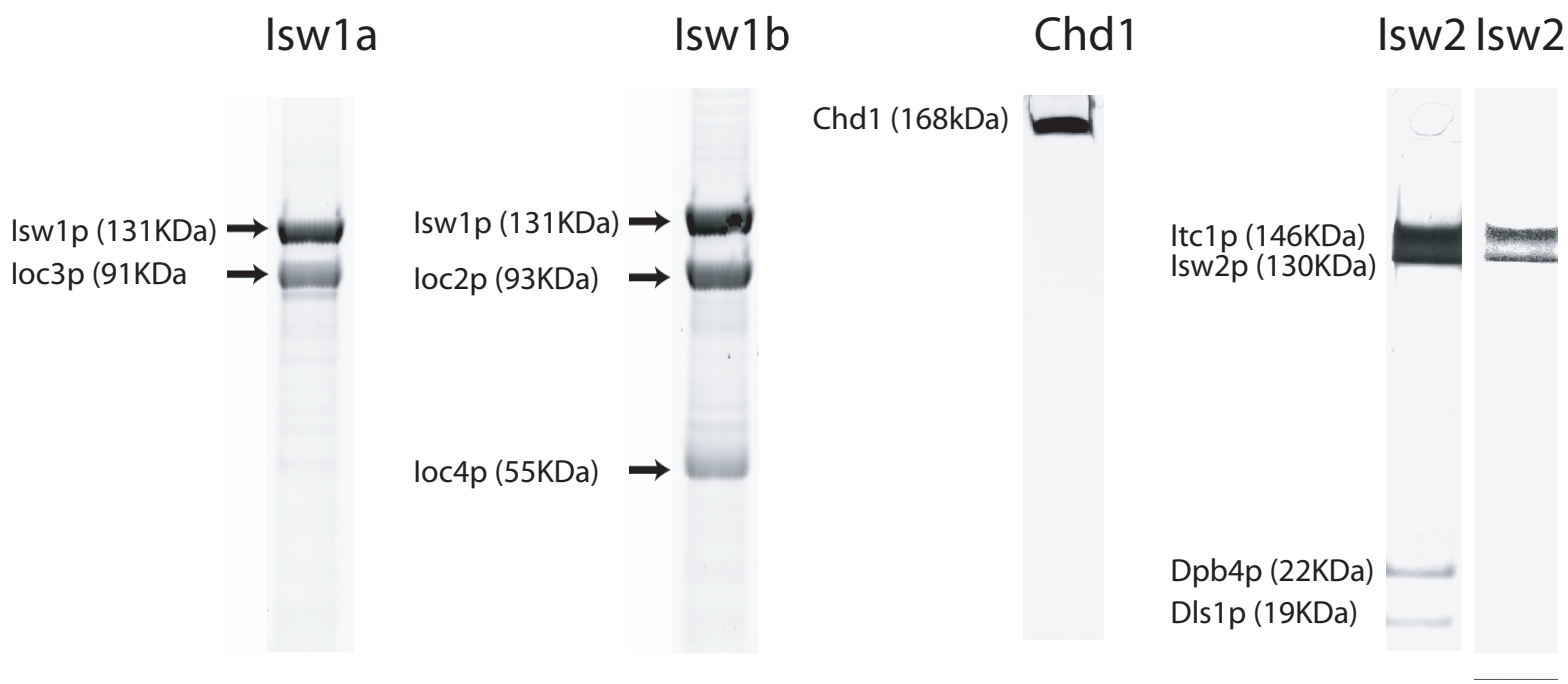
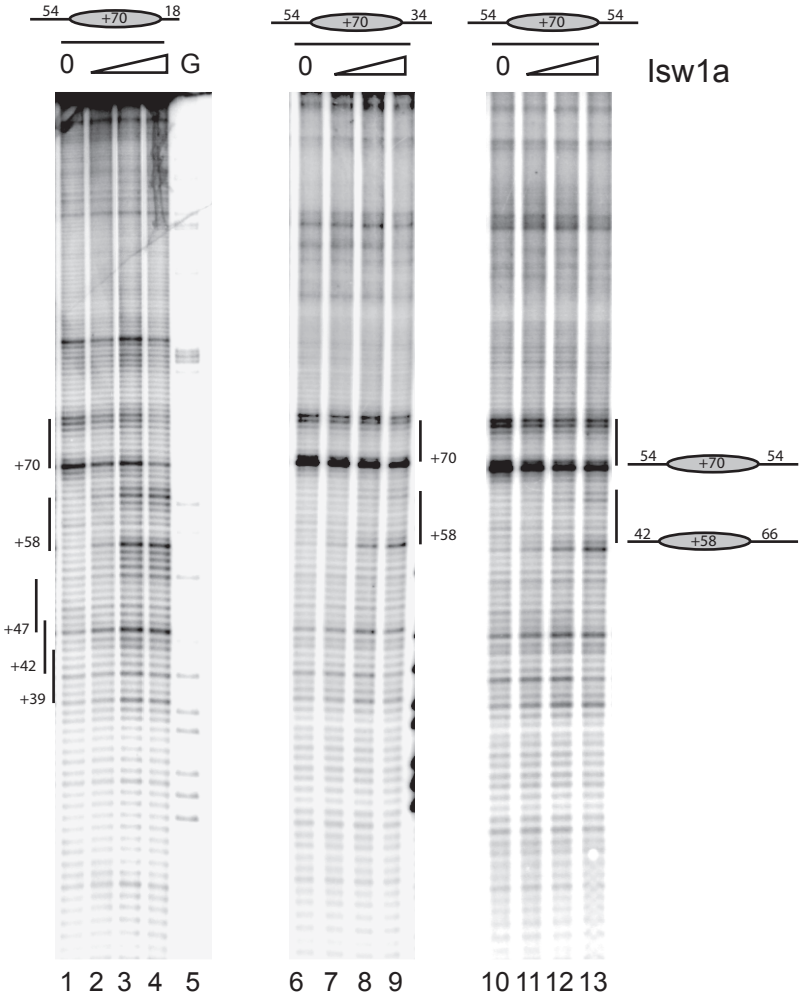
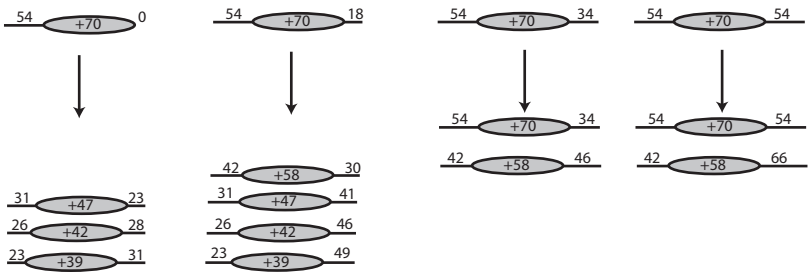

Isw1a
Isw1b
Chd1
Isw2
Isw2
Isw1p (131KDa)
Ioc3p (91KDa
Isw1p (131KDa)
Ioc2p (93KDa)
Ioc4p (55KDa)
Chd1 (168kDa)
Itc1p (146KDa)
Isw2p (130KDa)
Dpb4p (22KDa)
Dls1p (19KDa)

A


54 +70 18
0 G
54 +70 34
0
54 +70 54
0
Isw1a
+70
+58
+47
+42
+39
+70
+58
54 +70 54
42 +58 66
1 2 3 4 5
6 7 8 9
10 11 12 13

B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31 +47 23
26 +42 28
23 +39 31
54 +70 18
42 +58 30
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26 +42 46
23 +39 49
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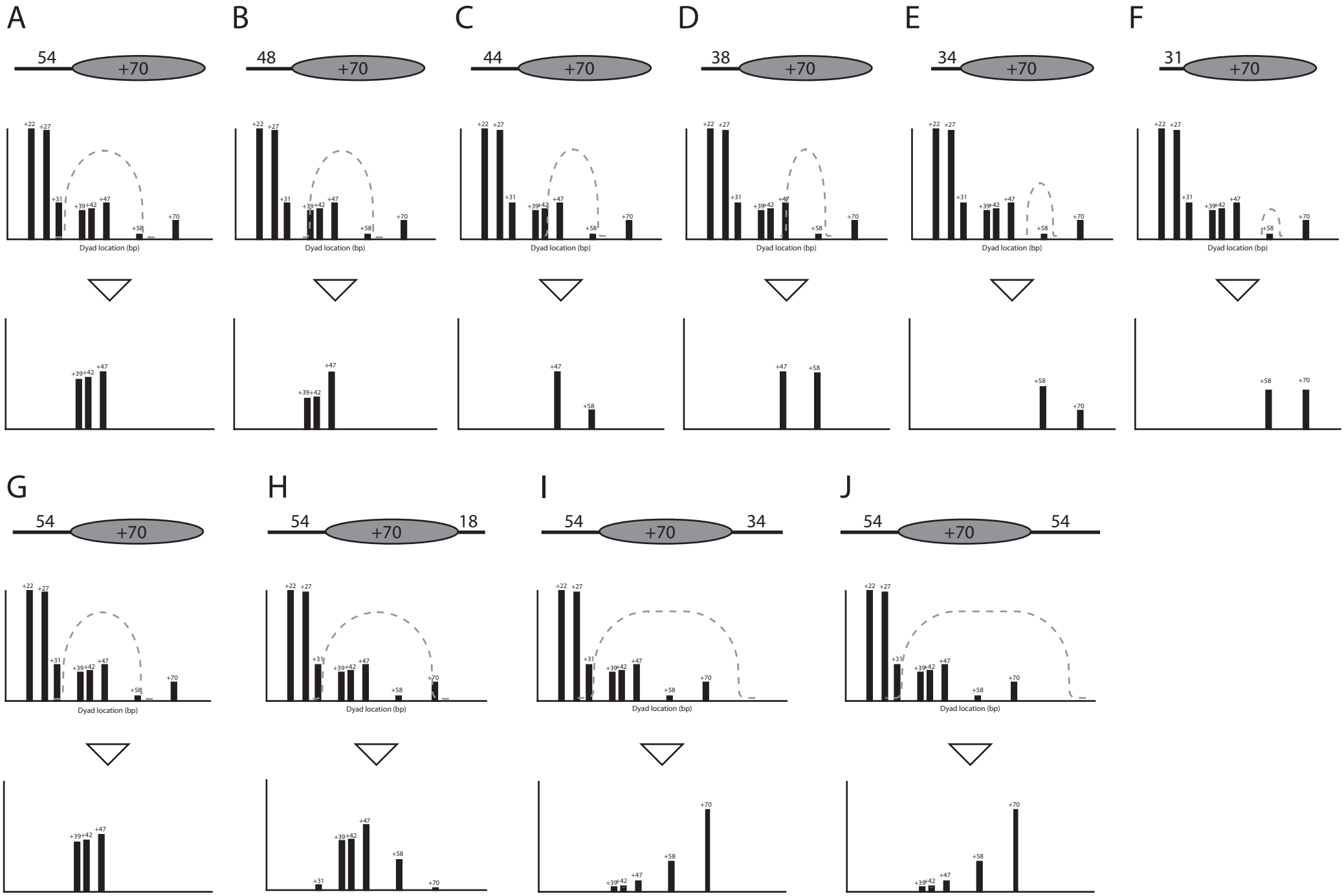
42 +58 46
54 +70 54
54 +70 54
42 +58 66


A
54
+70
B
48
+70
C
44
+70
D
38
+70
E
34
+70
F
31
+70
+22 +27 +31 +39 +42 +47 +58 +70
Dyad location (bp)
+39+42 +47
+39+42 +47
+47 +58
+47 +58
+58 +70
+58 +70
G
54
+70
H
54
+70
18
I
54
+70
34
J
54
+70
54
+39+42 +47
+31 +39+42 +47 +58 +70

Supplementary Figure 1. SDS polyacrylamide gels indicating the purity of the remodelling enzymes used in this study. The subunits present in each complex together with their molecular weights are indicated. The migration of the bands correlated well with their expected mobility in comparison to molecular weight markers (not shown). The gels for the Isw1a, Isw1b and Chd1 complexes were stained with Sypro Orange. The gel for Isw2 was silver stained. Two exposures are shown so that both the small subunits can be detected and the large subunits distinguished as separate species.

Supplementary Figure 2. The effect of progressive extension of the downstream linker DNA extension on redistribution by Isw1a. Nucleosomes were assembled onto DNA fragments with 54bp upstream extensions and 18 (Lanes 1-5), 34 lanes (6-9) and 54 bp (lanes 10-13) extensions on the downstream side. Repositioning reactions were carried out in the presence of Isw1a 100, 200, 400 fmoles lanes 2, 3 and 4; 36 fmoles, lanes 7 and 11, 107 fmoles lanes 8 and 12, 320 fmoles lanes 9 and 13. The positions to which nucleosomes are relocated are illustrated schematically in (B). The positions for a fragment with no downstream extension (obtained from Figure 2) are also illustrated.

Supplementary Figure 3. Superposition of nucleosome positioning preferences with the idealised Isw1a DNA end exclusion profile matches experimental observations on all DNA fragments used. Superposition of the nucleosome positioning preferences with the idealised Isw1a profile as described for Figure 6D, but scaled to fit each of the DNA fragments studied. In all cases the results fit well with the experimentally obtained data.