| H & E	CD56	EBV *in situ*

Supplementary figure 1. Histology of the primary biopsy specimens. Biopsied samples from brain lesion were stained with hematoxylin and eosin (left panel) or anti-CD56 antibody (middle panel). Sections of the same samples were also subjected to *in situ* hybridization staining for EBER (right panel). All images were shown at original magnification 400x.

a

b
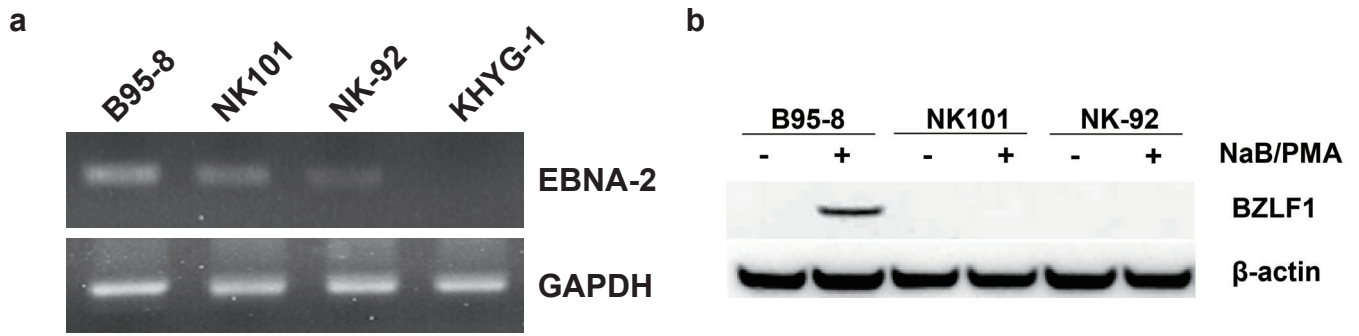
Supplementary figure 2. Analysis of a latent gene and a lytic protein expression of EBV in NK101 cell line. a PCR analysis of *EBNA-2* was performed with gDNAs isolated from B95-8, NK-92, KHYG-1, and NK101 cells. *GAPDH* was used as a loading control. **b** Indicated cells were incubated in the absence or presence of sodium butylate (NaB) and PMA as described in *Online Supplementary Methods*. Cell lysates were probed with an anti-BZLF1 or anti-β-actin antibody.
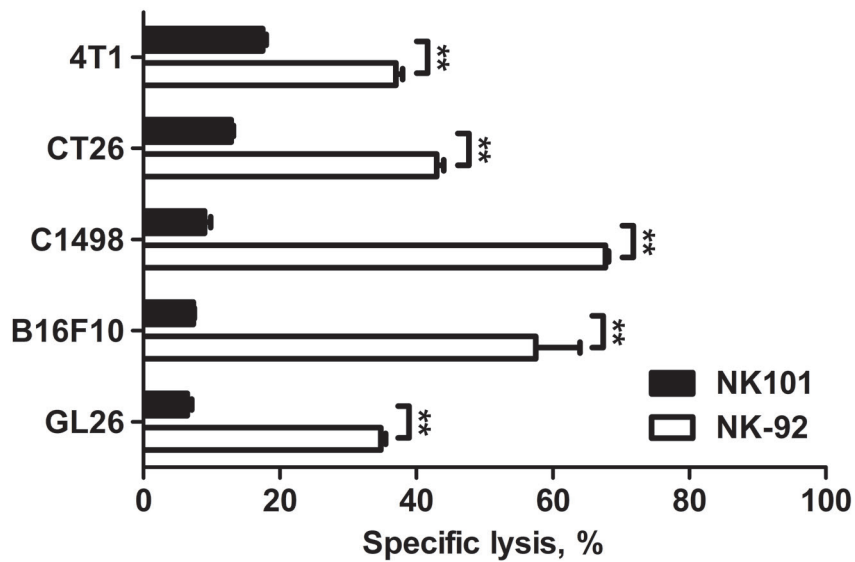
Supplementary figure 3. Comparative analysis of cytolytic activities of NK101 and NK-92 against murine tumor cell lines. Indicated murine cell lines were selected as target cells. Indicated cell lines were co-cultured with NK101 (black bar) and NK-92 (white bar) at an effector-to-target ratio of 4:1 for 24 hours. The percentages of apoptotic tumor cells were quantified by Annexin-V and fixable viability dye staining via flow cytometry. Percentage of specific lysis was calculated by the formula described in *Online Supplementary Methods*. **$p<0.01$.
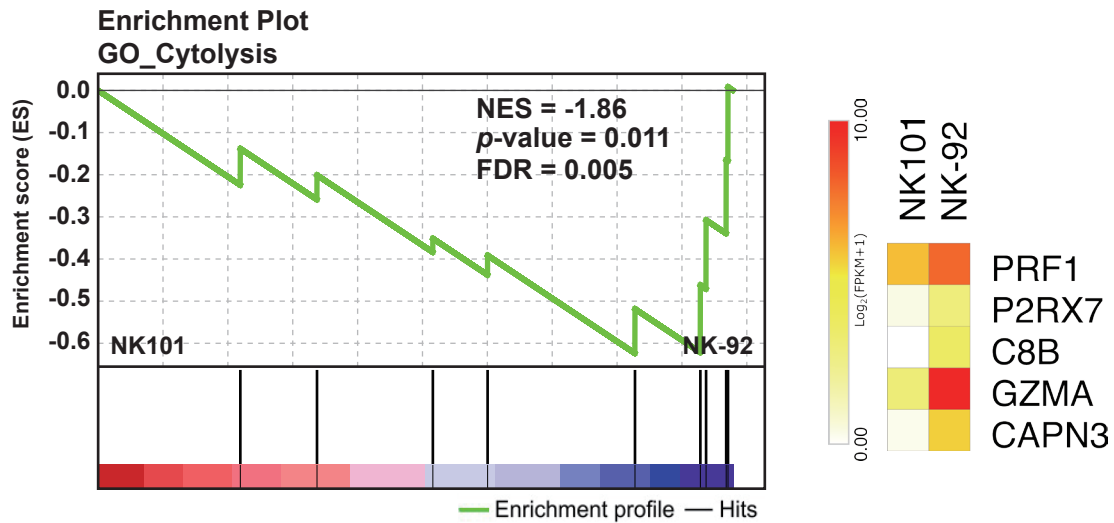
Supplementary figure 4. Cytolysis-related gene expression by NK101 and NK-92. GSEA between NK101 and NK-92 was performed in terms of 'cytolysis', and the enrichment plot was depicted with NES, *p*-value, and FDR. Expression levels of core genes were illustrated as the heatmap graph. A white-yellow-red color scale indicates expression level transformed as $Log_2(FPKM+1)$.
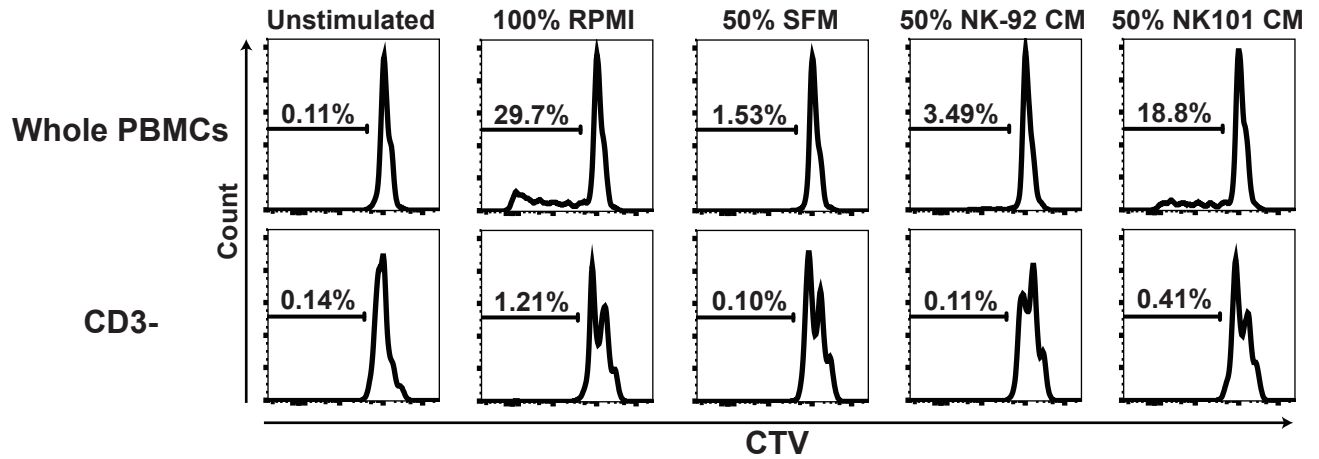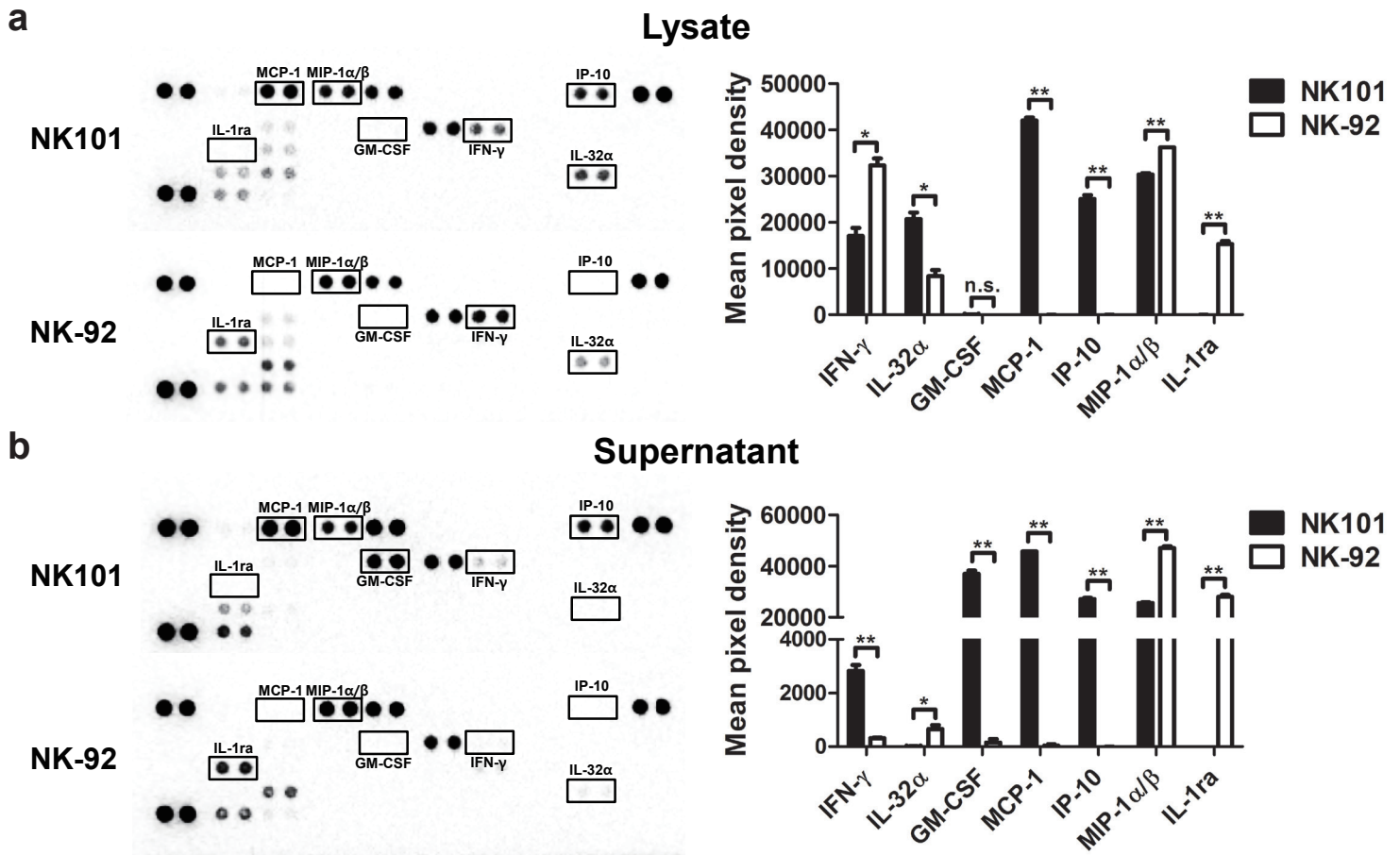
Supplementary figure 5. Effects of conditioned medium derived from NK-92 or NK101 on human peripheral blood mononuclear cells (PBMCs). Human PBMCs labeled with CellTrace Violet (CTV) were cultured under indicated conditions for 5 days. Total cells were stained using the Live/Dead Fixable Viability Dye and fluorochrome-conjugated antibodies specific to CD3, CD4, and CD8. Representative histograms for CTV in the gate of whole PBMCs and CD3- cells are displayed. The results are representative of 2 independent experiments from a single donor in triplicate. SFM, serum-free medium; CM, conditioned medium.
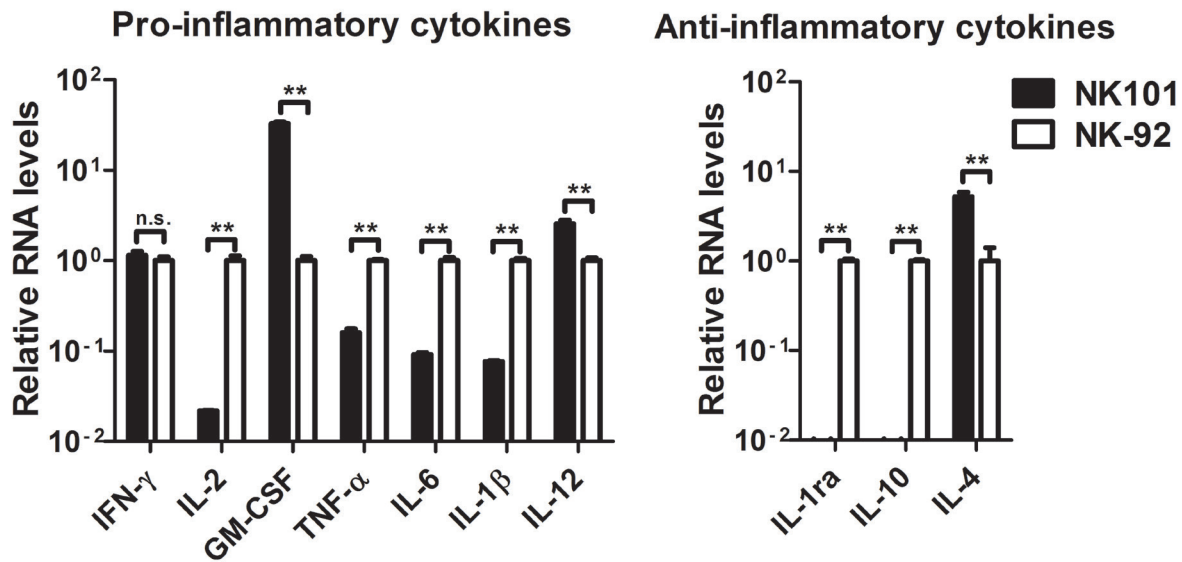
Supplementary figure 6. Pro-/anti-inflammatory gene expression profiles of NK101 and NK-92. Gene expression profiles of cultured NK101 and NK-92 cells were examined by real-time RT-PCR. RNA expression levels for all indicated genes were normalized with a reference gene, *RPL13A*, and calculated based on the 2^{-ddCt} methods as described in *Online Supplementary Methods*. Relative RNA levels were calculated as follows: 2^{-ddCt} (NK101 or NK-92 RNA level) /2^{-ddCt} (average NK-92 RNA level). Data represent mean ± SD of triplicate wells from 2 independent experiments. **$p<0.01$; n.s., not significant.

Supplementary figure 7. Expression profiles of cytokines/chemokines from lysates or supernatants of NK101 and NK-92. NK101 or NK-92 cells were cultured under serum-free condition for 72 hours. Both cellular lysates (a) and cultured supernatants (b) were subjected to Proteome Profiler Human Cytokine Array Kit. Differentially expressed cytokines/chemokines are highlighted in boxes. Out of 36 cytokines/chemokines quantified in the lysates and supernatants, levels of 7 proteins with significant difference between NK101 and NK-92 are shown as bar graphs. Data represent mean ± SD of duplicate dots from 2 independent experiments. *$p<0.05$; **$p<0.01$; n.s., not significant.