Supplementary Fig. 1 EBV-miR-BART11 and EBV-miR-BART17-3p upregulate PD-L1 expression in NPC and GC.

a) PD-L1 expression was analyzed in 31 NPCs and 10 NPEs of GSE12452 and 32 GC tissues and 32 normal gastric mucosa tissues of GSE65801. NPC, nasopharyngeal carcinoma; NPE, nasopharyngeal epithelial; GC, gastric adenocarcinoma.

b) PD-L1 expression was positively associated with EBV infection in GC samples based on data from the TCGA database and GSE51575.

c) EBER1 and PD-L1 expression was analyzed via qRT-PCR in NP69 and C666-1, HONE1 and HONE1-EBV, GES-1, SNU-719, AGS, and AGS-EBV cells. GAPDH was used as an internal control.

d) EBER1 and PD-L1 expression was analyzed via qRT-PCR in HNE2, CNE2 and HONE1 cells which were infected with EBV virions derived from Akata or B95-8 cell lines. GAPDH was used as an internal control.

e) Schematic diagram of the BART clusters in EBV derived from Akata and the differences with EBV derived from B95-8 cells.

f) qRT-PCR analysis of PD-L1 mRNA expression in HONE1 cells after transfection with different EBV miRNA (EBV-miR-BART17-3p, EBV-miR-BART11-3p, EBV-miR-BART11-5p, EBV-miR-BART10, EBV-miR-BART12, EBV-miR-BART17-5p, EBV-miR-BART22, or EBV-miR-BART6-3p) mimics. GAPDH and U6 were used as an internal control. n = 3 biologically independent samples.

g) Western blotting to quantify the protein levels of PD-L1 in HONE1 cells transfected with EBV-miR-BART10, EBV-miR-BART12, EBV-miR-BART17-5p, EBV-miR-BART22, or EBV-miR-BART6-3p mimics. GAPDH was used as an internal control.

h) qRT-PCR analysis of EBV-miR-BART17-3p, EBV-miR-BART11-3p, and EBV-miR-BART11-5p expression in EBV-negative HONE1 and AGS cells transfected with EBV-miR-BART17-3p, EBV-miR-BART11-3p or EBV-miR-BART11-5p mimics, and EBV-positive HONE1-EBV, AGS-EBV, C666-1, and SNU-719 cells transfected with EBV-miR-BART17-3p, EBV-miR-BART11-3p, or EBV-miR-BART11-5p inhibitors. U6 was used as an internal control. n = 3 biologically independent samples.

Data are presented as mean ± s.d, p values are calculated by unpaired two-sided t-test in a-d, f, h. Source data are provided as a Source Data file.
Supplementary Fig. 2

(a)

(b)

HONE1  HONE1-EBV  AGS  AGS-EBV  C666-1

IFN-γ  NC  BART11  NC  BART11  In  NC  BART11  In  NC  BART11  In

PD-L1

GAPDH

45kDa

38kDa
Supplementary Fig. 2 EBV further enhanced the effect of IFN-γ in upregulating PD-L1 expression.

a qRT-PCR and western blotting were performed to quantify PD-L1 expression after IFN-γ stimulation, respectively, in EBV-negative immortalized NPE cell line NP69 and EBV-positive NPC cell line C666-1, NPC cells HONE1 and HONE1-EBV stably transfected with EBV (Akata-derived), GC cells AGS and AGS-EBV stably transfected with EBV (Akata-derived), NPC cells HNE2, CNE2 and HNE2, CNE2 infected with EBV derived from Akata or B95-8. GAPDH was used as an internal control. n = 3 biologically independent samples.

b qRT-PCR and western blotting were used to detect PD-L1 expression after IFN-γ stimulation in HONE1 and AGS cells, respectively, transfected with EBV-miR-BART11 or EBV-miR-BART17-3p mimics, and EBV-positive HONE1-EBV, AGS-EBV, C666-1, and SNU-719 transfected with EBV-miR-BART11 or EBV-miR-BART17-3p inhibitors. GAPDH was used as an internal control. n = 3 biologically independent samples.

Data are presented as mean ± s.d, p values are calculated by unpaired two-sided t-test in a, b. Source data are provided as a Source Data file.
Supplementary Fig. 3  Bioinformatics strategies for screening the downstream genes targeted by EBV-miR-BART17-3p.

a  A total of 26 potential targets of EBV-miR-BART17-3p were predicted by miRNA databases such as miRanda and RNAhybrid.

b  EBV-miR-BART17-3p expression was high in 156 NPCs compared to 9 NPEs of GSE32960 and in 62 NPCs compared to 6 NPEs of GSE36682.

c  Screening of 511 significantly downregulated genes in NPCs in GSE12452 and GSE64634.

d  The heatmap of 511 genes that were simultaneously downregulated in GSE12452 and GSE64634.

e  PBRM1 and STK40 were predicted as EBV-miR-BART17-3p’s targets by miRanda and RNAhybrid and were also included in the 511 significantly downregulated genes in NPCs analyzed using the GSE12452 and GSE64634 datasets.

f  The correlation of PBRM1 or STK40 with PD-L1 expression was analyzed based on the data from GSE12452.

Data are presented as mean ± s.d, p values are calculated by unpaired two-sided t-test in b. f are calculated by linear regression. Source data are provided as a Source Data file.
Supplementary Fig. 4 EBV-miBART17-3p directly targets PBRM1.

a Using the digoxigenin-labeled probes for EBV-miR-BART17-3p, RNA FISH was performed to detect the expression of EBV-miR-BART17-3p in HONE1, HONE1-EBV, AGS, and AGS-EBV cells. DAPI-stained nucleus: blue, EBV-miR-BART17-3p: red, merge: DAPI and EBV-miR-BART17-3p signal superimposed image, magnification: 600×, scale = 20 µm.

b qRT-PCR analysis of the PBRM1 mRNA expression in EBV-negative HONE1 and AGS cells transfected with EBV-miR-BART17-3p mimics, EBV-positive HONE1-EBV, AGS-EBV, C666-1, and SNU-719 cells transfected with EBV-miR-BART17-3p inhibitors. GAPDH was used as an internal control. n = 3 biologically independent samples.

c Western blotting was performed to quantify the PBRM1 expression in EBV-negative HONE1 and AGS cells transfected with EBV-miR-BART17-3p mimics, and EBV-positive HONE1-EBV, AGS-EBV, C666-1, and SNU-719 cells transfected with EBV-miR-BART17-3p inhibitors. GAPDH was used as an internal control.

d qRT-PCR analysis of STK40 mRNA in EBV-negative HONE1 and AGS cells transfected with EBV-miR-BART17-3p mimics, and EBV-positive HONE1-EBV, AGS-EBV, C666-1, and SNU-719 cells transfected with EBV-miR-BART17-3p inhibitors. GAPDH was used as an internal control. n = 3 biologically independent samples.

e The binding site of EBV-miR-BART17-3p in the PBRM1 3’UTR region. The wild-type (PBRM1-WT) and mutant (PBRM1-MT) are indicated.

f RNA pull-down was performed after DNA electrophoresis of qRT-PCR products to verify the binding effect of EBV-miR-BART17-3p on the 3'UTR of PBRM1 in HONE1 and AGS cells transfected with the biotin-labeled or unlabeled EBV-miR-BART17-3p probes.

g After transfection of EBV-miR-BART17-3p mimics or negative control into EBV-negative HONE1 and AGS cells, the anti-AGO2 antibody was used for RIP experiments and DNA electrophoresis of qRT-PCR products was performed to identify whether EBV-miR-BART17-3p showed binding to the PBRM1 3’UTR via AGO2.
Data are presented as mean ± s.d, $p$ values are calculated by unpaired two-sided $t$-test in b, d. Source data are provided as a Source Data file.
Supplementary Fig. 5
Supplementary Fig. 5 EBV-miR-BART17-3p upregulates PD-L1 expression by targeting PBRM1.

a qRT-PCR analysis of EBV-miR-BART17-3p regulation of the PD-L1 mRNA via PBRM1 in HONE1, AGS, HONE1-EBV, AGS-EBV, C666-1, and SNU-719 cells transfected with the PBRM1 overexpression vector, siPBRM1, EBV-miR-BART17-3p mimics or inhibitors, or co-transfected with EBV-miR-BART17-3p mimics and the PBRM1 overexpression vector, or EBV-miR-BART17-3p inhibitors and siPBRM1. GAPDH was used as an internal control. n = 3 biologically independent samples.

b Flow cytometric analysis of PD-L1 expression in HONE1 and HONE1-EBV cells transfected with the PBRM1 overexpression vector, siPBRM1, EBV-miR-BART17-3p mimics or inhibitors, or co-transfected with EBV-miR-BART17-3p mimics and the PBRM1 overexpression vector, or EBV-miR-BART17-3p inhibitors and siPBRM1.
inhibitors and siPBRM1. n = 3 biologically independent samples, and the statistical results are shown in Fig. 2f.

Data are presented as mean ± s.d, p values are calculated by unpaired two-sided t-test in a. Source data are provided as a Source Data file.
Supplementary Fig. 6

(a) Normalized BART11 expression in NPE and NPC tissues of patients with gastric cancer. (b) Normalized FOXP1 expression in NPE and NPC tissues of patients with gastric cancer. (c) Immunofluorescence images showing the expression of BART11 and FOXP1 in HONE1, AGS, HONE1-EBV, AGS-EBV, CSE6-1, and SNU-719 cell lines. (d) Bar graphs showing the expression levels of FOXP1 in different cell lines. (e) Western blot analysis of FOXP1 and GAPDH levels in HONE1, AGS, HONE1-EBV, AGS-EBV, CSE6-1, and SNU-719 cell lines transfected with BART11 or control. (f) Bar graphs showing the expression levels of FOXP1 and GAPDH in different cell lines.
Supplementary Fig. 6 EBV-miBART11 directly targets FOXP1.

a EBV-miR-BART11-3p was highly expressed in 156 NPCs compared with the 9 NPE tissue samples from GSE32960, and EBV-miR-BART11-5p expression was high in 62 NPCs compared to 6 NPEs of GSE36682.

b FOXP1 expression and the correlation between FOXP1 and PD-L1 expression was analyzed in 31 NPCs and 10 NPEs from GSE12452.

c Using the digoxigenin-labeled probe for EBV-miR-BART11-3p and EBV-miR-BART11-5p, RNA FISH was performed to detect the expression of EBV-miR-BART11-3p and EBV-miR-BART11-5p in HONE1, HONE1-EBV, AGS, and AGS-EBV cells. DAPI-stained nucleus: blue, EBV-miR-BART11-3p or EBV-miR-BART11-5p: red, merge: DAPI and EBV-miR-BART11-3p or EBV-miR-BART11-5p signal superimposed image, magnification: 600×, scale = 20 µm.

d qRT-PCR analysis of FOXP1 mRNA in EBV-negative HONE1 and AGS cells transfected with EBV-miR-BART11 mimics, and EBV-positive HONE1-EBV, AGS-EBV, C666-1, and SNU-719 cells transfected with EBV-miR-BART11 inhibitors. GAPDH was used as an internal control. n = 3 biologically independent samples.

e Western blotting quantification of the FOXP1 protein in EBV-negative HONE1 and AGS cells transfected with EBV-miR-BART11 mimics, and EBV-positive HONE1-EBV, AGS-EBV, C666-1, and SNU-719 cells transfected with EBV-miR-BART11 inhibitors. GAPDH was used as an internal control.

f The luciferase reporter activity was measured in HONE1, AGS, HONE-EBV, AGS-EBV, C666-1, and SNU-719 cells were co-transfected with the FOXP1-WT vector or the FOXP1-MT vectors and EBV-miR-BART11-3p, EBV-miR-BART11-5p mimics or inhibitors. n = 3 biologically independent samples.

Data are presented as mean ± s.d, p values are calculated by unpaired two-sided t-test in a, b(left), d, f. b(right) are calculated by linear regression. Source data are provided as a Source Data file.
Supplementary Fig. 7 EBV-miR-BART11 upregulates PD-L1 expression by targeting FOXP1.

a RNA pull-down and subsequent DNA electrophoresis of qRT-PCR products to identify the binding effect of EBV-miR-BART11-3p and EBV-miR-BART11-5p on the 3′-UTR of FOXP1 in HONE1 and AGS cells transfected with the biotin-labeled or unlabeled EBV-miR-BART11-3p and EBV-miR-BART11-5p probes.

b After transfecting EBV-miR-BART11-3p, or EBV-miR-BART11-5p mimics or negative control into EBV-negative HONE1 and AGS cells, the anti-AGO2 antibody was used for the RIP experiment and DNA electrophoresis of qRT-PCR products was performed to analyze whether EBV-miR-BART11-3p and EBV-miR-BART11-5p bind the FOXP1 3′-UTR via AGO2.

c qRT-PCR analysis of EBV-miR-BART11 regulation of PD-L1 mRNA via FOXP1 in HONE1, AGS, HONE1-EBV, AGS-EBV, C666-1, and SNU-719 cells transfected with the FOXP1 overexpression vector, siFOXP1 EBV-miR-BART11 mimics or inhibitors, or co-transfected with EBV-miR-BART11 mimics
and the FOXP1 overexpression vector, or EBV-miR-BART11 inhibitors and siFOXP1. GAPDH was used as an internal control. n = 3 biologically independent samples.

d Flow cytometric analysis of PD-L1 expression in HONE1 and HONE1-EBV cells transfected with the FOXP1 overexpression vector, siFOXP1, EBV-miR-BART11 mimics or inhibitors, or co-transfected with EBV-miR-BART11 mimics and the FOXP1 overexpression vector, or EBV-miR-BART11 inhibitors and siFOXP1. n = 3 biologically independent samples, and the statistical results are shown in Fig. 3e.

Data are presented as mean ± s.d, p values are calculated by unpaired two-sided t-test in c. Source data are provided as a Source Data file.
Supplementary Fig. 8

(a) 

(b)
Supplementary Fig. 8 Expression and correlation analysis of EBV-miR-BART17-3p, PBRM1, EBV-miR-BART11-3p, EBV-miR-BART11-5p, and FOXP1 in NPC samples.

a The statistical analysis of EBV-miR-BART17-3p, EBV-miR-BART11-3p, EBV-miR-BART11-5p, FOXP1, and PBRM1 expression in 52 NPCs (13 EBV-negative and 39 EBV-positive) and 36 NPE samples and the correlation with EBV.
The correlation analysis between EBV-miR-BART17-3p, EBV-miR-BART11-3p, EBV-miR-BART11-5p, PBRM1, FOXP1, and PD-L1 was performed based on the ISH or IHC data in NPC.

The statistical analysis of EBV-miR-BART17-3p, EBV-miR-BART11-3p, EBV-miR-BART11-5p, FOXP1, and PBRM1 expression in 40 GCs (15 EBV-negative and 25 EBV-positive) and 20 normal gastric samples and the correlation with EBV.

The correlation analysis between EBV-miR-BART17-3p, EBV-miR-BART11-3p, EBV-miR-BART11-5p, PBRM1, FOXP1, and PD-L1 was performed based on the ISH or IHC data in gastric adenocarcinoma.

Flow cytometric analysis to detect the percentage of CD3$^+$ T cells in whole blood cells in 32 NPCs (8 EBV-negative and 24 EBV-positive) and samples from 36 normal people.

a, c are calculated by $F$-test. b, d are calculated by linear regression. e are calculated by unpaired two-sided $t$-test. Source data are provided as a Source Data file.
Supplementary Fig. 9 FOXP1 and PBRM1 do not inhibit PD-L1 transcription by binding to its promoter.

a A series of luciferase reporter gene vectors were constructed based on the PD-L1 transcription regulatory sequences (TRS) (-1,940 to +87 bp). The TRS activity was analyzed in HONE1 cells co-transfected with the corresponding TRS vector, the FOXP1 or PBRM1 overexpression vector, or siRNAs. n = 3 biologically independent samples.

b Prediction and primer design of the enhancer regions of PD-L1 (spanning -20,503 to +49,497 bp). The H3K27ac and H3K4me1 modifications in the ENCODE database and EBV negative NPC cell line
HNE1, EBV positive cell line C666-1 were shown using the UCSC browser. Based on the transcription start site (TSS), the 3C-anchor primers (red arrow) were designed according to the BamH I restriction site closest to the PD-L1 promoter (red area).

Data are presented as mean ± s.d, and calculated by unpaired two-sided t-test. Source data are provided as a Source Data file.
Supplementary Fig. 10

a

1C sample interaction: PD-L1 promoter + enhancer-B

b

FOXPI binding motif

| FOXPI binding site | Predicted sequence | Relative score | Mutated sequence |
|--------------------|-------------------|----------------|-----------------|
| B (1,703 – 1,803 bp) | AAAACAA AACA AAAAA | 0.8680820836536 | CCCCACC CCCCACCC |
| E (43,285 – 43,296 bp) | AGAAAAC ATGA | 0.807774036365 | CATCCCCACGTC |

c
d
Supplementary Fig. 10 EBV-miR-BART11 and EBV-miR-BART17-3p regulate the PD-L1 enhancer B and E regions by inhibiting FOXP1 and PBRM1, respectively.

a Sequencing verification of samples from the 3C experiments. Remote interactions were identified between the PD-L1 enhancer regions B, E, and the PD-L1 promoter regions. The blue area is the junction of the BamH I restriction site, the red area is the PD-L1 promoter area, and the green area is the PD-L1 enhancer area.

b The FOXP1 binding site was predicted in the enhancer B and E of PD-L1 by JASPAR. The table lists the location of binding sites, sequences, relative scores, and mutation sequences.

c ChIP experiments using the antibodies against FOXP1 or PBRM1 were performed to identify whether knockdown of FOXP1 or PBRM1 affected the binding of FOXP1 and PBRM1 in the PD-L1 enhancers A, B, C, D, and E in HONE1 cells. n = 3 biologically independent samples.

d ChIP experiments using the antibodies against FOXP1, PBRM1, H3K27ac, and H3K4me1 were performed to identify whether knockdown of FOXP1 or PBRM1 affected the binding of FOXP1 and PBRM1, and the H3K27ac and H3K4me1 modification in the PD-L1 enhancers B and E in AGS, C666-1, and SNU-719 cells transfected with FOXP1 or PBRM1 siRNA. n = 3 biologically independent samples.

e The EMSA assay was used to detect whether PBRM1 binds to the PD-L1 enhancers B and E in HONE1. Lane 1: only biotin-labeled probes were added; lane 2: nuclear protein and biotin-labeled region probes were added; lane 3: nuclear protein was added, biotin-labeled region probes and competitively bound unlabeled region probes were added in a ratio of 1:2; lane 4: nuclear protein was added and biotin-labeled probes and mutant unlabeled probes in a ratio of 1:2 were added; lane 5: nuclear protein, biotin-labeled probes and anti-PBRM1 antibodies were added simultaneously; lane 6: biotin-labeled probes and anti-PBRM1 antibody were added; lane 7: nuclear protein, nonspecific probe, and anti- PBRM1 antibody were added simultaneously.

f The 3C experiments were performed in HONE1, C666-1, and SNU-719 cells transfected with EBV-miR-BART11 or EBV-miR-BART17-3p mimics or inhibitors to detect the interaction frequency between the enhancers and the PD-L1 promoter. The relative interaction frequency was normalized to the closest BamH I digestion site. n = 3 biologically independent samples.
g Luciferase reporter gene assays showed that EBV-miR-BART11 or EBV-miR-BART17-3p affects the reporter activities of the *PD-L1* enhancer B and E regions *via* FOXP1 or PBRM1 in C666-1 and SNU-719 cells co-transfected with the B and E wild-types or the corresponding mutant vectors, and EBV-miR-BART11 or EBV-miR-BART17-3p inhibitors. n = 3 biologically independent samples.

h The modification of H3K27ac and H3K4me1 in C666-1 and SNU-719 cells was analyzed by ChIP experiments after transfection of EBV-miR-BART11 or EBV-miR-BART17-3p mimics or inhibitors. n = 3 biologically independent samples.

Data are presented as mean ± s.d, and calculated by unpaired two-sided *t*-test in c, d, f, h. Source data are provided as a Source Data file.
Supplementary Fig. 11

(a) M Input IgG FOXP1

(b) GSE12452

\[ p = 0.0156 \]
\[ r = -0.3752 \]
\[ n = 41 \]

Expression of DPF2

Expression of PBRM1

(c) HONE1 AG5 C666-1 SNU-719

GSE12452

\[ p = 0.0355 \]
\[ r = 0.3294 \]
\[ n = 41 \]

Expression of DPF2

Expression of PD-L1

(d) HONE1 AG5 C666-1 SNU-719

DPF2

1.0 0.51 1.0 0.53 1.0 0.48 1.0 0.37

GAPDH

1.0 0.51 1.0 0.53 1.0 0.48 1.0 0.37
Supplementary Fig. 11 FOXP1 interacts with PBRM1 of the PBAF complex and inhibits PD-L1 expression.

a The immunoprecipitate obtained using anti-FOXP1 antibody was resolved by SDS-PAGE and stained with Coomassie brilliant blue. The molecular weight is indicated on the left side of the figure.

b The correlation between DPF2 and PD-L1 expression and between DPF2 and PBRM1 expression was analyzed using the data from GSE12452.
c qRT-PCR was used to detect the mRNA for _DPF2_ in HONE1, AGS, C666-1, and SNU-719 cells after knockdown of _DPF2_. _GAPDH_ was used as an internal control. n = 3 biologically independent samples.

d Western blotting was used to detect the expression for _DPF2_ in HONE1, AGS, C666-1, and SNU-719 cells after knockdown of _DPF2_. _GAPDH_ was used as an internal.

e qRT-PCR was used to detect the mRNA for _PD-L1, FOXP1, PBRM1_, and _DPF2_ in HONE1, AGS, C666-1, and SNU-719 cells after knockdown of _FOXP1, PBRM1_, or _DPF2_. _GAPDH_ was used as an internal control. n = 3 biologically independent samples.

f ChIP experiments using antibodies against DPF2, H3K27ac, H3K4me1, FOXP1, and PBRM1 was performed to examine whether the knockdown of _DPF2_ affects the binding of DPF2, H3K27ac, H3K4me1, FOXP1, and PBRM1 in the _PD-L1_ enhancer regions B and E, and the H3K27ac and H3K4me1 modification in AGS, C666-1, and SNU-719 cells. n = 3 biologically independent samples. Data are presented as mean ± s.d, and calculated by unpaired two-sided _t_-test in c, e, f. b are calculated by _linear regression_. Source data are provided as a Source Data file.
Supplementary Fig. 12 EBV-miR-BART11 and EBV-miR-BART17-3p induce T-cell apoptosis by promoting PD-L1 expression in NPC and gastric carcinoma cells.

a A high-content screening system was used to track the activity status of primary T cells. The primary T cells were co-cultured with HONE1 or AGS cells after overexpression of EBV-miR-BART11 and EBV-miR-BART17-3p in the presence of PD-L1 blocking antibody; living tumor cells: red (CM-DiI), living T cells: green (CMFDA), living and apoptotic cells: bright field. The picture on the left shows the superimposed signals for red fluorescence, green fluorescence, and bright field. The statistical result is shown on the right. Magnification: 400×, scale bars = 20 μm.

b A high-content screening system was used to track the activity status of tumor cells. EBV-negative HONE1 or AGS cells were transfected with EBV-miR-BART11 and EBV-miR-BART17-3p mimics simultaneously and were subsequently co-cultured with primary T cells. Living tumor cells: blue (Hoechst), living and apoptotic cells: bright field. The picture on the left shows the superimposed signals for blue fluorescence and bright field. The statistical graph is shown on the right. Magnification: 400×, scale bars = 20 μm.

a, b are calculated by unpaired two-sided t-test. Source data are provided as a Source Data file.
Supplementary Fig. 13 Original flow cytometry results for Fig. 7b. Primary T cells were co-cultured with HONE1 or AGS cells after overexpression of EBV-miR-BART11 and EBV-miR-BART17-3p in the presence of PD-L1 blocking antibody. n = 3 biologically independent samples.

**Supplementary Fig. 14**

Supplementary Fig. 14 Original flow cytometry results for Fig. 7b. Primary T cells were co-cultured with HONE1-EBV or AGS-EBV after inhibition of EBV-miR-BART11 and EBV-miR-BART17-3p. n = 3 biologically independent samples.
Supplementary Fig. 15 EBV-miR-BART11 and EBV-miR-BART17-3p have no effect on the degree of T-cell apoptosis.

a Primary T cells were transfected with EBV-miR-BART11 and EBV-miR-BART17-3p mimics. qRT-PCR was used to confirm the transfection efficiency. n = 3 biologically independent samples.

b Flow cytometric analysis of T-cell apoptosis in T cells transfected with EBV-miR-BART11 and EBV-miR-BART17-3p mimics. Each group was analyzed using three independent replicates.

a, b are calculated by unpaired two-sided t-test. Source data are provided as a Source Data file.
Supplementary Fig. 16 Original flow cytometry results for Fig. 7e for detecting IFN-γ secretion. Primary T cells were co-cultured with HONE1 or AGS cells after overexpression of EBV-miR-BART11 and EBV-miR-BART17-3p, or co-cultured with HONE1-EBV or AGS-EBV cells after inhibition of EBV-miR-BART11 and EBV-miR-BART17-3p. n = 3 biologically independent samples.
Supplementary Fig. 17

![Bar chart showing apoptosis of CD3+ T cells with HONE1 and AGS control and treatment groups.](image)

The bar chart indicates a significant difference in apoptosis between the control and treatment groups for both HONE1 and AGS. The p-values are provided for each comparison, with values less than 0.001 indicating statistical significance.

![Flow cytometry plots for HONE1 and AGS control and treatment groups.](image)

The flow cytometry plots show the distribution of cells stained with Annexin-FITC and PI, with the percentage of cells in each quadrant indicated. The plots for HONE1 and AGS control and treatment groups are compared to assess the effect of the treatment on cell apoptosis.
Supplementary Fig. 17 Flow cytometric analysis of T-cell apoptosis in HONE1 and AGS cells treated with IFN-γ (10 ng/mL) and EBV-miR-BART11 and EBV-miR-BART17-3p mimics. Each group was analyzed using three independent replicates. Data are presented as mean ± s.d, and, $p$ values are calculated by unpaired two-sided $t$-test in a-f. Source data are provided as a Source Data file.
Supplementary Fig. 18

a

b

C

Jurkat co-cultured with HONE1

Jurkat co-cultured with HONE1-EBV

Jurkat co-cultured with HONE1

Jurkat co-cultured with HONE1-EBV

IL-2

IFN-γ

GZMB

IL-2

IFN-γ

GZMB

The concentration [pg/ml]

The concentration [pg/ml]
Supplementary Fig. 18 EBV-miR-BART17-3p enhances tumor cells to induce Jurkat T-cell apoptosis by inhibiting PBRM1.

a A confocal fluorescence microscope was used to show the activity status of activated Jurkat T cells. The cells were co-cultured with HONE1 cells transfected with the PBRM1 overexpression vector, siPBRM1 or EBV-miR-BART17-3p mimics, or co-transfected with EBV-miR-BART17-3p mimics and the PBRM1 overexpression vector. Living tumor cells: red (CM-DiI), living T cells: green (CMFDA), living and apoptotic cells: bright field. The picture on the left shows the superimposed signals for red fluorescence, green fluorescence, and bright field. The statistical graph is shown on the right. Magnification: 600×, scale bars = 20 µm. n = 3 biologically independent samples.

b qRT-PCR analysis for the expression of IL-2, IFN-γ, and GZMB in Jurkat cells. The cells were co-cultured with HONE1 or HONE1-EBV cells after the overexpression or inhibition of PBRM1 and EBV-miR-BART17-3p. GAPDH was used as an internal control. n = 3 biologically independent samples.

c ELISA analysis of the secretion of IL-2, IFN-γ, and GZMB proteins of Jurkat cells. The cells were co-cultured with HONE1 or HONE1-EBV cells after the overexpression or inhibition of PBRM1 and EBV-miR-BART17-3p. n = 3 biologically independent samples.

Data are presented as mean ± s.d, and, p values are calculated by unpaired two-sided t-test in a-c. Source data are provided as a Source Data file.
Supplementary Fig. 19

[Image of dot plots showing cell distribution across different conditions and treatments, with axes labeled for PI and Annexin-FITC, and numerical data points alongside each plot.]
Supplementary Fig. 19 Original flow cytometry results of Fig. 7f. EBV-miR-BART17-3p can induce Jurkat cells apoptosis through inhibiting PBRM1, each group was analyzed using three independent replicates.
Supplementary Fig. 20 EBV-miR-BART11 enhances tumor cells to induce Jurkat T-cell apoptosis by inhibiting FOXP1.

**a** Confocal fluorescence microscopy was used to show the activity status of activated Jurkat T cells. The cells were co-cultured with HONE1 or HONE1-EBV cells after the overexpression or inhibition of FOXP1 and EBV-miR-BART11. Living tumor cells: red (CM-DiI), living T cells: green (CMFDA), living and apoptotic cells: bright field. Left picture: superimposed signals for red fluorescence, green fluorescence, and bright field. The statistical graph is shown on the right. Magnification: 600×, scale bars = 20 µm. n = 3 biologically independent samples.

**b** qRT-PCR analysis for the mRNA levels of IL-2, IFN-γ, and GZMB in Jurkat cells. The cells were co-cultured with HONE1 or HONE1-EBV cells after the overexpression or inhibition of FOXP1 and EBV-miR-BART11. GAPDH was used as an internal control. n = 3 biologically independent samples.

**c** ELISA analysis of the secretion of IL-2, IFN-γ, and GZMB proteins. Jurkat T cells were co-cultured with HONE1 or HONE1-EBV cells after the overexpression or inhibition of FOXP1 and EBV-miR-BART11. n = 3 biologically independent samples.

Data are presented as mean ± s.d, and p values are calculated by unpaired two-sided t-test in a-c. Source data are provided as a Source Data file.
Supplementary Fig. 21
Supplementary Fig. 21 Original flow cytometry results for Fig. 7f. EBV-miR-BART11 can induce Jurkat cells apoptosis by inhibiting FOXP1. Each group was analyzed using three independent replicates.

**Supplementary Fig. 22**

![Diagram](image_url)

**a**
|       | AGS           | AGS-EBV       |
|-------|---------------|---------------|
| NC    | NC            | NC            |
| NC-T cells | NC-T cells   | NC-T cells   |
| BART11+ | BART11+      | BART11+      |
| BART17+5p | BART17+5p    | BART17+5p    |
| T-cells | T-cells       | T-cells       |
| PD-1   | PD-1          | PD-1          |
| PD-1L  | PD-1L         | PD-1L         |
| C10H8  | C10H8         | C10H8         |
| claudin-1 | claudin-1   | claudin-1    |
| PAP    | PAP           | PAP           |
| H&E    | H&E           | H&E           |
| BART11+ | BART11+      | BART11+      |
| BART17+5p | BART17+5p    | BART17+5p    |
| T-cells | T-cells       | T-cells       |
| 4'6-diamidino-2-phenylindole (DAPI) | 4'6-diamidino-2-phenylindole (DAPI) | 4'6-diamidino-2-phenylindole (DAPI) |

20 μm
Supplementary Fig. 22 The effects of EBV-miR-BART11 and EBV-miR-BART17-3p on tumor immune escape in xenograft mice models.

a A schematic diagram of the CDX mice models after injection of activated T cells. A density of $5 \times 10^6$ HONE1 or AGS cells were transfected with EBV-miR-BART11 and EBV-miR-BART17-3p mimics or negative control, HONE1-EBV or AGS-EBV cells were transfected with EBV-miR-BART11 and EBV-miR-BART17-3p inhibitors or negative control. Transfected cells were injected subcutaneously into the root of the right thigh of the mice. DCs and T cells were prepared and expanded simultaneously. DCs were first co-cultured with tumor cell lysate, and then co-cultured with T cells to present tumor cells specific tumor antigens to T cells, which enables them to produce tumor cells specific T cells. After 7 days, palpable tumors were formed, and $5 \times 10^7$ DiR ± T cells were infused into CDX mice through the tail vein. For the DiR-injected mice, the small animal live imaging system was used to observe the accumulation of DiR+T cells at the tumor-forming site. For one set of non-DiR-injected mice, activated T cells were injected into each tumor for another 7 days. Next, the peripheral blood of mice was extracted for flow cytometry, qRT-PCR, and ELISA. In another set, activated T cells were injected into each tumor for another 25 days and the tumor weight and volume were measured each day. The PD-L1 inhibitor (5 mg/kg, Atezolizumab) was injected to block the PD-L1/PD-1 immune checkpoint in mice and identify whether EBV miRNAs can induce tumor growth under PD-L1 inhibition after injection of HONE1 or AGS cells transfected with EBV-miR-BART11 and EBV-miR-BART17-3p mimics. Figure was created by PowerPoint (Microsoft Office 2016) and the materials of this figure were provided by the Servier Medical Art (https://smart.servier.com/) under the CC BY 3.0 license.

b The original flow cytometry results show the degree of T-cell apoptosis in each group after the injection of activated T cells for 14 days. n = 5 per group.

c The body weight of the mice was measured in each group after 25 days of activated T cells administration. n = 8 per group.

d The tumor weights for each group were measured after 25 days of activated T cells injection. n = 8 per group.

e Tumor volumes for each group after 25 days of injection with activated T cells. n = 8 per group.
Expression of EBV-miR-BART17-3p, EBV-miR-BART11-3p, and EBV-miR-BART11-5p analyzed ascertained via ISH and the expression of PBRM1, FOXP1, PD-L1, CD8, cleaved-Caspase 3, and cleaved-PARP proteins determined via IHC were examined in the CDX nude mice sections. Magnification: 400×; scale bars = 20 µm.

Statistical results for the expression of EBV-miR-BART17-3p, EBV-miR-BART11-3p, and EBV-miR-BART11-5p by ISH, and that of PBRM1, FOXP1, PD-L1, CD8, cleaved Caspase-3, and cleaved-PARP in the tissue sections were analyzed by IHC. Data are presented as mean ± s.d, and $p$ values are calculated by unpaired two-sided $t$-test in c-e, g. Source data are provided as a Source Data file.
Supplementary Fig. 23 The gating strategy for the detection of PD-L1 expression in tumor cells and the analysis of CD8+ T cells.

a FACS gating strategy shown with a representative example for the detection of PD-L1 expression in HONE1 or HONE1-EBV cells after transfected.

b Depicted is the gating path in Co-cultured cells or mouse peripheral blood cells. Depending on the respective experimental part, FITC-PI assay of cell apoptosis was analyzed in the human CD8+ T cells and IFN-γ as a marker for T cell killing function was only assessed in Co-cultured CD8+ T cells with the addition of Brefeldin A.
| Patient No. | Gender (M=Male, F=Female) | Age at Diagnosis | WHO histological diagnosis | T stage | N stage | M stage | Clinic stages |
|------------|--------------------------|-----------------|---------------------------|---------|---------|---------|--------------|
| Pat 040    | M:26, F:14               | less than 40 years old | 4                           | 1       | 2       | 0       | 1            |
| Pat 041    | M:36, F:16               | 40 years or older   | 5                           | 1       | 1       | 1       | 1            |
| Pat 042    | M:36, F:16               | less than 40 years old | 4                           | 1       | 2       | 0       | 1            |
| Pat 043    | M:36, F:16               | 40 years or older   | 3                           | 1       | 2       | 1       | 1            |
| Pat 044    | M:36, F:16               | less than 40 years old | 4                           | 1       | 2       | 0       | 1            |
| Pat 045    | M:36, F:16               | 40 years or older   | 4                           | 1       | 2       | 0       | 1            |
| Pat 046    | M:36, F:16               | less than 40 years old | 4                           | 1       | 2       | 0       | 1            |
| Pat 047    | M:36, F:16               | 40 years or older   | 3                           | 1       | 2       | 1       | 1            |
| Pat 048    | M:36, F:16               | less than 40 years old | 4                           | 1       | 2       | 0       | 1            |
| Pat 049    | M:36, F:16               | 40 years or older   | 4                           | 1       | 2       | 0       | 1            |
| Pat 050    | M:36, F:16               | less than 40 years old | 4                           | 1       | 2       | 0       | 1            |
| Pat 051    | M:36, F:16               | 40 years or older   | 3                           | 1       | 2       | 1       | 1            |
| Pat 052    | M:36, F:16               | less than 40 years old | 4                           | 1       | 2       | 0       | 1            |
| Pat 053    | M:36, F:16               | 40 years or older   | 4                           | 1       | 2       | 0       | 1            |
| Pat 054    | M:36, F:16               | less than 40 years old | 4                           | 1       | 2       | 0       | 1            |
| Pat 055    | M:36, F:16               | 40 years or older   | 3                           | 1       | 2       | 1       | 1            |
| Pat 056    | M:36, F:16               | less than 40 years old | 4                           | 1       | 2       | 0       | 1            |
| Pat 057    | M:36, F:16               | 40 years or older   | 4                           | 1       | 2       | 0       | 1            |
| Pat 058    | M:36, F:16               | less than 40 years old | 4                           | 1       | 2       | 0       | 1            |
| Pat 059    | M:36, F:16               | 40 years or older   | 3                           | 1       | 2       | 1       | 1            |
| Pat 060    | M:36, F:16               | less than 40 years old | 4                           | 1       | 2       | 0       | 1            |
| Pat 061    | M:36, F:16               | 40 years or older   | 4                           | 1       | 2       | 0       | 1            |

**WHO histological diagnosis**
- **WHO III = Nonkeratinizing undifferentiated carcinoma**
- **WHO II = Non keratinized poorly differentiated squamous cell carcinoma**

**Supplementary Table 1. Clinicopathological data on 52 paraffin-embedded nasopharyngeal carcinoma (NPC) and 36 nasopharyngeal adjacent epithelium (NPE) biopsies and the expression of PD-L1, FOXP1, PBRM1, and BART17-3p in these samples measured by immunohistochemistry (IHC) and in situ hybridization (ISH).**
Supplementary Table 2. Clinicopathological data on 40 paraffin-embedded gastric adenocarcinoma (GC) and 20 normal gastric mucosa biopsies and the expression of PD-L1, FOXP1, PBRM1, EBER, BART11-3p, BART11-5p, and BART17-3p in these samples measured by immunohistochemistry (IHC) and in situ hybridization (ISH).

| Patient No. | Gender (M:Male/F:Female) | Age at Diagnosis (less than 40 years old:1, 40 years or older:19) | WHO histological diagnosis | T stage | N stage | Stage 2 stage | Stages 3 | HIC score of PD-L1 | ISH score of FOXP1 | ISH score of PBRM1 | ISH score of EBER1 | ISH score of BART11-3p | ISH score of BART11-5p | ISH score of BART17-3p |
|-------------|--------------------------|-----------------------------------------------------------------|---------------------------|---------|---------|------------|--------|-------------------|-------------------|-----------------|-----------------|-----------------|-----------------|-----------------|-----------------|
| Pat 058     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 056     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 055     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 054     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 052     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 047     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 045     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 042     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 041     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 040     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 036     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 035     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 034     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 033     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 032     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 031     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 030     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 027     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 026     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 025     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 024     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 023     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 022     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 021     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |
| Pat 020     | M:31, F:9                | 6 less than 40 years old, 34 years or older:16                 | normal gastric mucosa tissues | NA      | NA      | NA         | 0      | 0                 | 0                 | 0               | 0               | 0               | 0               | 0               |

*Notes: T stage: I, II, III, IV; N stage: NA; Stage: normal gastric mucosa tissues, gastric adenocarcinoma.*
**Supplementary Table 3. List of qRT-PCR primers, siRNAs and probes sequences for ISH and EMSA.**

| siRNA     | sense                  | antisense               |
|-----------|------------------------|-------------------------|
| siNC      | 5'-UUCCUUGCGACUGUGUCCGAGCATT-3' | 5'-AGGUGACACGUUGUGAGAATT-3' |
| siFOXp1-1 | 5'-CCCAAGGCUUCCUGCUAUA-3'   | 5'-UAUAUCUGCUAGCUUGUGG-3'   |
| siFOXp1-2 | 5'-GAUGUGGAGUUGCUUULU-3'    | 5'-AAACAGUCAACUAAAGC-3'    |
| siPBRM1-1 | 5'-AGUUGAGGAGAGUGGCAUA-3'   | 5'-UUAAUCGCGACACUACCUACU-3' |
| siPBRM1-2 | 5'-GCAUCUGUCUCAGCUAUUA-3'   | 5'-AUAGUCGAGACAGAGCG-3'   |
| siDPF2-1  | 5'-GGUCACAAUUAAGAUGCU-3'    | 5'-AGCAUGUAUGUGUCCGAC-3'    |
| siDPF2-2  | 5'-GUCUCUCAAUUGGCUAU-3'     | 5'-AAUGCAUCUAAAUGGAGAGC-3' |

**Primers**

| Primers     | Forward                          | Reverse                          |
|-------------|----------------------------------|----------------------------------|
| PD-L1-F      | 5'-GTCATTGCTGAGGAGGAAG-3'        | 5'-CTCCCTCTGAGGAGGAGAAG-3'       |
| PD-L1-R      | 5'-GTCGGAGGGAAGGAGAAG-3'         | 5'-CCCGAGGAGGAGAAGGAGAAG-3'      |
| EBER1-F      | 5'-AGGACCTCACTGTCGCCCAA-3'       | 5'-AAAGAGGGAAGGAGAAGGAGAAG-3'    |
| EBER1-R      | 5'-AAAGAGGGAAGGAGAAGGAGAAG-3'    | 5'-CCCGAGGAGGAGAAGGAGAAG-3'      |
| FOXp1-F      | 5'-CCCGAGGAGGAGAAGGAGAAG-3'      | 5'-CCCGAGGAGGAGAAGGAGAAG-3'      |
| FOXp1-R      | 5'-CCCGAGGAGGAGAAGGAGAAG-3'      | 5'-CCCGAGGAGGAGAAGGAGAAG-3'      |
| PBRM1-F      | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| PBRM1-R      | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| STK40-F      | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| STK40-R      | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| DPF2-F       | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| DPF2-R       | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| IFN-γ-F      | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| IFN-γ-R      | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| IL-2-F       | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| IL-2-R       | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| GZMB-F       | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| GZMB-R       | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| U6-F         | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| U6-R         | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| GAPDH-F      | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| GAPDH-R      | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |

**Primers for RIP and RNA pull down**

| Primers     | Forward                          | Reverse                          |
|-------------|----------------------------------|----------------------------------|
| FOXp1 3'UTR(BART11-3p)-F | 5'-GACAGTGGAGGGAAG-3'        | 5'-GACAGTGGAGGGAAG-3'        |
| FOXp1 3'UTR(BART11-3p)-R | 5'-GACAGTGGAGGGAAG-3'        | 5'-GACAGTGGAGGGAAG-3'        |
| FOXp1 3'UTR(BART11-5p)-F | 5'-GACAGTGGAGGGAAG-3'        | 5'-GACAGTGGAGGGAAG-3'        |
| FOXp1 3'UTR(BART11-5p)-R | 5'-GACAGTGGAGGGAAG-3'        | 5'-GACAGTGGAGGGAAG-3'        |
| PBRM1 3'UTR(BART17-3p)-F | 5'-GACAGTGGAGGGAAG-3'        | 5'-GACAGTGGAGGGAAG-3'        |
| PBRM1 3'UTR(BART17-3p)-R | 5'-GACAGTGGAGGGAAG-3'        | 5'-GACAGTGGAGGGAAG-3'        |

**Primers for 3C**

| Primers     | Forward                          | Reverse                          |
|-------------|----------------------------------|----------------------------------|
| 3C-Anchor,A,B,C,D,E,F-F | 5'-GACAGTGGAGGGAAG-3'        | 5'-GACAGTGGAGGGAAG-3'        |
| 3C-Anchor-R  | 5'-GACAGTGGAGGGAAG-3'        | 5'-GACAGTGGAGGGAAG-3'        |
| 3C-A-R       | 5'-GACAGTGGAGGGAAG-3'        | 5'-GACAGTGGAGGGAAG-3'        |
| 3C-B-R       | 5'-GACAGTGGAGGGAAG-3'        | 5'-GACAGTGGAGGGAAG-3'        |
| 3C-C-R       | 5'-GACAGTGGAGGGAAG-3'        | 5'-GACAGTGGAGGGAAG-3'        |
| 3C-D-R       | 5'-GACAGTGGAGGGAAG-3'        | 5'-GACAGTGGAGGGAAG-3'        |
| 3C-F-R       | 5'-GACAGTGGAGGGAAG-3'        | 5'-GACAGTGGAGGGAAG-3'        |

**Primers for ChIP**

| Primers     | Forward                          | Reverse                          |
|-------------|----------------------------------|----------------------------------|
| ChIP-A-F    | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| ChIP-A-R    | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| ChIP-B-F    | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| ChIP-B-R    | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| ChIP-C-F    | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| ChIP-C-R    | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| ChIP-D-F    | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| ChIP-D-R    | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| ChIP-E-F    | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| ChIP-E-R    | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |

**Primers for the luciferase activities assay of PBRM1 3'UTR**

| Primers     | Forward                          | Reverse                          |
|-------------|----------------------------------|----------------------------------|
| PBRM1 WT-F  | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| PBRM1 MT-F  | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| PBRM1 MT-R  | 5'-GTCGTGTTAATGGAGGAG-3'         | 5'-GTCGTGTTAATGGAGGAG-3'         |
| Primers for the luciferase activities assay of PD-L1 enhancer |
|-------------------------------------------------------------|
| PD-L1 TRS1(-313bp+87bp)-Forward  | 5'-GGGGTACCCCCCATTTCAACTACCCAAA-3' |
| PD-L1 TRS1(-313bp+87bp)-Reverse | 5'-CCGCTCGAGCGGACAACGCTCCCTACCTGC-3' |
| PD-L1 TRS2(-1,567bp+87bp)-Forward | 5'-GGGGTACCCCCCATTTCAACTACCCAAA-3' |
| PD-L1 TRS2(-1,567bp+87bp)-Reverse | 5'-CCGCTCGAGCGGACAACGCTCCCTACCTGC-3' |
| PD-L1 TRS3(-1,940bp+87bp)-Forward  | 5'-GGGGTACCCCCCATTTCAACTACCCAAA-3' |
| PD-L1 TRS3(-1,940bp+87bp)-Reverse | 5'-CCGCTCGAGCGGACAACGCTCCCTACCTGC-3' |
| PD-L1 TRS4(-1,940bp-1,567bp)-Forward | 5'-CATGATGAACTAGCAGATCATAAAGGTTCAGATGTGTTGTTGAAATTCTTTTTT-3' |
| PD-L1 TRS4(-1,940bp-1,567bp)-Reverse | 5'-ATTTACAACAAGCCCAACACTCTGACCTTTTATGATCTGCTAGTCCATCATGACTCTTGGAG-3' |
| B-Forward | 5'-CATGATGAACTAGCAGATCATAAAGGTTCAGATGTGTTGTTGAAATTCTTTTTT-3' |
| B-Reverse | 5'-ATTTACAACAAGCCCAACACTCTGACCTTTTATGATCTGCTAGTCCCATCATGACTCTTGGAG-3' |
| B-MT-Forward | 5'-GGTACCCCTCCTGACCTTTTATGATCTGCTAGTCCCATCATGACTCTTGGAG-3' |
| B-MT-Reverse | 5'-TGGGATCCGGGACCAAGCTGACCTTTTATGATCTGCTAGTCCCATCATGACTCTTGGAG-3' |
| E-Forward | 5'-GACCGCCGAGCGCAACTGACCTTTTATGATCTGCTAGTCCCATCATGACTCTTGGAG-3' |
| E-Reverse | 5'-AGACACCGTCCTCACCCGAACCCAGGTGA-3' |
| E-MT-Forward | 5'-GGTACCCCTCCTGACCTTTTATGATCTGCTAGTCCCATCATGACTCTTGGAG-3' |
| E-MT-Reverse | 5'-GACCGCCGAGCGCAACTGACCTTTTATGATCTGCTAGTCCCATCATGACTCTTGGAG-3' |

| The probes for ISH and FISH |
|-----------------------------|
| EBER1 | 5'-AGACACCGTCCTCACCCGAACCCAGGTGA-3' |
| BART11-3p | 5'-GACCGCCGAGCGCAACTGACCTTTTATGATCTGCTAGTCCCATCATGACTCTTGGAG-3' |
| BART11-5p | 5'-GACCGCCGAGCGCAACTGACCTTTTATGATCTGCTAGTCCCATCATGACTCTTGGAG-3' |
| BART17-3p | 5'-GACCGCCGAGCGCAACTGACCTTTTATGATCTGCTAGTCCCATCATGACTCTTGGAG-3' |
| B-MT-Forward | 5'-GGTACCCCTCCTGACCTTTTATGATCTGCTAGTCCCATCATGACTCTTGGAG-3' |
| B-MT-Reverse | 5'-GACCGCCGAGCGCAACTGACCTTTTATGATCTGCTAGTCCCATCATGACTCTTGGAG-3' |
| E-MT-Forward | 5'-GGTACCCCTCCTGACCTTTTATGATCTGCTAGTCCCATCATGACTCTTGGAG-3' |
| E-MT-Reverse | 5'-GACCGCCGAGCGCAACTGACCTTTTATGATCTGCTAGTCCCATCATGACTCTTGGAG-3' |

| The probes for EMSA |
|--------------------|
| B-WT | 5'-GACCGCCGAGCGCAACTGACCTTTTATGATCTGCTAGTCCCATCATGACTCTTGGAG-3' |
| B-MT | 5'-GACCGCCGAGCGCAACTGACCTTTTATGATCTGCTAGTCCCATCATGACTCTTGGAG-3' |
| E-WT | 5'-GACCGCCGAGCGCAACTGACCTTTTATGATCTGCTAGTCCCATCATGACTCTTGGAG-3' |
| E-MT | 5'-GACCGCCGAGCGCAACTGACCTTTTATGATCTGCTAGTCCCATCATGACTCTTGGAG-3' |
| non-specific probe | 5'-GACCGCCGAGCGCAACTGACCTTTTATGATCTGCTAGTCCCATCATGACTCTTGGAG-3' |
| Antibody                                      | Catalog Number | Clone Number | Application               | Dilution/Working concentration | Company                        |
|-----------------------------------------------|----------------|--------------|---------------------------|--------------------------------|--------------------------------|
| PD-L1 (E1L3N®) XP® Rabbit Monoclonal antibody | 13684S         | E1L3N        | Western Blotting          | 1:1000                         | Cell Signaling Technology      |
| PD-L1/CD274 Mouse Monoclonal Antibody         | 66248-1-lg     | 2B11D11      | IF                        | 1:10                           | Proteintech Group, Inc         |
| PD-L1 Rabbit Monoclonal antibody               | ab213524       | EPR19759     | IHC                       | 1:200                          | abcam                          |
| PD-L1 Rabbit Monoclonal antibody               | RMA-0732       | MXR003       | IHC                       | 1:1                            | MXB biotechnologies            |
| PD-L1 Rabbit Monoclonal antibody               | M6101          | 1386723-44-3 | Blocking Cell line:5ug/ml | 1:50                           | AbMole                          |
| PD-L1 Rabbit Monoclonal antibody               | M8H1           |             | IF                        | 1:50                           | Cell Signaling Technology      |
| PE Mouse Anti-Human CD274 Monoclonal antibody  | 557924         |             | ChIP                      | 1:10                           | BD Pharmingen                   |
| FoxP1 Mouse Monoclonal antibody                | 4402S          | D35D10       | IHC                       | 1:200                          | ZENBIO                         |
| BAF180/BRM1 Rabbit Polyclonal antibody         | 382286         |             | IP                        | 1:200                          | ZENBIO                         |
| PBRM1/BAF180 (E9X2Z) Rabbit Monoclonal antibody| 89123          | E9X2Z        | ChIP                      | 1:50                           | Cell Signaling Technology      |
| ACO2 Rabbit Polyclonal antibody                | 10686-1-AP     |             | RIP                       | 1:100                          | Proteintech Group, Inc         |
| Histone H3k27Ac Mouse Monoclonal Antibody      | 39085          | MABI0339     | ChIP                      | 1:100                          | ZENBIO                         |
| BAF57/SMARCE1 Rabbit Polyclonal antibody       | 383214         |             | IP                        | 1:50                           | ZENBIO                         |
| Beta Actin Mouse Monoclonal antibody           | 66006-1-lg     | 2D4H5        | Western Blotting          | 1:200                          | Proteintech Group, Inc         |
| SMARCA4/BRG1 Rabbit Polyclonal antibody        | 21634-1-AP     |             | IP                        | 1:100                          | Proteintech Group, Inc         |
| DPF2 Rabbit Polyclonal antibody                | 12111-1-AP     |             | Western Blotting          | 1:1000                         | Proteintech Group, Inc         |
| DPF2 Rabbit Polyclonal antibody                | ab12849        |             | ChIP                      | 1:50                           | abcam                          |
| BV421 Mouse Anti-Human CD3 Monoclonal antibody | 563798         | SK7          | FACS                      | 1:10                           | BD Pharmingen                   |
| APC Mouse Anti-Human IFN-γ Monoclonal antibody  | 554702         | B27          | FACS                      | 1:10                           | BD Pharmingen                   |
| PE-Cy5® Mouse Anti-Human CD8 Monoclonal antibody| 557565         | RPA-T8       | FACS                      | 1:10                           | BD Pharmingen                   |
| C8 Rabbit Monoclonal antibody                  | RMA-0514       | SP16         | IHC                       | 1:1                            | MXB biotechnologies            |
| Cleaved PARP(Asp241)(gD44E10) XP6 Rabbit Monoclonal antibody | 5625T | D64E10 | IHC                       | 1:50                           | Cell Signaling Technology      |
| Cleaved Caspase-3(Asp175)(gD44E10) XP6 Rabbit Monoclonal antibody | 9664T | 5A1E | IHC                       | 1:200                          | Cell Signaling Technology      |
| GAPDH Rabbit Polyclonal antibody               | 10494-1-AP     |             | Western Blotting          | 1:5000                         | Proteintech Group, Inc         |
| Normal Mouse IgG Polyclonal Antibody           | 12-371         |             | IP                        | 1:200                          | Millipore                      |
| Normal Rabbit IgG Polyclonal Antibody          | 12-370         |             | IP                        | 1:200                          | Millipore                      |