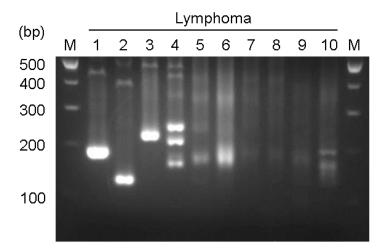


FIG S1 Flow cytometry analysis to assess cell-marker expression and population
diversity. Cell-marker expression of peripheral blood mononuclear cells from bovine
leukemia virus-uninfected cattle or cattle with lymphoma was analyzed by flow
cytometry. The results were evaluated as percentages of positive cells and numbers of
different cell populations.



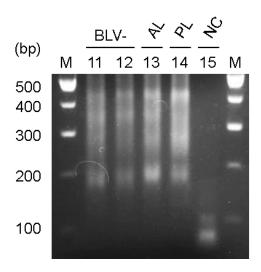


FIG S2 PCR-based IgH analysis to confirm B-cell clonality. Amplification of the gene encoding the IgH region of interest was performed using DNA extracted from peripheral blood mononuclear cells (PBMCs) and tissue samples of cattle with or without lymphoma. Representative PCR products run on an ethidium bromide-stained 3% Trisborate-EDTA agarose gel. Lane: 1, PBMCs; 2, solid tumor in heart; 3, superficial cervical lymph node; 4, PBMCs; 5, solid tumor in heart; 6–8, PBMCs; 9, solid mass in rib bone; 10, solid tumor in thymus; 11–14, PBMCs; 15, double-distilled water; M, 100-bp DNA ladder; AL, aleukemic; PL, persistent lymphocytosis; NC, negative control.

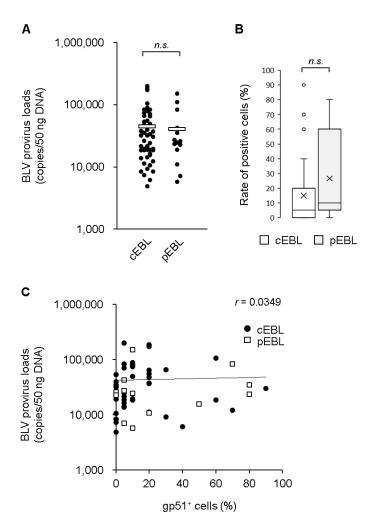


FIG S3 Difference in viral replication between two B-cell lymphomas. (A) Bovine leukemia virus (BLV) provirus loads were compared between the samples from classic enzootic bovine leukosis (cEBL; n = 42), polyclonal EBL (pEBL; n = 15). P = 0.7105, Wilcoxon rank sum test. (B) The expression levels of gp51 in cEBL (n = 41) and pEBL (n = 13) are shown as box-and-whisker plots. Each box indicates median, lower and upper quartiles, and whiskers indicate lower and upper extremes. The x-mark indicates the average, and dots represent outliers that are much greater than normal or much less than normal. P = 0.2236, Wilcoxon rank sum test. (C) Correlation between the BLV provirus loads and the positive percentages of gp51 expression. R = 0.0349.

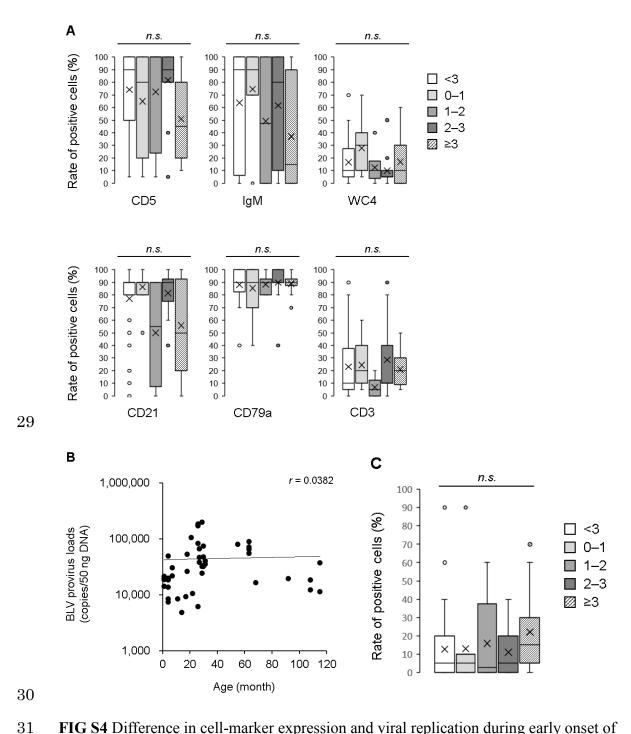


FIG S4 Difference in cell-marker expression and viral replication during early onset of classic enzootic bovine leukosis (cEBL). (A) The expression levels of six cell markers in the samples from different ages of cEBL cattle are shown as box-and-whisker plots. Each box indicates median, lower and upper quartiles, and whiskers indicate lower and upper extremes. The x-mark indicates the average, and dots represent outliers that are

much greater than normal or much less than normal. (B) Correlation between the bovine leukemia virus provirus loads and the age in months of cEBL cattle, R = 0.0382. (C)

The expression levels of gp51 in the samples from different ages of cEBL cattle are shown as box-and-whisker plots. Numbers indicate age in years of original cattle in each sample. <3, n = 32 (0–1, n = 11; 1–2, n = 6; 2–3, n = 15); ≥ 3 , n = 10.