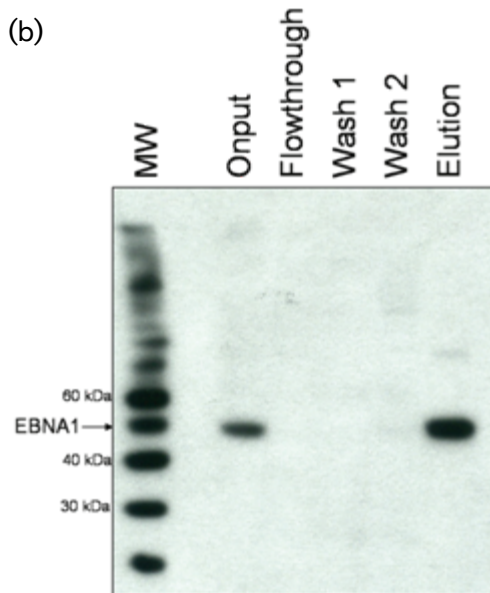
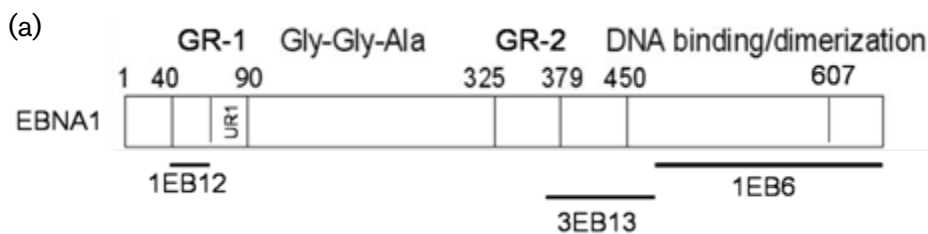
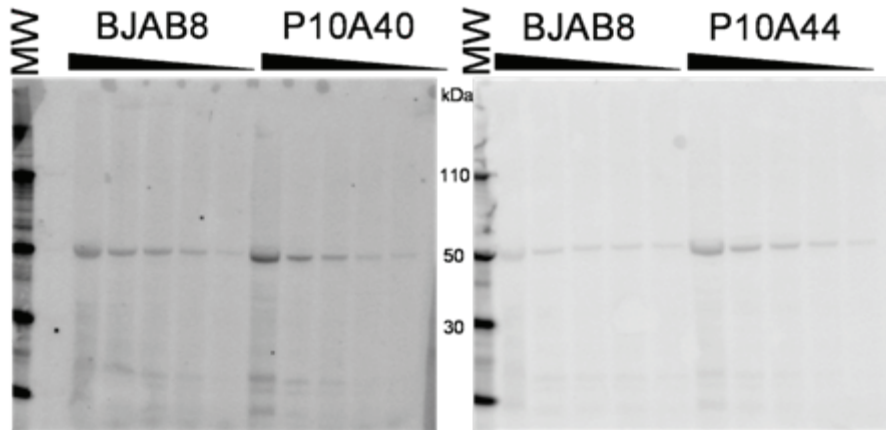


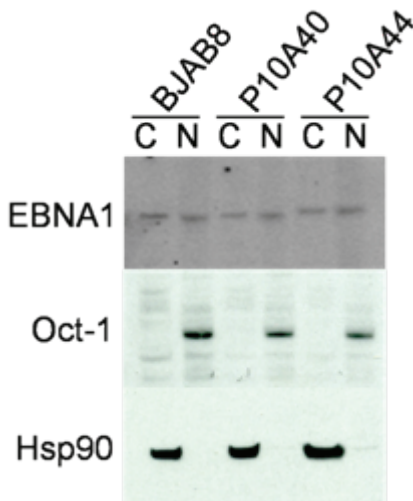
**Supplementary Fig. S1.** Expression level of EBNA1. Western blot comparing the expression level of EBNA1 between 721 lymphoblastoid cells and BJAB8 cells. Whole-cell extract from  $2 \times 10^6$  cells was loaded into the first lane for each cell type, followed by a 2-fold dilution series. The blot was probed with anti-EBNA1 mAb 1EB12. The difference in migration is due to the deletion of the majority of the GGA region in the BJAB8-expressed EBNA1 protein. The band at 90 kDa in the BJAB8 cell line is probably an EBNA1 dimer band, which is commonly seen.



**Supplementary Fig. S2.** Immunoprecipitation of EBNA1. (a) A cocktail of three mAbs (1EB6, 1EB12 and 3EB13) was used to immunoprecipitate EBNA1. The schematic shows the regions within EBNA1 where the epitopes for these mAbs are located. (b) Western blot, probed with mAb 1EB12, showing the immunoaffinity purification of EBNA1. The output is whole-cell extract from BJAB8 cells.



**Supplementary Fig. S3.** Expression-level analysis of EBNA1 and EBNA1P10A. A 2-fold dilution series, starting at  $2 \times 10^6$  cells for BJAB8 and  $5 \times 10^5$  cells for the P10A clones, was analysed by quantitative Western blotting, probed with anti-EBNA1 mAb 1EB12–Alexa Fluor 647. The bands were quantified and plotted and the resulting equations indicate that the expression level is 4.8-fold higher (clone 40) and 9.5-fold higher (clone 44) than that of the wild type.



**Supplementary Fig. S4.** Cytoplasmic and nuclear fractionation of EBNA1 and EBNA1P10A. Cell lysates from BJAB8 (encoding wild-type EBNA1) and P10A clones 40 and 44 (encoding EBNA1P10A) were fractionated into cytoplasmic (C) and nuclear (N) samples. EBNA1 was analysed by quantitative Western blotting, probed with anti-EBNA1 mAb 1EB12 conjugated to Alexa Fluor 647. Oct-1 is a nuclear marker and Hsp90 is a cytoplasmic marker. Detection of these proteins on the Western blot was performed by enhanced chemiluminescence.