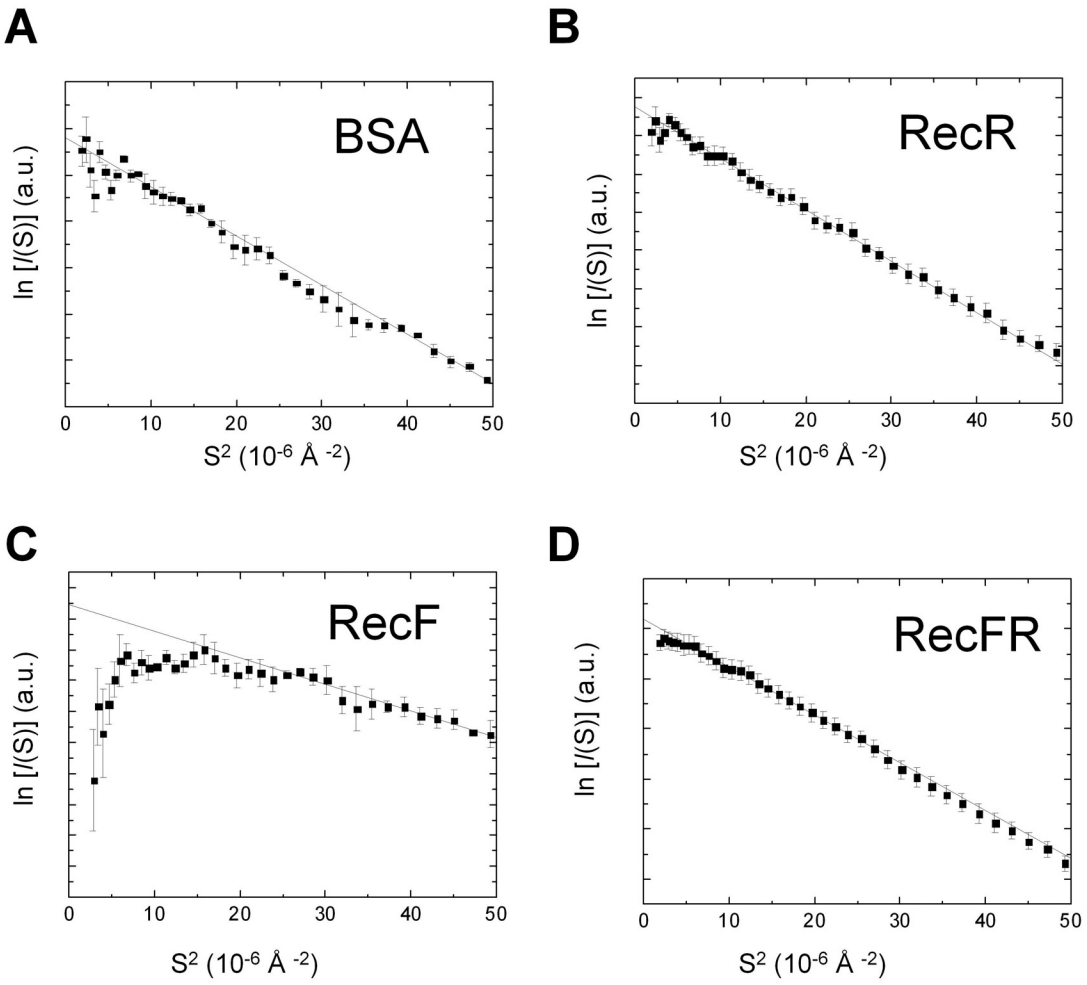
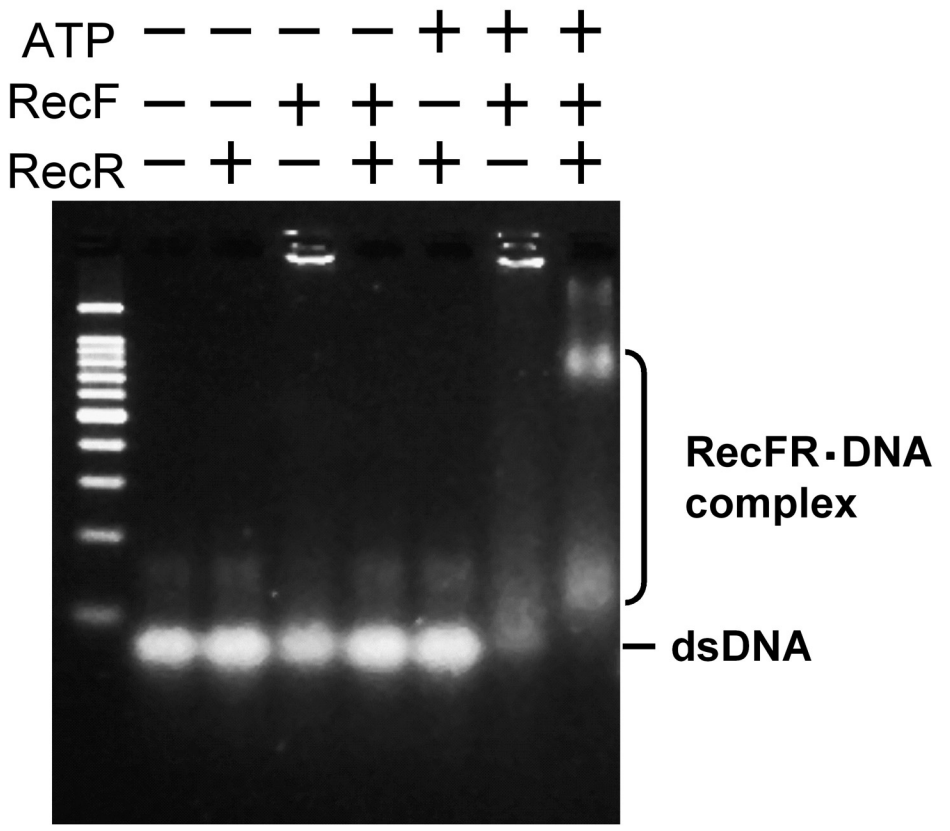
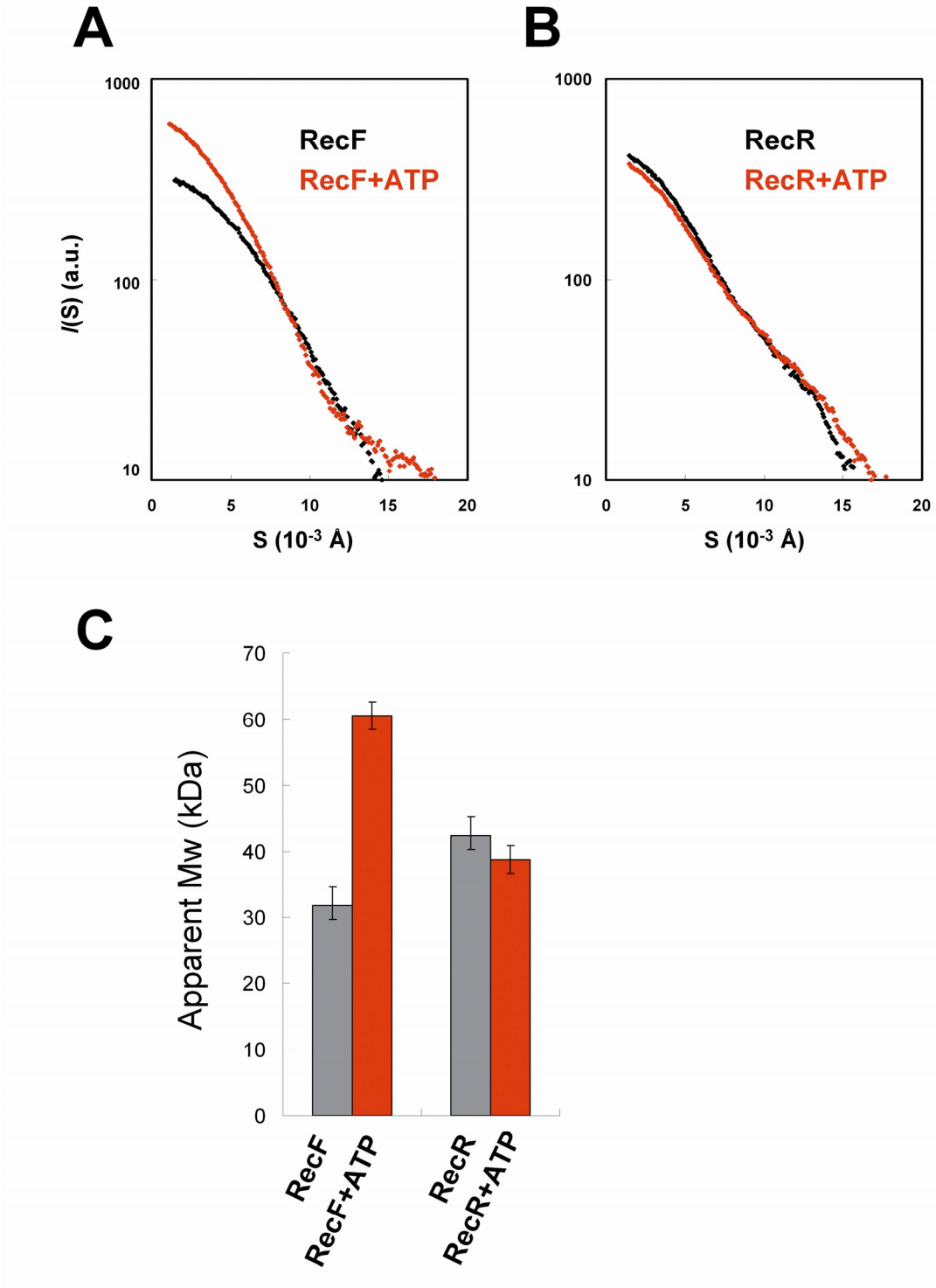


Supplementary Fig. 1. Zero-extrapolated Guinier plots of (A) BSA (B) ttRecR (C) ttRecF and (D) the ttRecFR complex. The continuous lines show a least-squares fit of Guinier approximation within an S range from 0.00226 $Å^{-1}$ to $S_{max}<1.3/2\pi Rg$. All plots are offset for the sake of clarity.



Supplementary Fig. 2. ATP-dependent dsDNA binding of the ttRecFR complex. ttRecF (5 μM), ttRecR (10 μM) or a mixture of ttRecF (5 μM) and ttRecR (10 μM) were incubated for 10 min in the presence of a 70 bp dsDNA (20 μM) with and without ATP (1 mM), and each mixture was then subjected to electrophoresis as described in Experimental Procedures. The dsDNA substrate is same as that in Figure 4B.


A
B
C
1000
100
10
I(S) (a.u.)
RecF
RecF+ATP
RecR
RecR+ATP
0
5
10
15
20
S (10-3 Å)
70
60
50
40
30
20
10
0
Apparent Mw (kDa)
RecF
RecF+ATP
RecR
RecR+ATP

Supplementary Fig. 3. Effect of ATP on oligomeric states of ttRecF and ttRecR. (A) A SAXS profile of ttRecF with and without 10 mM ATP (red and black lines, respectively). Significant difference was observed in the plot with and without ATP, which suggests oligomerization was occurred. (B) A SAXS profile of ttRecR with and without 10 mM ATP. (C) The ATP effect on the apparent molecular weights of both RecF and RecR. Molecular weights were estimated from the normalized forward intensity, $I(0)$, of ttRecF and ttRecR at a concentration of 1.2 mg/ml. The doubling apparent Mw corresponds to dimer formation of ttRecF that was induced by ATP. BSA was used as a standard as described in the legend of Table 1e.