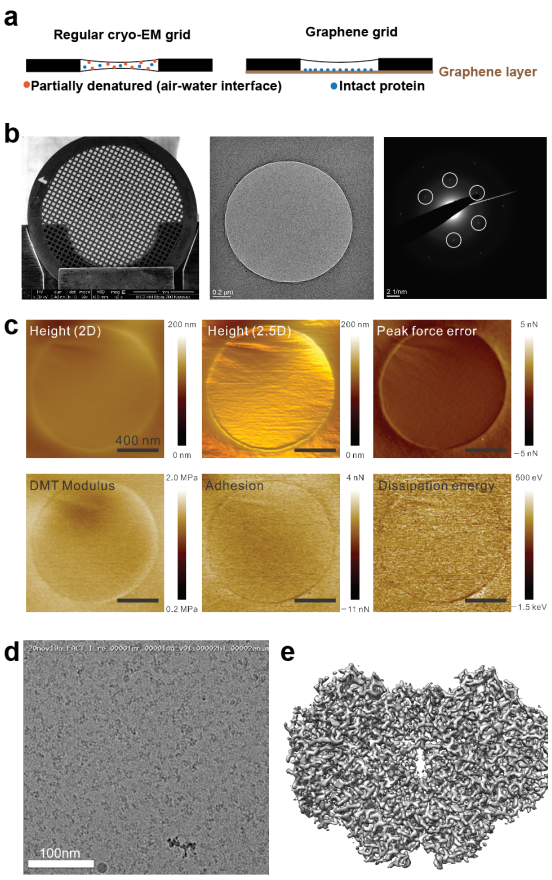

Figure 1. **a.** Schematic comparison of regular vs. graphene grids. **b,** Scanned electron microscopic and diffraction images of the graphene grid. **c,** Atomic force microscopy of the graphene grid. **d,** cryo-EM image of *M.caps* MMOH using the graphene grid. **e,** the 2.1Å cryo-EM map of *M.caps* MMOH.

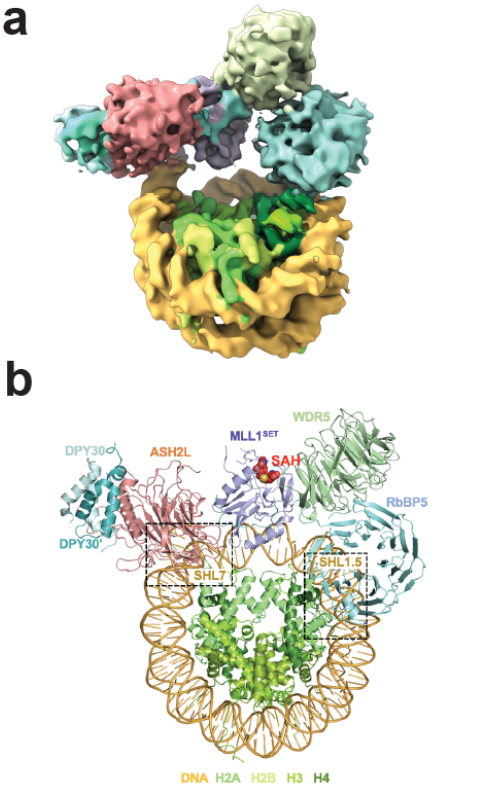

Figure 2. **a.** Cryo-EM 3D reconstruction of the MLL1^{RWSAD}-NCP complex. **b,** Top view of the MLL1^{RWSAD}-NCP structure. The S-adenosyl-L-homocysteine (SAH) was represented as a sphere (red) and the MLL1 core components shown in cartoon representation (RbBP5: cyan, WDR5: green, MLL1^{SET}: slate, ASH2L: orange, and DPY30 dimer: cerulean and teal). Widom 601 DNA and four histones were colored as indicated on bottom. Two black dashed squares highlighted the nucleosome contact points near SHL1.5 and SHL7 by MLL1^{RWSAD}.

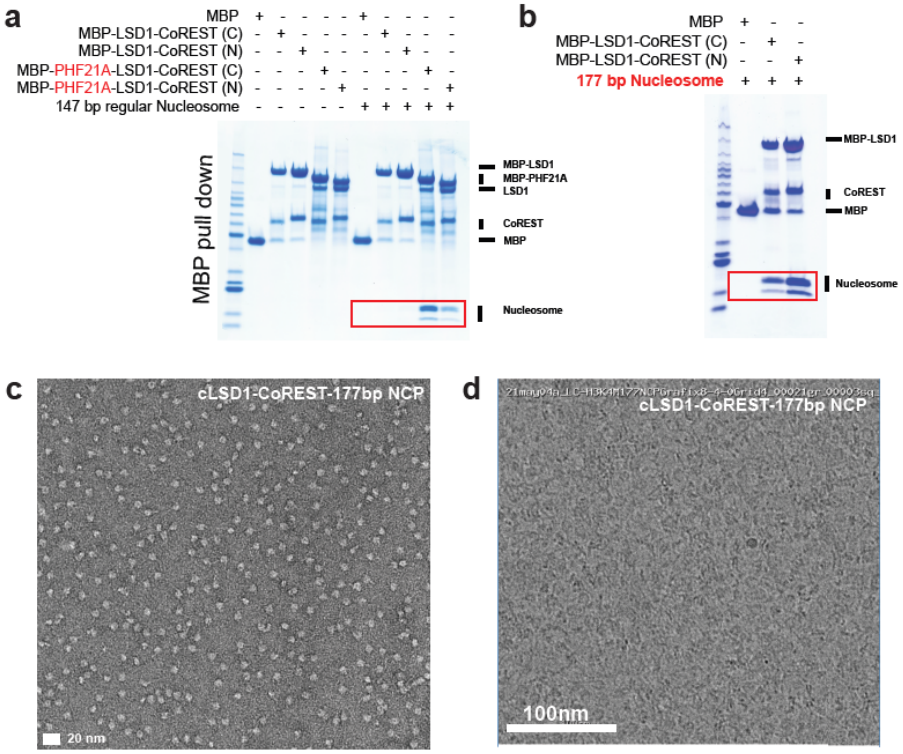

Figure 3. **a.** MBP pull-down using either MBP-LSD1 or MBP-PHF21. Canonical (C) and neuronal (N) forms of LSD1 and PHF21A were used. **b.** MBP pull-down using MBP-c/n LSD1 toward to 177bp nucleosome. **d.** Negative stain EM image of canonical LSD1-CoREST complex bound to the 177bp nucleosome. **e.** Cryo-EM image (200KeV Talos Arctica) of the canonical LSD1-CoREST complex bound to the 177bp H3 K4M nucleosome.

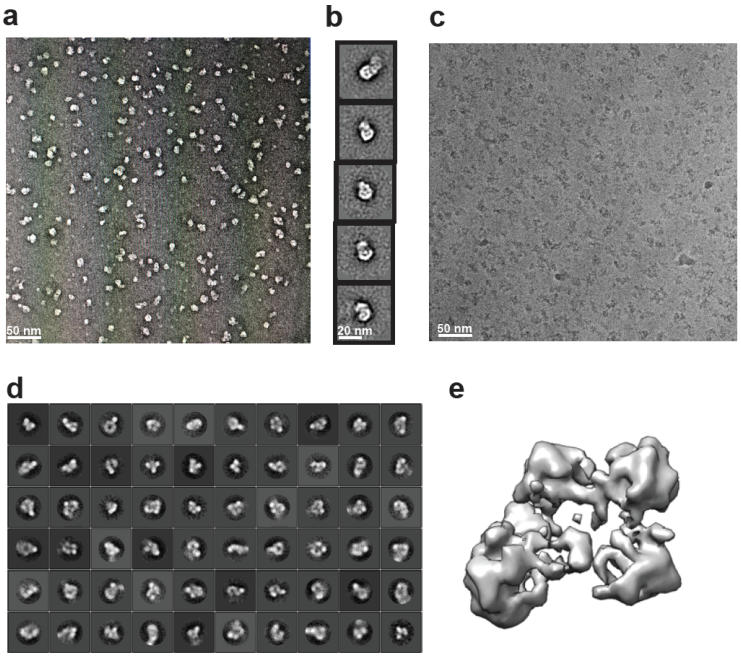

Figure 4. **a.** Negative stain EM images of the endogenous FACT-histone complex demonstrate the presence of large and homogenous particles. **b.** 2-D class averages of negative stain EM data. **c.** The volta-phase plate cryo-EM micrograph of the FACT-histone complex. **d.** 2D-classification of the FACT-histone complex. **e.** Three-dimensional reconstruction of the FACT-histone complex with ~12Å resolution.