Supplementary information, Data S1 Materials and Methods

Protein Expression and Purification

Human MOF_{HAT} (residue 170-458) and $MSL3_{MRG}$ (residue 160-521) were cloned into a modified pET28b vector with a SUMO protein fused at the N terminus after a His_6 tag. NSL1 and MSL1 fragments were cloned into a GST fusion protein expression vector, pGEX6p-1 (GE healthcare).

The MOF-NSL1 complexes were co-expressed in *E. coli* Rosetta strains (Novagen) and purified by sequential affinity chromatography with Ni-NTA agarose beads (Qiagen) and glutathione sepharose 4B beads (GE Healthcare). After removal of the SUMO tag and GST tag respectively with Ulp1 and Protease 3C, they were further purified with gel-filtration chromatography on a Hiload Superdex 75. The MSL1-MSL3 complex and MOF itself were individually expressed in *E. coli* Rosetta strains. After affinity purification with Ni-NTA agarose beads, the MSL1-MSL3 proteins were mixed with excess MOF proteins and further purified with glutathione sepharose 4B beads. After tag removal, they were finally purified with gel-filtration chromatography on a Hiload Superdex 200.

Histone Acetyltransferase (HAT) Assays

For each HAT assay, 1 μg of HeLa nucleosomes was used as substrates and the MOF complexes were calibrated to have equal amount of MOF protein (500 ng). Reactions were carried out at 30°C for 1 hr in the presence of [^{3}H] acetyl-CoA and finally visualized by autoradiography.

Crystallization, Data Collection, and Structure Determination

Crystals of the MOF_{HAT}-$MSL1_{MBM}$ complex were grown by sitting drop vapor diffusion at 4°C. The well solution contained 0.05 M HEPES pH 7.0, 0.05 M $MgSO_4$ and 1.6 M Li_2SO_4. Crystals were gradually transferred into a harvesting solution (0.05 M HEPES pH 7.0, 0.05 M $MgSO_4$, 0.3 M Li_2SO_4 and 5 M Sodium formate) before flash-frozen in liquid nitrogen for storage and data collection under cryogenic conditions (100 K). Data sets were collected at beam line 21ID-D at APS and processed using HKL2000 [1]. Models were built by molecular replacement of the PDB dataset 2PQ8 using Phaser [2], and further refined using simulated annealing and positional refinement in CNS [3] as well as manual rebuilding in program O [4].

References

1 Otwinowski Z, Minor W. Processing of X-ray diffraction data collected in oscillation mode. Method in enzymology. San Diego: Academic Press 1997:307-326.

2 McCoy AJ, Grosse-Kunstleve RW, Adams PD, Winn MD, Storoni LC, Read RJ. Phaser crystallographic software. *J Appl Crystallogr* 2007; **40**:658-674.

3 Brunger AT, Adams PD, Clore GM *et al.* Crystallography & NMR system: A new software suite for macromolecular structure determination. *Acta Crystallogr D Biol Crystallogr* 1998; **54**:905-921.

4 Jones TA, Zou JY, Cowan SW, Kjeldgaard M. Improved methods for building protein models in electron density maps and the location of errors in these models. *Acta Crystallogr A* 1991; **47 (Pt 2)**:110-119.