

10

15 ~~58.~~ The antibody according to any one of claims ~~55 to 56~~, 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*.

~~59-36.~~ 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.

20

~~60-37.~~ 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.

25

~~61-38.~~ 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.

30 ~~62-39.~~ 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.

~~63-40.~~ The antibody according to any one of the preceding claims, wherein said antibody comprises a kappa (κ) light chain.

5 ~~64-41.~~ The antibody according to any one of the preceding claims, wherein said antibody comprises a lambda (λ) light chain.

~~65-42.~~ 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.

10 43. The bispecific antibody according to any one of claims 14, 19-21, 24-26, 29, and 32 to 42, comprising

an antigen-binding region capable of binding 5T4, which comprises a heavy chain variable region (VH) sequence as set forth in SEQ ID NO: 40, and a light chain variable region (VL) sequence as set forth in SEQ ID NO: 44 [207],

15 an 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,

a first and a second heavy chain, wherein

20 in said first heavy chain the amino acids in the positions corresponding to positions L234, L235, D265 and K409 in a human IgG1 heavy chain, are F, E, A and R respectively, the amino acid positions being numbered according to EU numbering,

in said second heavy chain the amino acids in the positions corresponding to positions L234, L235, D265 and F405 in a human IgG1 heavy chain, are F, E, A and L respectively, the amino acid positions being numbered according to EU numbering,

25 an Fc region, which is a human IgG1 isotype; and

a kappa light chain constant region consisting of the sequence set forth in SEQ ID NO: 95, and a lambda light chain constant region consisting of the sequence set forth in Seq ID NO: 96.

~~66~~44. _____ 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.

~~67~~45. _____ A nucleic acid construct comprising

- 5 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-~~43~~66, and/or
- 10 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 14 to 43~~35 to 66~~.

~~68~~46. _____ The nucleic acid construct according to claim ~~45~~67, further comprising

- 15 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 14 to 43~~35 to 66~~; 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 14 to 43~~35 to 66~~.

~~69~~47. _____ An expression vector comprising

- 20 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 ~~43~~65, and/or
- 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 ~~43~~65.

~~70~~48. _____ An expression vector according to claim 69, further comprising

- 25 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 14 to 43~~35 to 65~~; and/or
- 30 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 14 to 43~~35 to 65~~.

- ~~71-49.~~ A cell comprising a nucleic acid construct as defined in any one of claims ~~45 to 46~~~~67 to 68~~, or an expression vector as defined in claim ~~47 to 48~~~~69 or 70~~, 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.
- 5 ~~72-50.~~ The cell according to claim ~~49~~~~71~~, 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.
- ~~73-51.~~ A composition comprising an antibody or immunoconjugate or antibody-drug conjugate (ADC) as defined in any one of claims 1 to ~~44~~~~65~~.
- 10 ~~74-52.~~ A pharmaceutical composition comprising an antibody or immunoconjugate or antibody-drug conjugate (ADC) as defined in any one of claims 1 to ~~44~~~~65~~ and a pharmaceutically acceptable carrier.
- ~~75.~~ Use of an antibody or immunoconjugate or antibody-drug conjugate (ADC) as defined in any of claims 1 to ~~44~~~~65~~ for the manufacture of a medicament for the treatment of cancer.
- 15 ~~76-53.~~ The use according to claim ~~75~~, wherein the cancer is characterized by expression of 5T4 in at least some of the tumor cells.
- ~~77-54.~~ The use according to any one of claims ~~55 to 56~~~~75 to 76~~, 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.
- 20
- ~~78-55.~~ A method for producing an antibody as defined in any of claims 1 to ~~43~~~~65~~, comprising the steps of
- 25 a) culturing a host cell comprising an expression vector as defined in claim ~~51 or 52~~~~69 or 70~~; and
- b) and purifying said antibody from the culture medium.
- ~~79-56.~~ A method for producing an antibody as defined in any one of claims ~~14 to 43~~~~65~~, comprising the steps of
- 30 a) Providing an antibody capable of binding to 5T4 by culturing a host cell comprising an expression vector as defined in claim ~~47 or 48~~~~69 or 70~~ 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;

b) Providing an antibody capable of binding to CD3 by culturing a host cell comprising an expression vector comprising

5 I) 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 ~~14-4335 to 54~~; and

10 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 ~~14-4335 to 65~~;

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;

15 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.

20 ~~80-57.~~ A kit-of-parts, such as a kit for use as a companion diagnostic/for identifying within a population of patients those patients which have a propensity to respond to treatment with an antibody as defined in any one of claims 1 to ~~4365~~ or an immunoconjugate or antibody-drug conjugate (ADC) as defined in claim ~~4466~~, 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 ~~4365~~; and instructions for use of said kit.

25 ~~81-58.~~ 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 ~~4365~~.