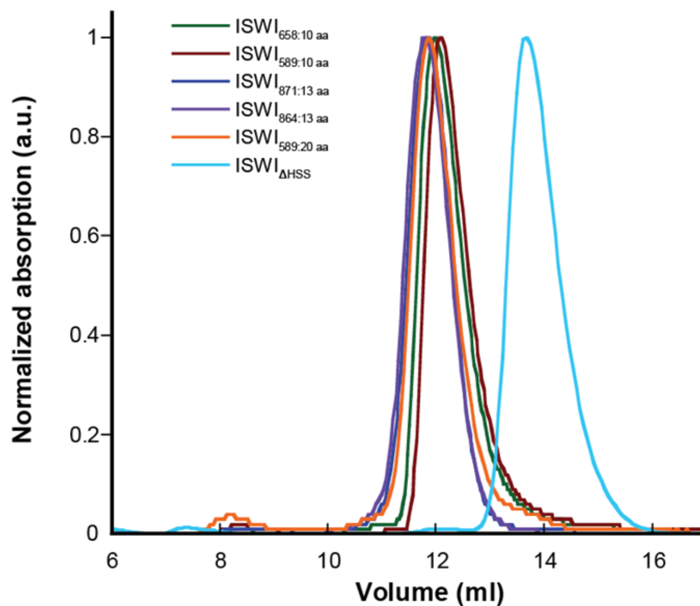
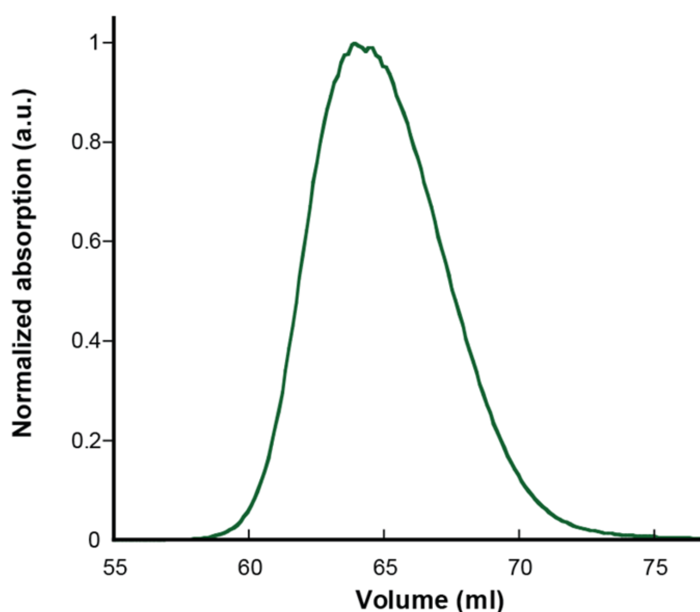
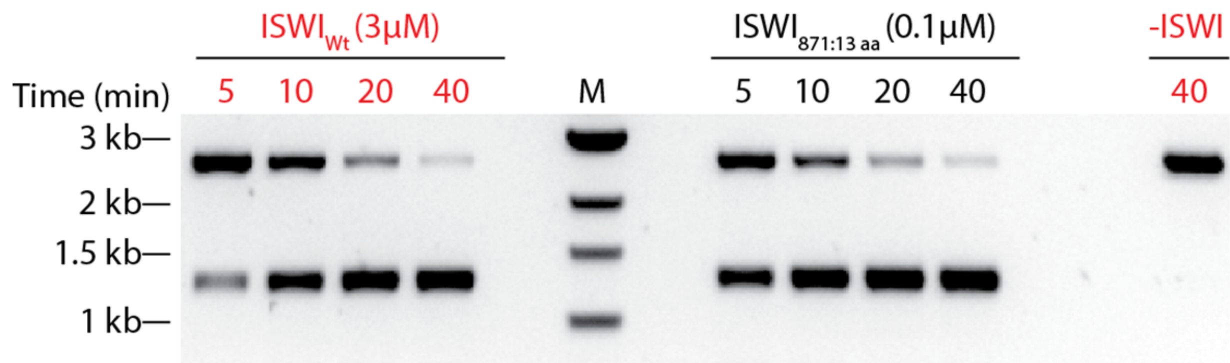
A



B



Supplementary Figure 1: Proteins of this study analyzed by size exclusion chromatography (SEC). All proteins were purified by metal affinity and ion exchange chromatography prior to SEC (see Methods). (**A**) ISWI mutants (1 to 1.6 mg of insertion mutants and 3.4 mg of $ISWI_{\Delta HSS}$) were separated over a Superdex 200 10/300 GL column (GE Healthcare). UV absorption was measured at 280 nm except for $ISWI_{\Delta HSS}$ (254 nm) to prevent saturation of the UV detector. (**B**) $ISWI_{Wt}$ (7 mg) was separated over a HiLoad 16/600 Superdex 200 column (GE Healthcare). Absorption was measured at 280 nm. The mobile phase contained 50 mM Hepes-KOH pH 7.6, 0.2 mM EDTA, 200 mM potassium acetate and 1 mM dithiothreitol for all insertion mutants and $ISWI_{Wt,}$ and 25 mM Hepes-KOH pH 7.6, 1.5 mM magnesium acetate, 0.1 mM EDTA, 100 mM potassium chloride, 10% glycerol and 10 mM beta-mercaptoethanol for $ISWI_{\Delta HSS}$.



Supplementary Figure 2: Original agarose gel used to generate Figure 3A. Remodeling time courses were obtained for ISWI$_{Wt}$ and ISWI$_{871:13\ aa}$ as explained in Figure 3. Mock-treated sample (-ISWI) served as a control. Red labeled lanes are shown in Figure 3A. M: molecular weight marker; kb: kilobases.