Fig.S1 HDAC gene family was extensively higher expressed in dedifferentiated liposarcoma(DDLPS) and leiomyosarcoma(LMS). (A). HDAC1/2/3/4/5/6/7/8/9/10/11 was highly expressed in tumor compared to normal tissues(386 adipose tissue from GETx database) in the cohort of liposarcoma. (B). HDAC1/2/3/4/5/6/7/8/9/11 was highly expressed in tumor compared to normal tissues(478 muscle tissues in GETx database) in the cohort of leiomyosarcoma patients.

Red squares indicate upregulated genes, blue squares indicate downregulated genes, and white squares indicate genes without difference. The p values were showed as: ***p < 0.001.

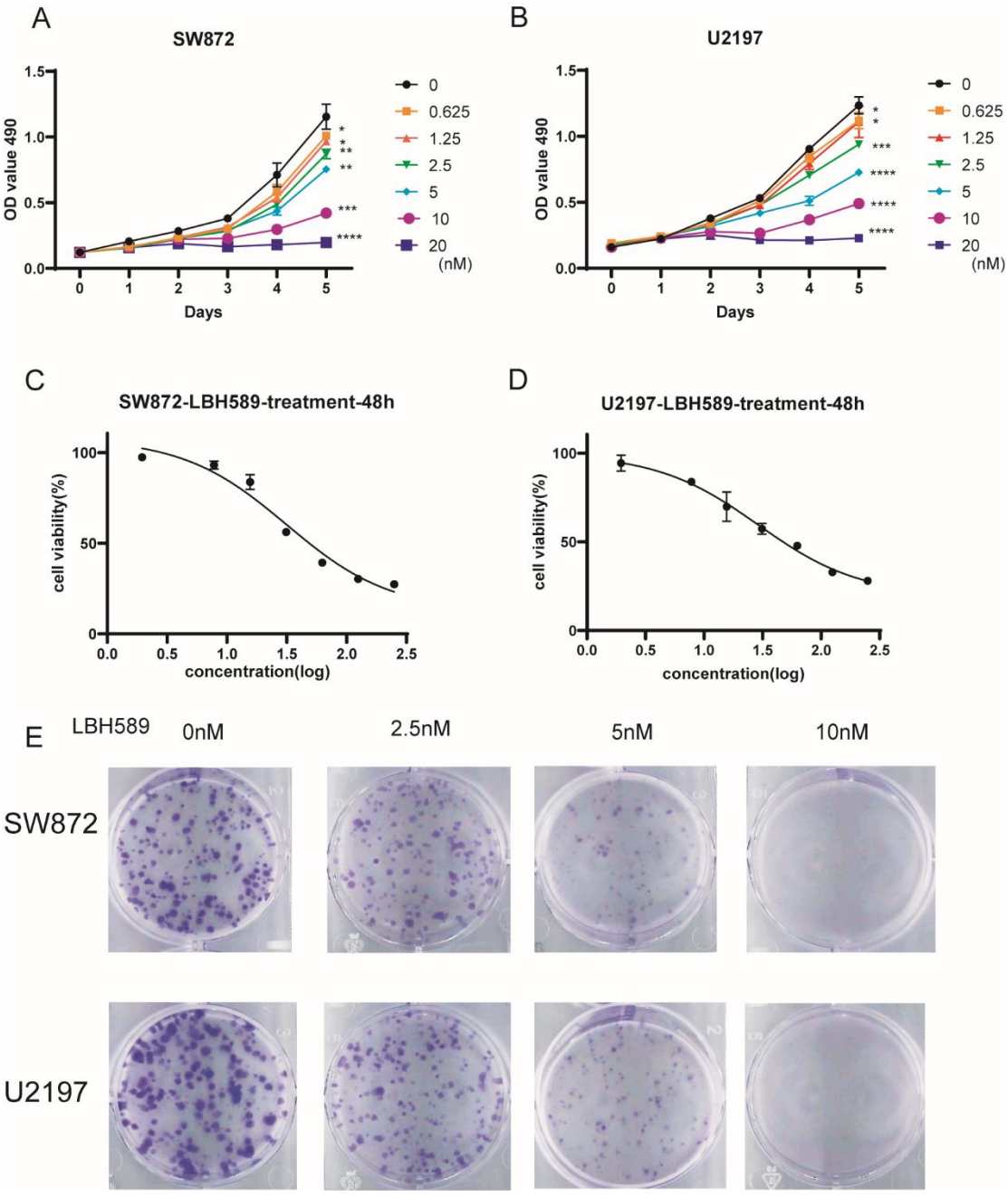

Fig.S2 LBH589 suppresses the proliferation of STS cells in vitro. (A-B) Human soft tissue sarcoma cell lines SW872 and U2197 were treated with LBH589 (0, 0.625, 1.25, 2.5, 5, 10, and 20 nM) for 5 days. (C-D) Cell viability was measured by MTT assays. (E) A colony formation assay was performed using SW872 and U2197 cells treated with LBH589 (0, 2.5, 5, and 10 nM) to assess proliferation. Colonies were imaged.

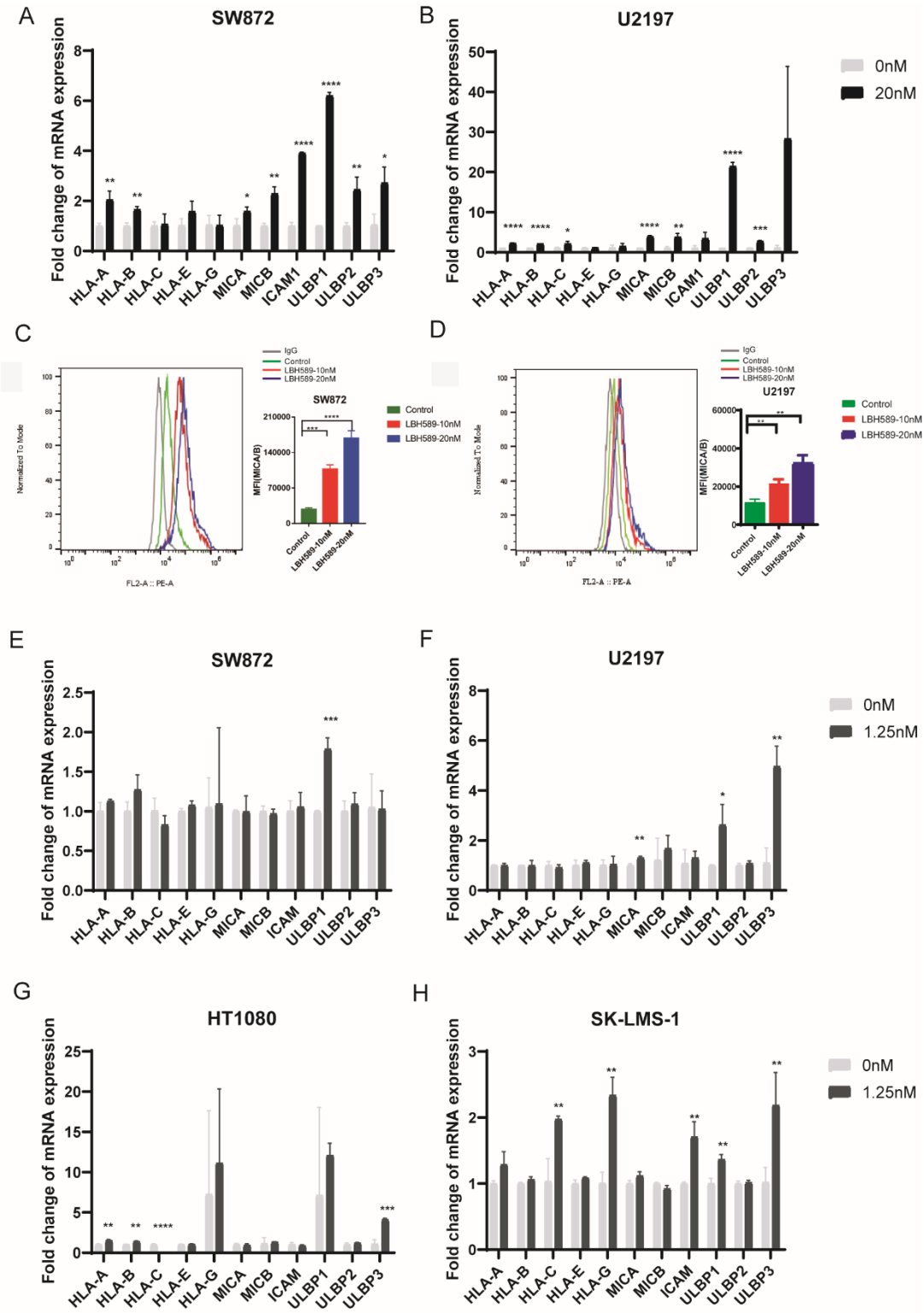

Fig.S3 LBH589 increases NK cell mediated cytotoxicity. (A-B) Real-time q-PCR analysis shows the effects of LBH589 treatment on the expression of NKG2DL in STS cells (mean ± SD, n = 3). (C-D). Flow cytometry analysis of surface levels of MICA/B on LBH589(10 and 20nM) treatment SW872 cells (left) and U2197 cells (right) and quantification. (E-H) Real-time q-PCR analysis shows the effects of LBH589 treatment

at low concentration of 1.25nM on the expression of NKG2D in STS cells (mean ± SD, n = 3). Data are mean±SD of three independent experiments. * $p < 0.05$, **$P < 0.01$, ***$P < 0.001$ (two-tailed unpaired t-test).