CLAIMS

1. An antigen binding protein, an antigen binding variant, or an antigen binding fragment thereof that binds specifically to Epithelial Cellular Adhesion Molecule (EpCAM), wherein the antigen binding protein, variant or fragment thereof comprises a heavy chain variable region and/or a light chain variable region selected from the group consisting of:

(i) a heavy chain variable region comprising:

a CDR-H1 comprising GGTFSSYA (**SEQ ID NO: 1**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-H2 comprising IIPIFGTA (**SEQ ID NO: 2)** or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-H3 comprising ARSLGGRFRY (**SEQ ID NO: 3**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

(ii) a heavy chain variable region comprising:

a CDR-H1 comprising GDSISSNSVA (**SEQ ID NO: 5)** or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-H2 comprising TYYRSKWYS (**SEQ ID NO: 6)** or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-H3 comprising AREVEGSSYDAFDI (**SEQ ID NO: 7)** or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

(iii) a light chain variable region comprising:

a CDR-L1 comprising:

- QSLLHSNGYNY (**SEQ ID NO: 9**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,
- QSLLHSNRYNY (**SEQ ID NO: 17**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, or
- QSISDF (**SEQ ID NO: 19**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

a CDR-L2 comprising:

- LGS (**SEQ ID NO: 10**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, or
- AAS (**SEQ ID NO: 20**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-L3 comprising:

- MQALQTPYT (**SEQ ID NO: 11**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,
- MQGLQSPWT (**SEQ ID NO: 15**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,
- QQSYIMPDT (**SEQ ID NO: 21**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, or
- MQGLQTPYT (**SEQ ID NO: 23**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto; and

(iv) a heavy chain variable region comprising:

a CDR-H1 comprising:

- GSIFSGND (**SEQ ID NO: 25**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, or
- GSSERFTS (**SEQ ID NO: 29**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

a CDR-H2 comprising:

- ITSGGST (**SEQ ID NO: 26**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, or
- ITNGGST (**SEQ ID NO: 30**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto and

a CDR-H3 comprising:

- TNGRWSGDTYYAHH (**SEQ ID NO: 27**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,
- MAGTS (**SEQ ID NO: 31**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, or
- TNGRWSGDTYYAHL (**SEQ ID NO: 33**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto.

2. The antigen binding protein, variant or fragment thereof of claim 1, wherein the antigen binding protein, variant or fragment thereof of comprises a heavy chain variable region selected from the group consisting of:

(i) a heavy chain variable region comprising:

a CDR-H1 comprising GGTFSSYA (**SEQ ID NO: 1**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-H2 comprising IIPIFGTA (**SEQ ID NO: 2)** or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-H3 comprising ARSLGGRFRY (**SEQ ID NO: 3**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

(ii) a heavy chain variable region comprising:

a CDR-H1 comprising GDSISSNSVA (**SEQ ID NO: 5)** or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-H2 comprising TYYRSKWYS (**SEQ ID NO: 6)** or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-H3 comprising AREVEGSSYDAFDI (**SEQ ID NO: 7)** or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto; and

comprises a light chain variable region comprising:

a CDR-L1 comprising:

- QSLLHSNGYNY (**SEQ ID NO: 9**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,
- QSLLHSNRYNY (**SEQ ID NO: 17**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, or
- QSISDF (**SEQ ID NO: 19**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

a CDR-L2 comprising:

- LGS (**SEQ ID NO: 10**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, or
- AAS (**SEQ ID NO: 20**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-L3 comprising:

- MQALQTPYT (**SEQ ID NO: 11**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,
- MQGLQSPWT (**SEQ ID NO: 15**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,
- QQSYIMPDT (**SEQ ID NO: 21**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, or
- MQGLQTPYT (**SEQ ID NO: 23**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto.

3. The antigen binding protein, variant or fragment thereof of claim 1, wherein the antigen binding protein, variant or binding fragment thereof comprises a heavy chain variable region comprising:

a CDR-H1 comprising:

- GSIFSGND (**SEQ ID NO: 25**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, or
- GSSERFTS (**SEQ ID NO: 29**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

a CDR-H2 comprising:

- ITSGGST (**SEQ ID NO: 26**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, or
- ITNGGST (**SEQ ID NO: 30**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto; and

a CDR-H3 comprising:

- TNGRWSGDTYYAHH (**SEQ ID NO: 27**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,
- MAGTS (**SEQ ID NO: 31**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, or
- TNGRWSGDTYYAHL (**SEQ ID NO: 33**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto.

4. The antigen binding protein, variant or fragment thereof of any one of the preceding claims, wherein

(a) the antigen binding protein, variant or fragment thereof comprises a heavy chain variable region and/or a light chain variable region selected from the group consisting of:

(i) a heavy chain variable region comprising:

a CDR-H1 comprising GGTFSSYA (**SEQ ID NO: 1**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-H2 comprising IIPIFGTA (**SEQ ID NO: 2**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-H3 comprising ARSLGGRFRY (**SEQ ID NO: 3**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

(ii) a heavy chain variable region comprising:

a CDR-H1 comprising GDSISSNSVA (**SEQ ID NO: 5**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-H2 comprising TYYRSKWYS (**SEQ ID NO: 6**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-H3 comprising AREVEGSSYDAFDI (**SEQ ID NO: 7**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

(iii) a light chain variable region comprising:

a CDR-L1 comprising QSLLHSNGYNY (**SEQ ID NO: 9**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-L2 comprising LGS (**SEQ ID NO: 10**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-L3 comprising MQALQTPYT (**SEQ ID NO: 11**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

(iv) a light chain variable region comprising:

a CDR-L1 comprising QSLLHSNGYNY (**SEQ ID NO: 9**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-L2 comprising LGS (**SEQ ID NO: 10**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-L3 comprising MQGLQSPWT (**SEQ ID NO: 15**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

(v) a light chain variable region comprising:

a CDR-L1 comprising QSLLHSNRYNY (**SEQ ID NO: 17**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-L2 comprising LGS (**SEQ ID NO: 10**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-L3 comprising MQALQTPYT (**SEQ ID NO: 11**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

(vi) a light chain variable region comprising:

a CDR-L1 comprising QSISDF (**SEQ ID NO: 19**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-L2 comprising AAS (**SEQ ID NO: 20**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-L3 comprising QQSYIMPDT (**SEQ ID NO: 21**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

(vii) a light chain variable region comprising:

a CDR-L1 comprising QSLLHSNGYNY (**SEQ ID NO: 9**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-L2 comprising LGS (**SEQ ID NO: 10**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-L3 comprising MQGLQTPYT (**SEQ ID NO: 23**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

(viii) a heavy chain variable region comprising:

a CDR-H1 comprising GSIFSGND (**SEQ ID NO: 25**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-H2 comprising ITSGGST (**SEQ ID NO: 26**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-H3 comprising TNGRWSGDTYYAHH (**SEQ ID NO: 27**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

(ix) a heavy chain variable region comprising:

a CDR-H1 comprising GSSERFTS (**SEQ ID NO: 29**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-H2 comprising ITNGGST (**SEQ ID NO: 30**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-H3 comprising MAGTS (**SEQ ID NO: 31**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto; and

(x) a heavy chain variable region comprising:

a CDR-H1 comprising GSIFSGND (**SEQ ID NO: 25**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-H2 comprising ITSGGST (**SEQ ID NO: 26**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-H3 comprising TNGRWSGDTYYAHL (**SEQ ID NO: 33**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto; and/or

(b) the antigen binding protein, variant or fragment thereof comprises a heavy chain variable region and a light chain variable region selected from the group consisting of:

(i) a heavy chain variable region comprising:

a CDR-H1 comprising GGTFSSYA (**SEQ ID NO: 1**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-H2 comprising IIPIFGTA (**SEQ ID NO: 2**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-H3 comprising ARSLGGRFRY (**SEQ ID NO: 3**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto; and

a light chain variable region comprising:

a CDR-L1 comprising QSLLHSNGYNY (**SEQ ID NO: 9**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-L2 comprising LGS (**SEQ ID NO: 10**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-L3 comprising MQALQTPYT (**SEQ ID NO: 11**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

(ii) a heavy chain variable region comprising:

a CDR-H1 comprising GGTFSSYA (**SEQ ID NO: 1**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-H2 comprising IIPIFGTA (**SEQ ID NO: 2**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-H3 comprising ARSLGGRFRY (**SEQ ID NO: 3**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto; and

a light chain variable region comprising:

a CDR-L1 comprising QSLLHSNGYNY (**SEQ ID NO: 9**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-L2 comprising LGS (**SEQ ID NO: 10**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-L3 comprising MQGLQSPWT (**SEQ ID NO: 15**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

(iii) a heavy chain variable region comprising:

a CDR-H1 comprising GGTFSSYA (**SEQ ID NO: 1**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-H2 comprising IIPIFGTA (**SEQ ID NO: 2**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-H3 comprising ARSLGGRFRY (**SEQ ID NO: 3**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto; and

a light chain variable region comprising:

a CDR-L1 comprising QSLLHSNRYNY (**SEQ ID NO: 17**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-L2 comprising LGS (**SEQ ID NO: 10**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-L3 comprising MQALQTPYT (**SEQ ID NO: 11**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

(iv) a heavy chain variable region comprising:

a CDR-H1 comprising GGTFSSYA (**SEQ ID NO: 1**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-H2 comprising IIPIFGTA (**SEQ ID NO: 2**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-H3 comprising ARSLGGRFRY (**SEQ ID NO: 3**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto; and

a light chain variable region comprising:

a CDR-L1 comprising QSLLHSNGYNY (**SEQ ID NO: 9**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-L2 comprising LGS (**SEQ ID NO: 10**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-L3 comprising MQGLQTPYT (**SEQ ID NO: 23**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto; and

(v) a heavy chain variable region comprising:

a CDR-H1 comprising GDSISSNSVA (**SEQ ID NO: 5**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-H2 comprising TYYRSKWYS (**SEQ ID NO: 6**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-H3 comprising AREVEGSSYDAFDI (**SEQ ID NO: 7**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto; and

a light chain variable region comprising:

a CDR-L1 comprising QSISDF (**SEQ ID NO: 19**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-L2 comprising AAS (**SEQ ID NO: 20**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-L3 comprising QQSYIMPDT (**SEQ ID NO: 21**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto.

5. The antigen binding protein, variant or fragment thereof of any one of the preceding claims, wherein

(a) the antigen binding protein, variant or fragment thereof comprises a heavy chain variable region selected from the group consisting of:

(i) a heavy chain variable region comprising:

a CDR-H1 comprising GSIFSGND (**SEQ ID NO: 25**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-H2 comprising ITSGGST (**SEQ ID NO: 26**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-H3 comprising TNGRWSGDTYYAHH (**SEQ ID NO: 27**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto

(ii) a heavy chain variable region comprising:

a CDR-H1 comprising GSSERFTS (**SEQ ID NO: 29**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-H2 comprising ITNGGST (**SEQ ID NO: 30**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-H3 comprising MAGTS (**SEQ ID NO: 31**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto; and

(iii) a heavy chain variable region comprising:

a CDR-H1 comprising GSIFSGND (**SEQ ID NO: 25**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto,

a CDR-H2 comprising ITSGGST (**SEQ ID NO: 26**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto, and

a CDR-H3 comprising TNGRWSGDTYYAHL (**SEQ ID NO: 33**) or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto; and/or

(b) the antigen binding protein, variant or fragment thereof comprises a heavy chain variable domain and/or a light chain variable domain selected from the group consisting of:

(i) a heavy chain variable domain comprising EVQLVQSGAEVKKPGSSVKVSCKAS**GGTFSSYA**ISWVRQAPGQGLEWMGG**II PIFGTA**NYAQNFQGRVTMTADTSISTAYMELSSLRSEDTAVYYC**ARSLGGRFR Y**WGQGTL (**SEQ ID NO: 4** - 1B6, 1C1, 1C11, 1D4 and 1H6) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions

(ii) a heavy chain variable domain comprising QVQLQQSGPGLVKPSQTLSLTCAIS**GDSISSNSVA**WNWIRQSPSRGLEWLGR**T YYRSKWYS**DYAISVKGRLDINPDTSKNQFSLQLNSVTPEDTAVYYC**AREVEGS SYDAFDI**WGQGTM (**SEQ ID NO: 8**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions,

(iii) a light chain variable domain comprising DVVMTQSPLSLPVTPGEPASISCRSS**QSLLHSNGYNY**LDWYLQKPGQSPQLLI Y**LGS**NRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQALQTPYT**FGQ GTK (**SEQ ID NO: 12**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions

(iv) a light chain variable domain comprising EIVLTQSPLSLPVTPGEPASISCRSS**QSLLHSNGYNY**LDWYLQKPGQSPQLLIY**L GS**NRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQGLQSPWT**FGQGT K (**SEQ ID NO: 16**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions

(v) a light chain variable domain comprising DVVMTQSPLSLPVTPGESASISCRSS**QSLLHSNRYNY**LDWYLQKPGQSPQLLI Y**LGS**NRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQALQTPYT**FGQ GTK (**SEQ ID NO: 18**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions

(vi) a light chain variable domain comprising DIQLTQSPSSLSASVGDRVTITCRAS**QSISDF**LNWYQQKPGKAPKLLIY**AAS**SLQ TGVPSRFGGSGSGTEFTLTISSLQPEDLGTYYC**QQSYIMPDT**FGQGTK (**SEQ**

ID NO: 22) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions

(vii) a light chain variable domain comprising DVVMTQSPLSLPVTPGEPASISCRSS**QSLLHSNGYNY**LDWYLQKPGQSPQLLI Y**LGS**NRASGVPDRFSGSGSGTDFTLQISRVEAEDAGVYYC**MQGLQTPYT**FGQ GTK (**SEQ ID NO: 24**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions

(viii) a heavy chain variable domain comprising QVQLQESGGGLVQPGGSLRLSCADS**GSIFSGND**MAWYRRAPGVERELVAV**IT SGGST**HYADSVKGRFTISRDNAQKTVYLQTNDLKPEDTAVYYC**TNGRWSGDT YYAHH**WGQGTQ (**SEQ ID NO: 28**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions

(ix) a heavy chain variable domain comprising QVQLQESGGGLVQPGGSLRLSCAAS**GSSERFTS**VAWYRQAPGKERELVAF**IT NGGST**RYTDPVKGRFTISRDNAKNTVYLQMNSLKAEDTAVYYC**MAGTS**WGQG TQ (**SEQ ID NO: 32**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions

(x) a heavy chain variable domain comprising QVQLQESGGGLVQPGGSLRLSCADS**GSIFSGND**MAWYRRAPGVERELVAV**IT SGGST**HYADSVKGRFTISRDNAQKTVYLQTNDLKPEDTAVYYC**TNGRWSGDT YYAHL**WGQGTQ (**SEQ ID NO: 34**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions

(xi) a heavy chain variable domain comprising QVQLQESGGGLVQAGGSLRLSCADS**GSIFSGND**MAWYRRAPGVERELVAV**IT SGGST**HYADSVKGRFTISRDNAQKTVYLQTNDLKPEDTAVYYC**TNGRWSGDT YYAHH**WGQGTQ (**SEQ ID NO: 35**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions

(xii) a heavy chain variable domain comprising QVQLQESGGGLVQAGDSLRLSCADS**GSIFSGND**MAWYRRAPGVERELVAV**IT SGGST**HYADSVKGRFTISRDNAQKTVYLQTNDLKPEDTAVYYC**TNGRWSGDT YYAHH**WGQGTQ (**SEQ ID NO: 36**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions; and
a heavy chain variable domain comprising QVQLVESGGGLVQAGGSLRLSCAAS**GSIFSGND**MSWYRQAPGKGLELVAV**ITS GGST**YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC**TNGRWSGDTY YAHH**WGQGTL (**SEQ ID NO: 37**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions; and/or

(c) the antigen binding protein, variant or fragment thereof comprises a heavy chain variable domain and a light chain variable domain selected from the group consisting of:

(i) a heavy chain variable domain comprising: EVQLVQSGAEVKKPGSSVKVSCKAS**GGTFSSYA**ISWVRQAPGQGLEWMGG**IIPIF GTA**NYAQNFQGRVTMTADTSISTAYMELSSLRSEDTAVYYC**ARSLGGRFRY**WGQ GTL (**SEQ ID NO: 4**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions, and
a light chain variable domain comprising DVVMTQSPLSLPVTPGEPASISCRSS**QSLLHSNGYNY**LDWYLQKPGQSPQLLIY**LG S**NRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQALQTPYT**FGQGTK (**SEQ ID NO: 12**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions

(ii) a heavy chain variable domain comprising: EVQLVQSGAEVKKPGSSVKVSCKAS**GGTFSSYA**ISWVRQAPGQGLEWMGG**IIPIF GTA**NYAQNFQGRVTMTADTSISTAYMELSSLRSEDTAVYYC**ARSLGGRFRY**WGQ GTL (**SEQ ID NO: 4**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions, and
a light chain variable domain comprising EIVLTQSPLSLPVTPGEPASISCRSS**QSLLHSNGYNY**LDWYLQKPGQSPQLLIY**LGS**

NRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQGLQSPWT**FGQGTK (**SEQ ID NO: 16**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions

(iii) a heavy chain variable domain comprising:
EVQLVQSGAEVKKPGSSVKVSCKAS**GGTFSSYA**ISWVRQAPGQGLEWMGG**IIPIF GTA**NYAQNFQGRVTMTADTSISTAYMELSSLRSEDTAVYYC**ARSLGGRFRY**WGQ GTL (**SEQ ID NO: 4**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions, and
a light chain variable domain comprising
DVVMTQSPLSLPVTPGESASISCRSS**QSLLHSNRYNY**LDWYLQKPGQSPQLLIY**LG S**NRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQALQTPYT**FGQGTK (**SEQ ID NO: 18**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions

(iv) a heavy chain variable domain comprising:
QVQLQQSGPGLVKPSQTLSLTCAIS**GDSISSNSVA**WNWIRQSPSRGLEWLGR**T YYRSKWYS**DYAISVKGRLDINPDTSKNQFSLQLNSVTPEDTAVYYC**AREVEGS SYDAFDI**WGQGTM (**SEQ ID NO: 8**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions, and
a light chain variable domain comprising
DIQLTQSPSSLSASVGDRVTITCRAS**QSISDF**LNWYQQKPGKAPKLLIY**AAS**SLQTG VPSRFGGSGSGTEFTLTISSLQPEDLGTYYC**QQSYIMPDT**FGQGTK (**SEQ ID NO: 22**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions, or

(v) a heavy chain variable domain comprising:
EVQLVQSGAEVKKPGSSVKVSCKAS**GGTFSSYA**ISWVRQAPGQGLEWMGG**IIPIF GTA**NYAQNFQGRVTMTADTSISTAYMELSSLRSEDTAVYYC**ARSLGGRFRY**WGQ GTL (**SEQ ID NO: 4**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions, and

a light chain variable domain DVVMTQSPLSLPVTPGEPASISCRSS**QSLLHSNGYNY**LDWYLQKPGQSPQLLIY**LGS**NRASGVPDRFSGSGSGTDFTLQISRVEAEDAGVYYC**MQGLQTPYT**FGQGTK (**SEQ ID NO: 24**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions; and/or

(d) the antigen binding protein, variant or fragment thereof comprises a single domain heavy chain variable domain having a sequence:

(i) QVQLQESGGGLVQPGGSLRLSCADS**GSIFSGND**MAWYRRAPGVERELVAV**ITSGGST**HYADSVKGRFTISRDNAQKTVYLQTNDLKPEDTAVYYC**TNGRWSGDTYYAHH**WGQGTQ (**SEQ ID NO: 28**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions, or

(ii) QVQLQESGGGLVQPGGSLRLSCAAS**GSSERFTS**VAWYRQAPGKERELVAF**ITNGGST**RYTDPVKGRFTISRDNAKNTVYLQMNSLKAEDTAVYYC**MAGTS**WGQGTQ (**SEQ ID NO: 32**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions, or

(iii) QVQLQESGGGLVQPGGSLRLSCADS**GSIFSGND**MAWYRRAPGVERELVAV**ITSGGST**HYADSVKGRFTISRDNAQKTVYLQTNDLKPEDTAVYYC**TNGRWSGDTYYAHL**WGQGTQ (**SEQ ID NO: 34**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions, or

(iv) QVQLQESGGGLVQAGGSLRLSCADS**GSIFSGND**MAWYRRAPGVERELVAV**ITSGGST**HYADSVKGRFTISRDNAQKTVYLQTNDLKPEDTAVYYC**TNGRWSGDTYYAHH**WGQGTQ (**SEQ ID NO: 35**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions, or

(v) QVQLQESGGGLVQAGDSLRLSCADS**GSIFSGND**MAWYRRAPGVERELVAV**ITSGGST**HYADSVKGRFTISRDNAQKTVYLQTNDLKPEDTAVYYC**TNGRWSGDTYYAHH**WGQGTQ (**SEQ ID NO: 36**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions, or

(vi) QVQLVESGGGLVQAGGSLRLSCAAS**GSIFSGND**MSWYRQAPGKGLELVAV**ITS GGST**YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC**TNGRWSGDTY YAHH**WGQGTL (**SEQ ID NO: 37**) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions; and/or

(e) the antigen binding protein, variant or fragment thereof comprises a light chain constant domain having a sequence:

(i) RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VAEQDSKDSTYSLSSTLTLSKADYEKHKLYACEVTHQGLSSPVTKSFNRGEC (SEQ ID NO: 13) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions, or

(ii) RTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQES VTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFSRGEC (SEQ ID NO: 14) or a fragment, variant or sequence thereof at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having two or three amino acids substitutions.

6. The antigen binding protein, variant or fragment thereof according to any one of the preceding claims, wherein the antigen binding protein, variant or fragment thereof is

(i) an IgG antibody

(ii) an IgG1 antibody

(iii) a multi-specific antigen binding protein, variant or fragment thereof

(iv) a bispecific antibody

(v) a bispecific T cell engager (BiTE); and/or

(vi) a bispecific T cell engager (BiTE) comprising an anti-EpCAM heavy chain antibody variable region (VHH) or a single chain variable fragment (scFv).

7. The antigen binding protein, variant or fragment thereof according to claim 6, wherein the multi-specific antigen binding protein, variant or fragment thereof binds to an immune marker selected from the group consisting of CD3, NKG2D, CD4, CD8, CD16 and CD64.

8. The antigen binding protein, variant or fragment thereof according to any one of the preceding claims, wherein the antigen binding protein, variant or fragment thereof comprises a Fc region.

9. A polynucleotide encoding the antigen binding protein, variant or fragment thereof of any one of the preceding claims; or a vector expressing the polynucleotide; or a host cell comprising the vector; or a cell expressing/secreting the antigen binding protein, variant of fragment thereof; or a cell expressing/secreting an immune cell engager specific to EpCAM; or a composition comprising the antigen binding protein, variant or fragment thereof and/or the cell.

10. The polynucleotide of claim 9, wherein

(a) the heavy chain variable domain is encoded by a nucleotide sequence comprising:

(i) GAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTC GGTGAAGGTCTCCTGCAAGGCTTCT**GGAGGCACCTTCAGCAGCTATGCT**AT CAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGG **ATCATCCCTATCTTTGGTACAGCA**AACTACGCACAGAACTTCCAGGGCAGA GTCACCATGACCGCAGACACCTCCATAAGCACAGCCTACATGGAGCTGAGC AGCCTGAGATCTGAGGACACGGCCGTGTATTACTGT**GCGAGATCGTTGGGT GGGAGATTTCGCTAC**TGGGGCCAGGGAACCCTG (**SEQ ID NO:** 41) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions, or

(ii) CAGGTACAGCTGCAGCAGTCAGGTCCAGGGCTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCC**GGGGACAGTATCTCTAGTAACAGTGT TGCT**TGGAACTGGATCAGGCAGTCCCCATCGAGAGGCCTTGAGTGGCTGG GAAGG**ACATACTACAGGTCCAAGTGGTACAGT**GATTATGCAATATCTGTGA AAGGTCGATTAGACATCAACCCAGACACATCCAAGAACCAGTTCTCCCTGC AGCTGAACTCTGTGACTCCCGAGGACACGGCTGTGTATTATTGT**GCAAGAG AAGTTGAGGGCAGCAGCTATGATGCTTTTGATATC**TGGGGCCAAGGGACA ATG (**SEQ ID NO: 45**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions;

(iii) CAGGTGCAGCTGCAGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGAGGGT CTCTGAGACTCTCCTGTGCAGACTCT**GGAAGCATCTTCAGTGGCAATGAC**A

TGGCCTGGTACCGCCGGGCTCCAGGGGTGGAGCGCGAGTTGGTCGCGGT T**ATTACTAGCGGTGGTAGTACA**CACTATGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATGCCCAGAAGACCGTATATCTGCAAACGAACGA CTTGAAACCTGAGGACACGGCCGTGTATTACTGC**ACAAACGGAAGATGGT CAGGCGATACTTACTATGCCCATCAC**TGGGGCCAGGGGACCCAG (**SEQ ID NO: 65**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions,

(iv) CAGGTGCAGCTGCAGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGGGGGT CTCTGAGACTCTCCTGTGCAGCCTCT**GGAAGCTCCGAAAGATTCACATCA**G TGGCCTGGTACCGCCAGGCTCCAGGAAAGGAGCGCGAGTTGGTCGCATTT **ATTACTAATGGTGGTAGCACA**AGATATACAGACCCCGTGAAGGGCCGATTC ACCATCTCCAGAGACAACGCCAAGAACACGGTGTATCTGCAAATGAACAGC CTGAAAGCTGAGGACACGGCCGTCTATTATTGT**ATGGCGGGTACGTCC**TGG GGCCAGGGGACCCAG (**SEQ ID NO: 69**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions,

(v) CAGGTGCAGCTGCAGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGAGGGT CTCTGAGACTCTCCTGTGCAGACTCT**GGAAGCATCTTCAGTGGCAATGAC**A TGGCCTGGTACCGCCGGGCTCCAGGGGTGGAGCGCGAGTTGGTCGCGGT T**ATTACTAGCGGTGGTAGTACA**CACTATGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATGCCCAGAAGACCGTATATCTGCAAACGAACGA CCTGAAACCTGAGGACACGGCCGTGTATTACTGC**ACAAACGGAAGATGGT CAGGCGATACTTACTATGCCCATCTC**TGGGGCCAGGGGACCCAG (**SEQ ID NO: 71**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions,

(vi) CAGGTGCAGCTGCAGGAGTCTGGGGGAGGATTGGTGCAGGCTGGGGGCT CTCTGAGACTCTCCTGTGCAGACTCT**GGAAGCATCTTCAGTGGCAATGAC**A TGGCCTGGTACCGCCGGGCTCCAGGGGTGGAGCGCGAGTTGGTCGCGGT T**ATTACTAGCGGTGGTAGTACA**CACTATGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATGCCCAGAAGACCGTATATCTGCAAACGAACGA CCTGAAACCTGAGGACACGGCCGTGTATTACTGC**ACAAACGGAAGATGGT CAGGCGATACTTACTATGCCCATCAC**TGGGGCCAGGGGACCCAG (**SEQ ID NO: 72**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions,

(vii)CAGGTGCAGCTGCAGGAGTCTGGGGGAGGATTGGTGCAGGCTGGGGACT CTCTGAGACTCTCCTGTGCAGACTCT**GGAAGCATCTTCAGTGGCAATGAC**A TGGCCTGGTACCGCCGGGCTCCAGGGGTGGAGCGCGAGTTGGTCGCGGT T**ATTACTAGCGGTGGTAGTACA**CACTATGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATGCCCAGAAGACCGTATATCTGCAAACGAACGA CCTGAAACCTGAGGACACGGCCGTGTATTACTGC**ACAAACGGAAGATGGT CAGGCGATACTTACTATGCCCATCAC**TGGGGCCAGGGGACCCAG (**SEQ ID NO: 73**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions, or

(viii) CAGGTGCAGCTGGTGGAGTCTGGGGGAGGATTGGTGCAGGCTGGG GGCTCTCTGAGACTCTCCTGTGCAGCCTCT**GGAAGCATCTTCAGTGGCAAT GAC**ATGTCCTGGTACCGCCAGGCTCCAGGGAAGGGACTCGAGTTGGTCGC GGTT**ATTACTAGCGGTGGTAGTACA**TACTATGCAGACTCCGTGAAGGGCCG ATTCACCATCTCCAGAGACAATTCCaAGAAcACCcTATATCTGCAAATGAACA GCCTGAGAGCTGAGGACACGGCCGTGTATTACTGC**ACAAACGGAAGATGG TCAGGCGATACTTACTATGCCCATCAC**TGGGGCCAGGGGACCCTG (**SEQ ID NO: 74**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions; and/or

the light chain variable domain is encoded by a nucleotide sequence comprising:

(i) GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAG CCGGCCTCCATCTCCTGCAGGTCTAGT**CAGAGCCTCCTGCATAGTAATGGA TACAACTAT**TTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTC CTGATCTAT**TTGGGTTCT**AATCGGGCCTCCGGGGTCCCTGACAGGTTCAGT GGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCT GAGGATGTTGGGGTTTATTACTGC**ATGCAAGCTCTACAAACTCCGTACACT** TTTGGCCAGGGGACCAAG (**SEQ ID NO: 49**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions, or

(ii) GAAATTGTGCTGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAG CCGGCCTCCATCTCCTGCAGGTCTAGT**CAGAGCCTCCTGCATAGTAATGGA TACAACTAT**TTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTC CTGATCTAT**TTGGGTTCT**AATCGGGCCTCCGGGGTCCCTGACAGGTTCAGT GGCAGTGGATCAGGTACAGATTTTACACTGAAAATAAGCAGAGTGGAGGCT GAGGATGTTGGGGTTTATTACTGC**ATGCAAGGTCTACAAAGTCCCTGGACG**

TTCGGCCAAGGGACCAAG (**SEQ ID NO: 53**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions, or

(iii) GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAG TCGGCCTCCATCTCCTGCAGGTCTAGT**CAGAGCCTCCTGCATAGTAATAGA TACAACTAT**TTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTC CTGATCTAT**TTGGGTTCT**AATCGGGCCTCCGGGGTCCCTGACAGGTTCAGT GGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCT GAGGATGTTGGGGTTTATTACTGC**ATGCAAGCTCTACAAACTCCGTACACT** TTTGGCCAGGGGACCAAG (**SEQ ID NO: 55**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions, or

(iv) GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGAC AGAGTCACCATCACTTGCCGGGCAAGT**CAGAGTATTAGCGACTTT**TTAAATT GGTACCAGCAGAAACCAGGTAAAGCCCCGAAGCTCCTGATCTAT**GCTGCAT CG**AGTTTACAAACTGGGGTCCCCTCAAGATTCGGTGGCAGTGGATCTGGGA CAGAATTCACTCTCACCATAAGCAGTCTACAACCTGAAGATTTGGGAACTTA TTACTGT**CAACAGAGTTACATTATGCCCGACACT**TTTGGCCAGGGGACGAA A (**SEQ ID NO: 59**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions, or GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAG CCGGCCTCCATCTCCTGCAGGTCTAGT**CAGAGCCTCCTGCATAGTAATGGA TACAACTAT**TTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTC CTGATCTAT**TTGGGTTCT**AATCGGGCCTCCGGGGTCCCTGACAGGTTCAGT GGCAGTGGATCAGGCACAGATTTTACACTGCAAATCAGCAGAGTGGAGGCT GAGGATGCTGGGGTTTATTACTGC**ATGCAAGGTCTACAGACTCCGTACACT** TTTGGCCAGGGGACCAAG (**SEQ ID NO: 61**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions; and/or

(b) the heavy chain and light chain variable domains are encoded by nucleotide sequences selected from the group consisting of:

(i) a heavy chain variable domain encoded by the nucleotide sequence comprising: GAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTC GGTGAAGGTCTCCTGCAAGGCTTCT**GGAGGCACCTTCAGCAGCTATGCT**AT

CAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGG
ATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAACTTCCAGGGCAGA
GTCACCATGACCGCAGACACCTCCATAAGCACAGCCTACATGGAGCTGAGC
AGCCTGAGATCTGAGGACACGGCCGTGTATTACTGT**GCGAGATCGTTGGGT**
GGGAGATTTCGCTACTGGGGCCAGGGAACCCTG (**SEQ ID NO: 41**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions, and

a light chain variable domain encoded by the nucleotide sequence comprising:
GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAG
CCGGCCTCCATCTCCTGCAGGTCTAGT**CAGAGCCTCCTGCATAGTAATGGA**
TACAACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTC
CTGATCTAT**TTGGGTTCT**AATCGGGCCTCCGGGGTCCCTGACAGGTTCAGT
GGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCT
GAGGATGTTGGGGTTTATTACTGC**ATGCAAGCTCTACAAACTCCGTACACT**
TTTGGCCAGGGGACCAAG (**SEQ ID NO: 49**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions

(ii) a heavy chain variable domain encoded by the nucleotide sequence comprising:
GAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTC
GGTGAAGGTCTCCTGCAAGGCTTCT**GGAGGCACCTTCAGCAGCTATGCT**AT
CAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGG
ATCATCCCTATCTTTGGTACAGCAAACTACGCACAGAACTTCCAGGGCAGA
GTCACCATGACCGCAGACACCTCCATAAGCACAGCCTACATGGAGCTGAGC
AGCCTGAGATCTGAGGACACGGCCGTGTATTACTGT**GCGAGATCGTTGGGT**
GGGAGATTTCGCTACTGGGGCCAGGGAACCCTG (**SEQ ID NO: 41**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions, and

a light chain variable domain encoded by the nucleotide sequence comprising:
GAAATTGTGCTGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAG
CCGGCCTCCATCTCCTGCAGGTCTAGT**CAGAGCCTCCTGCATAGTAATGGA**
TACAACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTC
CTGATCTAT**TTGGGTTCT**AATCGGGCCTCCGGGGTCCCTGACAGGTTCAGT
GGCAGTGGATCAGGTACAGATTTTACACTGAAAATAAGCAGAGTGGAGGCT
GAGGATGTTGGGGTTTATTACTGC**ATGCAAGGTCTACAAAGTCCCTGGACG**

TTCGGCCAAGGGACCAAG (**SEQ ID NO: 53**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions

(iii) a heavy chain variable domain encoded by the nucleotide sequence comprising:

GAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTC GGTGAAGGTCTCCTGCAAGGCTTCT**GGAGGCACCTTCAGCAGCTATGCT**AT CAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGG **ATCATCCCTATCTTTGGTACAGCA**AACTACGCACAGAACTTCCAGGGCAGA GTCACCATGACCGCAGACACCTCCATAAGCACAGCCTACATGGAGCTGAGC AGCCTGAGATCTGAGGACACGGCCGTGTATTACTGT**GCGAGATCGTTGGGT GGGAGATTTCGCTAC**TGGGGCCAGGGAACCCTG (**SEQ ID NO: 41**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions, and

a light chain variable domain encoded by the nucleotide sequence comprising:

GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAG TCGGCCTCCATCTCCTGCAGGTCTAGT**CAGAGCCTCCTGCATAGTAATAGA TACAACTAT**TTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTC CTGATCTAT**TTGGGTTCT**AATCGGGCCTCCGGGGTCCCTGACAGGTTCAGT GGCAGTGGATCAGGCACAGATTTTACACTGAAAATCAGCAGAGTGGAGGCT GAGGATGTTGGGGTTTATTACTGC**ATGCAAGCTCTACAAACTCCGTACACT** TTTGGCCAGGGGACCAAG (**SEQ ID NO: 55**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions

(iv) a heavy chain variable domain encoded by the nucleotide sequence comprising:

GAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTC GGTGAAGGTCTCCTGCAAGGCTTCT**GGAGGCACCTTCAGCAGCTATGCT**AT CAGCTGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGG **ATCATCCCTATCTTTGGTACAGCA**AACTACGCACAGAACTTCCAGGGCAGA GTCACCATGACCGCAGACACCTCCATAAGCACAGCCTACATGGAGCTGAGC AGCCTGAGATCTGAGGACACGGCCGTGTATTACTGT**GCGAGATCGTTGGGT GGGAGATTTCGCTAC**TGGGGCCAGGGAACCCTG (**SEQ ID NO: 41**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions, and

a light chain variable domain encoded by the nucleotide sequence comprising:

GATGTTGTGATGACTCAGTCTCCACTCTCCCTGCCCGTCACCCCTGGAGAG
CCGGCCTCCATCTCCTGCAGGTCTAGT**CAGAGCCTCCTGCATAGTAATGGA**
TACAACTATTTGGATTGGTACCTGCAGAAGCCAGGGCAGTCTCCACAGCTC
CTGATCTAT**TTGGGTTCT**AATCGGGCCTCCGGGGTCCCTGACAGGTTCAGT
GGCAGTGGATCAGGCACAGATTTTACACTGCAAATCAGCAGAGTGGAGGCT
GAGGATGCTGGGGTTTATTACTGC**ATGCAAGGTCTACAGACTCCGTACACT**
TTTGGCCAGGGGACCAAG (**SEQ ID NO: 61**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions; and

(v) a heavy chain variable domain encoded by the nucleotide sequence comprising:

CAGGTACAGCTGCAGCAGTCAGGTCCAGGGCTGGTGAAGCCCTCGCAGAC
CCTCTCACTCACCTGTGCCATCTCC**GGGGACAGTATCTCTAGTAACAGTGT**
TGCTTGGAACTGGATCAGGCAGTCCCCATCGAGAGGCCTTGAGTGGCTGG
GAAGG**ACATACTACAGGTCCAAGTGGTACAGT**GATTATGCAATATCTGTGA
AAGGTCGATTAGACATCAACCCAGACACATCCAAGAACCAGTTCTCCCTGC
AGCTGAACTCTGTGACTCCCGAGGACACGGCTGTGTATTATTGT**GCAAGAG**
AAGTTGAGGGCAGCAGCTATGATGCTTTTGATATCTGGGGCCAAGGGACA
ATG (**SEQ ID NO: 45**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions, and

a light chain variable domain encoded by the nucleotide sequence comprising:

GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGAC
AGAGTCACCATCACTTGCCGGGCAAGT**CAGAGTATTAGCGACTTT**TTAAATT
GGTACCAGCAGAAACCAGGTAAAGCCCCGAAGCTCCTGATCTAT**GCTGCAT**
CGAGTTTACAAACTGGGGTCCCCTCAAGATTCGGTGGCAGTGGATCTGGGA
CAGAATTCACTCTCACCATAAGCAGTCTACAACCTGAAGATTTGGGAACTTA
TTACTGT**CAACAGAGTTACATTATGCCCGACACT**TTTGGCCAGGGGACGAA
A (**SEQ ID NO: 59**)

or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions; and/or

(c) the single domain heavy chain variable domain is encoded by a nucleotide sequence comprising

(i) CAGGTGCAGCTGCAGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGAGGGT
CTCTGAGACTCTCCTGTGCAGACTCT**GGAAGCATCTTCAGTGGCAATGAC**A

TGGCCTGGTACCGCCGGGCTCCAGGGGTGGAGCGCGAGTTGGTCGCGGT T**ATTACTAGCGGTGGTAGTACA**CACTATGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATGCCCAGAAGACCGTATATCTGCAAACGAACGA CTTGAAACCTGAGGACACGGCCGTGTATTACTGC**ACAAACGGAAGATGGT CAGGCGATACTTACTATGCCCATCAC**TGGGGCCAGGGGACCCAG (**SEQ ID NO: 65**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions,

(ii) CAGGTGCAGCTGCAGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGGGGGT CTCTGAGACTCTCCTGTGCAGCCTCT**GGAAGCTCCGAAAGATTCACATCA**G TGGCCTGGTACCGCCAGGCTCCAGGAAAGGAGCGCGAGTTGGTCGCATTT **ATTACTAATGGTGGTAGCACA**AGATATACAGACCCCGTGAAGGGCCGATTC ACCATCTCCAGAGACAACGCCAAGAACACGGTGTATCTGCAAATGAACAGC CTGAAAGCTGAGGACACGGCCGTCTATTATTGT**ATGGCGGGTACGTCC**TGG GGCCAGGGGACCCAG (**SEQ ID NO: 69**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions,

(iii) CAGGTGCAGCTGCAGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGAGGGT CTCTGAGACTCTCCTGTGCAGACTCT**GGAAGCATCTTCAGTGGCAATGAC**A TGGCCTGGTACCGCCGGGCTCCAGGGGTGGAGCGCGAGTTGGTCGCGGT T**ATTACTAGCGGTGGTAGTACA**CACTATGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATGCCCAGAAGACCGTATATCTGCAAACGAACGA CCTGAAACCTGAGGACACGGCCGTGTATTACTGC**ACAAACGGAAGATGGT CAGGCGATACTTACTATGCCCATCTC**TGGGGCCAGGGGACCCAG (**SEQ ID NO: 71**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions,

(iv) CAGGTGCAGCTGCAGGAGTCTGGGGGAGGATTGGTGCAGGCTGGGGGCT CTCTGAGACTCTCCTGTGCAGACTCT**GGAAGCATCTTCAGTGGCAATGAC**A TGGCCTGGTACCGCCGGGCTCCAGGGGTGGAGCGCGAGTTGGTCGCGGT T**ATTACTAGCGGTGGTAGTACA**CACTATGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATGCCCAGAAGACCGTATATCTGCAAACGAACGA CCTGAAACCTGAGGACACGGCCGTGTATTACTGC**ACAAACGGAAGATGGT CAGGCGATACTTACTATGCCCATCAC**TGGGGCCAGGGGACCCAG (**SEQ ID NO: 72**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions,

(v) CAGGTGCAGCTGCAGGAGTCTGGGGGAGGATTGGTGCAGGCTGGGGACT CTCTGAGACTCTCCTGTGCAGACTCT**GGAAGCATCTTCAGTGGCAATGAC**A TGGCCTGGTACCGCCGGGCTCCAGGGGTGGAGCGCGAGTTGGTCGCGGT T**ATTACTAGCGGTGGTAGTACA**CACTATGCAGACTCCGTGAAGGGCCGATT CACCATCTCCAGAGACAATGCCCAGAAGACCGTATATCTGCAAACGAACGA CCTGAAACCTGAGGACACGGCCGTGTATTACTGC**ACAAACGGAAGATGGT CAGGCGATACTTACTATGCCCATCAC**TGGGGCCAGGGGACCCAG (**SEQ ID NO: 73**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions, or

(vi) CAGGTGCAGCTGGTGGAGTCTGGGGGAGGATTGGTGCAGGCTGGGGGCT CTCTGAGACTCTCCTGTGCAGCCTCT**GGAAGCATCTTCAGTGGCAATGAC**A TGTCCTGGTACCGCCAGGCTCCAGGGAAGGGACTCGAGTTGGTCGCGGTT **ATTACTAGCGGTGGTAGTACA**TACTATGCAGACTCCGTGAAGGGCCGATTC ACCATCTCCAGAGACAATTCCaAGAAcACCcTATATCTGCAAATGAACAGCCT GAGAGCTGAGGACACGGCCGTGTATTACTGC**ACAAACGGAAGATGGTCAG GCGATACTTACTATGCCCATCAC**TGGGGCCAGGGGACCCTG (**SEQ ID NO: 74**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions; and/or

(d) the light chain constant domain is encoded by a nucleotide sequence comprising

(i) CGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGT TGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAG AGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTC CCAGGAGAGTGTCGCAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCA GCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAACTCTACG CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA ACAGGGGAGAGTGT (**SEQ ID NO: 50**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions, or

(ii) CGAACTGTGGCTGCACCATCTGTCTTCATCTTCCCGCCATCTGATGAGCAGT TGAAATCTGGAACTGCCTCTGTTGTGTGCCTGCTGAATAACTTCTATCCCAG AGAGGCCAAAGTACAGTGGAAGGTGGATAACGCCCTCCAATCGGGTAACTC CCAGGAGAGTGTCACAGAGCAGGACAGCAAGGACAGCACCTACAGCCTCA GCAGCACCCTGACGCTGAGCAAAGCAGACTACGAGAAACACAAAGTCTACG CCTGCGAAGTCACCCATCAGGGCCTGAGCTCGCCCGTCACAAAGAGCTTCA

GCAGGGGAGAGTGT (**SEQ ID NO: 51**) or a sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identical thereto and/or having 10-20 nucleic acid substitutions.

11. The cell according to claim 9, wherein the immune cell engager is selected from the group comprising
(i) a T cell engager, an NK cell engager, a monocyte engager and a macrophage engager
(ii) a bispecific T cell engager (BiTE)
(iii) an inducible BiTE
(iv) a non-inducible BiTE; and/or
(v) a constitutive expression BiTE,
comprising the antigen binding protein, variant or fragment thereof of any one of claims 1 to 8.

12. The cell of any one of claims 9 and 11, wherein
(i) the cell is an immune cell, for example selected from the group comprising a T cell, a macrophage, a monocyte, and an NK cell;and/or
(ii) the immune cell is a T-cell, in particular a CAR T-cell; and/or
(iii) the cell is a stem cell, for example selected from the group comprising a mesenchymal stem cell, a neural stem cell and a pluripotent stem cell, such as an induced pluripotent stem cell (iPSC).

13. An antigen binding protein, variant or fragment thereof of any one of claims 1 to 8, cell of any one of claims 9, 11, 12, or a composition of claim 9 for use in treatment of a disease.

14. Use of the antigen binding protein, variant or fragment thereof of any one of claims 1 to 8, a cell according to any one of claims 9, 11, 12 or the composition of 9 in the manufacture of a medicament for preventing and/or treating a disease,

optionally wherein the disease is a proliferative disease such as a tumor or cancer.

15. A method of diagnosis / determining the prognosis or presence of a solid tumor originating from epithelium comprising detecting the expression of high EpCAM on the

solid tumor using the antigen binding protein, variant or fragment thereof of any one of claims 1 to 8 or a composition of claim 9.