

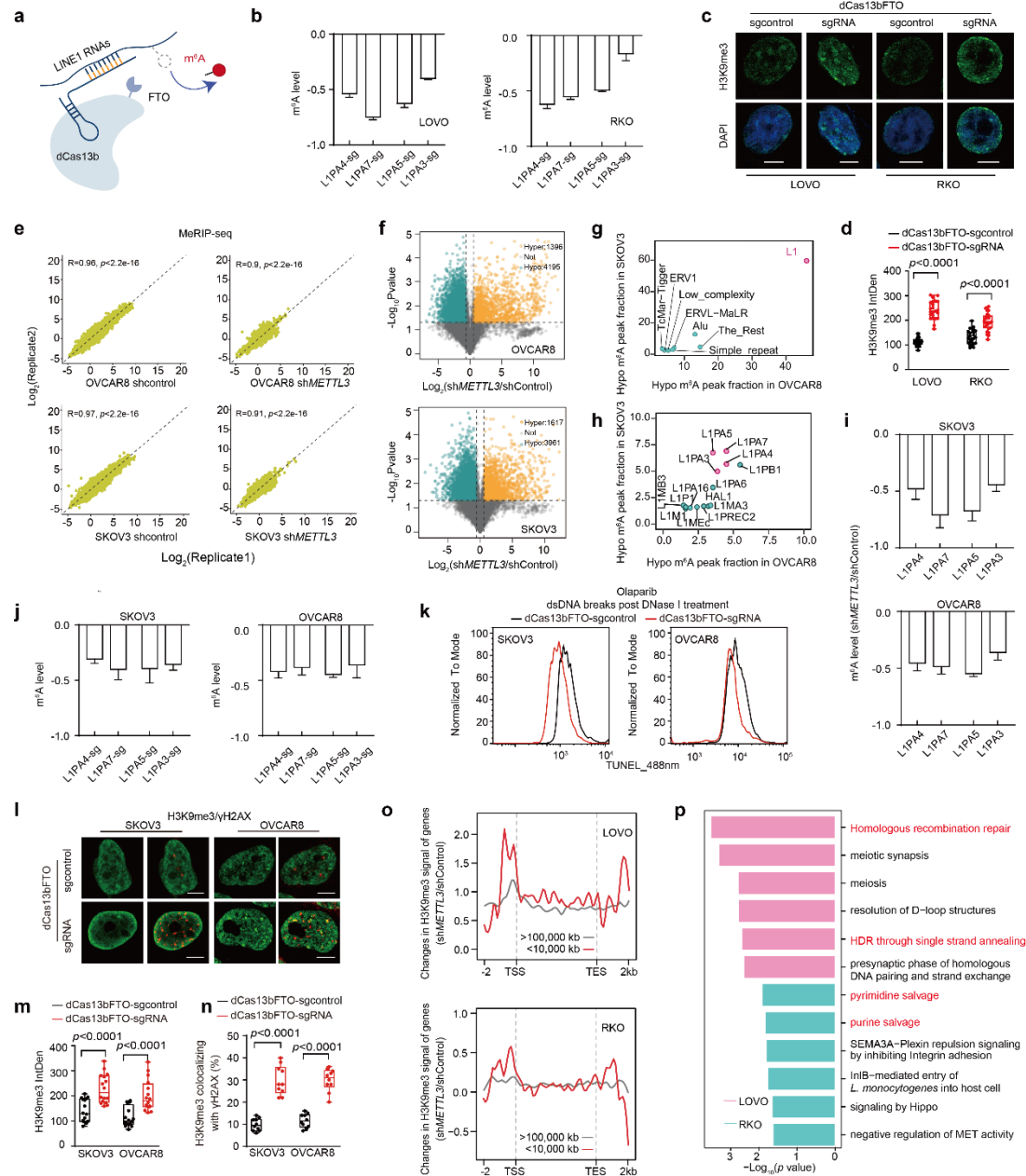


Fig. S5 m⁶A-marked L1PA promotes chromatin accessibility in *BRCA*^{wt} and *BRCA*^{-/-} cells. (a) Schematic model of the dCas13b-FTO site-specific demethylation system. (b) Relative m⁶A levels of L1 quantified with RT-qPCR in dCas13b-FTO constructs with gRNA targeting m⁶A-marked L1 or nontarget LOVO and RKO cells. (c, d) Detection (c) and quantification (d) of H3K9me3 fluorescence intensity in dCas13b-FTO constructs with gRNA targeting m⁶A-marked L1 or nontarget LOVO and RKO cells; scale bar, 5 μ m. (e) The correlation of m⁶A levels on m⁶A peak regions between two replicates showed high reproducibility. The R value refers to Pearson's correlation coefficient. P values were calculated by Student's *t* test. (f) Scatter plots showing differential m⁶A peaks in *METTL3*-knockdown SKOV3 and OVCAR8 cells compared with control cells using caRNA MeRIP-seq data. Each point represents a peak. Hypermethylated (m⁶A log₂ [fold change] > 0.58 and *P* < 0.05) and hypomethylated (m⁶A log₂ [fold change] < -0.58 and *P* < 0.05) peaks are shown in

yellow and green, respectively. *P* values were calculated by Student's *t* test. **(g, h)** Percentage of hypo-m⁶A peaks ($m^6A \log_2 [\text{sh}METTL3/\text{shControl}] < -0.58$ and $P < 0.05$) distributed at various repeat families **(g)** and distinct LINE1 subfamilies **(h)** in SKOV3 and OVCAR8 cells. **(i)** Relative m⁶A levels of L1 quantified with RT-qPCR in *METTL3*-knockdown and control SKOV3 and OVCAR8 cells. **(j)** Relative m⁶A levels of L1 quantified with RT-qPCR in dCas13b-FTO constructs with gRNA targeting m⁶A-marked L1 or nontarget SKOV3 and OVCAR8 cells. **(k)** DNase I-treated TUNEL assays were performed to analyze chromatin accessibility in dCas13b-FTO constructs with gRNA targeting m⁶A-marked L1 or nontarget SKOV3 and OVCAR8 cells. **(l)** Immunofluorescence of olaparib-treated L1 dCas13b-FTO constructs with gRNA targeting m⁶A-marked L1 or nontarget SKOV3 and OVCAR8 cells stained with anti- γ H2AX (red) and anti-H3K9me3 (green). Scale bars, 5 μ m. **(m, n)** Quantification of H3K9me3 fluorescence intensity **(m)** and proportion of γ H2AX foci colocalizing with H3K9me3 **(n)**. **(o)** Profiles of H3K9me3 enrichment on promoters of genes near (red line; the distance is smaller than 10,000 kb) or far (gray line; the distance is larger than 100,000 kb) from *LIPA5* RNA loci with hypo-m⁶A peaks and its flanking 1 kb following *METTL3* knockdown in LOVO and RKO cells. **(p)** Functional enrichment analysis of genes near *LIPA5* RNA loci with hypo-m⁶A peaks. **(b, d, i, j, m, n)** Statistical analyses were performed using a *t* test. *n* = 3 biological replicates. Data are shown as mean $\pm$ SEM.