

**Supplementary Figure S5. Genome-wide localization of KDM5A in MM.1S cells**

**A,** ChIP was carried out with KDM5A antibody (rabbit polyclonal) or control normal rabbit IgG, followed by immunoblot analysis for KDM5A in MM.1S cells.

**B,** Genome-wide KDM5A-bound sites were determined by ChIP-seq in MM.1S cells. Distribution of KDM5A-bound sites in MM.1S cells.

**C,** Heatmap representing enrichment of KDM5A around the transcriptional start site (TSS). H3K4me3-, H3K27Ac-, or H3K27me3-marked regions in MM.1S cells. + 5 kb from TSS or each histone modification-marked region is shown.

**D,** Motif analysis of KDM5A-bound sites (top 200) was performed by MEME\_ChIP. Shown is the position-weight matrix of the most enriched motif, which includes KDM5A consensus motif (CCGCCC).

**E,** Volcano plot depicting the expression changes of KDM5A-bound genes after treatment with JQKD82 at 1 µM for 48h in MM.1S cells, compared with DMSO control. Red indicates KDM5A-bound genes, and blue indicates genes not bound by KDM5A. L2FC = log2 fold change.

**F,** Gene tracks representing enrichment of KDM5A, H3K4me3, MYC, CDK7, CDK9, and RNAPII at the representative MYC target gene loci in MM.1S cells.