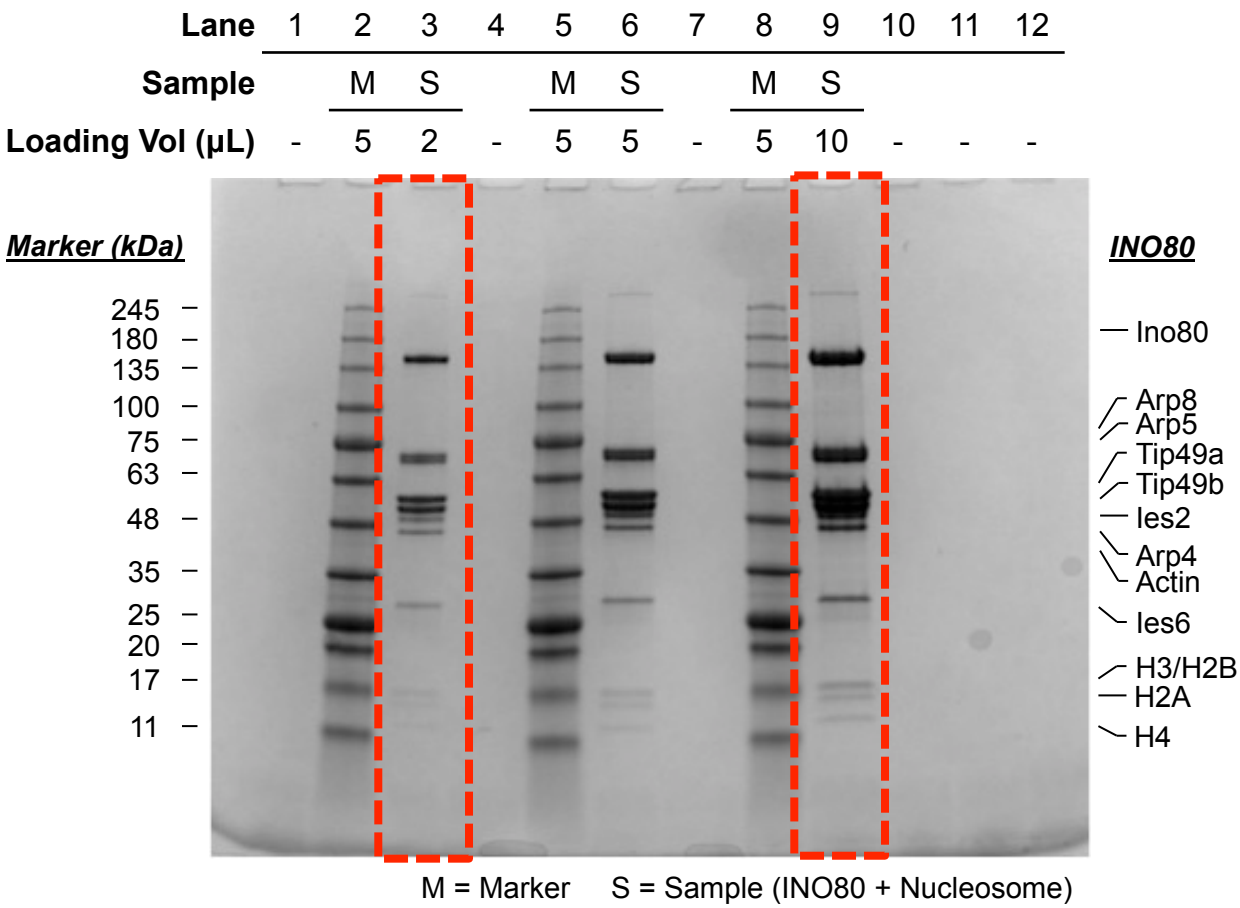
Supplementary Information 1

Original Gel for Extended Data 1b

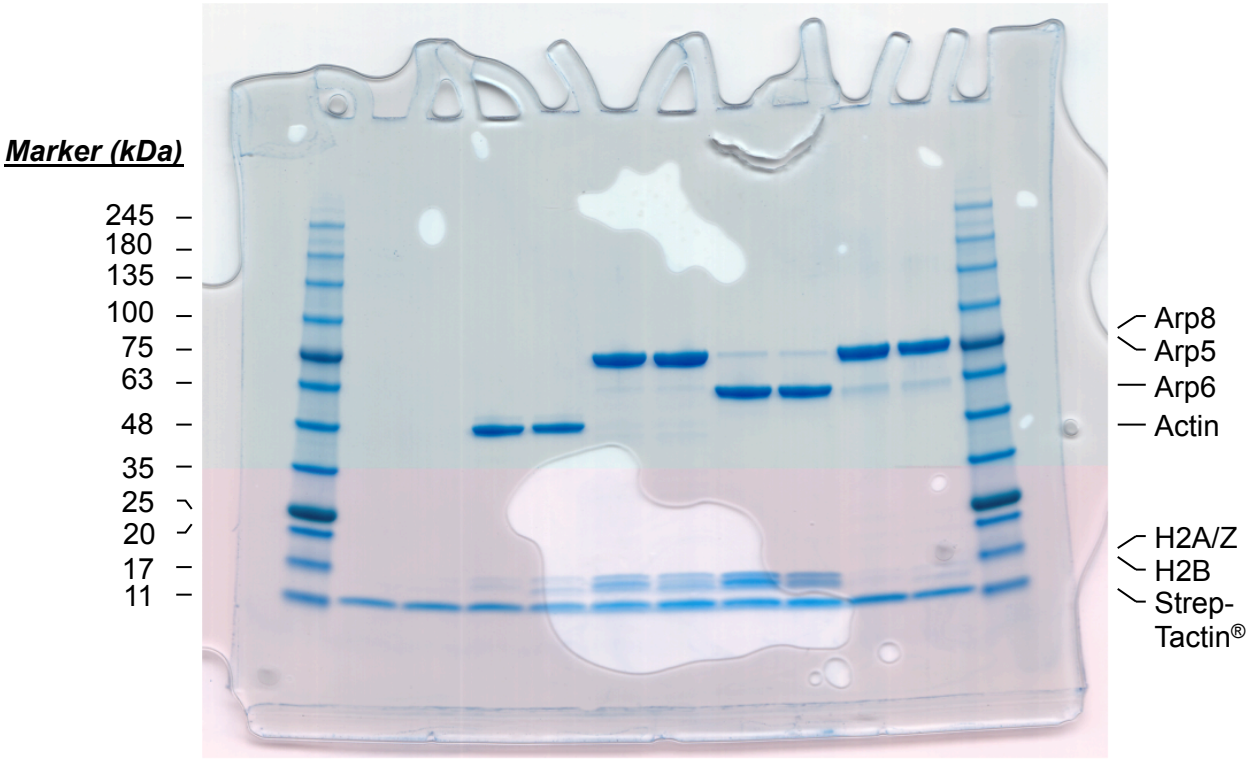


Extended Data 1b. Analysis of INO80-nucleosome complex sample. Varying quantities of INO80-nucleosome complex were analysed by SDS-PAGE on a 4-20% Tris-Glycine gel. Bands were visualised by Coomassie staining. Dashed boxes indicate the crop in the final version of this image, which includes only the 2 and 10 µL loadings.

Supplementary Information 1

Original Gel for Extended Data 6a

Lane	1	2	3	4	5	6	7	8	9	10	11	12
Bait Protein	M	-		Actin		Arp5		Arp6		Arp8		M
H2A/H2A.Z	-	A	Z	A	Z	A	Z	A	Z	A	Z	-

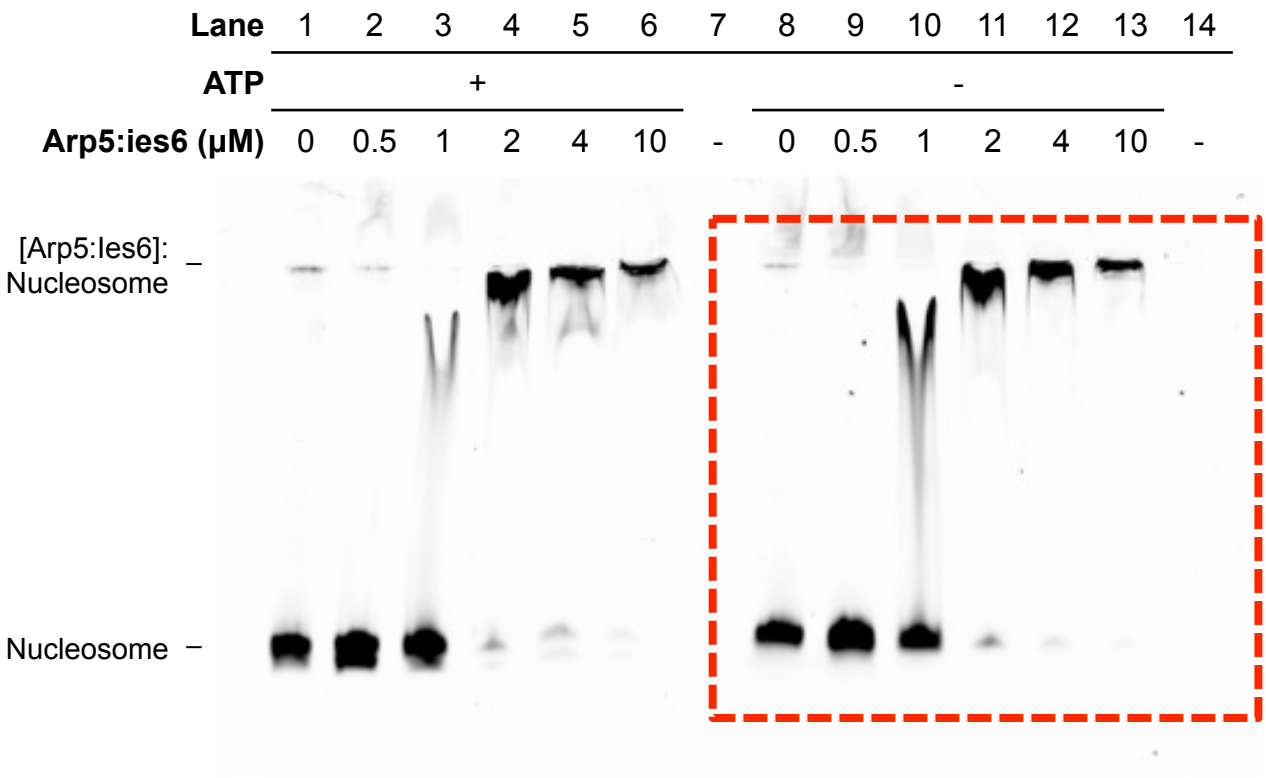


M = Marker

Extended Data 6. Interaction of human Actin, Arp5 and Arp8 with human H2A-H2B dimers assessed by *in vitro* pulldown. a, SDS-PAGE analysis highlighting the interaction of Actin, Arp5 and Arp8 with H2A:H2B dimers. The original experiment also assessed the interaction with free H2A.Z:H2B histone dimers, and also included human Arp6 as an additional bait protein (a component of the human SRCAP complex). Denatured polypeptide bands were resolved on a 4-20% Tris-Glycine gel and visualised by Coomassie staining. The final crop shows only the H2A:H2B containing lanes for Actin, Arp5 and Arp8.

Supplementary Information 1

Original Gel for Extended Data 6b



Extended Data 6. Interaction of human Actin, Arp5 and Arp8 with human H2A-H2B dimers assessed by *in vitro* pulldown. b, EMSA analysis of Arp5:Ies6 interaction with nucleosomes. The nucleosomes in this experiment were fluorescently labelled with a Cy5 fluorophore. EMSA products were resolved by native PAGE on a 6% acrylamide, 0.5x TBE gel run in 0.5x TBE buffer, and then visualised by fluorescent scan on a flatbed scanner. The original experiment compared the effect of ATP on binding to the nucleosome substrate. The final crop contains only the right-hand side of this image, showing the electrophoretic mobility change in the absence of ATP (red dashed box).