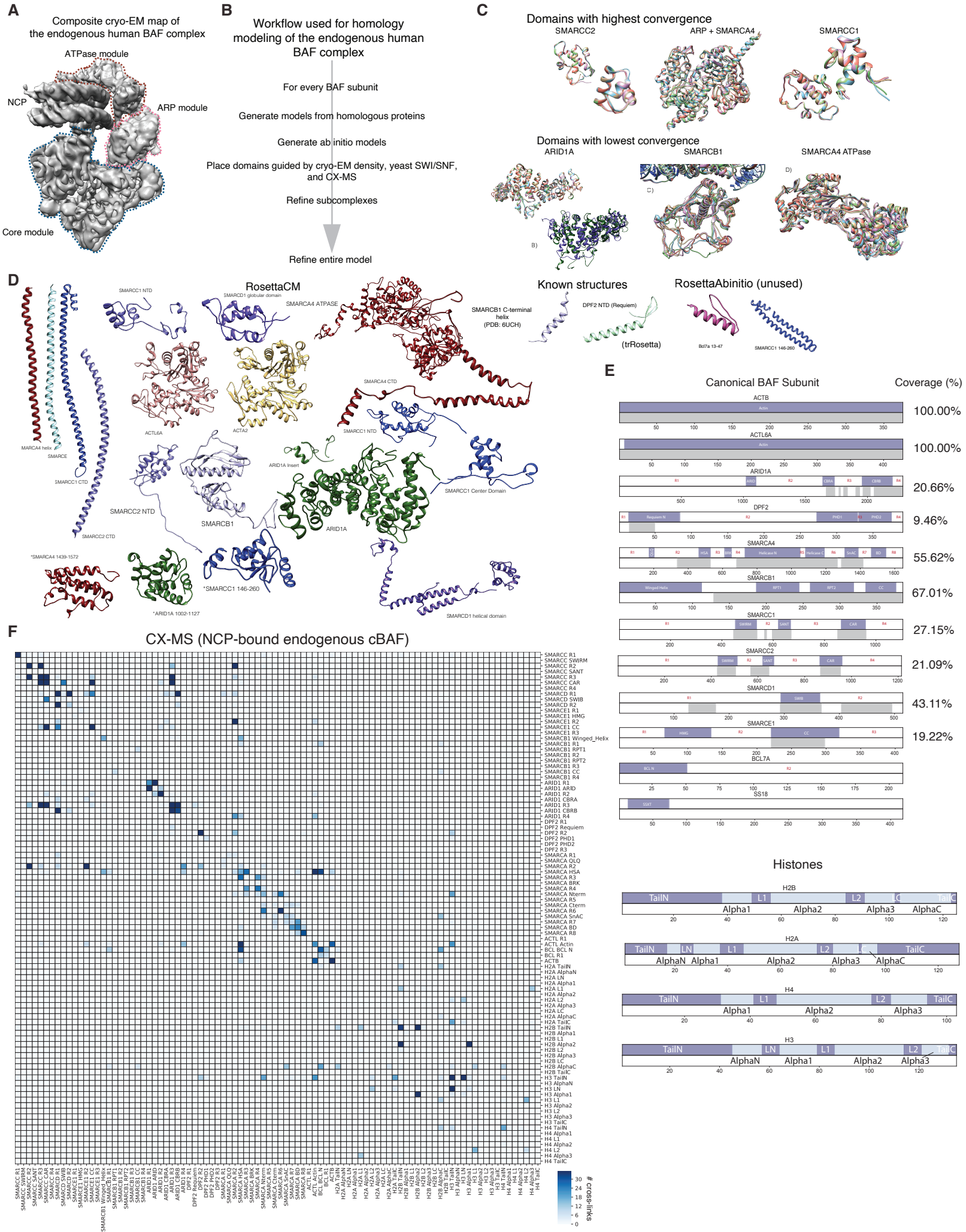
Figure S3


A
Composite cryo-EM map of the endogenous human BAF complex
ATPase module
NCP
ARP module
Core module
B
Workflow used for homology modeling of the endogenous human BAF complex
For every BAF subunit
Generate models from homologous proteins
Generate ab initio models
Place domains guided by cryo-EM density, yeast SWI/SNF, and CX-MS
Refine subcomplexes
Refine entire model
C
Domains with highest convergence
SMARCC2
ARP + SMARCA4
SMARCC1
Domains with lowest convergence
ARID1A
SMARCB1
SMARCA4 ATPase
D
RosettaCM
SMARCC1 NTD
SMARCD1 globular domain
SMARCA4 ATPASE
SMARCB1 C-terminal helix (PDB: 6UCH)
SMARCA4 CTD
SMARCC1 NTD
ACTL6A
ACTA2
MARCA4 helix
SMARCE
SMARCC1 CTD
ARID1A Insert
SMARCC1 Center Domain
SMARCC2 NTD
SMARCB1
ARID1A
SMARCC2 CTD
*SMARCA4 1439-1572
*ARID1A 1002-1127
*SMARCC1 146-260
SMARCD1 helical domain
Known structures
DPF2 NTD (Requiem)
(trRosetta)
RosettaAbinitio (unused)
Bcl7a 13-47
SMARCC1 146-260
E
Canonical BAF Subunit
Coverage (%)
ACTB 100.00%
ACTL6A 100.00%
ARID1A 20.66%
DPF2 9.46%
SMARCA4 55.62%
SMARCB1 67.01%
SMARCC1 27.15%
SMARCC2 21.09%
SMARCD1 43.11%
SMARCE1 19.22%
BCL7A
SS18
Histones
H2B
H2A
H4
H3
F
CX-MS (NCP-bound endogenous cBAF)
cross-links