CLAIMS

1. An anti-Trop2 antibody or antigen-binding fragment thereof, comprising the complementarity determining region (CDR) sequences selected from the group comprising:

(i) a CDRH1 sequence of GGSISSGGYY (**SEQ ID NO: 1**),
a CDRH2 sequence of IYYSGST (**SEQ ID NO: 5**),
a CDRH3 sequence of AREEGIAAAAFDI (**SEQ ID NO: 9**),
a CDRL1 sequence of QSVGSF (**SEQ ID NO: 13**),
a CDRL2 sequence of GAS (**SEQ ID NO: 17**), and
a CDRL3 sequence of QQSDSSPFT (**SEQ ID NO: 19**);

(ii) a CDRH1 sequence of GYTFTSYG (**SEQ ID NO: 2**),
a CDRH2 sequence of ISAYNGNT (**SEQ ID NO: 6**),
a CDRH3 sequence of ARKYSGFDY (**SEQ ID NO: 10**)
a CDRL1 sequence of QSLLHSNGYNY (**SEQ ID NO: 14**)
a CDRL2 sequence of LGS (**SEQ ID NO: 18**); and
a CDRL3 sequence of MQNLQTPWT (**SEQ ID NO: 20**)

(iii) a CDRH1 sequence of GFTFSSYS (**SEQ ID NO: 3**),
a CDRH2 sequence of ISSSSSYI (**SEQ ID NO: 7**),
a CDRH3 sequence of ARDYYDSSGYPYYYYGMDV (**SEQ ID NO: 11**),
a CDRL1 sequence of QSVSSSY (**SEQ ID NO: 15**),
a CDRL2 sequence of GAS (**SEQ ID NO: 17**), and
a CDRL3 sequence of HQSGSSLRT (**SEQ ID NO: 21**); and

(iv) a CDRH1 sequence of GFTFSSYW (**SEQ ID NO: 4**),
a CDRH2 sequence of IKQDGSEK (**SEQ ID NO: 8**),
a CDRH3 sequence of ARDFVDWSATPFDY (**SEQ ID NO: 12**),
a CDRL1 sequence of RSLLHSNGYNY (**SEQ ID NO: 16**),
a CDRL2 sequence of LGS (**SEQ ID NO: 18**), and
a CDRL3 sequence of MQALQIPKT (**SEQ ID NO: 22**).

2. The antibody or antigen-binding fragment thereof according to claim 1, wherein the antibody or antigen-binding fragment thereof is a germline configured counterpart thereof.

3. The antibody or antigen-binding fragment thereof according to any one of the preceding claims, comprising

(a) a VH domain sequence selected from the group comprising:

QVQLQESGPGLVKPSQTLSLTCAVSGGSISSGGYYWSWIRQPPGKGLEWIGYIYYSGS TYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREEGIAAAAFDIWGQGTM **(SEQ ID NO: 23)**,

QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNG NTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARKYSGFDYWGQGTL **(SEQ ID NO: 24)**,

EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWISAYNG NTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARKYSGFDYWGQGTL **(SEQ ID NO: 25)**, and

EVQLVQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSISSSSSY IYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDYYDSSGYPYYYYGMDV WGQGTT **(SEQ ID NO: 26)**,

EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGS EKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDFVDWSATPFDYWGQ GTL **(SEQ ID NO: 27)**,

or a variant thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical thereto;

(b) a VL domain sequence selected from the group comprising:

DIQMTQSPSSLSASVGDRVTITCRASQSVGSFLNWYQQKPGKAPKLLIYGASSLQSGV PSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSDSSPFTFGGGTK **(SEQ ID NO: 28)**,

EIVLTQSPSSLSASVGDRVTITCRASQSVGSFLNWYQQKPGKAPQVLIFGASNLESGVP SRFSGRGSGSEFTLTINSLQPEDFATYYCQQSDSSPFTFGGGTK **(SEQ ID NO: 29)**,

DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNR ASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQNLQTPWTFGQGTK **(SEQ ID NO: 30)**,

EIVLTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYLGSNR ASGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCMQNLQTPWTFGQGTK **(SEQ ID NO: 31)**,

ETTLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGASSRATGI PDRFSGSGSGTDFNLTISRLEPEDFAVYYCHQSGSSLRTFGQGTT **(SEQ ID NO: 32)**, and

DVVMTQSPLSLPVTPGEPASISCRSSRSLLHSNGYNYLDWYVQKPGQSPQLLIYLGSY RASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQIPKTFGQGTK **(SEQ ID NO: 33)**,

or a variant thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical thereto; and/or

(c) a VH domain and a VL domain selected from the group comprising:

(i) a VH domain sequence of:
QVQLQESGPGLVKPSQTLSLTCAVSGGSISSGGYYWSWIRQPPGKGLEWIGYI YYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREEGIAAAAF DIWGQGTM **(SEQ ID NO: 23)** or a variant thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical thereto, and
a VL domain sequence of:
DIQMTQSPSSLSASVGDRVTITCRASQSVGSFLNWYQQKPGKAPKLLIYGASSL QSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSDSSPFTFGGGTK **(SEQ ID NO: 28)** or a variant thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical thereto;

(ii) a VH domain sequence of:
QVQLQESGPGLVKPSQTLSLTCAVSGGSISSGGYYWSWIRQPPGKGLEWIGYI YYSGSTYYNPSLKSRVTISVDTSKNQFSLKLSSVTAADTAVYYCAREEGIAAAAF DIWGQGTM **(SEQ ID NO: 23)** or a variant thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical thereto, and
a VL domain sequence of:
EIVLTQSPSSLSASVGDRVTITCRASQSVGSFLNWYQQKPGKAPQVLIFGASNL ESGVPSRFSGRGSGSEFTLTINSLQPEDFATYYCQQSDSSPFTFGGGTK **(SEQ ID NO: 29)** or a variant thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical thereto;

(iii) a VH domain sequence of:
QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWIS AYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARKYSGFDY WGQGTL **(SEQ ID NO: 24)** or a variant thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical thereto, and
a VL domain sequence of:
DIVMTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIY LGSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQNLQTPWTFGQG

TK **(SEQ ID NO: 30)** or a variant thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical thereto;

(iv) a VH domain sequence of:
EVQLVQSGAEVKKPGASVKVSCKASGYTFTSYGISWVRQAPGQGLEWMGWIS AYNGNTNYAQKLQGRVTMTTDTSTSTAYMELRSLRSDDTAVYYCARKYSGFDY WGQGTL **(SEQ ID NO: 25)** or a variant thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical thereto, and
a VL domain sequence of:
EIVLTQSPLSLPVTPGEPASISCRSSQSLLHSNGYNYLDWYLQKPGQSPQLLIYL GSNRASGVPDRFSGSGSGTDFTLKISRVEAEDVGIYYCMQNLQTPWTFGQGT K **(SEQ ID NO: 31)** or a variant thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical thereto;

(v) a VH domain sequence of:
EVQLVQSGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSIS SSSSYIYYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDYYDSSGY PYYYYGMDVWGQGTT **(SEQ ID NO: 26)** or a variant thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical thereto, and
a VL domain sequence of:
ETTLTQSPGTLSLSPGERATLSCRASQSVSSSYLAWYQQKPGQAPRLLIYGAS SRATGIPDRFSGSGSGTDFNLTISRLEPEDFAVYYCHQSGSSLRTFGQGTT **(SEQ ID NO: 32)** or a variant thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical thereto; and

(vi) a VH domain sequence of:
EVQLVQSGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANI KQDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDFVDWS ATPFDYWGQGTL **(SEQ ID NO: 27)** or a variant thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical thereto, and
a VL domain sequence of:
DVVMTQSPLSLPVTPGEPASISCRSSRSLLHSNGYNYLDWYVQKPGQSPQLLIY LGSYRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYCMQALQIPKTFGQGT K **(SEQ ID NO: 33)** or a variant thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identical thereto.

4. The antibody or antigen-binding fragment thereof according to any one of the preceding claims, wherein the antibody is a full-length antibody; or

wherein the antibody is an IgG antibody; or

wherein the antibody or antigen-binding fragment thereof is a fully human antibody or antigen-binding fragment thereof; or

wherein the antibody or antigen-binding fragment thereof is specific to human Trop2.

5. The antibody or antigen-binding fragment thereof according to any one of the preceding claims, wherein the antibody or antigen-binding fragment thereof exhibits cross-reactivity with two or more different species, and/or

wherein the antibody or antigen-binding fragment thereof binds to human Trop2 and cynomolgus Trop2.

6. The antibody or antigen-binding fragment thereof according to any one of the preceding claims, wherein the antibody or antigen-binding fragment thereof is conjugated to a therapeutic agent;

wherein the therapeutic agent is an anti-cancer agent; optionally

wherein the therapeutic agent is selected from the group comprising MMAE (vedotin), PNU-159682, DX-8951 (exatecan), PBD (pyrrolobenzodiazepine) and DMDM.

7. An antibody-drug conjugate (ADC) comprising the antibody or antigen binding fragment thereof according to any one of the preceding claims.

8. A multi-specific antibody comprising an anti-Trop2 binding domain, wherein the anti-Trop2 binding domain is an antibody or antigen-binding fragment thereof according to any one of the preceding claims,

optionally wherein the multi-specific antibody is an immune cell engager;

optionally wherein the immune cell engager binds to an immune marker selected from the group consisting of CD3, NKG2D, CD4, CD8, CD16 and CD64;

optionally wherein the immune cell engager is selected from the group comprising a T cell engager, an NK cell engager, a monocyte engager and a macrophage engager; and

optionally wherein the immune engager is a bispecific T cell engager (BiTE).

9. An immune cell comprising an anti-Trop2 antibody or antigen-binding fragment thereof according to any one of claims 1 to 6, an antibody-drug conjugate (ADC) according to claim 7, or multi-specific antibody according to claim 8,

optionally wherein the immune cell is selected from the group comprising a T-cell, a CAR T-cell, a natural killer (NK) cell, a monocyte and a macrophage.

10. A pharmaceutical composition comprising the antibody or antigen-binding fragment thereof, the antibody drug conjugate, the multi-specific antibody, or the immune cell according to any one of the preceding claims, wherein the composition optionally comprises a pharmaceutically acceptable excipient, buffer and/or additive.

11. A polynucleotide encoding an anti-Trop2 antibody or antigen-binding fragment thereof according to any one of claims 1 to 6, an antibody drug conjugate according to claim 7, or a multi-specific antibody according to claim 8.

12. The polynucleotide according to claim 11, comprising a sequence selected from the group comprising:

i. CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGAC CCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCCATCAGCAGTGGTGGTTA CTACTGGAGTTGGATCCGCCAGCCCCCCGGGAAGGGCCTGGAGTGGATTG GGTACATCTATTACAGTGGGAGCACCTACTACAACCCGTCCCTCAAGAGTC GAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAG CTCTGTGACTGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGAAGAGG GTATAGCAGCAGCTGCTTTTGATATCTGGGGCCAAGGGACAATG (**SEQ ID NO: 34)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto,

ii. CAGGTCCAGCTGGTACAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGCTACGGTATC AGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGAT CAGCGCTTACAATGGTAACACAAACTATGCACAGAAGCTCCAGGGCAGAGT CACCATGACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAG CCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAAAATACAGTGG CTTTGACTACTGGGGCCAGGGCACCCTG **(SEQ ID NO: 35)** or a variant

thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto,

iii. GAGGTCCAGCTGGTaCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTC AGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGCTACGGTATC AGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGAT CAGCGCTTACAATGGTAACACAAACTATGCACAGAAGCTCCAGGGCAGAGT CACCATGACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAG CCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAAAATACAGTGG CTTTGACTACTGGGGCCAGGGCACCCTG **(SEQ ID NO: 36)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto,

iv. GAGGTCCAGCTGGTGCAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGT CCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCAT GAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCA TTAGTAGTAGTAGTAGTTACATATACTACGCAGACTCAGTGAAGGGCCGATT CACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAG CCTGAGAGCCGAGGACACGGCTGTTTATTACTGTGCGAGAGATTACTATGA TAGTAGTGGCTATCCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGG GACCACG **(SEQ ID NO: 37)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto,

v. GAGGTCCAGCTGGTACAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTC CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATG AGCTGGGTCCGCCAGGCTCCAGGGAAAGGGCTGGAGTGGGTGGCCAACAT AAAGCAAGATGGAAGTGAGAAATACTATGTGGACTCTGTGAAGGGCCGATT CACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAG CCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGGGATTTTGTGGA CTGGTCCGCCACACCCTTTGACTACTGGGGCCAGGGCACCCTG **(SEQ ID NO: 38)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto,

vi. GACATTCAGATGACGCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGAC AGAGTCACCATCACTTGCCGGGCAAGTCAGAGCGTTGGCTCTTTTTTAAATT GGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGGTGCCT CCAGTTTACAGAGTGGGGTCCCATCAAGGTTCAGTGGCAGTGGATCTGGGA CAGATTTCACTCTCACCATCAGCAGTCTGCAACCCGAAGATTTTGCAACTTA

CTACTGTCAACAGAGTGACAGTTCCCCCTTCACTTTCGGCGGAGGGACCAA G **(SEQ ID NO: 39)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto,

vii. GAAATTGTGTTGACGCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACA GAGTCACCATCACTTGCCGGGCAAGTCAGAGCGTTGGCTCTTTTTTAAATTG GTATCAGCAGAAACCAGGGAAAGCCCCTCAGGTCCTGATCTTTGGTGCCTC CAATTTAGAAAGTGGGGTCCCATCAAGGTTCAGTGGCAGAGGATCTGGGTC AGAATTCACTCTCACCATCAACAGTCTGCAACCCGAAGATTTTGCAACTTAC TACTGTCAACAGAGTGACAGTTCCCCCTTCACTTTCGGCGGAGGGACCAAG **(SEQ ID NO: 40)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto,

viii. GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAG CCGGCCTCCATCTCCTGCAGGTCTAGTCAGAGTCTCCTGCATAGTAATGGA TACAACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTC CTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCAGT GGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCT GAGGATGTTGGGGTTTATTACTGCATGCAAAATCTTCAAACTCCGTGGACGT TCGGCCAAGGGACCAAG **(SEQ ID NO: 41)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto,

ix. GAAATTGTGCTGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAG CCGGCCTCCATCTCCTGCAGGTCTAGTCAGAGTCTCCTGCATAGTAATGGA TACAACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTC CTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCAGT GGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCT GAGGATGTTGGGATTTATTACTGCATGCAAAATCTTCAAACTCCGTGGACGT TCGGCCAAGGGACCAAG **(SEQ ID NO: 42)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto,

x. GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAA AGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTA GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGT GCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTC TGGGACAGACTTCAATCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGC AGTGTATTACTGTCACCAGTCTGGCAGTTCACTTCGGACGTTCGGCCAAGG

GACCACG **(SEQ ID NO: 43)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

xi. GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAG CCGGCCTCCATCTCCTGCAGGTCTAGTCGGAGCCTCCTACATAGTAATGGA TACAACTATTTGGATTGGTACGTGCAGAAGCCAGGGCAGTCTCCACAGCTC CTGATCTATTTGGGTTCATATCGGGCCTCCGGGGTCCCTGACAGGTTTAGT GGCAGTGGATCAGGCACAGATTTTACACTGAAGATCAGCAGGGTGGAGGCT GAGGATGTTGGAGTTTATTACTGCATGCAAGCTTTACAAATTCCGAAGACGT TCGGCCAAGGGACCAAG **(SEQ ID NO: 44)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto**.**

13. A vector comprising one or more polynucleotides according to any one of claims 11 or 12 or a host cell comprising the vector.

14. The vector according to claim 13, comprising a polynucleotide selected from the group comprising:

(i) a polynucleotide having the sequence:
CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGAC CCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCCATCAGCAGTGGTGGTTA CTACTGGAGTTGGATCCGCCAGCCCCCCGGGAAGGGCCTGGAGTGGATTG GGTACATCTATTACAGTGGGAGCACCTACTACAACCCGTCCCTCAAGAGTC GAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAG CTCTGTGACTGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGAAGAGG GTATAGCAGCAGCTGCTTTTGATATCTGGGGCCAAGGGACAATG (**SEQ ID NO: 34)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and
a polynucleotide having the sequence:
GACATTCAGATGACGCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGAC AGAGTCACCATCACTTGCCGGGCAAGTCAGAGCGTTGGCTCTTTTTTAAATT GGTATCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCTATGGTGCCT CCAGTTTACAGAGTGGGGTCCCATCAAGGTTCAGTGGCAGTGGATCTGGGA CAGATTTCACTCTCACCATCAGCAGTCTGCAACCCGAAGATTTTGCAACTTA CTACTGTCAACAGAGTGACAGTTCCCCCTTCACTTTCGGCGGAGGGACCAA

G **(SEQ ID NO: 39)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto;

(ii) a polynucleotide having the sequence:
CAGGTGCAGCTGCAGGAGTCGGGCCCAGGACTGGTGAAGCCTTCACAGAC
CCTGTCCCTCACCTGCGCTGTCTCTGGTGGCTCCATCAGCAGTGGTGGTTA
CTACTGGAGTTGGATCCGCCAGCCCCCCGGGAAGGGCCTGGAGTGGATTG
GGTACATCTATTACAGTGGGAGCACCTACTACAACCCGTCCCTCAAGAGTC
GAGTTACCATATCAGTAGACACGTCTAAGAACCAGTTCTCCCTGAAGCTGAG
CTCTGTGACTGCCGCGGACACGGCCGTGTATTACTGTGCGAGAGAAGAGG
GTATAGCAGCAGCTGCTTTTGATATCTGGGGCCAAGGGACAATG (**SEQ ID NO: 34)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and
a polynucleotide having the sequence:
GAAATTGTGTTGACGCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACA
GAGTCACCATCACTTGCCGGGCAAGTCAGAGCGTTGGCTCTTTTTTAAATTG
GTATCAGCAGAAACCAGGGAAAGCCCCTCAGGTCCTGATCTTTGGTGCCTC
CAATTTAGAAAGTGGGGTCCCATCAAGGTTCAGTGGCAGAGGATCTGGGTC
AGAATTCACTCTCACCATCAACAGTCTGCAACCCGAAGATTTTGCAACTTAC
TACTGTCAACAGAGTGACAGTTCCCCCTTCACTTTCGGCGGAGGGACCAAG
(SEQ ID NO: 40) or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto;

(iii) a polynucleotide having the sequence:
CAGGTCCAGCTGGTACAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGCTACGGTATC
AGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGAT
CAGCGCTTACAATGGTAACACAAACTATGCACAGAAGCTCCAGGGCAGAGT
CACCATGACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAG
CCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAAAATACAGTGG
CTTTGACTACTGGGGCCAGGGCACCCTG **(SEQ ID NO: 35)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and
a polynucleotide having the sequence:
GATATTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAG
CCGGCCTCCATCTCCTGCAGGTCTAGTCAGAGTCTCCTGCATAGTAATGGA

TACAACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTC
CTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCAGT
GGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCT
GAGGATGTTGGGGTTTATTACTGCATGCAAAATCTTCAAACTCCGTGGACGT
TCGGCCAAGGGACCAAG **(SEQ ID NO: 41)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto;

(iv) a polynucleotide having the sequence:
GAGGTCCAGCTGGTaCAGTCTGGAGCTGAGGTGAAGAAGCCTGGGGCCTC
AGTGAAGGTCTCCTGCAAGGCTTCTGGTTACACCTTTACCAGCTACGGTATC
AGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGATGGAT
CAGCGCTTACAATGGTAACACAAACTATGCACAGAAGCTCCAGGGCAGAGT
CACCATGACCACAGACACATCCACGAGCACAGCCTACATGGAGCTGAGGAG
CCTGAGATCTGACGACACGGCCGTGTATTACTGTGCGAGAAAATACAGTGG
CTTTGACTACTGGGGCCAGGGCACCCTG **(SEQ ID NO: 36)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and
a polynucleotide having the sequence:
GAAATTGTGCTGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAG
CCGGCCTCCATCTCCTGCAGGTCTAGTCAGAGTCTCCTGCATAGTAATGGA
TACAACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTC
CTGATCTATTTGGGTTCTAATCGGGCCTCCGGGGTCCCTGACAGGTTCAGT
GGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCT
GAGGATGTTGGGATTTATTACTGCATGCAAAATCTTCAAACTCCGTGGACGT
TCGGCCAAGGGACCAAG **(SEQ ID NO: 42)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto;

(v) a polynucleotide having the sequence:
GAGGTCCAGCTGGTGCAGTCTGGGGGAGGCCTGGTCAAGCCTGGGGGGT
CCCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCAT
GAACTGGGTCCGCCAGGCTCCAGGGAAGGGGCTGGAGTGGGTCTCATCCA
TTAGTAGTAGTAGTAGTTACATATACTACGCAGACTCAGTGAAGGGCCGATT
CACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAG
CCTGAGAGCCGAGGACACGGCTGTTTATTACTGTGCGAGAGATTACTATGA
TAGTAGTGGCTATCCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGG

GACCACG **(SEQ ID NO: 37)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a polynucleotide having the sequence:

GAAACGACACTCACGCAGTCTCCAGGCACCCTGTCTTTGTCTCCAGGGGAA
AGAGCCACCCTCTCCTGCAGGGCCAGTCAGAGTGTTAGCAGCAGCTACTTA
GCCTGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATCTATGGT
GCATCCAGCAGGGCCACTGGCATCCCAGACAGGTTCAGTGGCAGTGGGTC
TGGGACAGACTTCAATCTCACCATCAGCAGACTGGAGCCTGAAGATTTTGCA
GTGTATTACTGTCACCAGTCTGGCAGTTCACTTCGGACGTTCGGCCAAGGG
ACCACG **(SEQ ID NO: 43)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto; and

(vi) a polynucleotide having the sequence:

GAGGTCCAGCTGGTACAGTCTGGGGGAGGCTTGGTCCAGCCTGGGGGGTC
CCTGAGACTCTCCTGTGCAGCCTCTGGATTCACCTTTAGTAGCTATTGGATG
AGCTGGGTCCGCCAGGCTCCAGGGAAAGGGCTGGAGTGGGTGGCCAACAT
AAAGCAAGATGGAAGTGAGAAATACTATGTGGACTCTGTGAAGGGCCGATT
CACCATCTCCAGAGACAACGCCAAGAACTCACTGTATCTGCAAATGAACAG
CCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGGGATTTTGTGGA
CTGGTCCGCCACACCCTTTGACTACTGGGGCCAGGGCACCCTG **(SEQ ID NO: 38)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto, and

a polynucleotide having the sequence:

GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAG
CCGGCCTCCATCTCCTGCAGGTCTAGTCGGAGCCTCCTACATAGTAATGGA
TACAACTATTTGGATTGGTACGTGCAGAAGCCAGGGCAGTCTCCACAGCTC
CTGATCTATTTGGGTTCATATCGGGCCTCCGGGGTCCCTGACAGGTTTAGT
GGCAGTGGATCAGGCACAGATTTTACACTGAAGATCAGCAGGGTGGAGGCT
GAGGATGTTGGAGTTTATTACTGCATGCAAGCTTTACAAATTCCGAAGACGT
TCGGCCAAGGGACCAAG **(SEQ ID NO: 44)** or a variant thereof having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity thereto.

15. An antibody or antigen-binding fragment thereof, an antibody drug conjugate, a multi-specific antibody, an immune cell or a pharmaceutical composition according to any one of claims 1 to 10 for use in the treatment of a patient.

16. Use of an antibody or antigen-binding fragment thereof, an antibody drug conjugate, a multi-specific antibody, an immune cell or a pharmaceutical composition according to any one of claims 1 to 10 in the manufacture of a medicament for the treatment of a patient.

17. The method, antibody or antigen-binding fragment thereof, antibody drug conjugate, multi-specific antibody, immune cell or a pharmaceutical composition for use or use according to any one of the claims 15 to 16, wherein the patient has cancer; wherein the cancer is Trop2+.

18. A method of diagnosing a tumor expressing Trop2 comprising contacting the tumor with an antibody or antigen-binding fragment thereof according to any one of claims 1 to 6, an antibody-drug conjugate (ADC) according to claim 7, a multi-specific antibody according to claim 8 or a composition according to claim 10.

19. The method, antibody or antigen-binding fragment thereof, an antibody drug conjugate, multi-specific antibody, immune cell or pharmaceutical composition for use, or use according to any one of claims 16 to 18, wherein the cancer is selected from the group comprising gastric adenocarcinoma, colon cancer, pancreatic cancer and breast cancer.