CLAIMS

1. A modified cell expressing

(a) a chimeric antigen receptor targeting GPC3 or CD19, and

(b) a multi-specific antigen binding protein, variant or binding fragment thereof that binds one or more target, comprising a first antigen binding protein, variant or binding fragment thereof that binds to EpCAM (epithelial cell adhesion molecule) and a second antigen binding protein, variant or binding fragment thereof that binds to an immune cell marker,

wherein the first antigen binding protein, variant or binding fragment thereof that binds to EpCAM 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:

- 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**)

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,

(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,

(iii) 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,

(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,
- 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** - 1E4) 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.

2. The cell of claim 1, wherein the first antigen binding protein, variant or binding fragment thereof that binds to EpCAM 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 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 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,

(iii) 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,

(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 MQALQTPYT (**SEQ ID NO: 11**) 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 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,

(vi) 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,

(vii) 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,

(viii) 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

(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.

3. The cell of any one of the preceding claims, wherein the first antigen binding protein, variant or binding fragment thereof that binds to EpCAM 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 fragment, variant 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 fragment, variant 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 fragment, variant or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto; and/or

a light chain variable region comprising:

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

a light chain variable region comprising:

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

a light chain variable region comprising:

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

a light chain variable region comprising:

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

a light chain variable region comprising:

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

4. The cell of any one of the preceding claims, wherein the first antigen binding protein, variant or binding fragment thereof that binds to EpCAM 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.

5. The cell of any one of the preceding claims, wherein the first antigen binding protein, variant or binding fragment thereof that binds to EpCAM 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.

6. The cell of any one of the preceding claims, wherein the first antigen binding protein, variant or binding fragment thereof that binds to EpCAM 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

QVQLVESGGGLVQAGGSLRLSCAAS**GSIFSGND**MSWYRQAPGKGLELVAV**ITS GGST**YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYC**TNGRWSGDTY**

YAHHWGQGTL (**SEQ ID NO: 37**) or a fragment, variant or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto and/or having two or three amino acids substitutions

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

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

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

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

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

(viii) a light chain variable domain comprising DIQLTQSPSSLSASVGDRVTITCRAS**QSISDF**LNWYQQKPGKAPKLLIY**AAS**SLQ TGVPSRFGGSGSGTEFTLTISSLQPEDLGTYYC**QQSYIMPDT**FGQGTK (**SEQ ID NO: 22**) or a fragment, variant or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto and/or having two or three amino acids substitutions

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

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

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

(xii) a heavy chain variable domain comprising QVQLQESGGGLVQPGGSLRLSCADS**GSIFSGND**MAWYRRAPGVERELVAV**IT SGGST**HYADSVKGRFTISRDNAQKTVYLQTNDLKPEDTAVYYC**TNGRWSGDT YYAHL**WGQGTQ (**SEQ ID NO: 34**) or a fragment, variant or a sequence having

at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto and/or having two or three amino acids substitutions

(xiii) a heavy chain variable domain comprising QVQLQESGGGLVQAGDSLRLSCADS**GSIFSGND**MAWYRRAPGVERELVAV**IT SGGST**HYADSVKGRFTISRDNAQKTVYLQTNDLKPEDTAVYYC**TNGRWSGDT YYAHH**WGQGTQ (**SEQ ID NO: 36**) or a fragment, variant or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto and/or having two or three amino acids substitutions.

7. The cell of any one of the preceding claims, wherein the first antigen binding protein, variant or binding fragment thereof that binds to EpCAM 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**ARSLGGR FRY**WGQGTL (**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/or

a light chain variable domain comprising DVVMTQSPLSLPVTPGEPASISCRSS**QSLLHSNGYNY**LDWYLQKPGQSPQ LLIY**LGS**NRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQALQTPY T**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**II PIFGTA**NYAQNFQGRVTMTADTSISTAYMELSSLRSEDTAVYYC**ARSLGGR FRY**WGQGTL (**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/or

a light chain variable domain comprising EIVLTQSPLSLPVTPGEPASISCRSS**QSLLHSNGYNY**LDWYLQKPGQSPQL LIY**LGS**NRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQGLQSPW T**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**II**
PIFGTANYAQNFQGRVTMTADTSISTAYMELSSLRSEDTAVYYC**ARSLGGR**
FRYWGQGTL (**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/or

a light chain variable domain comprising

DVVMTQSPLSLPVTPGESASISCRSS**QSLLHSNRYNY**LDWYLQKPGQSPQ
LLIY**LGS**NRASGVPDRFSGSGSGTDFTLKISRVEAEDVGVYYC**MQALQTPY**
TFGQGTK (**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**WNWIRQSPSRGLEWL
GR**TYYRSKWYS**DYAISVKGRLDINPDTSKNQFSLQLNSVTPEDTAVYYC**AR**
EVEGSSYDAFDIWGQGTM (**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/or

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, or

(v) a heavy chain variable domain comprising:

EVQLVQSGAEVKKPGSSVKVSCKAS**GGTFSSYA**ISWVRQAPGQGLEWMGG**II**
PIFGTANYAQNFQGRVTMTADTSISTAYMELSSLRSEDTAVYYC**ARSLGGR**
FRYWGQGTL (**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/or

a light chain variable domain

DVVMTQSPLSLPVTPGEPASISCRSS**QSLLHSNGYNY**LDWYLQKPGQSPQLLI Y**LGS**NRASGVPDRFSGSGSGTDFTLQISRVEAEDAGVYYC**MQGLQTPYT**F GQGTK (**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).

8. The cell of any one of the preceding claims, wherein the first antigen binding protein, variant or binding fragment thereof that binds to EpCAM comprises a single domain heavy chain variable domain having a sequence:

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

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

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

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

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

(vi) QVQLQESGGGLVQAGDSLRLSCADS**GSIFSGND**MAWYRRAPGVERELVAV**IT SGGST**HYADSVKGRFTISRDNAQKTVYLQTNDLKPEDTAVYYC**TNGRWSGDT YYAHH**WGQGTQ (**SEQ ID NO: 36**) or a fragment, variant or a sequence having at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto and/or having two or three amino acids substitutions.

9. The cell of any one of the preceding claims, wherein the first antigen binding protein, variant or binding fragment thereof that binds to EpCAM comprises a heavy chain variable domain encoded by a nucleotide sequence comprising:

(i) a heavy chain variable region comprising:

a CDR-H1 comprising GGAAGCATCTTCAGTGGCAATGAC (**SEQ ID NO: 62**),
a CDR-H2 comprising ATTACTAGCGGTGGTAGTACA (**SEQ ID NO: 63**), and
a CDR-H3 comprising ACAAACGGAAGATGGTCAGGCGATACTTACTATGCCCATCAC (**SEQ ID NO: 64**)

(ii) a heavy chain variable region comprising:

a CDR-H1 comprising GGAAGCTCCGAAAGATTCACATCA (**SEQ ID NO: 66**),
a CDR-H2 comprising ATTACTAATGGTGGTAGCACA (**SEQ ID NO: 67**), and
a CDR-H3 comprising ATGGCGGGTACGTCC (**SEQ ID NO: 68**); and

(iii) a heavy chain variable region comprising:

a CDR-H1 comprising GGAAGCATCTTCAGTGGCAATGAC (**SEQ ID NO: 62**),
a CDR-H2 comprising ATTACTAGCGGTGGTAGTACA (**SEQ ID NO: 63**), and
a CDR-H3 comprising ACAAACGGAAGATGGTCAGGCGATACTTACTATGCCCATCTC (**SEQ ID NO: 70**)

or fragment or variation or sequence at least 80%, 85%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% identity thereto.

10. The cell of any one of the preceding claims, wherein the first antigen binding protein, variant or binding fragment thereof that binds to EpCAM comprises a heavy chain variable domain encoded by a nucleotide sequence comprising:

(i) CAGGTGCAGCTGCAGGAGTCTGGGGGAGGATTGGTGCAGGCTGGGGGCT CTCTGAGACTCTCCTGTGCAGACTCT**GGAAGCATCTTCAGTGGCAATGAC**A TGGCCTGGTACCGCCGGGCTCCAGGGGTGGAGCGCGAGTTGGTCGCGGT

T**ATTACTAGCGGTGGTAGTACA**CACTATGCAGACTCCGTGAAGGGCCGATT
CACCATCTCCAGAGACAATGCCCAGAAGACCGTATATCTGCAAACGAACGA
CCTGAAACCTGAGGACACGGCCGTGTATTACTGC**ACAAACGGAAGATGGT**
CAGGCGATACTTACTATGCCCATCACTGGGGCCAGGGGACCCAG (**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, or

(ii) CAGGTGCAGCTGGTGGAGTCTGGGGGAGGATTGGTGCAGGCTGGGGGCT
CTCTGAGACTCTCCTGTGCAGCCTCT**GGAAGCATCTTCAGTGGCAATGAC**A
TGTCCTGGTACCGCCAGGCTCCAGGGAAGGGACTCGAGTTGGTCGCGGTT
ATTACTAGCGGTGGTAGTACATACTATGCAGACTCCGTGAAGGGCCGATTC
ACCATCTCCAGAGACAATTCCaAGAAcACCcTATATCTGCAAATGAACAGCCT
GAGAGCTGAGGACACGGCCGTGTATTACTGC**ACAAACGGAAGATGGTCAG**
GCGATACTTACTATGCCCATCACTGGGGCCAGGGGACCCTG (**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; or

(iii) 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, or

(iv) 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; or

(v) 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, or

(vi) 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, or

(vii) 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, or

(viii) CAGGTGCAGCTGCAGGAGTCTGGGGGAGGATTGGTGCAGGCTGGG GACTCTCTGAGACTCTCCTGTGCAGACTCT**GGAAGCATCTTCAGTGGCAAT GAC**ATGGCCTGGTACCGCCGGGCTCCAGGGGTGGAGCGCGAGTTGGTCG CGGTT**ATTACTAGCGGTGGTAGTACA**CACTATGCAGACTCCGTGAAGGGCC GATTCACCATCTCCAGAGACAATGCCCAGAAGACCGTATATCTGCAAACGA ACGACCTGAAACCTGAGGACACGGCCGTGTATTACTGC**ACAAACGGAAGA TGGTCAGGCGATACTTACTATGCCCATCAC**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, 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**

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, or

(v) 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.

11. The cell of any one of the preceding claims, wherein the first antigen binding protein, variant or binding fragment thereof that binds to EpCAM comprises heavy chain and/or light chain variable domains 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 **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/or

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

(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/or
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
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/or

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/or

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

(v) a heavy chain variable domain encoded by the nucleotide sequence comprising: CAGGTACAGCTGCAGCAGTCAGGTCCAGGGCTGGTGAAGCCCTCGCAGAC CCTCTCACTCACCTGTGCCATCTCC**GGGGACAGTATCTCTAGTAACAGTGT TGCT**TGGAACTGGATCAGGCAGTCCCCATCGAGAGGCCTTGAGTGGCTGG

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/or

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.

12. The cell of any one of the preceding claims, wherein the first antigen binding protein, variant or binding fragment thereof that binds to EpCAM comprises a heavy chain variable domain encoded by the nucleotide sequence comprising:

(i) CAGGTGCAGCTGGTGGAGTCTGGGGGAGGATTGGTGCAGGCTGGGGGCTCTC
TGAGACTCTCCTGTGCAGCCTCT**GGAAGCATCTTCAGTGGCAATGAC**ATGTCC
TGGTACCGCCAGGCTCCAGGGAAGGGACTCGAGTTGGTCGCGGTT**ATTACTAG**
CGGTGGTAGTACATACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCCA
GAGACAATTCCaAGAAcACCcTATATCTGCAAATGAACAGCCTGAGAGCTGAGG
ACACGGCCGTGTATTACTGC**ACAAACGGAAGATGGTCAGGCGATACTTACTAT**
GCCCATCACTGGGGCCAGGGGACCCTG (**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; or

(ii) CAGGTGCAGCTGCAGGAGTCTGGGGGAGGATTGGTGCAGGCTGGGGGCTCTC
TGAGACTCTCCTGTGCAGACTCT**GGAAGCATCTTCAGTGGCAATGAC**ATGGCC
TGGTACCGCCGGGCTCCAGGGGTGGAGCGCGAGTTGGTCGCGGTT**ATTACTA**
GCGGTGGTAGTACACACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCC
AGAGACAATGCCCAGAAGACCGTATATCTGCAAACGAACGACCTGAAACCTGA

GGACACGGCCGTGTATTACTGC**ACAAACGGAAGATGGTCAGGCGATACTTAC TATGCCCATCAC**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, or

(iii) CAGGTGCAGCTGCAGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGAGGGTCTC TGAGACTCTCCTGTGCAGACTCT**GGAAGCATCTTCAGTGGCAATGAC**ATGGCC TGGTACCGCCGGGCTCCAGGGGTGGAGCGCGAGTTGGTCGCGGTT**ATTACTA GCGGTGGTAGTACA**CACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCC AGAGACAATGCCCAGAAGACCGTATATCTGCAAACGAACGACTTGAAACCTGAG GACACGGCCGTGTATTACTGC**ACAAACGGAAGATGGTCAGGCGATACTTACTA TGCCCATCAC**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, or

(iv) CAGGTGCAGCTGCAGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGGGGGTCTC TGAGACTCTCCTGTGCAGCCTCT**GGAAGCTCCGAAAGATTCACATCA**GTGGCC TGGTACCGCCAGGCTCCAGGAAAGGAGCGCGAGTTGGTCGCATTT**ATTACTAA TGGTGGTAGCACA**AGATATACAGACCCCGTGAAGGGCCGATTCACCATCTCCA GAGACAACGCCAAGAACACGGTGTATCTGCAAATGAACAGCCTGAAAGCTGAG GACACGGCCGTCTATTATTGT**ATGGCGGGTACGTCC**TGGGGCCAGGGGACCC AG (**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, or

(v) CAGGTGCAGCTGCAGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGAGGGTCTC TGAGACTCTCCTGTGCAGACTCT**GGAAGCATCTTCAGTGGCAATGAC**ATGGCC TGGTACCGCCGGGCTCCAGGGGTGGAGCGCGAGTTGGTCGCGGTT**ATTACTA GCGGTGGTAGTACA**CACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCC AGAGACAATGCCCAGAAGACCGTATATCTGCAAACGAACGACCTGAAACCTGA GGACACGGCCGTGTATTACTGC**ACAAACGGAAGATGGTCAGGCGATACTTAC TATGCCCATCTC**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, or

(vi) CAGGTGCAGCTGCAGGAGTCTGGGGGAGGATTGGTGCAGGCTGGGGACTCTC TGAGACTCTCCTGTGCAGACTCT**GGAAGCATCTTCAGTGGCAATGAC**ATGGCC TGGTACCGCCGGGCTCCAGGGGTGGAGCGCGAGTTGGTCGCGGTT**ATTACTA GCGGTGGTAGTACA**CACTATGCAGACTCCGTGAAGGGCCGATTCACCATCTCC

AGAGACAATGCCCAGAAGACCGTATATCTGCAAACGAACGACCTGAAACCTGA GGACACGGCCGTGTATTACTGC**ACAAACGGAAGATGGTCAGGCGATACTTAC TATGCCCATCAC**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, GAGGTCCAGCTGGTGCAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCGG TGAAGGTCTCCTGCAAGGCTTCT**GGAGGCACCTTCAGCAGCTATGCT**ATCAGC TGGGTGCGACAGGCCCCTGGACAAGGGCTTGAGTGGATGGGAGGG**ATCATCC CTATCTTTGGTACAGCA**AACTACGCACAGAACTTCCAGGGCAGAGTCACCATG ACCGCAGACACCTCCATAAGCACAGCCTACATGGAGCTGAGCAGCCTGAGATC TGAGGACACGGCCGTGTATTACTGT**GCGAGATCGTTGGGTGGGAGATTTCGCT AC**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

(vii) CAGGTACAGCTGCAGCAGTCAGGTCCAGGGCTGGTGAAGCCCTCGCAGACCC TCTCACTCACCTGTGCCATCTCC**GGGGACAGTATCTCTAGTAACAGTGTTGCT**T GGAACTGGATCAGGCAGTCCCCATCGAGAGGCCTTGAGTGGCTGGGAAGG**AC ATACTACAGGTCCAAGTGGTACAGT**GATTATGCAATATCTGTGAAAGGTCGATT AGACATCAACCCAGACACATCCAAGAACCAGTTCTCCCTGCAGCTGAACTCTGT GACTCCCGAGGACACGGCTGTGTATTATTGT**GCAAGAGAAGTTGAGGGCAGC AGCTATGATGCTTTTGATATC**TGGGGCCAAGGGACAATG (**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.

13. The cell of any one of the preceding claims, wherein the multi-specific antigen binding protein, variant or fragment thereof is a bispecific antibody.

14. The cell of any one of the preceding claims, wherein the multi-specific antigen binding protein, variant or fragment thereof is an immune cell engager selected from the group comprising a T cell engager, an NK cell engager, a monocyte engager and a macrophage engager.

15. The cell of any one of the preceding claims, wherein the multi-specific antigen binding protein, variant or fragment thereof is a bispecific T cell engager (BiTE), such as an inducible BiTE, a non-inducible BiTE or a constitutive expression BiTE.

16. The cell of any one of the preceding claims, wherein the second antigen binding protein, variant or binding fragment thereof binds to the immune marker selected from the group consisting of CD3, NKG2D, CD4, CD8, CD16, and CD64.

17. The cell of any one of the preceding claims, wherein the multispecific antigen binding protein is an inducible bispecific T cell engager comprising a Heavy chain antibody variable region (i.e. VHH) or a single chain variable fragment (scFv).

18. The cell of any one of the preceding claims, wherein the cell is selected from the group consisting of a T cell, a macrophage, a monocyte, and an NK cell.

19. The cell of any one of the preceding claims, wherein the cell is a T cell, optionally a CAR T-cell.

20. The cell of any one of the preceding claims, wherein the cell

i. binds to GPC3 and secretes an inducible bispecific T cell engager that targets EpCAM and CD3 (GE CAR-BiTE T); or

ii. binds to CD19 and secretes an inducible bispecific T cell engager that targets EpCAM and CD3 (CD19 CAR-BiTE T).

21. A polynucleotide encoding the cell of any one of the preceding claims.

22. A vector expressing the polynucleotide of claim 21.

23. A host cell comprising the vector of claim 22.

24. A method of producing / generating the cell of any one of claims 1 to 20, comprising introducing the polynucleotide of claim 21 into the cell.

25. A composition comprising the cell of any one of claims 1 to 20.

26. Use of the cell of any one of claims 1 to 20 or the composition of claim 25 in the manufacture of a medicament for treating a disease in a subject in need thereof, optionally the disease is a proliferative disease, optionally a cancer.